jc813 U.S. PTO
06/27/00

06-28-00

A
Box Seq.

Customer No. 000959
Case Docket No. BGI-129CP

jc062 U.S. PTO
09/605703
06/27/00

Assistant Commissioner for Patents
BOX PATENT APPLICATION
Washington, D.C. 20231

"Express Mail" Mailing Label Number EL 373 207 171 US

Date of Deposit June 27, 2000

I hereby certify that this transmittal letter and the papers referred to as being enclosed therein are being deposited with the United States Postal Service "Express Mail Post Office to Addressee" service under 37 CFR 1.10 on the date indicated above and is addressed to the Assistant Commissioner for Patents, Box Patent Application, Washington, DC 20231.

Larry Taylor
Signature

Larry Taylor
Please Print Name of Person Signing

Sir:

Transmitted herewith for filing is the patent application of:

Inventors: Markus Pompejus *et al.*

For: *"Corynebacterium Glutamicum Genes Encoding Novel Proteins"*

Enclosed are:

- ☒ 58 pages of specification, 5 pages of claims and 1 page of abstract;
- ☒ 26 pages of Table 1;
- ☒ 16 pages of Table 2;
- ☒ 6 pages of Table 3;
- ☒ 95 pages of Table 4;
- ☒ 535 pages of Appendix A;
- ☒ 162 pages of Appendix B;
- ☒ 3331 pages of Sequence Listing;
- ☒ Zip Disk Containing Sequence Listing;
- ☒ Transmittal Letter for Zip Disk Containing Sequence Listing;
- ☒ An *unexecuted* Declaration, Petition and Power of Attorney;
- ☒ A pre-paid acknowledgment postcard.

The filing fee has been calculated as shown below:

	(Col. 1)	(Col. 2)
FOR:	NO. FILED	NO. EXTRA
BASIC FEE	////////////////////////////////	
TOTAL CLAIMS	52 - 20	= 32
INDEP. CLAIMS	15 - 3	= 12
☒ MULTIPLE DEPENDENT CLAIMS PRESENTED		

* If the difference in Col. 2 is less than zero, enter "0" in Col. 2.

SMALL ENTITY			OTHER THAN SMALL ENTITY	
RATE	FEE	OR	RATE	FEE
//////////	$	OR	/////////	$ 690
x 9=	$	OR	x 18=	$ 576
x 39	$	OR	x 78	$ 936
+130	$	OR	+260	$ 260
TOTAL	0	OR	TOTAL	$2462.00

☒ **FILING FEES ARE NOT BEING PAID AT THIS TIME.**

☐ The Commissioner is hereby authorized to charge payment of the following fees associated with this communication or credit any overpayment to Deposit Account No..

- ☐ Any additional filing fees required under 37 C.F.R. 1.16.
- ☐ Any patent application processing fees under 37 C.F.R. 1.17.

☐ The Commissioner is hereby authorized to charge payment of the following fees during the pendency of this application or credit any overpayment to Deposit Account No..
A duplicate copy of this sheet is enclosed.

- ☐ Any patent application processing fees under 37 C.F.R. 1.17.
- ☐ The issue fee set in 37 C.F.R. 1.18 at or before mailing of the Notice of Allowance, pursuant to 37 C.F.R 1.311(b).
- ☐ Any filing fees under 37 C.F.R. 1.16 for presentation of extra claims.

☐ A check in the amount of $_____ to cover the recording of assignment documents is also enclosed.

☒ Address all future communications (May only be completed by applicant, or attorney or agent of record) to **Elizabeth A. Hanley, Esq. at Customer Number: 000959** whose address is:

Lahive & Cockfield, LLP
28 State Street
Boston, Massachusetts 02109

Date: **June 27, 2000**

28 State Street
Boston, MA 02109
(617) 227-7400 (Tel.)
(617) 742-4214 (Fax)

LAHIVE & COCKFIELD, LLP

Attorneys at Law

By: _____

Elizabeth A. Hanley, Esq.
Registration No. 33,505
Attorney for Applicants

CORYNEBACTERIUM GLUTAMICUM GENES ENCODING NOVEL PROTEINS

Related Applications

This application claims priority to prior filed U.S. Provisional Patent Application Serial No. 60/142764, filed July 8, 1999, and U.S. Provisional Patent Application Serial No. 60/152,318, filed September 3, 1999. The entire contents of both of the aforementioned applications are hereby expressly incorporated herein by reference.

Background of the Invention

Certain products and by-products of naturally-occurring metabolic processes in cells have utility in a wide array of industries, including the food, feed, cosmetics, and pharmaceutical industries. These molecules, collectively termed 'fine chemicals', include organic acids, both proteinogenic and non-proteinogenic amino acids, nucleotides and nucleosides, lipids and fatty acids, diols, carbohydrates, aromatic compounds, vitamins and cofactors, and enzymes. Their production is most conveniently performed through the large-scale culture of bacteria developed to produce and secrete large quantities of one or more desired molecules. One particularly useful organism for this purpose is *Corynebacterium glutamicum*, a gram positive, nonpathogenic bacterium. Through strain selection, a number of mutant strains have been developed which produce an array of desirable compounds. However, selection of strains improved for the production of a particular molecule is a time-consuming and difficult process.

Summary of the Invention

The invention provides novel bacterial nucleic acid molecules which have a variety of uses. These uses include the identification of microorganisms which can be used to produce fine chemicals, the modulation of fine chemical production in *C. glutamicum* or related bacteria, the typing or identification of *C. glutamicum* or related bacteria, as reference points for mapping the *C. glutamicum* genome, and as markers for transformation. These novel nucleic acid molecules encode proteins, referred to herein as marker and fine chemical production (MCP) proteins.

C. glutamicum is a gram positive, aerobic bacterium which is commonly used in industry for the large-scale production of a variety of fine chemicals, and also for the degradation of hydrocarbons (such as in petroleum spills) and for the oxidation of terpenoids. The MCP nucleic acid molecules of the invention, therefore, can be used to identify microorganisms which can be used to produce fine chemicals, *e.g.*, by

fermentation processes. Modulation of the expression of the MCP nucleic acids of the invention, or modification of the sequence of the MCP nucleic acid molecules of the invention, can be used to modulate the production of one or more fine chemicals from a microorganism (*e.g.*, to improve the yield or production of one or more fine chemicals from a Corynebacterium or Brevibacterium species).

The MCP nucleic acids of the invention may also be used to identify an organism as being *Corynebacterium glutamicum* or a close relative thereof, or to identify the presence of *C. glutamicum* or a relative thereof in a mixed population of microorganisms. The invention provides the nucleic acid sequences of a number of *C. glutamicum* genes; by probing the extracted genomic DNA of a culture of a unique or mixed population of microorganisms under stringent conditions with a probe spanning a region of a *C. glutamicum* gene which is unique to this organism, one can ascertain whether this organism is present. Although *Corynebacterium glutamicum* itself is nonpathogenic, it is related to species pathogenic in humans, such as *Corynebacterium diphtheriae* (the causative agent of diphtheria); the detection of such organisms is of significant clinical relevance.

The MCP nucleic acid molecules of the invention may also serve as reference points for mapping of the *C. glutamicum* genome, or of genomes of related organisms. Similarly, these molecules, or variants or portions thereof, may serve as markers for genetically engineered Corynebacterium or Brevibacterium species.

The MCP proteins encoded by the novel nucleic acid molecules of the invention may be involved, for example, in the direct or indirect production of one or more fine chemicals from *C. glutamicum*. The MCP proteins of the invention may also participate in the degradation of hydrocarbons or the oxidation of terpenoids. These proteins may also be utilized for the identification of *Corynebacterium glutamicum* or organisms related to *C. glutamicum*; the presence of an MCP protein specific to *C. glutamicum* and related species in a mixture of proteins may indicate the presence of one of these bacteria in the sample. Further, these MCP proteins may have homologues in plants or animals which are involved in a disease state or condition; these proteins thus may serve as useful pharmaceutical targets for drug screening and the development of therapeutic compounds.

Given the availability of cloning vectors for use in *Corynebacterium glutamicum*, such as those disclosed in Sinskey *et al.*, U.S. Patent No. 4,649,119, and techniques for genetic manipulation of *C. glutamicum* and the related *Brevibacterium* species (*e.g.*, *lactofermentum*) (Yoshihama et al, *J. Bacteriol.* 162: 591-597 (1985); Katsumata *et al.*, *J. Bacteriol.* 159: 306-311 (1984); and Santamaria *et al.*, *J. Gen. Microbiol.* 130: 2237-2246 (1984)), the nucleic acid molecules of the invention may be

utilized in the genetic engineering of this organism to modulate the production of one or more fine chemicals. This modulation may be due to a direct effect of manipulation of a gene of the invention, or it may be due to an indirect effect of such manipulation. For example, by modifying the activity of a protein involved in the biosynthesis or degradation of a fine chemical (*i.e.*, through mutagenesis of the corresponding gene), one may directly modulate the ability of the cell to synthesize or to degrade this compound, thereby modulating the yield and/or efficiency of production of the fine chemical. Similarly, by modulating the activity of a protein which regulates a fine chemical metabolic pathway, one may directly influence whether the production of the desired compound is up- or down-regulated, either of which will modulate the yield or efficiency of production of the fine chemical from the cell.

Indirect modulation of fine chemical production may also result by modifying the activity of a protein of the invention (*i.e.*, by mutagenesis of the corresponding gene) such that the overall ability of the cell to grow and divide or to remain viable and productive is increased. The production of fine chemicals from *C. glutamicum* is generally accomplished by the large-scale fermentative culture of these microorganisms, conditions which are frequently suboptimal for growth and cell division. By engineering a protein of the invention (*e.g.*, a stress response protein, a cell wall protein, or proteins involved in the metabolism of compounds necessary for cell growth and division to occur, such as nucleotides and amino acids) such that it is better able to survive, grow, and multiply in such conditions, it may be possible to increase the number and productivity of such engineered *C. glutamicum* cells in large-scale culture, which in turn should result in increased yields and/or efficiency of production of one or more desired fine chemicals. Further, the metabolic pathways of any cell are necessarily interrelated and coregulated. By altering the activity or regulation of any one metabolic pathway in *C. glutamicum* (*i.e.*, by altering the activity of one of the proteins of the invention which participates in such a pathway), it is possible to concomitantly alter the activity or regulation of other metabolic pathways in this microorganism, which may be directly involved in the synthesis or degradation of a fine chemical.

The invention provides novel nucleic acid molecules which encode proteins, referred to herein as MCP proteins, which are capable of, for example, modulating the production or efficiency of production of one or more fine chemicals from *C. glutamicum*, or of serving as identifying markers for *C. glutamicum* or related organisms. Nucleic acid molecules encoding an MCP protein are referred to herein as MCP nucleic acid molecules. In a preferred embodiment, the MCP protein is capable of modulating the production or efficiency of production of one or more fine chemicals from *C. glutamicum*, or of serving as identifying markers for *C. glutamicum* or related

organisms. Examples of such proteins include those encoded by the genes set forth in Table 1.

Accordingly, one aspect of the invention pertains to isolated nucleic acid molecules (*e.g.*, cDNAs, DNAs, or RNAs) comprising a nucleotide sequence encoding an MCP protein or biologically active portions thereof, as well as nucleic acid fragments suitable as primers or hybridization probes for the detection or amplification of MCP-encoding nucleic acid (*e.g.*, DNA or mRNA). In particularly preferred embodiments, the isolated nucleic acid molecule comprises one of the nucleotide sequences set forth in Appendix A or the coding region or a complement thereof of one of these nucleotide sequences. In other particularly preferred embodiments, the isolated nucleic acid molecule of the invention comprises a nucleotide sequence which hybridizes to or is at least about 50%, preferably at least about 60%, more preferably at least about 70%, 80% or 90%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to a nucleotide sequence set forth in Appendix A, or a portion thereof. In other preferred embodiments, the isolated nucleic acid molecule encodes one of the amino acid sequences set forth in Appendix B. The preferred MCP proteins of the present invention also preferably possess at least one of the MCP activities described herein.

In another embodiment, the isolated nucleic acid molecule encodes a protein or portion thereof wherein the protein or portion thereof includes an amino acid sequence which is sufficiently homologous to an amino acid sequence of Appendix B, *e.g.*, sufficiently homologous to an amino acid sequence of Appendix B such that the protein or portion thereof maintains an MCP activity. Preferably, the protein or portion thereof encoded by the nucleic acid molecule maintains the ability to modulate the production or efficiency of production of one or more fine chemicals from *C. glutamicum*, or of serving as an identifying marker for *C. glutamicum* or related organisms. In one embodiment, the protein encoded by the nucleic acid molecule is at least about 50%, preferably at least about 60%, and more preferably at least about 70%, 80%, or 90% and most preferably at least about 95%, 96%, 97%, 98%, or 99% or more homologous to an amino acid sequence of Appendix B (*e.g.*, an entire amino acid sequence selected from those sequences set forth in Appendix B). In another preferred embodiment, the protein is a full length *C. glutamicum* protein which is substantially homologous to an entire amino acid sequence of Appendix B (encoded by an open reading frame shown in Appendix A).

In another preferred embodiment, the isolated nucleic acid molecule is derived from *C. glutamicum* and encodes a protein (*e.g.*, an MCP fusion protein) which includes a biologically active domain which is at least about 50% or more homologous to one of

the amino acid sequences of Appendix B and is able to modulate the yield, production, and/or efficiency of production of one or more fine chemicals from *C. glutamicum*, to degrade hydrocarbons, to oxidize terpenoids, to serve as a target for drug development, or to serve as an identifying marker for *C. glutamicum* or related organisms, and which also includes heterologous nucleic acid sequences encoding a heterologous polypeptide or regulatory regions.

In another embodiment, the isolated nucleic acid molecule is at least 15 nucleotides in length and hybridizes under stringent conditions to a nucleic acid molecule comprising a nucleotide sequence of Appendix A. Preferably, the isolated nucleic acid molecule corresponds to a naturally-occurring nucleic acid molecule. More preferably, the isolated nucleic acid encodes a naturally-occurring *C. glutamicum* MCP protein, or a biologically active portion thereof.

Another aspect of the invention pertains to vectors, *e.g.*, recombinant expression vectors, containing the nucleic acid molecules of the invention, and host cells into which such vectors have been introduced. In one embodiment, such a host cell is used to produce an MCP protein by culturing the host cell in a suitable medium. The MCP protein can then be isolated from the medium or the host cell.

Yet another aspect of the invention pertains to a genetically altered microorganism in which an MCP gene has been introduced or altered. In one embodiment, the genome of the microorganism has been altered by introduction of a nucleic acid molecule of the invention encoding wild-type or mutated MCP sequence as a transgene. In another embodiment, an endogenous MCP gene within the genome of the microorganism has been altered, *e.g.*, functionally disrupted, by homologous recombination with an altered MCP gene. In another embodiment, an endogenous or introduced MCP gene in a microorganism has been altered by one or more point mutations, deletions, or inversions, but still encodes a functional MCP protein. In still another embodiment, one or more of the regulatory regions (*e.g.*, a promoter, repressor, or inducer) of an MCP gene in a microorganism has been altered (*e.g.*, by deletion, truncation, inversion, or point mutation) such that the expression of the MCP gene is modulated. In a preferred embodiment, the microorganism belongs to the genus *Corynebacterium* or *Brevibacterium*, with *Corynebacterium glutamicum* being particularly preferred. In a preferred embodiment, the microorganism is also utilized for the production of a desired compound, such as an amino acid, with lysine being particularly preferred.

In another aspect, the invention provides a method of identifying the presence or activity of *Cornyebacterium diphtheriae* in a subject. This method includes detection of one or more of the nucleic acid or amino acid sequences of the invention (*e.g.*, the

sequences set forth in Appendix A or Appendix B) in a subject, thereby detecting the presence or activity of *Corynebacterium diphtheriae* in the subject.

Still another aspect of the invention pertains to an isolated MCP protein or a portion, *e.g.*, a biologically active portion, thereof. In a preferred embodiment, the isolated MCP protein or portion thereof is capable of modulating the production or efficiency of production of one or more fine chemicals from *C. glutamicum*, or of serving as an identifying marker for *C. glutamicum* or related organisms. In another preferred embodiment, the isolated MCP protein or portion thereof is sufficiently homologous to an amino acid sequence of Appendix B such that the protein or portion thereof maintains the ability to, for example, modulate the production or efficiency of production of one or more fine chemicals from *C. glutamicum*, or to serve as identifying markers for *C. glutamicum* or related organisms.

The invention also provides an isolated preparation of an MCP protein. In preferred embodiments, the MCP protein comprises an amino acid sequence of Appendix B. In another preferred embodiment, the invention pertains to an isolated full length protein which is substantially homologous to an entire amino acid sequence of Appendix B (encoded by an open reading frame set forth in Appendix A). In yet another embodiment, the protein is at least about 50%, preferably at least about 60%, and more preferably at least about 70%, 80%, or 90%, and most preferably at least about 95%, 96%, 97%, 98%, or 99% or more homologous to an entire amino acid sequence of Appendix B. In other embodiments, the isolated MCP protein comprises an amino acid sequence which is at least about 50% or more homologous to one of the amino acid sequences of Appendix B and is able to modulate the yield, production, and/or efficiency of production of one or more fine chemicals from *C. glutamicum*, to degrade hydrocarbons, to oxidize terpenoids, to serve as a target for drug development, or to serve as an identifying marker for *C. glutamicum* or related organisms.

Alternatively, the isolated MCP protein can comprise an amino acid sequence which is encoded by a nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, or is at least about 50%, preferably at least about 60%, more preferably at least about 70%, 80%, or 90%, and even more preferably at least about 95%, 96%, 97%, 98,%, or 99% or more homologous, to a nucleotide sequence of Appendix B. It is also preferred that the preferred forms of MCP proteins also have one or more of the MCP bioactivities described herein.

The MCP polypeptide, or a biologically active portion thereof, can be operatively linked to a non-MCP polypeptide to form a fusion protein. In preferred embodiments, this fusion protein has an activity which differs from that of the MCP protein alone. In other preferred embodiments, this fusion protein is capable of

modulating the yield, production and/or efficiency of production of one or more fine chemicals from *C. glutamicum*, or of serving as an identifying marker for *C. glutamicum* or related organisms. In particularly preferred embodiments, integration of this fusion protein into a host cell modulates production of a desired compound from the cell.

In another aspect, the invention provides methods for screening molecules which modulate the activity of an MCP protein, either by interacting with the protein itself or a substrate or binding partner of the MCP protein, or by modulating the transcription or translation of an MCP nucleic acid molecule of the invention.

Another aspect of the invention pertains to a method for producing a fine chemical. This method involves the culturing of a cell containing a vector directing the expression of an MCP nucleic acid molecule of the invention, such that a fine chemical is produced. In a preferred embodiment, this method further includes the step of obtaining a cell containing such a vector, in which a cell is transfected with a vector directing the expression of an MCP nucleic acid. In another preferred embodiment, this method further includes the step of recovering the fine chemical from the culture. In a particularly preferred embodiment, the cell is from the genus *Corynebacterium* or *Brevibacterium*, or is selected from those strains set forth in Table 3.

Another aspect of the invention pertains to methods for modulating production of a molecule from a microorganism. Such methods include contacting the cell with an agent which modulates MCP protein activity or MCP nucleic acid expression such that a cell associated activity is altered relative to this same activity in the absence of the agent. In a preferred embodiment, the cell is modulated for one or more *C. glutamicum* MCP protein activities, such that the yield, production, and/or efficiency of production of a desired fine chemical by this microorganism is improved. The agent which modulates MCP protein activity can be an agent which stimulates MCP protein activity or MCP nucleic acid expression. Examples of agents which stimulate MCP protein activity or MCP nucleic acid expression include small molecules, active MCP proteins, and nucleic acids encoding MCP proteins that have been introduced into the cell. Examples of agents which inhibit MCP activity or expression include small molecules and antisense MCP nucleic acid molecules.

Another aspect of the invention pertains to methods for modulating yields, production, and/or efficiency of production of a desired compound from a cell, involving the introduction of a wild-type or mutant MCP gene into a cell, either maintained on a separate plasmid or integrated into the genome of the host cell. If integrated into the genome, such integration can be random, or it can take place by homologous recombination such that the native gene is replaced by the introduced copy, causing the production of the desired compound from the cell to be modulated. In a

preferred embodiment, said yields are increased. In another preferred embodiment, said chemical is a fine chemical. In a particularly preferred embodiment, said fine chemical is an amino acid. In especially preferred embodiments, said amino acid is L-lysine.

Detailed Description of the Invention

The present invention provides MCP nucleic acid and protein molecules. These MCP nucleic acid molecules may be utilized in the identification of *Corynebacterium glutamicum* or related organisms, in the mapping of the *C. glutamicum* genome (or a genome of a closely related organism), or in the identification of microorganisms which may be used to produce fine chemicals, *e.g.*, by fermentation processes. The proteins encoded by these nucleic acids may be utilized in the direct or indirect modulation of the production or efficiency of production of one or more fine chemicals from *C. glutamicum*, as identifying markers for *C. glutamicum* or related organisms, in the oxidation of terpenoids or the degradation of hydrocarbons, or as targets for the development of therapeutic pharmaceutical compounds. Aspects of the invention are further explicated below.

I. Fine Chemicals

The term 'fine chemical' is art-recognized and includes molecules produced by an organism which have applications in various industries, such as, but not limited to, the pharmaceutical, agriculture, and cosmetics industries. Such compounds include organic acids, such as tartaric acid, itaconic acid, and diaminopimelic acid, both proteinogenic and non-proteinogenic amino acids, purine and pyrimidine bases, nucleosides, and nucleotides (as described *e.g.* in Kuninaka, A. (1996) Nucleotides and related compounds, p. 561-612, in Biotechnology vol. 6, Rehm *et al.*, eds. VCH: Weinheim, and references contained therein), lipids, both saturated and unsaturated fatty acids (*e.g.*, arachidonic acid), diols (*e.g.*, propane diol, and butane diol), carbohydrates (*e.g.*, hyaluronic acid and trehalose), aromatic compounds (*e.g.*, aromatic amines, vanillin, and indigo), vitamins and cofactors (as described in Ullmann's Encyclopedia of Industrial Chemistry, vol. A27, "Vitamins", p. 443-613 (1996) VCH: Weinheim and references therein; and Ong, A.S., Niki, E. & Packer, L. (1995) "Nutrition, Lipids, Health, and Disease" Proceedings of the UNESCO/Confederation of Scientific and Technological Associations in Malaysia, and the Society for Free Radical Research – Asia, held Sept. 1-3, 1994 at Penang, Malaysia, AOCS Press, (1995)), enzymes, polyketides (Cane *et al.* (1998) *Science* 282: 63-68), and all other chemicals described in Gutcho (1983) Chemicals by Fermentation, Noyes Data Corporation, ISBN:

0818805086 and references therein. The metabolism and uses of certain of these fine chemicals are further explicated below.

A. *Amino Acid Metabolism and Uses*

Amino acids comprise the basic structural units of all proteins, and as such are essential for normal cellular functioning in all organisms. The term "amino acid" is art-recognized. The proteinogenic amino acids, of which there are 20 species, serve as structural units for proteins, in which they are linked by peptide bonds, while the nonproteinogenic amino acids (hundreds of which are known) are not normally found in proteins (see Ulmann's Encyclopedia of Industrial Chemistry, vol. A2, p. 57-97 VCH: Weinheim (1985)). Amino acids may be in the D- or L- optical configuration, though L-amino acids are generally the only type found in naturally-occurring proteins. Biosynthetic and degradative pathways of each of the 20 proteinogenic amino acids have been well characterized in both prokaryotic and eukaryotic cells (see, for example, Stryer, L. Biochemistry, 3rd edition, pages 578-590 (1988)). The 'essential' amino acids (histidine, isoleucine, leucine, lysine, methionine, phenylalanine, threonine, tryptophan, and valine), so named because they are generally a nutritional requirement due to the complexity of their biosyntheses, are readily converted by simple biosynthetic pathways to the remaining 11 'nonessential' amino acids (alanine, arginine, asparagine, aspartate, cysteine, glutamate, glutamine, glycine, proline, serine, and tyrosine). Higher animals do retain the ability to synthesize some of these amino acids, but the essential amino acids must be supplied from the diet in order for normal protein synthesis to occur.

Aside from their function in protein biosynthesis, these amino acids are interesting chemicals in their own right, and many have been found to have various applications in the food, feed, chemical, cosmetics, agriculture, and pharmaceutical industries. Lysine is an important amino acid in the nutrition not only of humans, but also of monogastric animals such as poultry and swine. Glutamate is most commonly used as a flavor additive (mono-sodium glutamate, MSG) and is widely used throughout the food industry, as are aspartate, phenylalanine, glycine, and cysteine. Glycine, L-methionine and tryptophan are all utilized in the pharmaceutical industry. Glutamine, valine, leucine, isoleucine, histidine, arginine, proline, serine and alanine are of use in both the pharmaceutical and cosmetics industries. Threonine, tryptophan, and D/ L-methionine are common feed additives. (Leuchtenberger, W. (1996) Amino aids – technical production and use, p. 466-502 in Rehm *et al.* (eds.) Biotechnology vol. 6, chapter 14a, VCH: Weinheim). Additionally, these amino acids have been found to be useful as precursors for the synthesis of synthetic amino acids and proteins, such as N-acetylcysteine, S-carboxymethyl-L-cysteine, (S)-5-hydroxytryptophan, and others

described in Ulmann's Encyclopedia of Industrial Chemistry, vol. A2, p. 57-97, VCH: Weinheim, 1985.

The biosynthesis of these natural amino acids in organisms capable of producing them, such as bacteria, has been well characterized (for review of bacterial amino acid biosynthesis and regulation thereof, see Umbarger, H.E.(1978) *Ann. Rev. Biochem.* 47: 533-606). Glutamate is synthesized by the reductive amination of α-ketoglutarate, an intermediate in the citric acid cycle. Glutamine, proline, and arginine are each subsequently produced from glutamate. The biosynthesis of serine is a three-step process beginning with 3-phosphoglycerate (an intermediate in glycolysis), and resulting in this amino acid after oxidation, transamination, and hydrolysis steps. Both cysteine and glycine are produced from serine; the former by the condensation of homocysteine with serine, and the latter by the transferal of the side-chain β-carbon atom to tetrahydrofolate, in a reaction catalyzed by serine transhydroxymethylase. Phenylalanine, and tyrosine are synthesized from the glycolytic and pentose phosphate pathway precursors erythrose 4-phosphate and phosphoenolpyruvate in a 9-step biosynthetic pathway that differ only at the final two steps after synthesis of prephenate. Tryptophan is also produced from these two initial molecules, but its synthesis is an 11-step pathway. Tyrosine may also be synthesized from phenylalanine, in a reaction catalyzed by phenylalanine hydroxylase. Alanine, valine, and leucine are all biosynthetic products of pyruvate, the final product of glycolysis. Aspartate is formed from oxaloacetate, an intermediate of the citric acid cycle. Asparagine, methionine, threonine, and lysine are each produced by the conversion of aspartate. Isoleucine is formed from threonine. A complex 9-step pathway results in the production of histidine from 5-phosphoribosyl-1-pyrophosphate, an activated sugar.

Amino acids in excess of the protein synthesis needs of the cell cannot be stored, and are instead degraded to provide intermediates for the major metabolic pathways of the cell (for review see Stryer, L. Biochemistry 3rd ed. Ch. 21 "Amino Acid Degradation and the Urea Cycle" p. 495-516 (1988)). Although the cell is able to convert unwanted amino acids into useful metabolic intermediates, amino acid production is costly in terms of energy, precursor molecules, and the enzymes necessary to synthesize them. Thus it is not surprising that amino acid biosynthesis is regulated by feedback inhibition, in which the presence of a particular amino acid serves to slow or entirely stop its own production (for overview of feedback mechanisms in amino acid biosynthetic pathways, see Stryer, L. Biochemistry, 3rd ed. Ch. 24: "Biosynthesis of Amino Acids and Heme" p. 575-600 (1988)). Thus, the output of any particular amino acid is limited by the amount of that amino acid present in the cell.

B. Vitamin, Cofactor, and Nutraceutical Metabolism and Uses

Vitamins, cofactors, and nutraceuticals comprise another group of molecules which the higher animals have lost the ability to synthesize and so must ingest, although they are readily synthesized by other organisms such as bacteria. These molecules are either bioactive substances themselves, or are precursors of biologically active substances which may serve as electron carriers or intermediates in a variety of metabolic pathways. Aside from their nutritive value, these compounds also have significant industrial value as coloring agents, antioxidants, and catalysts or other processing aids. (For an overview of the structure, activity, and industrial applications of these compounds, see, for example, Ullman's Encyclopedia of Industrial Chemistry, "Vitamins" vol. A27, p. 443-613, VCH: Weinheim, 1996.) The term "vitamin" is art-recognized, and includes nutrients which are required by an organism for normal functioning, but which that organism cannot synthesize by itself. The group of vitamins may encompass cofactors and nutraceutical compounds. The language "cofactor" includes nonproteinaceous compounds required for a normal enzymatic activity to occur. Such compounds may be organic or inorganic; the cofactor molecules of the invention are preferably organic. The term "nutraceutical" includes dietary supplements having health benefits in plants and animals, particularly humans. Examples of such molecules are vitamins, antioxidants, and also certain lipids (*e.g.*, polyunsaturated fatty acids).

The biosynthesis of these molecules in organisms capable of producing them, such as bacteria, has been largely characterized (Ullman's Encyclopedia of Industrial Chemistry, "Vitamins" vol. A27, p. 443-613, VCH: Weinheim, 1996; Michal, G. (1999) Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology, John Wiley & Sons; Ong, A.S., Niki, E. & Packer, L. (1995) "Nutrition, Lipids, Health, and Disease" Proceedings of the UNESCO/Confederation of Scientific and Technological Associations in Malaysia, and the Society for Free Radical Research – Asia, held Sept. 1-3, 1994 at Penang, Malaysia, AOCS Press: Champaign, IL X, 374 S).

Thiamin (vitamin B_1) is produced by the chemical coupling of pyrimidine and thiazole moieties. Riboflavin (vitamin B_2) is synthesized from guanosine-5'-triphosphate (GTP) and ribose-5'-phosphate. Riboflavin, in turn, is utilized for the synthesis of flavin mononucleotide (FMN) and flavin adenine dinucleotide (FAD). The family of compounds collectively termed 'vitamin B_6' (*e.g.*, pyridoxine, pyridoxamine, pyridoxa-5'-phosphate, and the commercially used pyridoxin hydrochloride) are all derivatives of the common structural unit, 5-hydroxy-6-methylpyridine. Pantothenate (pantothenic acid, (R)-(+)-N-(2,4-dihydroxy-3,3-dimethyl-1-oxobutyl)-β-alanine) can be produced either by chemical synthesis or by fermentation. The final steps in pantothenate

biosynthesis consist of the ATP-driven condensation of β-alanine and pantoic acid. The enzymes responsible for the biosynthesis steps for the conversion to pantoic acid, to β-alanine and for the condensation to panthotenic acid are known. The metabolically active form of pantothenate is Coenzyme A, for which the biosynthesis proceeds in 5 enzymatic steps. Pantothenate, pyridoxal-5'-phosphate, cysteine and ATP are the precursors of Coenzyme A. These enzymes not only catalyze the formation of panthothante, but also the production of (R)-pantoic acid, (R)-pantolacton, (R)-panthenol (provitamin B_5), pantetheine (and its derivatives) and coenzyme A.

Biotin biosynthesis from the precursor molecule pimeloyl-CoA in microorganisms has been studied in detail and several of the genes involved have been identified. Many of the corresponding proteins have been found to also be involved in Fe-cluster synthesis and are members of the nifS class of proteins. Lipoic acid is derived from octanoic acid, and serves as a coenzyme in energy metabolism, where it becomes part of the pyruvate dehydrogenase complex and the α-ketoglutarate dehydrogenase complex. The folates are a group of substances which are all derivatives of folic acid, which is turn is derived from L-glutamic acid, p-amino-benzoic acid and 6-methylpterin. The biosynthesis of folic acid and its derivatives, starting from the metabolism intermediates guanosine-5'-triphosphate (GTP), L-glutamic acid and p-amino-benzoic acid has been studied in detail in certain microorganisms.

Corrinoids (such as the cobalamines and particularly vitamin B_{12}) and porphyrines belong to a group of chemicals characterized by a tetrapyrole ring system. The biosynthesis of vitamin B_{12} is sufficiently complex that it has not yet been completely characterized, but many of the enzymes and substrates involved are now known. Nicotinic acid (nicotinate), and nicotinamide are pyridine derivatives which are also termed 'niacin'. Niacin is the precursor of the important coenzymes NAD (nicotinamide adenine dinucleotide) and NADP (nicotinamide adenine dinucleotide phosphate) and their reduced forms.

The large-scale production of these compounds has largely relied on cell-free chemical syntheses, though some of these chemicals have also been produced by large-scale culture of microorganisms, such as riboflavin, Vitamin B_6, pantothenate, and biotin. Only Vitamin B_{12} is produced solely by fermentation, due to the complexity of its synthesis. *In vitro* methodologies require significant inputs of materials and time, often at great cost.

C. Purine, Pyrimidine, Nucleoside and Nucleotide Metabolism and Uses

Purine and pyrimidine metabolism genes and their corresponding proteins are important targets for the therapy of tumor diseases and viral infections. The language

"purine" or "pyrimidine" includes the nitrogenous bases which are constituents of nucleic acids, co-enzymes, and nucleotides. The term "nucleotide" includes the basic structural units of nucleic acid molecules, which are comprised of a nitrogenous base, a pentose sugar (in the case of RNA, the sugar is ribose; in the case of DNA, the sugar is D-deoxyribose), and phosphoric acid. The language "nucleoside" includes molecules which serve as precursors to nucleotides, but which are lacking the phosphoric acid moiety that nucleotides possess. By inhibiting the biosynthesis of these molecules, or their mobilization to form nucleic acid molecules, it is possible to inhibit RNA and DNA synthesis; by inhibiting this activity in a fashion targeted to cancerous cells, the ability of tumor cells to divide and replicate may be inhibited. Additionally, there are nucleotides which may serve as energy stores (*e.g.*, ADP, ATP) or as coenzymes (*i.e.*, FAD and NAD).

Several publications have described the use of these chemicals for these medical indications, by influencing purine and/or pyrimidine metabolism (*e.g.* Christopherson, R.I. and Lyons, S.D. (1990) "Potent inhibitors of *de novo* pyrimidine and purine biosynthesis as chemotherapeutic agents." *Med. Res. Reviews* 10: 505-548). Studies of enzymes involved in purine and pyrimidine metabolism have been focused on the development of new drugs which can be used, for example, as immunosuppressants or anti-proliferants (Smith, J.L., (1995) "Enzymes in nucleotide synthesis." *Curr. Opin. Struct. Biol.* 5: 752-757; (1995) *Biochem Soc. Transact.* 23: 877-902). However, purine and pyrimidine bases, nucleosides and nucleotides have other utilities: as intermediates in the biosynthesis of several fine chemicals (*e.g.*, thiamine, S-adenosyl-methionine, folates, or riboflavin), as energy carriers for the cell (*e.g.*, ATP or GTP), and for chemicals themselves, commonly used as flavor enhancers (*e.g.*, IMP or GMP) or for several medicinal applications (see, for example, Kuninaka, A. (1996) Nucleotides and Related Compounds in Biotechnology vol. 6, Rehm *et al.*, eds. VCH: Weinheim, p. 561-612). Also, enzymes involved in purine, pyrimidine, nucleoside, or nucleotide metabolism are increasingly serving as targets against which chemicals for crop protection, including fungicides, herbicides and insecticides, are developed.

The metabolism of these compounds in bacteria has been characterized (for reviews see, for example, Zalkin, H. and Dixon, J.E. (1992) "*de novo* purine nucleotide biosynthesis", in: Progress in Nucleic Acid Research and Molecular Biology, vol. 42, Academic Press:, p. 259-287; and Michal, G. (1999) "Nucleotides and Nucleosides", Chapter 8 in: Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology, Wiley: New York). Purine metabolism has been the subject of intensive research, and is essential to the normal functioning of the cell. Impaired purine metabolism in higher animals can cause severe disease, such as gout. Purine nucleotides are synthesized from

ribose-5-phosphate, in a series of steps through the intermediate compound inosine-5'-phosphate (IMP), resulting in the production of guanosine-5'-monophosphate (GMP) or adenosine-5'-monophosphate (AMP), from which the triphosphate forms utilized as nucleotides are readily formed. These compounds are also utilized as energy stores, so their degradation provides energy for many different biochemical processes in the cell. Pyrimidine biosynthesis proceeds by the formation of uridine-5'-monophosphate (UMP) from ribose-5-phosphate. UMP, in turn, is converted to cytidine-5'-triphosphate (CTP). The deoxy- forms of all of these nucleotides are produced in a one step reduction reaction from the diphosphate ribose form of the nucleotide to the diphosphate deoxyribose form of the nucleotide. Upon phosphorylation, these molecules are able to participate in DNA synthesis.

D. Trehalose Metabolism and Uses

Trehalose consists of two glucose molecules, bound in α, α-1,1 linkage. It is commonly used in the food industry as a sweetener, an additive for dried or frozen foods, and in beverages. However, it also has applications in the pharmaceutical, cosmetics and biotechnology industries (see, for example, Nishimoto *et al.*, (1998) U.S. Patent No. 5,759,610; Singer, M.A. and Lindquist, S. (1998) *Trends Biotech.* 16: 460-467; Paiva, C.L.A. and Panek, A.D. (1996) *Biotech. Ann. Rev.* 2: 293-314; and Shiosaka, M. (1997) J. Japan 172: 97-102). Trehalose is produced by enzymes from many microorganisms and is naturally released into the surrounding medium, from which it can be collected using methods known in the art.

II. Elements and Methods of the Invention

The present invention is based, at least in part, on the discovery of novel molecules, referred to herein as MCP nucleic acid molecules. These MCP nucleic acid molecules are useful not only for the identification of *C. glutamicum* or related bacterial species, but also as markers for the mapping of the *C. glutamicum* genome and in the identification of bacteria useful for the production of fine chemicals by, *e.g.*, fermentative processes. The present invention is also based, at least in part, on the MCP protein molecules encoded by these MCP nucleic acid molecules. These MCP proteins are capable of modulating the yield, production, and/or efficiency of production of one or more fine chemicals from *C. glutamicum*, of serving as identifying markers for *C. glutamicum* or related organisms, of degrading hydrocarbons, and of serving as targets for the development of therapeutic pharmaceutical compounds. In one embodiment, the MCP molecules of the invention directly or indirectly participate in one or more fine chemical metabolic pathways in *C. glutamicum*. In a preferred embodiment, the activity

of the MCP molecules of the invention to indirectly or directly participate in such metabolic pathways has an impact on the production of a desired fine chemical by this microorganism. In a particularly preferred embodiment, the MCP molecules of the invention are modulated in activity, such that the *C. glutamicum* metabolic pathways in which the MCP proteins of the invention participate are modulated in efficiency or output, which either directly or indirectly modulates the production or efficiency of production of a desired fine chemical by *C. glutamicum*.

The language, "MCP protein" or "MCP polypeptide" includes proteins which are able to modulate the yield, production, and/or efficiency of production of one or more fine chemicals from *C. glutamicum*, to degrade hydrocarbons, to oxidize terpenoids, to serve as a target protein for drug screening or design, or to serve as identifying markers for *C. glutamicum* or related organisms. Examples of MCP proteins include those encoded by the MCP genes set forth in Table 1 and Appendix A. The terms "MCP gene" or "MCP nucleic acid sequence" include nucleic acid sequences encoding an MCP protein, which consist of a coding region and also corresponding untranslated 5' and 3' sequence regions. Examples of MCP genes include those set forth in Table 1. The terms "production" or "productivity" are art-recognized and include the concentration of the fermentation product (for example, the desired fine chemical) formed within a given time and a given fermentation volume (*e.g.*, kg product per hour per liter). The term "efficiency of production" includes the time required for a particular level of production to be achieved (for example, how long it takes for the cell to attain a particular rate of output of a fine chemical). The term "yield" or "product/carbon yield" is art-recognized and includes the efficiency of the conversion of the carbon source into the product (*i.e.*, fine chemical). This is generally written as, for example, kg product per kg carbon source. By increasing the yield or production of the compound, the quantity of recovered molecules, or of useful recovered molecules of that compound in a given amount of culture over a given amount of time is increased. The terms "biosynthesis" or a "biosynthetic pathway" are art-recognized and include the synthesis of a compound, preferably an organic compound, by a cell from intermediate compounds in what may be a multistep and highly regulated process. The terms "degradation" or a "degradation pathway" are art-recognized and include the breakdown of a compound, preferably an organic compound, by a cell to degradation products (generally speaking, smaller or less complex molecules) in what may be a multistep and highly regulated process. The language "metabolism" is art-recognized and includes the totality of the biochemical reactions that take place in an organism. The metabolism of a particular compound, then, (*e.g.*, the metabolism of an amino acid such as glycine) comprises the overall

biosynthetic, modification, and degradation pathways in the cell related to this compound.

In another embodiment, the MCP molecules of the invention are capable of modulating the production of a desired molecule, such as a fine chemical, in a microorganism such as *C. glutamicum*, either directly or indirectly. Using recombinant genetic techniques, one or more of the MCP proteins of the invention may be manipulated such that its function is modulated. Such modulation of function may result in the modulation of the yield, production, and/or efficiency of production of one or more fine chemicals from *C. glutamicum*.

For example, by modifying the activity of a protein involved in the biosynthesis or degradation of a fine chemical (*i.e.*, through mutagenesis of the corresponding gene), one may directly modulate the ability of the cell to synthesize or to degrade this compound, thereby modulating the yield and/or efficiency of production of the fine chemical. Similarly, by modulating the activity of a protein which regulates a fine chemical metabolic pathway, one may directly influence whether the production of the desired compound is up- or down-regulated, either of which will modulate the yield or efficiency of production of the fine chemical from the cell.

Indirect modulation of fine chemical production may also result by modifying the activity of a protein of the invention (*i.e.*, by mutagenesis of the corresponding gene) such that the overall ability of the cell to grow and divide or to remain viable and productive is increased. The production of fine chemicals from *C. glutamicum* is generally accomplished by the large-scale fermentative culture of these microorganisms, conditions which are frequently suboptimal for growth and cell division. By engineering a protein of the invention (*e.g.*, a stress response protein, a cell wall protein, or proteins involved in the metabolism of compounds necessary for cell growth and division to occur, such as nucleotides and amino acids) such that it is better able to survive, grow, and multiply in such conditions, it may be possible to increase the number and productivity of such engineered *C. glutamicum* cells in large-scale culture, which in turn should result in increased yields and/or efficiency of production of one or more desired fine chemicals. Further, the metabolic pathways of any cell are necessarily interrelated and coregulated. By altering the activity or regulation of any one metabolic pathway in *C. glutamicum* (*i.e.*, by altering the activity of one of the proteins of the invention which participates in such a pathway), it is possible to concomitantly alter the activity or regulation of other metabolic pathways in this microorganism, which may be directly involved in the synthesis or degradation of a fine chemical.

The isolated nucleic acid sequences of the invention are contained within the genome of a *Corynebacterium glutamicum* strain available through the American Type

Culture Collection, given designation ATCC 13032. The nucleotide sequences of the isolated *C. glutamicum* MCP nucleic acid molecules and the predicted amino acid sequences of the *C. glutamicum* MCP proteins are shown in Appendices A and B, respectively. Computational analyses were performed which classified and/or identified many of these nucleotide sequences as sequences having homology to *E. co*li or *Bacillus subtilis* genes.

The present invention also pertains to proteins which have an amino acid sequence which is substantially homologous to an amino acid sequence of Appendix B. As used herein, a protein which has an amino acid sequence which is substantially homologous to a selected amino acid sequence is least about 50% homologous to the selected amino acid sequence, *e.g.*, the entire selected amino acid sequence. A protein which has an amino acid sequence which is substantially homologous to a selected amino acid sequence can also be least about 50-60%, preferably at least about 60-70%, and more preferably at least about 70-80%, 80-90%, or 90-95%, and most preferably at least about 96%, 97%, 98%, 99% or more homologous to the selected amino acid sequence.

The MCP protein or a biologically active portion or fragment thereof of the invention is able to modulate the yield, production, and/or efficiency of production of one or more fine chemicals from *C. glutamicum*, to degrade hydrocarbons, to oxidize terpenoids, to serve as a target for drug development, or to serve as an identifying marker for *C. glutamicum* or related organisms.

Various aspects of the invention are described in further detail in the following subsections:

A. Isolated Nucleic Acid Molecules

One aspect of the invention pertains to isolated nucleic acid molecules that encode MCP polypeptides or biologically active portions thereof, as well as nucleic acid fragments sufficient for use as hybridization probes or primers for the identification or amplification of MCP-encoding nucleic acid (*e.g.*, MCP DNA). These nucleic acid molecules may be used to identify *C. glutamicum* or related organisms, to map the genome of *C. glutamicum* or closely related bacteria, or to identify microorganisms useful for the production of fine chemicals, *e.g.*, by fermentative processes. As used herein, the term "nucleic acid molecule" is intended to include DNA molecules (*e.g.*, cDNA or genomic DNA) and RNA molecules (*e.g.*, mRNA) and analogs of the DNA or RNA generated using nucleotide analogs. This term also encompasses untranslated sequence located at both the 3' and 5' ends of the coding region of the gene: at least about 100 nucleotides of sequence upstream from the 5' end of the coding region and at

least about 20 nucleotides of sequence downstream from the 3'end of the coding region of the gene. The nucleic acid molecule can be single-stranded or double-stranded, but preferably is double-stranded DNA. An "isolated" nucleic acid molecule is one which is separated from other nucleic acid molecules which are present in the natural source of the nucleic acid. Preferably, an "isolated" nucleic acid is free of sequences which naturally flank the nucleic acid (*i.e.*, sequences located at the 5' and 3' ends of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. For example, in various embodiments, the isolated MCP nucleic acid molecule can contain less than about 5 kb, 4kb, 3kb, 2kb, 1 kb, 0.5 kb or 0.1 kb of nucleotide sequences which naturally flank the nucleic acid molecule in genomic DNA of the cell from which the nucleic acid is derived (e.g, a *C. glutamicum* cell). Moreover, an "isolated" nucleic acid molecule, such as a DNA molecule, can be substantially free of other cellular material, or culture medium when produced by recombinant techniques, or chemical precursors or other chemicals when chemically synthesized.

A nucleic acid molecule of the present invention, *e.g.*, a nucleic acid molecule having a nucleotide sequence of Appendix A, or a portion thereof, can be isolated using standard molecular biology techniques and the sequence information provided herein. For example, a *C. glutamicum* MCP DNA can be isolated from a *C. glutamicum* library using all or portion of one of the sequences of Appendix A as a hybridization probe and standard hybridization techniques (*e.g.*, as described in Sambrook, J., Fritsh, E. F., and Maniatis, T. *Molecular Cloning: A Laboratory Manual. 2nd, ed., Cold Spring Harbor Laboratory,* Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989). Moreover, a nucleic acid molecule encompassing all or a portion of one of the sequences of Appendix A can be isolated by the polymerase chain reaction using oligonucleotide primers designed based upon this sequence (*e.g.*, a nucleic acid molecule encompassing all or a portion of one of the sequences of Appendix A can be isolated by the polymerase chain reaction using oligonucleotide primers designed based upon this same sequence of Appendix A). For example, mRNA can be isolated from normal endothelial cells (*e.g.*, by the guanidinium-thiocyanate extraction procedure of Chirgwin *et al.* (1979) *Biochemistry* 18: 5294-5299) and DNA can be prepared using reverse transcriptase (*e.g.*, Moloney MLV reverse transcriptase, available from Gibco/BRL, Bethesda, MD; or AMV reverse transcriptase, available from Seikagaku America, Inc., St. Petersburg, FL) and random polynucleotide primers or oligonucleotide primers based upon one of the nucleotide sequences shown in Appendix A. Synthetic oligonucleotide primers for polymerase chain reaction amplification can be designed based upon one of the nucleotide sequences shown in Appendix A. A nucleic acid of the invention can be amplified using cDNA or, alternatively, genomic DNA, as a template and appropriate

oligonucleotide primers according to standard PCR amplification techniques. The nucleic acid so amplified can be cloned into an appropriate vector and characterized by DNA sequence analysis. Furthermore, oligonucleotides corresponding to an MCP nucleotide sequence can be prepared by standard synthetic techniques, *e.g.*, using an automated DNA synthesizer.

In a preferred embodiment, an isolated nucleic acid molecule of the invention comprises one of the nucleotide sequences shown in Appendix A. The sequences of Appendix A correspond to the *Corynebacterium glutamicum* MCP DNAs of the invention. This cDNA comprises sequences encoding MCP proteins (*i.e.*, the "coding region", indicated in each sequence in Appendix A), as well as 5' untranslated sequences and 3' untranslated sequences, also indicated in Appendix A. Alternatively, the nucleic acid molecule can comprise only the coding region of any of the sequences in Appendix A.

For the purposes of this application, it will be understood that each of the sequences set forth in Appendix A has an identifying RXA or RXN number having the designation "RXA" or "RXN" followed by 5 digits (*i.e.*, RXA00003 or RXN00022). Each of these sequences comprises up to three parts: a 5' upstream region, a coding region, and a downstream region. Each of these three regions is identified by the same RXA or RXN designation to eliminate confusion. The recitation "one of the sequences in Appendix A", then, refers to any of the sequences in Appendix A, which may be distinguished by their differing RXA or RXN designations. The coding region of each of these sequences is translated into a corresponding amino acid sequence, which is set forth in Appendix B. The sequences of Appendix B are identified by the same RXA or RXN designations as Appendix A, such that they can be readily correlated. For example, the amino acid sequence in Appendix B designated RXA00003 is a translation of the coding region of the nucleotide sequence of nucleic acid molecule RXA00003 in Appendix A, and the amino acid sequence in Appendix B designated RXN00022 is a translation of the coding region of the nucleotide sequence of nucleic acid molecule RXN00022 in Appendix A. Each of the RXA and RXN nucleotide and amino acid sequences of the invention has also been assigned a SEQ ID NO, as indicated in Table 1.

Several of the genes of the invention are "F-designated genes". An F-designated gene includes those genes set forth in Table 1 which have an 'F' in front of the RXA designation. For example, SEQ ID NO:3, designated, as indicated on Table 1, as "F RXA01638", is an F-designated gene, as are SEQ ID NOs: 5, 9, and 11 (designated on Table 1 as "F RXA01639", "F RXA01590", and "F RXA01542", respectively).

In one embodiment, the nucleic acid molecules of the present invention are not intended to include those compiled in Table 2.

In another preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleic acid molecule which is a complement of one of the nucleotide sequences shown in Appendix A, or a portion thereof. A nucleic acid molecule which is complementary to one of the nucleotide sequences shown in Appendix A is one which is sufficiently complementary to one of the nucleotide sequences shown in Appendix A such that it can hybridize to one of the nucleotide sequences shown in Appendix A, thereby forming a stable duplex.

In still another preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleotide sequence which is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to a nucleotide sequence shown in Appendix A, or a portion thereof. Ranges and identity values intermediate to the above-recited ranges, (*e.g.*, 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included. In an additional preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, to one of the nucleotide sequences shown in Appendix A, or a portion thereof.

Moreover, the nucleic acid molecule of the invention can comprise only a portion of the coding region of one of the sequences in Appendix A, for example a fragment which can be used as a probe or primer or a fragment encoding a biologically active portion of an MCP protein. The nucleotide sequences determined from the cloning of the MCP genes from *C. glutamicum* allows for the generation of probes and primers designed for use in identifying and/or cloning MCP homologues in other cell types and organisms, as well as MCP homologues from other *Corynebacteria* or related species. The probe/primer typically comprises substantially purified oligonucleotide. The oligonucleotide typically comprises a region of nucleotide sequence that hybridizes under stringent conditions to at least about 12, preferably about 25, more preferably about 40, 50 or 75 consecutive nucleotides of a sense strand of one of the sequences set forth in Appendix A, an anti-sense sequence of one of the sequences set forth in Appendix A, or naturally occurring mutants thereof. Primers based on a nucleotide sequence of Appendix A can be used in PCR reactions to clone MCP homologues. Probes based on the MCP nucleotide sequences can be used to detect transcripts or

genomic sequences encoding the same or homologous proteins. In preferred embodiments, the probe further comprises a label group attached thereto, *e.g.* the label group can be a radioisotope, a fluorescent compound, an enzyme, or an enzyme co-factor. Such probes can be used as a part of a diagnostic test kit for identifying cells which misexpress an MCP protein, such as by measuring a level of an MCP-encoding nucleic acid in a sample of cells, *e.g.*, detecting MCP mRNA levels or determining whether a genomic MCP gene has been mutated or deleted.

In one embodiment, the nucleic acid molecule of the invention encodes a protein or portion thereof which includes an amino acid sequence which is sufficiently homologous to an amino acid sequence of Appendix B such that the protein or portion thereof maintains the ability to modulate the yield, production, and/or efficiency of production of one or more fine chemicals from *C. glutamicum*, to degrade hydrocarbons, to oxidize terpenoids, to serve as a target for drug development, or to serve as an identifying marker for *C. glutamicum* or related organisms. As used herein, the language "sufficiently homologous" refers to proteins or portions thereof which have amino acid sequences which include a minimum number of identical or equivalent (*e.g.*, an amino acid residue which has a similar side chain as an amino acid residue in one of the sequences of Appendix B) amino acid residues to an amino acid sequence of Appendix B such that the protein or portion thereof is able to modulate the yield, production, and/or efficiency of production of one or more fine chemicals from *C. glutamicum*, to degrade hydrocarbons, to oxidize terpenoids, to serve as a target for drug development, or to serve as an identifying marker for *C. glutamicum* or related organisms. Examples of such activities are also described herein. Thus, "the function of an MCP protein" contributes to the overall regulation of one or more fine chemical metabolic pathways, or to the degradation of a hydrocarbon, or to the oxidation of a terpenoid.

In another embodiment, the protein is at least about 50-60%, preferably at least about 60-70%, and more preferably at least about 70-80%, 80-90%, 90-95%, and most preferably at least about 96%, 97%, 98%, 99% or more homologous to an entire amino acid sequence of Appendix B.

Portions of proteins encoded by the MCP nucleic acid molecules of the invention are preferably biologically active portions of one of the MCP proteins. As used herein, the term "biologically active portion of an MCP protein" is intended to include a portion, *e.g.*, a domain/motif, of an MCP protein that modulates the yield, production, and/or efficiency of production of one or more fine chemicals from *C. glutamicum*, that degrades hydrocarbons, that oxidizes terpenoids, that may serve as a target for drug development, or that may serve as an identifying marker for *C. glutamicum* or related

organisms. To determine whether an MCP protein or a biologically active portion thereof can modulate the yield, production, and/or efficiency of production of one or more fine chemicals from *C. glutamicum*, can degrade hydrocarbons, or can oxidize terpenoids, an assay of activity may be performed. Such assay methods are well known to those of ordinary skill in the art, as detailed in Example 8 of the Exemplification.

Additional nucleic acid fragments encoding biologically active portions of an MCP protein can be prepared by isolating a portion of one of the sequences in Appendix B, expressing the encoded portion of the MCP protein or peptide (*e.g.*, by recombinant expression *in vitro*) and assessing the activity of the encoded portion of the MCP protein or peptide.

The invention further encompasses nucleic acid molecules that differ from one of the nucleotide sequences shown in Appendix A (and portions thereof) due to degeneracy of the genetic code and thus encode the same MCP protein as that encoded by the nucleotide sequences shown in Appendix A. In another embodiment, an isolated nucleic acid molecule of the invention has a nucleotide sequence encoding a protein having an amino acid sequence shown in Appendix B. In a still further embodiment, the nucleic acid molecule of the invention encodes a full length *C. glutamicum* protein which is substantially homologous to an amino acid sequence of Appendix B (encoded by an open reading frame shown in Appendix A).

It will be understood by one of ordinary skill in the art that in one embodiment the sequences of the invention are not meant to include the sequences of the prior art, such as those Genbank sequences set forth in Tables 2 or 4 which were available prior to the present invention. In one embodiment, the invention includes nucleotide and amino acid sequences having a percent identity to a nucleotide or amino acid sequence of the invention which is greater than that of a sequence of the prior art (*e.g.*, a Genbank sequence (or the protein encoded by such a sequence) set forth in Tables 2 or 4). For example, the invention includes a nucleotide sequence which is greater than and/or at least 39% identical to the nucleotide sequence designated RXA00008 (SEQ ID NO:1549), a nucleotide sequence which is greater than and/or at least 42% identical to the nucleotide sequence designated RXA00059 (SEQ ID NO:1571), and a nucleotide sequence which is greater than and/or at least 39% identical to the nucleotide sequence designated RXA00096 (SEQ ID NO:93). One of ordinary skill in the art would be able to calculate the lower threshold of percent identity for any given sequence of the invention by examining the GAP-calculated percent identity scores set forth in Table 4 for each of the three top hits for the given sequence, and by subtracting the highest GAP-calculated percent identity from 100 percent. One of ordinary skill in the art will also appreciate that nucleic acid and amino acid sequences having percent identities

greater than the lower threshold so calculated (*e.g.*, at least 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more identical) are also encompassed by the invention.

In addition to the *C. glutamicum* MCP nucleotide sequences shown in Appendix A, it will be appreciated by those of ordinary skill in the art that DNA sequence polymorphisms that lead to changes in the amino acid sequences of MCP proteins may exist within a population (*e.g.*, the *C. glutamicum* population). Such genetic polymorphism in the MCP gene may exist among individuals within a population due to natural variation. As used herein, the terms "gene" and "recombinant gene" refer to nucleic acid molecules comprising an open reading frame encoding an MCP protein, preferably a *C. glutamicum* MCP protein. Such natural variations can typically result in 1-5% variance in the nucleotide sequence of the MCP gene. Any and all such nucleotide variations and resulting amino acid polymorphisms in MCP that are the result of natural variation and that do not alter the functional activity of MCP proteins are intended to be within the scope of the invention.

Nucleic acid molecules corresponding to natural variants and non-*C. glutamicum* homologues of the *C. glutamicum* MCP DNA of the invention can be isolated based on their homology to the *C. glutamicum* MCP nucleic acid disclosed herein using the *C. glutamicum* DNA, or a portion thereof, as a hybridization probe according to standard hybridization techniques under stringent hybridization conditions. Accordingly, in another embodiment, an isolated nucleic acid molecule of the invention is at least 15 nucleotides in length and hybridizes under stringent conditions to the nucleic acid molecule comprising a nucleotide sequence of Appendix A. In other embodiments, the nucleic acid is at least 30, 50, 100, 250 or more nucleotides in length. As used herein, the term "hybridizes under stringent conditions" is intended to describe conditions for hybridization and washing under which nucleotide sequences at least 60% homologous to each other typically remain hybridized to each other. Preferably, the conditions are such that sequences at least about 65%, more preferably at least about 70%, and even more preferably at least about 75% or more homologous to each other typically remain hybridized to each other. Such stringent conditions are known to those of ordinary skill in the art and can be found in *Current Protocols in Molecular Biology*, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6. A preferred, non-limiting example of stringent hybridization conditions are hybridization in 6X sodium chloride/sodium citrate (SSC) at about 45°C, followed by one or more washes in 0.2 X SSC, 0.1% SDS at 50-65°C.

Preferably, an isolated nucleic acid molecule of the invention that hybridizes under stringent conditions to a sequence of Appendix A corresponds to a naturally-occurring nucleic acid molecule. As used herein, a "naturally-occurring" nucleic acid molecule refers to an RNA or DNA molecule having a nucleotide sequence that occurs in nature (*e.g.*, encodes a natural protein). In one embodiment, the nucleic acid encodes a natural *C. glutamicum* MCP protein.

In addition to naturally-occurring variants of the MCP sequence that may exist in the population, one of ordinary skill in the art will further appreciate that changes can be introduced by mutation into a nucleotide sequence of Appendix A, thereby leading to changes in the amino acid sequence of the encoded MCP protein, without altering the functional ability of the MCP protein. For example, nucleotide substitutions leading to amino acid substitutions at "non-essential" amino acid residues can be made in a sequence of Appendix A. A "non-essential" amino acid residue is a residue that can be altered from the wild-type sequence of one of the MCP proteins (Appendix B) without altering the activity of said MCP protein, whereas an "essential" amino acid residue is required for MCP protein activity. Other amino acid residues, however, (*e.g.*, those that are not conserved or only semi-conserved in the domain having MCP activity) may not be essential for activity and thus are likely to be amenable to alteration without altering MCP activity.

Accordingly, another aspect of the invention pertains to nucleic acid molecules encoding MCP proteins that contain changes in amino acid residues that are not essential for MCP activity. Such MCP proteins differ in amino acid sequence from a sequence contained in Appendix B yet retain at least one of the MCP activities described herein. In one embodiment, the isolated nucleic acid molecule comprises a nucleotide sequence encoding a protein, wherein the protein comprises an amino acid sequence at least about 50% homologous to an amino acid sequence of Appendix B and is able to modulate the yield, production, and/or efficiency of production of one or more fine chemicals from *C. glutamicum*, to degrade hydrocarbons, to oxidize terpenoids, to serve as a target for drug development, or to serve as an identifying marker for *C. glutamicum* or related organisms. Preferably, the protein encoded by the nucleic acid molecule is at least about 50-60% homologous to one of the sequences in Appendix B, more preferably at least about 60-70% homologous to one of the sequences in Appendix B, even more preferably at least about 70-80%, 80-90%, 90-95% homologous to one of the sequences in Appendix B, and most preferably at least about 96%, 97%, 98%, or 99% homologous to one of the sequences in Appendix B.

To determine the percent homology of two amino acid sequences (*e.g.*, one of the sequences of Appendix B and a mutant form thereof) or of two nucleic acids, the

sequences are aligned for optimal comparison purposes (*e.g.*, gaps can be introduced in the sequence of one protein or nucleic acid for optimal alignment with the other protein or nucleic acid). The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in one sequence (*e.g.*, one of the sequences of Appendix B) is occupied by the same amino acid residue or nucleotide as the corresponding position in the other sequence (*e.g.*, a mutant form of the sequence selected from Appendix B), then the molecules are homologous at that position (*i.e.*, as used herein amino acid or nucleic acid "homology" is equivalent to amino acid or nucleic acid "identity"). The percent homology between the two sequences is a function of the number of identical positions shared by the sequences (*i.e.*, % homology = # of identical positions/total # of positions x 100).

An isolated nucleic acid molecule encoding an MCP protein homologous to a protein sequence of Appendix B can be created by introducing one or more nucleotide substitutions, additions or deletions into a nucleotide sequence of Appendix A such that one or more amino acid substitutions, additions or deletions are introduced into the encoded protein. Mutations can be introduced into one of the sequences of Appendix A by standard techniques, such as site-directed mutagenesis and PCR-mediated mutagenesis. Preferably, conservative amino acid substitutions are made at one or more predicted non-essential amino acid residues. A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (*e.g.*, lysine, arginine, histidine), acidic side chains (*e.g.*, aspartic acid, glutamic acid), uncharged polar side chains (*e.g.*, glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (*e.g.*, alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (*e.g.*, threonine, valine, isoleucine) and aromatic side chains (*e.g.*, tyrosine, phenylalanine, tryptophan, histidine). Thus, a predicted nonessential amino acid residue in an MCP protein is preferably replaced with another amino acid residue from the same side chain family. Alternatively, in another embodiment, mutations can be introduced randomly along all or part of an MCP coding sequence, such as by saturation mutagenesis, and the resultant mutants can be screened for an MCP activity described herein to identify mutants that retain MCP activity. Following mutagenesis of one of the sequences of Appendix A, the encoded protein can be expressed recombinantly and the activity of the protein can be determined using, for example, assays described herein (see Example 8 of the Exemplification).

In addition to the nucleic acid molecules encoding MCP proteins described above, another aspect of the invention pertains to isolated nucleic acid molecules which are antisense thereto. An "antisense" nucleic acid comprises a nucleotide sequence which is complementary to a "sense" nucleic acid encoding a protein, *e.g.*, complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence. Accordingly, an antisense nucleic acid can hydrogen bond to a sense nucleic acid. The antisense nucleic acid can be complementary to an entire MCP coding strand, or to only a portion thereof. In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence encoding an MCP protein. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid residues (*e.g.*, the entire coding region of SEQ ID NO. 1 (RXN01638) comprises nucleotides 1 to900). In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence encoding MCP. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding MCP disclosed herein (*e.g.*, the sequences set forth in Appendix A), antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of MCP mRNA, but more preferably is an oligonucleotide which is antisense to only a portion of the coding or noncoding region of MCP mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of MCP mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed by chemical synthesis and enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used. Examples of modified nucleotides which can be used to generate the antisense nucleic acid include 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxylmethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-

methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

The antisense nucleic acid molecules of the invention are typically administered to a cell or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding an MCP protein to thereby inhibit expression of the protein, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule which binds to DNA duplexes, through specific interactions in the major groove of the double helix. The antisense molecule can be modified such that it specifically binds to a receptor or an antigen expressed on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecule to a peptide or an antibody which binds to a cell surface receptor or antigen. The antisense nucleic acid molecule can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of the antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong prokaryotic, viral, or eukaryotic promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an α-anomeric nucleic acid molecule. An α-anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β-units, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids. Res.* 15:6625-6641). The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue *et al.* (1987) *Nucleic Acids Res.* 15:6131-6148) or a chimeric RNA-DNA analogue (Inoue *et al.* (1987) *FEBS Lett.* 215:327-330).

In still another embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity which are capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which they have a complementary region. Thus, ribozymes (*e.g.*, hammerhead ribozymes

(described in Haselhoff and Gerlach (1988) *Nature* 334:585-591)) can be used to catalytically cleave MCP mRNA transcripts to thereby inhibit translation of MCP mRNA. A ribozyme having specificity for an MCP-encoding nucleic acid can be designed based upon the nucleotide sequence of an MCP DNA disclosed herein (*i.e.*, SEQ ID NO. 1 (RXN01368) in Appendix A). For example, a derivative of a *Tetrahymena* L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in an MCP-encoding mRNA. See, *e.g.*, Cech *et al.* U.S. Patent No. 4,987,071 and Cech *et al.* U.S. Patent No. 5,116,742. Alternatively, MCP mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, *e.g.*, Bartel, D. and Szostak, J.W. (1993) *Science* 261:1411-1418.

Alternatively, MCP gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region of an MCP nucleotide sequence (*e.g.*, an MCP promoter and/or enhancers) to form triple helical structures that prevent transcription of an MCP gene in target cells. See generally, Helene, C. (1991) *Anticancer Drug Des.* 6(6):569-84; Helene, C. *et al.* (1992) *Ann. N.Y. Acad. Sci.* 660:27-36; and Maher, L.J. (1992) *Bioassays* 14(12):807-15.

B. Recombinant Expression Vectors and Host Cells

Another aspect of the invention pertains to vectors, preferably expression vectors, containing a nucleic acid encoding an MCP protein (or a portion thereof). As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid", which refers to a circular double stranded DNA loop into which additional DNA segments can be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (*e.g.*, bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (*e.g.*, non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors are capable of directing the expression of genes to which they are operatively linked. Such vectors are referred to herein as "expression vectors". In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. In the present specification, "plasmid" and "vector" can be used interchangeably as the plasmid is the most commonly used form of vector. However, the invention is intended to include such other forms of expression vectors,

such as viral vectors (*e.g.*, replication defective retroviruses, adenoviruses and adeno-associated viruses), which serve equivalent functions.

The recombinant expression vectors of the invention comprise a nucleic acid of the invention in a form suitable for expression of the nucleic acid in a host cell, which means that the recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, which is operatively linked to the nucleic acid sequence to be expressed. Within a recombinant expression vector, "operably linked" is intended to mean that the nucleotide sequence of interest is linked to the regulatory sequence(s) in a manner which allows for expression of the nucleotide sequence (*e.g.*, in an *in vitro* transcription/translation system or in a host cell when the vector is introduced into the host cell). The term "regulatory sequence" is intended to include promoters, repressor binding sites, activator binding sites, enhancer regions and other expression control elements (*e.g.*, terminators, other elements of mRNA secondary structure, or polyadenylation signals). Such regulatory sequences are described, for example, in Goeddel; *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, CA (1990). Regulatory sequences include those which direct constitutive expression of a nucleotide sequence in many types of host cell and those which direct expression of the nucleotide sequence only in certain host cells. Preferred regulatory sequences are, for example, promoters such as cos-, tac-, trp-, tet-, trp-tet-, lpp-, lac-, lpp-lac-, $lacI^q$-, T7-, T5-, T3-, gal-, trc-, ara-, SP6-, arny, SPO2, λ-P_R- or λ P_L, which are used preferably in bacteria. Additional regulatory sequences are, for example, promoters from yeasts and fungi, such as ADC1, MFα, AC, P-60, CYC1, GAPDH, TEF, rp28, ADH, promoters from plants such as CaMV/35S, SSU, OCS, lib4, usp, STLS1, B33, nos or ubiquitin- or phaseolin-promoters. It is also possible to use artificial promoters. It will be appreciated by those of ordinary skill in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed, the level of expression of protein desired, etc. The expression vectors of the invention can be introduced into host cells to thereby produce proteins or peptides, including fusion proteins or peptides, encoded by nucleic acids as described herein (*e.g.*, MCP proteins, mutant forms of MCP proteins, fusion proteins, etc.).

The recombinant expression vectors of the invention can be designed for expression of MCP proteins in prokaryotic or eukaryotic cells. For example, MCP genes can be expressed in bacterial cells such as *C. glutamicum*, insect cells (using baculovirus expression vectors), yeast and other fungal cells (see Romanos, M.A. *et al.* (1992) "Foreign gene expression in yeast: a review", *Yeast* 8: 423-488; van den Hondel, C.A.M.J.J. *et al.* (1991) "Heterologous gene expression in filamentous fungi" in: More

Gene Manipulations in Fungi, J.W. Bennet & L.L. Lasure, eds., p. 396-428: Academic Press: San Diego; and van den Hondel, C.A.M.J.J. & Punt, P.J. (1991) "Gene transfer systems and vector development for filamentous fungi, in: Applied Molecular Genetics of Fungi, Peberdy, J.F. *et al.*, eds., p. 1-28, Cambridge University Press: Cambridge), algae and multicellular plant cells (see Schmidt, R. and Willmitzer, L. (1988) High efficiency *Agrobacterium tumefactiens* –mediated transformation of *Arabidopsis thaliana* leaf and cotyledon explants" *Plant Cell Rep.*: 583-586), or mammalian cells. Suitable host cells are discussed further in Goeddel, *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, CA (1990). Alternatively, the recombinant expression vector can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase.

Expression of proteins in prokaryotes is most often carried out with vectors containing constitutive or inducible promoters directing the expression of either fusion or non-fusion proteins. Fusion vectors add a number of amino acids to a protein encoded therein, usually to the amino terminus of the recombinant protein. Such fusion vectors typically serve three purposes: 1) to increase expression of recombinant protein; 2) to increase the solubility of the recombinant protein; and 3) to aid in the purification of the recombinant protein by acting as a ligand in affinity purification. Often, in fusion expression vectors, a proteolytic cleavage site is introduced at the junction of the fusion moiety and the recombinant protein to enable separation of the recombinant protein from the fusion moiety subsequent to purification of the fusion protein. Such enzymes, and their cognate recognition sequences, include Factor Xa, thrombin and enterokinase.

Typical fusion expression vectors include pGEX (Pharmacia Biotech Inc; Smith, D.B. and Johnson, K.S. (1988) *Gene* 67:31-40), pMAL (New England Biolabs, Beverly, MA) and pRIT5 (Pharmacia, Piscataway, NJ) which fuse glutathione S-transferase (GST), maltose E binding protein, or protein A, respectively, to the target recombinant protein. In one embodiment, the coding sequence of the MCP protein is cloned into a pGEX expression vector to create a vector encoding a fusion protein comprising, from the N-terminus to the C-terminus, GST-thrombin cleavage site-X protein. The fusion protein can be purified by affinity chromatography using glutathione-agarose resin. Recombinant MCP protein unfused to GST can be recovered by cleavage of the fusion protein with thrombin.

Examples of suitable inducible non-fusion *E. coli* expression vectors include pTrc (Amann *et al.*, (1988) *Gene* 69:301-315), pLG338, pACYC184, pBR322, pUC18, pUC19, pKC30, pRep4, pHS1, pHS2, pPLc236, pMBL24, pLG200, pUR290, pIN-III113-B1, λgt11, pBdCl, and pET 11d (Studier *et al.*, *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, California (1990) 60-89 ; and

Pouwels *et al.*, eds. (1985) Cloning Vectors. Elsevier: New York IBSN 0 444 904018). Target gene expression from the pTrc vector relies on host RNA polymerase transcription from a hybrid trp-lac fusion promoter. Target gene expression from the pET 11d vector relies on transcription from a T7 gn10-lac fusion promoter mediated by a coexpressed viral RNA polymerase (T7 gn1). This viral polymerase is supplied by host strains BL21(DE3) or HMS174(DE3) from a resident λ prophage harboring a T7 gn1 gene under the transcriptional control of the lacUV 5 promoter. For transformation of other varieties of bacteria, appropriate vectors may be selected. For example, the plasmids pIJ101, pIJ364, pIJ702 and pIJ361 are known to be useful in transforming Streptomyces, while plasmids pUB110, pC194, or pBD214 are suited for transformation of Bacillus species. Several plasmids of use in the transfer of genetic information into Corynebacterium include pHM1519, pBL1, pSA77, or pAJ667 (Pouwels *et al.*, eds. (1985) Cloning Vectors. Elsevier: New York IBSN 0 444 904018).

One strategy to maximize recombinant protein expression is to express the protein in a host bacteria with an impaired capacity to proteolytically cleave the recombinant protein (Gottesman, S., *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, California (1990) 119-128). Another strategy is to alter the nucleic acid sequence of the nucleic acid to be inserted into an expression vector so that the individual codons for each amino acid are those preferentially utilized in the bacterium chosen for expression, such as *C. glutamicum* (Wada *et al.* (1992) *Nucleic Acids Res.* 20:2111-2118). Such alteration of nucleic acid sequences of the invention can be carried out by standard DNA synthesis techniques.

In another embodiment, the MCP protein expression vector is a yeast expression vector. Examples of vectors for expression in yeast *S. cerevisiae* include pYepSec1 (Baldari, *et al.*, (1987) *Embo J.* 6:229-234), 2 μ, pAG-1, Yep6, Yep13, pEMBLYe23, pMFa (Kurjan and Herskowitz, (1982) *Cell* 30:933-943), pJRY88 (Schultz *et al.*, (1987) *Gene* 54:113-123), and pYES2 (Invitrogen Corporation, San Diego, CA). Vectors and methods for the construction of vectors appropriate for use in other fungi, such as the filamentous fungi, include those detailed in: van den Hondel, C.A.M.J.J. & Punt, P.J. (1991) "Gene transfer systems and vector development for filamentous fungi, in: Applied Molecular Genetics of Fungi, J.F. Peberdy, *et al.*, eds., p. 1-28, Cambridge University Press: Cambridge, and Pouwels *et al.*, eds. (1985) Cloning Vectors. Elsevier: New York (IBSN 0 444 904018).

Alternatively, the MCP proteins of the invention can be expressed in insect cells using baculovirus expression vectors. Baculovirus vectors available for expression of proteins in cultured insect cells (*e.g.*, Sf 9 cells) include the pAc series (Smith *et al.*

(1983) *Mol. Cell Biol.* 3:2156-2165) and the pVL series (Lucklow and Summers (1989) *Virology* 170:31-39).

In another embodiment, the MCP proteins of the invention may be expressed in unicellular plant cells (such as algae) or in plant cells from higher plants (*e.g.*, the spermatophytes, such as crop plants). Examples of plant expression vectors include those detailed in: Becker, D., Kemper, E., Schell, J. and Masterson, R. (1992) "New plant binary vectors with selectable markers located proximal to the left border", *Plant Mol. Biol.* 20: 1195-1197; and Bevan, M.W. (1984) "Binary *Agrobacterium* vectors for plant transformation", *Nucl. Acid. Res.* 12: 8711-8721, and include pLGV23, pGHlac+, pBIN19, pAK2004, and pDH51 (Pouwels *et al.*, eds. (1985) Cloning Vectors. Elsevier: New York IBSN 0 444 904018).

In yet another embodiment, a nucleic acid of the invention is expressed in mammalian cells using a mammalian expression vector. Examples of mammalian expression vectors include pCDM8 (Seed, B. (1987) *Nature* 329:840) and pMT2PC (Kaufman *et al.* (1987) *EMBO J.* 6:187-195). When used in mammalian cells, the expression vector's control functions are often provided by viral regulatory elements. For example, commonly used promoters are derived from polyoma, Adenovirus 2, cytomegalovirus and Simian Virus 40. For other suitable expression systems for both prokaryotic and eukaryotic cells see chapters 16 and 17 of Sambrook, J., Fritsh, E. F., and Maniatis, T. *Molecular Cloning: A Laboratory Manual. 2nd, ed., Cold Spring Harbor Laboratory,* Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989.

In another embodiment, the recombinant mammalian expression vector is capable of directing expression of the nucleic acid preferentially in a particular cell type (*e.g.*, tissue-specific regulatory elements are used to express the nucleic acid). Tissue-specific regulatory elements are known in the art. Non-limiting examples of suitable tissue-specific promoters include the albumin promoter (liver-specific; Pinkert *et al.* (1987) *Genes Dev.* 1:268-277), lymphoid-specific promoters (Calame and Eaton (1988) *Adv. Immunol.* 43:235-275), in particular promoters of T cell receptors (Winoto and Baltimore (1989) *EMBO J.* 8:729-733) and immunoglobulins (Banerji *et al.* (1983) *Cell* 33:729-740; Queen and Baltimore (1983) *Cell* 33:741-748), neuron-specific promoters (*e.g.*, the neurofilament promoter; Byrne and Ruddle (1989) *PNAS* 86:5473-5477), pancreas-specific promoters (Edlund *et al.* (1985) *Science* 230:912-916), and mammary gland-specific promoters (*e.g.*, milk whey promoter; U.S. Patent No. 4,873,316 and European Application Publication No. 264,166). Developmentally-regulated promoters are also encompassed, for example the murine hox promoters (Kessel and Gruss (1990)

Science 249:374-379) and the α-fetoprotein promoter (Campes and Tilghman (1989) *Genes Dev.* 3:537-546).

The invention further provides a recombinant expression vector comprising a DNA molecule of the invention cloned into the expression vector in an antisense orientation. That is, the DNA molecule is operatively linked to a regulatory sequence in a manner which allows for expression (by transcription of the DNA molecule) of an RNA molecule which is antisense to MCP mRNA. Regulatory sequences operatively linked to a nucleic acid cloned in the antisense orientation can be chosen which direct the continuous expression of the antisense RNA molecule in a variety of cell types, for instance viral promoters and/or enhancers, or regulatory sequences can be chosen which direct constitutive, tissue specific or cell type specific expression of antisense RNA. The antisense expression vector can be in the form of a recombinant plasmid, phagemid or attenuated virus in which antisense nucleic acids are produced under the control of a high efficiency regulatory region, the activity of which can be determined by the cell type into which the vector is introduced. For a discussion of the regulation of gene expression using antisense genes see Weintraub, H. *et al.* (1986) "Antisense RNA as a molecular tool for genetic analysis", *Reviews - Trends in Genetics*, Vol. 1(1).

Another aspect of the invention pertains to host cells into which a recombinant expression vector of the invention has been introduced. The terms "host cell" and "recombinant host cell" are used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

A host cell can be any prokaryotic or eukaryotic cell. For example, an MCP protein can be expressed in bacterial cells such as *C. glutamicum*, insect cells, yeast or mammalian cells (such as Chinese hamster ovary cells (CHO) or COS cells). Other suitable host cells are known to those of ordinary skill in the art. Microorganisms related to *Corynebacterium glutamicum* which may be conveniently used as host cells for the nucleic acid and protein molecules of the invention are set forth in Table 3.

Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional transformation or transfection techniques. As used herein, the terms "transformation", "transfection", "conjugation" and "transduction" are intended to refer to a variety of art-recognized techniques for introducing foreign nucleic acid (*e.g.*, linear DNA or RNA (*e.g.*, a linearized vector or a gene construct alone without a vector) or nucleic acid in the form of a vector (*e.g.*, a plasmid, phage, phasmid, phagemid,

transposon or other DNA) into a host cell, including using natural competence, chemical mediated transfer, calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, lipofection, or electroporation. Suitable methods for transforming or transfecting host cells can be found in Sambrook, *et al.* (*Molecular Cloning: A Laboratory Manual. 2nd, ed., Cold Spring Harbor Laboratory,* Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989), and other laboratory manuals.

For stable transfection of mammalian cells, it is known that, depending upon the expression vector and transfection technique used, only a small fraction of cells may integrate the foreign DNA into their genome. In order to identify and select these integrants, a gene that encodes a selectable marker (*e.g.*, resistance to antibiotics) is generally introduced into the host cells along with the gene of interest. Preferred selectable markers include those which confer resistance to drugs, such as G418, hygromycin and methotrexate. Nucleic acid encoding a selectable marker can be introduced into a host cell on the same vector as that encoding an MCP protein or can be introduced on a separate vector. Cells stably transfected with the introduced nucleic acid can be identified by, for example, drug selection (*e.g.*, cells that have incorporated the selectable marker gene will survive, while the other cells die).

To create a homologous recombinant microorganism, a vector is prepared which contains at least a portion of an MCP gene into which a deletion, addition or substitution has been introduced to thereby alter, *e.g.*, functionally disrupt, the MCP gene. Preferably, this MCP gene is a *Corynebacterium glutamicum* MCP gene, but it can be a homologue from a related bacterium or even from a mammalian, yeast, or insect source. In a preferred embodiment, the vector is designed such that, upon homologous recombination, the endogenous MCP gene is functionally disrupted (*i.e.*, no longer encodes a functional protein; also referred to as a "knock out" vector). Alternatively, the vector can be designed such that, upon homologous recombination, the endogenous MCP gene is mutated or otherwise altered but still encodes functional protein (*e.g.*, the upstream regulatory region can be altered to thereby alter the expression of the endogenous MCP protein). In the homologous recombination vector, the altered portion of the MCP gene is flanked at its 5' and 3' ends by additional nucleic acid of the MCP gene to allow for homologous recombination to occur between the exogenous MCP gene carried by the vector and an endogenous MCP gene in a microorganism. The additional flanking MCP nucleic acid is of sufficient length for successful homologous recombination with the endogenous gene. Typically, less than one kilobase of flanking DNA (both at the 5' and 3' ends) is included in the vector (see *e.g.*, Thomas, K.R., and Capecchi, M.R. (1987) Cell 51: 503 for a description of homologous recombination vectors). The vector is introduced into a microorganism (*e.g.*, by electroporation) and

cells in which the introduced MCP gene has homologously recombined with the endogenous MCP gene are selected, using art-known techniques.

In another embodiment, recombinant microorganisms can be produced which contain selected systems which allow for regulated expression of the introduced gene. For example, inclusion of an MCP gene on a vector placing it under control of the lac operon permits expression of the MCP gene in the presence of IPTG. Such regulatory systems are well known in the art.

In another embodiment, an endogenous MCP gene in a host cell is disrupted (*e.g.*, by homologous recombination or other genetic means known in the art) such that expression of its protein product does not occur. In another embodiment, an endogenous or introduced MCP gene in a host cell has been altered by one or more point mutations, deletions, or inversions, but still encodes a functional MCP protein. In still another embodiment, one or more of the regulatory regions (*e.g.*, a promoter, repressor, or inducer) of an MCP gene in a microorganism has been altered (*e.g.*, by deletion, truncation, inversion, or point mutation) such that the expression of the MCP gene is modulated. One of ordinary skill in the art will appreciate that host cells containing more than one of the described MCP gene and protein modifications may be readily produced using the methods of the invention, and are meant to be included in the present invention.

A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce (*i.e.*, express) an MCP protein. Accordingly, the invention further provides methods for producing MCP proteins using the host cells of the invention. In one embodiment, the method comprises culturing the host cell of invention (into which a recombinant expression vector encoding an MCP protein has been introduced, or into which genome has been introduced a gene encoding a wild-type or altered MCP protein) in a suitable medium until MCP protein is produced. In another embodiment, the method further comprises isolating MCP proteins from the medium or the host cell.

C. Isolated MCP Proteins

Another aspect of the invention pertains to isolated MCP proteins, and biologically active portions thereof. An "isolated" or "purified" protein or biologically active portion thereof is substantially free of cellular material when produced by recombinant DNA techniques, or chemical precursors or other chemicals when chemically synthesized. The language "substantially free of cellular material" includes preparations of MCP protein in which the protein is separated from cellular components of the cells in which it is naturally or recombinantly produced. In one embodiment, the

language "substantially free of cellular material" includes preparations of MCP protein having less than about 30% (by dry weight) of non-MCP protein (also referred to herein as a "contaminating protein"), more preferably less than about 20% of non-MCP protein, still more preferably less than about 10% of non-MCP protein, and most preferably less than about 5% non-MCP protein. When the MCP protein or biologically active portion thereof is recombinantly produced, it is also preferably substantially free of culture medium, *i.e.*, culture medium represents less than about 20%, more preferably less than about 10%, and most preferably less than about 5% of the volume of the protein preparation. The language "substantially free of chemical precursors or other chemicals" includes preparations of MCP protein in which the protein is separated from chemical precursors or other chemicals which are involved in the synthesis of the protein. In one embodiment, the language "substantially free of chemical precursors or other chemicals" includes preparations of MCP protein having less than about 30% (by dry weight) of chemical precursors or non-MCP chemicals, more preferably less than about 20% chemical precursors or non-MCP chemicals, still more preferably less than about 10% chemical precursors or non-MCP chemicals, and most preferably less than about 5% chemical precursors or non-MCP chemicals. In preferred embodiments, isolated proteins or biologically active portions thereof lack contaminating proteins from the same organism from which the MCP protein is derived. Typically, such proteins are produced by recombinant expression of, for example, a *C. glutamicum* MCP protein in a microorganism such as *C. glutamicum.*

An isolated MCP protein or a portion thereof of the invention is able to modulate the yield, production, and/or efficiency of production of one or more fine chemicals from *C. glutamicum*, to degrade hydrocarbons, to oxidize terpenoids, to serve as a target for drug development, or to serve as an identifying marker for *C. glutamicum* or related organisms. In preferred embodiments, the protein or portion thereof comprises an amino acid sequence which is sufficiently homologous to an amino acid sequence of Appendix B such that the protein or portion thereof maintains the ability to modulate the yield, production, and/or efficiency of production of one or more fine chemicals from *C. glutamicum*, to degrade hydrocarbons, to oxidize terpenoids, to serve as a target for drug development, or to serve as an identifying marker for *C. glutamicum* or related organisms. The portion of the protein is preferably a biologically active portion as described herein. In another preferred embodiment, an MCP protein of the invention has an amino acid sequence shown in Appendix B. In yet another preferred embodiment, the MCP protein has an amino acid sequence which is encoded by a nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, to a nucleotide sequence of Appendix A. In still another preferred embodiment, the MCP

protein has an amino acid sequence which is encoded by a nucleotide sequence that is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99%or more homologous to one of the nucleic acid sequences of Appendix A, or a portion thereof. Ranges and identity values intermediate to the above-recited values, (*e.g.*, 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included. The preferred MCP proteins of the present invention also preferably possess at least one of the MCP activities described herein. For example, a preferred MCP protein of the present invention includes an amino acid sequence encoded by a nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, to a nucleotide sequence of Appendix A, and which is able to modulate the yield, production, and/or efficiency of production of one or more fine chemicals from *C. glutamicum*, to degrade hydrocarbons, to oxidize terpenoids, to serve as a target for drug development, or to serve as an identifying marker for *C. glutamicum* or related organisms.

In other embodiments, the MCP protein is substantially homologous to an amino acid sequence of Appendix B and retains the functional activity of the protein of one of the sequences of Appendix B yet differs in amino acid sequence due to natural variation or mutagenesis, as described in detail in subsection I above. Accordingly, in another embodiment, the MCP protein is a protein which comprises an amino acid sequence which is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to an entire amino acid sequence of Appendix B and which has at least one of the MCP activities described herein. Ranges and identity values intermediate to the above-recited values, (*e.g.*, 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included. In another embodiment, the invention pertains to a full length *C. glutamicum* protein which is substantially homologous to an entire amino acid sequence of Appendix B.

Biologically active portions of an MCP protein include peptides comprising amino acid sequences derived from the amino acid sequence of an MCP protein, *e.g.*, an amino acid sequence shown in Appendix B or the amino acid sequence of a protein homologous to an MCP protein, which include fewer amino acids than a full length MCP protein or the full length protein which is homologous to an MCP protein, and exhibit at least one activity of an MCP protein. Typically, biologically active portions (peptides, *e.g.*, peptides which are, for example, 5, 10, 15, 20, 30, 35, 36, 37, 38, 39, 40, 50, 100 or more amino acids in length) comprise a domain or motif with at least one activity of an MCP protein. Moreover, other biologically active portions, in which other regions of the protein are deleted, can be prepared by recombinant techniques and evaluated for one or more of the activities described herein. Preferably, the biologically active portions of an MCP protein include one or more selected domains/motifs or portions thereof having biological activity.

MCP proteins are preferably produced by recombinant DNA techniques. For example, a nucleic acid molecule encoding the protein is cloned into an expression vector (as described above), the expression vector is introduced into a host cell (as described above) and the MCP protein is expressed in the host cell. The MCP protein can then be isolated from the cells by an appropriate purification scheme using standard protein purification techniques. Alternative to recombinant expression, an MCP protein, polypeptide, or peptide can be synthesized chemically using standard peptide synthesis techniques. Moreover, native MCP protein can be isolated from cells (*e.g.*, endothelial cells, bacterial cells, fungal cells or other cells), for example using an anti-MCP antibody, which can be produced by standard techniques utilizing an MCP protein or fragment thereof of this invention.

The invention also provides MCP chimeric or fusion proteins. As used herein, an MCP "chimeric protein" or "fusion protein" comprises an MCP polypeptide operatively linked to a non-MCP polypeptide. An "MCP polypeptide" refers to a polypeptide having an amino acid sequence corresponding to an MCP protein, whereas a "non-MCP polypeptide" refers to a polypeptide having an amino acid sequence corresponding to a protein which is not substantially homologous to the MCP protein, *e.g.*, a protein which is different from the MCP protein and which is derived from the same or a different organism. Within the fusion protein, the term "operatively linked" is intended to indicate that the MCP polypeptide and the non-MCP polypeptide are fused in-frame to each other. The non-MCP polypeptide can be fused to the N-terminus or C-terminus of the MCP polypeptide. For example, in one embodiment the fusion protein is a GST-MCP fusion protein in which the MCP sequences are fused to the C-terminus of the GST sequences. Such fusion proteins can facilitate the purification of

recombinant MCP proteins. In another embodiment, the fusion protein is an MCP protein containing a heterologous signal sequence at its N-terminus. In certain host cells (*e.g.*, mammalian host cells, bacterial host cells, fungal host cells), expression and/or secretion of an MCP protein can be increased through use of a heterologous signal sequence.

Preferably, an MCP chimeric or fusion protein of the invention is produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, for example by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers which give rise to complementary overhangs between two consecutive gene fragments which can subsequently be annealed and reamplified to generate a chimeric gene sequence (see, for example, *Current Protocols in Molecular Biology*, eds. Ausubel *et al.* John Wiley & Sons: 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (*e.g.*, a GST polypeptide). An MCP-encoding nucleic acid can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the MCP protein.

Homologues of the MCP protein can be generated by mutagenesis, *e.g.*, discrete point mutation or truncation of the MCP protein. As used herein, the term "homologue" refers to a variant form of the MCP protein which acts as an agonist or antagonist of the activity of the MCP protein. An agonist of the MCP protein can retain substantially the same, or a subset, of the biological activities of the MCP protein. An antagonist of the MCP protein can inhibit one or more of the activities of the naturally occurring form of the MCP protein, by, for example, competitively binding to a downstream or upstream member of a biochemical pathway which includes the MCP protein.

In an alternative embodiment, homologues of the MCP protein can be identified by screening combinatorial libraries of mutants, *e.g.*, truncation mutants, of the MCP protein for MCP protein agonist or antagonist activity. In one embodiment, a variegated library of MCP variants is generated by combinatorial mutagenesis at the nucleic acid level and is encoded by a variegated gene library. A variegated library of MCP variants can be produced by, for example, enzymatically ligating a mixture of synthetic oligonucleotides into gene sequences such that a degenerate set of potential MCP sequences is expressible as individual polypeptides, or alternatively, as a set of larger

fusion proteins (*e.g.*, for phage display) containing the set of MCP sequences therein. There are a variety of methods which can be used to produce libraries of potential MCP homologues from a degenerate oligonucleotide sequence. Chemical synthesis of a degenerate gene sequence can be performed in an automatic DNA synthesizer, and the synthetic gene then ligated into an appropriate expression vector. Use of a degenerate set of genes allows for the provision, in one mixture, of all of the sequences encoding the desired set of potential MCP sequences. Methods for synthesizing degenerate oligonucleotides are known in the art (see, *e.g.*, Narang, S.A. (1983) *Tetrahedron* 39:3; Itakura *et al.* (1984) *Annu. Rev. Biochem.* 53:323; Itakura *et al.* (1984) *Science* 198:1056; Ike *et al.* (1983) *Nucleic Acid Res.* 11:477.

In addition, libraries of fragments of the MCP protein coding can be used to generate a variegated population of MCP fragments for screening and subsequent selection of homologues of an MCP protein. In one embodiment, a library of coding sequence fragments can be generated by treating a double stranded PCR fragment of an MCP coding sequence with a nuclease under conditions wherein nicking occurs only about once per molecule, denaturing the double stranded DNA, renaturing the DNA to form double stranded DNA which can include sense/antisense pairs from different nicked products, removing single stranded portions from reformed duplexes by treatment with S1 nuclease, and ligating the resulting fragment library into an expression vector. By this method, an expression library can be derived which encodes N-terminal, C-terminal and internal fragments of various sizes of the MCP protein.

Several techniques are known in the art for screening gene products of combinatorial libraries made by point mutations or truncation, and for screening cDNA libraries for gene products having a selected property. Such techniques are adaptable for rapid screening of the gene libraries generated by the combinatorial mutagenesis of MCP homologues. The most widely used techniques, which are amenable to high through-put analysis, for screening large gene libraries typically include cloning the gene library into replicable expression vectors, transforming appropriate cells with the resulting library of vectors, and expressing the combinatorial genes under conditions in which detection of a desired activity facilitates isolation of the vector encoding the gene whose product was detected. Recrusive ensemble mutagenesis (REM), a new technique which enhances the frequency of functional mutants in the libraries, can be used in combination with the screening assays to identify MCP homologues (Arkin and Yourvan (1992) *PNAS 89*:7811-7815; Delgrave *et al.* (1993) *Protein Engineering* 6(3):327-331).

In another embodiment, cell based assays can be exploited to analyze a variegated MCP library, using methods well known in the art.

D. Uses and Methods of the Invention

The nucleic acid molecules, proteins, protein homologues, fusion proteins, primers, vectors, and host cells described herein can be used in one or more of the following methods: identification of *C. glutamicum* and related organisms; mapping of genomes of organisms related to *C. glutamicum*; identification and localization of *C. glutamicum* sequences of interest; evolutionary studies; determination of MCP protein regions required for function; modulation of an MCP protein activity; modulation of the activity of one or more metabolic pathways; and modulation of cellular production of a desired compound, such as a fine chemical.

The MCP nucleic acid molecules of the invention have a variety of uses. First, they may be used to identify an organism as being *Corynebacterium glutamicum* or a close relative thereof. Also, they may be used to identify the presence of *C. glutamicum* or a relative thereof in a mixed population of microorganisms. The invention provides the nucleic acid sequences of a number of *C. glutamicum* genes, and probes based thereon; by probing the extracted genomic DNA of a culture of a unique or mixed population of microorganisms under stringent conditions with a probe spanning a region of a *C. glutamicum* gene which is unique to this organism, one can ascertain whether this organism is present. Although *Corynebacterium glutamicum* itself is nonpathogenic, it is related to pathogenic species, such as *Corynebacterium diphtheriae*. *Corynebacterium diphtheriae* is the causative agent of diphtheria, a rapidly developing, acute, febrile infection which involves both local and systemic pathology. In this disease, a local lesion develops in the upper respiratory tract and involves necrotic injury to epithelial cells; the bacilli secrete toxin which is disseminated through this lesion to distal susceptible tissues of the body. Degenerative changes brought about by the inhibition of protein synthesis in these tissues, which include heart, muscle, peripheral nerves, adrenals, kidneys, liver and spleen, result in the systemic pathology of the disease. Diphtheria continues to have high incidence in many parts of the world, including Africa, Asia, Eastern Europe and the independent states of the former Soviet Union. An ongoing epidemic of diphtheria in the latter two regions has resulted in at least 5,000 deaths since 1990.

In one embodiment, the invention provides a method of identifying the presence or activity of *Corynebacterium diphtheriae* in a subject. This method includes detection of one or more of the nucleic acid or amino acid sequences of the invention (*e.g.*, the sequences set forth in Appendix A or Appendix B) in a subject, thereby detecting the presence or activity of *Corynebacterium diphtheriae* in the subject. *C. glutamicum* and *C. diphtheriae* are related bacteria, and many of the nucleic acid and protein molecules

in *C. glutamicum* are homologous to *C. diphtheriae* nucleic acid and protein molecules, and can therefore be used to detect *C. diphtheriae* in a subject.

To detect the presence of *C. glutamicum* in a sample, techniques well known in the art may be employed. Specifically, the cells in the sample may optionally first be cultured in a suitable liquid or on a suitable solid culture medium to increase the number of cells in the sample. These cells are lysed, and the total DNA content extracted and optionally purified to remove debris and protein material which may interfere with subsequent analysis. The polymerase chain reaction or a similar technique known in the art is performed (for general reference on methodologies commonly used for the amplification of nucleic acid sequences, see Mullis *et al.*, U.S. Patent No. 4,683,195, Mullis *et al.*, U.S. Patent No. 4,965,188, and Innis, M.A., and Gelfand, D. H., (1989) PCR Protocols, A guide to Methods and Applications, Academic Press, p. 3-12, and (1988) Biotechnology 6:1197, and International Patent Application No. WO89/01050) in which primers specific to an MCP nucleic acid molecule of the invention are incubated with the nucleic acid sample such that, if present in the sample, that particular MCP nucleic acid sequence will be amplified. The particular MCP nucleic acid to be amplified is selected based on its uniqueness to the *C. glutamicum* genome, or to the genomes of *C. glutamicum* and only a few closely related bacteria. The presence of the desired amplified product is thus indicative of the presence of *C. glutamicum*, or an organism closely related to *C. glutamicum*.

Further, the nucleic acid and protein molecules of the invention may serve as markers for specific regions of the genome. It is possible, using techniques well known in the art, to ascertain the physical location on the *C. glutamicum* genome of the MCP nucleic acid molecules of the invention, which in turn provides markers on the genome which can be used to aid in the placement of other nucleic acid molecules and genes on the genome map. Also, the nucleic acid molecules of the invention may be sufficiently homologous to the sequences of related bacterial species that these nucleic acid molecules may similarly permit the construction of a genomic map in such bacteria (*e.g.*, *Brevibacterium lactofermentum*).

The nucleic acid molecules of the invention have utility not only in the mapping of the genome, but also for functional studies of *C. glutamicum* proteins. For example, to identify the region of the genome to which a particular *C. glutamicum* DNA-binding protein binds, the *C. glutamicum* genome could be digested, and the fragments incubated with the DNA-binding protein. Those which bind the protein may be additionally probed with the nucleic acid molecules of the invention, preferably with readily detectable labels; binding of such a nucleic acid molecule to the genome fragment enables the localization of the fragment to the genome map of *C. glutamicum*, and, when performed

multiple times with different enzymes, facilitates a rapid determination of the nucleic acid sequence to which the protein binds.

The MCP nucleic acid molecules of the invention are also useful for evolutionary and protein structural studies. The metabolic processes in which the molecules of the invention participate are utilized by a wide variety of prokaryotic and eukaryotic cells; by comparing the sequences of the nucleic acid molecules of the present invention to those encoding similar enzymes from other organisms, the evolutionary relatedness of the organisms can be assessed. Similarly, such a comparison permits an assessment of which regions of the sequence are conserved and which are not, which may aid in determining those regions of the protein which are essential for the functioning of the enzyme. This type of determination is of value for protein engineering studies and may give an indication of what the protein can tolerate in terms of mutagenesis without losing function.

The MCP protein molecules of the invention may also be utilized as markers for the classification of an unknown bacterium as *C. glutamicum*, or for the identification of *C. glutamicum* or closely related bacteria in a sample. For example, using techniques well known in the art, cells in a sample may optionally be amplified (*e.g.*, by culturing in an appropriate medium) to increase the sample size, and then may be lysed to release proteins contained therein. This sample may optionally be purified to remove debris and nucleic acid molecules which may interfere with subsequent analysis. Antibodies specific for a selected MCP protein of the invention may be incubated with the protein sample in a typical Western assay format (see, *e.g.*, Ausubel *et al.*, (1988) Current Protocols in Molecular Biology, Wiley: New York) in which the antibody will bind to its target protein if this protein is present in the sample. An MCP protein is selected for this type of assay if it is unique or nearly unique to *C. glutamicum* or *C. glutamicum* and bacteria very closely related to *C. glutamicum*. Proteins in the sample are then separated by gel electrophoresis, and transferred to a suitable matrix, such as nitrocellulose. An appropriate secondary antibody having a detectable label (*e.g.*, chemiluminescent or colorimetric) is incubated with this matrix, followed by stringent washing. The presence or absence of the label is indicative of the presence or absence of the target protein in the sample. If the protein is present, then this is indicative of the presence of *C. glutamicum*. A similar process enables the classification of an unknown bacterium as *C. glutamicum*; if a panel of proteins specific to *C. glutamicum* are not detected in protein samples prepared from the unknown bacterium, then that bacterium is not likely to be *C. glutamicum*.

The invention provides methods for screening molecules which modulate the activity of an MCP protein, either by interacting with the protein itself or a substrate or

binding partner of the MCP protein, or by modulating the transcription or translation of an MCP nucleic acid molecule of the invention. In such methods, a microorganism expressing one or more MCP proteins of the invention is contacted with one or more test compounds, and the effect of each test compound on the activity or level of expression of the MCP protein is assessed.

Genetic manipulation of the MCP nucleic acid molecules of the invention may result in the production of MCP proteins having functional differences from the wild-type MCP proteins. These proteins may be improved in efficiency or activity, may be present in greater numbers in the cell than is usual, or may be decreased in efficiency or activity.

Such changes in activity may directly modulate the yield, production, and/or efficiency of production of one or more fine chemicals from *C. glutamicum*. For example, by modifying the activity of a protein involved in the biosynthesis or degradation of a fine chemical (*i.e.*, through mutagenesis of the corresponding gene), one may directly modulate the ability of the cell to synthesize or to degrade this compound, thereby modulating the yield and/or efficiency of production of the fine chemical. Similarly, by modulating the activity of a protein which regulates a fine chemical metabolic pathway, one may directly influence whether the production of the desired compound is up- or down-regulated, either of which will modulate the yield or efficiency of production of the fine chemical from the cell.

Indirect modulation of fine chemical production may also result by modifying the activity of a protein of the invention (*i.e.*, by mutagenesis of the corresponding gene) such that the overall ability of the cell to grow and divide or to remain viable and productive is increased. The production of fine chemicals from *C. glutamicum* is generally accomplished by the large-scale fermentative culture of these microorganisms, conditions which are frequently suboptimal for growth and cell division. By engineering a protein of the invention (*e.g.*, a stress response protein, a cell wall protein, or proteins involved in the metabolism of compounds necessary for cell growth and division to occur, such as nucleotides and amino acids) such that it is better able to survive, grow, and multiply in such conditions, it may be possible to increase the number and productivity of such engineered *C. glutamicum* cells in large-scale culture, which in turn should result in increased yields and/or efficiency of production of one or more desired fine chemicals. Further, the metabolic pathways of any cell are necessarily interrelated and coregulated. By altering the activity or regulation of any one metabolic pathway in *C. glutamicum* (*i.e.*, by altering the activity of one of the proteins of the invention which participates in such a pathway), it is possible to concomitantly alter the

activity or regulation of other metabolic pathways in this microorganism, which may be directly involved in the synthesis or degradation of a fine chemical.

The aforementioned mutagenesis strategies for MCP proteins to result in increased yields of a fine chemical from *C. glutamicum* are not meant to be limiting; variations on these strategies will be readily apparent to one of ordinary skill in the art. Using such strategies, and incorporating the mechanisms disclosed herein, the nucleic acid and protein molecules of the invention may be utilized to generate *C. glutamicum* or related strains of bacteria expressing mutated MCP nucleic acid and protein molecules such that the yield, production, and/or efficiency of production of a desired compound is improved. This desired compound may be any natural product of *C. glutamicum*, which includes the final products of biosynthesis pathways and intermediates of naturally-occurring metabolic pathways, as well as molecules which do not naturally occur in the metabolism of *C. glutamicum*, but which are produced by a *C. glutamicum* strain of the invention.

This invention is further illustrated by the following examples which should not be construed as limiting. The contents of all references, patent applications, patents, published patent applications, Tables, Appendices, and the sequence listing cited throughout this application are hereby incorporated by reference.

Exemplification

Example 1: Preparation of total genomic DNA of *Corynebacterium glutamicum* ATCC 13032

A culture of *Corynebacterium glutamicum* (ATCC 13032) was grown overnight at 30°C with vigorous shaking in BHI medium (Difco). The cells were harvested by centrifugation, the supernatant was discarded and the cells were resuspended in 5 ml buffer-I (5% of the original volume of the culture — all indicated volumes have been calculated for 100 ml of culture volume). Composition of buffer-I: 140.34 g/l sucrose, 2.46 g/l $MgSO_4 \times 7H_2O$, 10 ml/l KH_2PO_4 solution (100 g/l, adjusted to pH 6.7 with KOH), 50 ml/l M12 concentrate (10 g/l $(NH_4)_2SO_4$, 1 g/l NaCl, 2 g/l $MgSO_4 \times 7H_2O$, 0.2 g/l $CaCl_2$, 0.5 g/l yeast extract (Difco), 10 ml/l trace-elements-mix (200 mg/l $FeSO_4 \times H_2O$, 10 mg/l $ZnSO_4 \times 7\ H_2O$, 3 mg/l $MnCl_2 \times 4\ H_2O$, 30 mg/l H_3BO_3 20 mg/l $CoCl_2 \times 6\ H_2O$, 1 mg/l $NiCl_2 \times 6\ H_2O$, 3 mg/l $Na_2MoO_4 \times 2\ H_2O$, 500 mg/l complexing agent (EDTA or critic acid), 100 ml/l vitamins-mix (0.2 mg/l biotin, 0.2 mg/l folic acid, 20 mg/l p-amino benzoic acid, 20 mg/l riboflavin, 40 mg/l ca-panthothenate, 140 mg/l nicotinic acid, 40 mg/l pyridoxole hydrochloride, 200 mg/l myo-inositol). Lysozyme

was added to the suspension to a final concentration of 2.5 mg/ml. After an approximately 4 h incubation at 37°C, the cell wall was degraded and the resulting protoplasts are harvested by centrifugation. The pellet was washed once with 5 ml buffer-I and once with 5 ml TE-buffer (10 mM Tris-HCl, 1 mM EDTA, pH 8). The pellet was resuspended in 4 ml TE-buffer and 0.5 ml SDS solution (10%) and 0.5 ml NaCl solution (5 M) are added. After adding of proteinase K to a final concentration of 200 µg/ml, the suspension is incubated for ca.18 h at 37°C. The DNA was purified by extraction with phenol, phenol-chloroform-isoamylalcohol and chloroform-isoamylalcohol using standard procedures. Then, the DNA was precipitated by adding 1/50 volume of 3 M sodium acetate and 2 volumes of ethanol, followed by a 30 min incubation at -20°C and a 30 min centrifugation at 12,000 rpm in a high speed centrifuge using a SS34 rotor (Sorvall). The DNA was dissolved in 1 ml TE-buffer containing 20 µg/ml RNaseA and dialysed at 4°C against 1000 ml TE-buffer for at least 3 hours. During this time, the buffer was exchanged 3 times. To aliquots of 0.4 ml of the dialysed DNA solution, 0.4 ml of 2 M LiCl and 0.8 ml of ethanol are added. After a 30 min incubation at -20°C, the DNA was collected by centrifugation (13,000 rpm, Biofuge Fresco, Heraeus, Hanau, Germany). The DNA pellet was dissolved in TE-buffer. DNA prepared by this procedure could be used for all purposes, including southern blotting or construction of genomic libraries.

Example 2: Construction of genomic libraries in *Escherichia coli* of *Corynebacterium glutamicum* ATCC13032.

Using DNA prepared as described in Example 1, cosmid and plasmid libraries were constructed according to known and well established methods (*see e.g.,* Sambrook, J. *et al.* (1989) "Molecular Cloning : A Laboratory Manual", Cold Spring Harbor Laboratory Press, or Ausubel, F.M. *et al.* (1994) "Current Protocols in Molecular Biology", John Wiley & Sons.)

Any plasmid or cosmid could be used. Of particular use were the plasmids pBR322 (Sutcliffe, J.G. (1979) *Proc. Natl. Acad. Sci. USA*, 75:3737-3741); pACYC177 (Change & Cohen (1978) *J. Bacteriol* 134:1141-1156), plasmids of the pBS series (pBSSK+, pBSSK- and others; Stratagene, LaJolla, USA), or cosmids as SuperCos1 (Stratagene, LaJolla, USA) or Lorist6 (Gibson, T.J., Rosenthal A. and Waterson, R.H. (1987) *Gene* 53:283-286. Gene libraries specifically for use in *C. glutamicum* may be constructed using plasmid pSL109 (Lee, H.-S. and A. J. Sinskey (1994) *J. Microbiol. Biotechnol.* 4: 256-263).

Example 3: DNA Sequencing and Computational Functional Analysis

Genomic libraries as described in Example 2 were used for DNA sequencing according to standard methods, in particular by the chain termination method using ABI377 sequencing machines (see *e.g.*, Fleischman, R.D. *et al.* (1995) "Whole-genome Random Sequencing and Assembly of Haemophilus Influenzae Rd., *Science*, 269:496-512). Sequencing primers with the following nucleotide sequences were used: 5'-GGAAACAGTATGACCATG-3' or 5'-GTAAAACGACGGCCAGT-3'.

Example 4: *In vivo* Mutagenesis

In vivo mutagenesis of *Corynebacterium glutamicum* can be performed by passage of plasmid (or other vector) DNA through *E. coli* or other microorganisms (*e.g. Bacillus* spp. or yeasts such as *Saccharomyces cerevisiae*) which are impaired in their capabilities to maintain the integrity of their genetic information. Typical mutator strains have mutations in the genes for the DNA repair system (*e.g.*, mutHLS, mutD, mutT, etc.; for reference, see Rupp, W.D. (1996) DNA repair mechanisms, in: *Escherichia col*i and *Salmonella*, p. 2277-2294, ASM: Washington.) Such strains are well known to those of ordinary skill in the art. The use of such strains is illustrated, for example, in Greener, A. and Callahan, M. (1994) *Strategies* 7: 32-34.

Example 5: DNA Transfer Between *Escherichia coli* and *Corynebacterium glutamicum*

Several *Corynebacterium* and *Brevibacterium* species contain endogenous plasmids (as *e.g.*, pHM1519 or pBL1) which replicate autonomously (for review see, *e.g.*, Martin, J.F. *et al.* (1987) Biotechnology, 5:137-146). Shuttle vectors for *Escherichia coli* and *Corynebacterium glutamicum* can be readily constructed by using standard vectors for *E. coli* (Sambrook, J. *et al.* (1989), "Molecular Cloning: A Laboratory Manual", Cold Spring Harbor Laboratory Press or Ausubel, F.M. *et al.* (1994) "Current Protocols in Molecular Biology", John Wiley & Sons) to which a origin or replication for and a suitable marker from *Corynebacterium glutamicum* is added. Such origins of replication are preferably taken from endogenous plasmids isolated from *Corynebacterium* and *Brevibacterium* species. Of particular use as transformation markers for these species are genes for kanamycin resistance (such as those derived from the Tn5 or Tn903 transposons) or chloramphenicol (Winnacker, E.L. (1987) "From Genes to Clones — Introduction to Gene Technology, VCH, Weinheim). There are numerous examples in the literature of the construction of a wide variety of shuttle vectors which replicate in both *E. coli and C. glutamicum*, and which can be used for several purposes, including gene over-expression (for reference, see *e.g.*, Yoshihama, M. *et al.* (1985) *J. Bacteriol. 162:591-597,*

Martin J.F. et al. (1987) Biotechnology, 5:137-146 and Eikmanns, B.J. et al. (1991) Gene, 102:93-98).

Using standard methods, it is possible to clone a gene of interest into one of the shuttle vectors described above and to introduce such a hybrid vectors into strains of *Corynebacterium glutamicum*. Transformation of *C. glutamicum* can be achieved by protoplast transformation (Kastsumata, R. *et al.* (1984) J. Bacteriol. 159306-311), electroporation (Liebl, E. *et al.* (1989) *FEMS Microbiol. Letters*, 53:399-303) and in cases where special vectors are used, also by conjugation (as described *e.g.* in Schäfer, A *et al.* (1990) *J. Bacteriol.* 172:1663-1666). It is also possible to transfer the shuttle vectors for *C. glutamicum* to *E. coli* by preparing plasmid DNA from *C. glutamicum* (using standard methods well-known in the art) and transforming it into *E. coli*. This transformation step can be performed using standard methods, but it is advantageous to use an Mcr-deficient *E. coli* strain, such as NM522 (Gough & Murray (1983) *J. Mol. Biol.* 166:1-19).

Genes may be overexpressed in *C. glutamicum* strains using plasmids which comprise pCG1 (U.S. Patent No. 4,617,267) or fragments thereof, and optionally the gene for kanamycin resistance from TN903 (Grindley, N.D. and Joyce, C.M. (1980) *Proc. Natl. Acad. Sci. USA* 77(12): 7176-7180). In addition, genes may be overexpressed in *C. glutamicum* strains using plasmid pSL109 (Lee, H.-S. and A. J. Sinskey (1994) *J. Microbiol. Biotechnol.* 4: 256-263).

Aside from the use of replicative plasmids, gene overexpression can also be achieved by integration into the genome. Genomic integration in *C. glutamicum* or other Corynebacterium or Brevibacterium species may be accomplished by well-known methods, such as homologous recombination with genomic region(s), restriction endonuclease mediated integration (REMI) (see, *e.g.*, DE Patent 19823834), or through the use of transposons. It is also possible to modulate the activity of a gene of interest by modifying the regulatory regions (*e.g.*, a promoter, a repressor, and/or an enhancer) by sequence modification, insertion, or deletion using site-directed methods (such as homologous recombination) or methods based on random events (such as transposon mutagenesis or REMI). Nucleic acid sequences which function as transcriptional terminators may also be inserted 3' to the coding region of one or more genes of the invention; such terminators are well-known in the art and are described, for example, in Winnacker, E.L. (1987) From Genes to Clones – Introduction to Gene Technology. VCH: Weinheim.

Example 6: Assessment of the Expression of the Mutant Protein

Observations of the activity of a mutated protein in a transformed host cell rely on the fact that the mutant protein is expressed in a similar fashion and in a similar quantity

to that of the wild-type protein. A useful method to ascertain the level of transcription of the mutant gene (an indicator of the amount of mRNA available for translation to the gene product) is to perform a Northern blot (for reference see, for example, Ausubel *et al.* (1988) Current Protocols in Molecular Biology, Wiley: New York), in which a primer designed to bind to the gene of interest is labeled with a detectable tag (usually radioactive or chemiluminescent), such that when the total RNA of a culture of the organism is extracted, run on gel, transferred to a stable matrix and incubated with this probe, the binding and quantity of binding of the probe indicates the presence and also the quantity of mRNA for this gene. This information is evidence of the degree of transcription of the mutant gene. Total cellular RNA can be prepared from *Corynebacterium glutamicum* by several methods, all well-known in the art, such as that described in Bormann, E.R. *et al.* (1992) *Mol. Microbiol.* 6: 317-326.

To assess the presence or relative quantity of protein translated from this mRNA, standard techniques, such as a Western blot, may be employed (see, for example, Ausubel *et al.* (1988) Current Protocols in Molecular Biology, Wiley: New York). In this process, total cellular proteins are extracted, separated by gel electrophoresis, transferred to a matrix such as nitrocellulose, and incubated with a probe, such as an antibody, which specifically binds to the desired protein. This probe is generally tagged with a chemiluminescent or colorimetric label which may be readily detected. The presence and quantity of label observed indicates the presence and quantity of the desired mutant protein present in the cell.

Example 7: Growth of Genetically Modified *Corynebacterium glutamicum* — Media and Culture Conditions

Genetically modified *Corynebacteria* are cultured in synthetic or natural growth media. A number of different growth media for Corynebacteria are both well-known and readily available (Lieb *et al.* (1989) *Appl. Microbiol. Biotechnol.*, 32:205-210; von der Osten *et al.* (1998) *Biotechnology Letters*, 11:11-16; Patent DE 4,120,867; Liebl (1992) "The Genus *Corynebacterium*, in: The Procaryotes, Volume II, Balows, A. *et al.*, eds. Springer-Verlag). These media consist of one or more carbon sources, nitrogen sources, inorganic salts, vitamins and trace elements. Preferred carbon sources are sugars, such as mono-, di-, or polysaccharides. For example, glucose, fructose, mannose, galactose, ribose, sorbose, ribulose, lactose, maltose, sucrose, raffinose, starch or cellulose serve as very good carbon sources. It is also possible to supply sugar to the media via complex compounds such as molasses or other by-products from sugar refinement. It can also be advantageous to supply mixtures of different carbon sources. Other possible carbon

sources are alcohols and organic acids, such as methanol, ethanol, acetic acid or lactic acid. Nitrogen sources are usually organic or inorganic nitrogen compounds, or materials which contain these compounds. Exemplary nitrogen sources include ammonia gas or ammonia salts, such as NH_4Cl or $(NH_4)_2SO_4$, NH_4OH, nitrates, urea, amino acids or complex nitrogen sources like corn steep liquor, soy bean flour, soy bean protein, yeast extract, meat extract and others.

Inorganic salt compounds which may be included in the media include the chloride-, phosphorous- or sulfate- salts of calcium, magnesium, sodium, cobalt, molybdenum, potassium, manganese, zinc, copper and iron. Chelating compounds can be added to the medium to keep the metal ions in solution. Particularly useful chelating compounds include dihydroxyphenols, like catechol or protocatechuate, or organic acids, such as citric acid. It is typical for the media to also contain other growth factors, such as vitamins or growth promoters, examples of which include biotin, riboflavin, thiamin, folic acid, nicotinic acid, pantothenate and pyridoxin. Growth factors and salts frequently originate from complex media components such as yeast extract, molasses, corn steep liquor and others. The exact composition of the media compounds depends strongly on the immediate experiment and is individually decided for each specific case. Information about media optimization is available in the textbook "Applied Microbiol. Physiology, A Practical Approach (*eds.* P.M. Rhodes, P.F. Stanbury, IRL Press (1997) pp. 53-73, ISBN 0 19 963577 3). It is also possible to select growth media from commercial suppliers, like standard 1 (Merck) or BHI (grain heart infusion, DIFCO) or others.

All medium components are sterilized, either by heat (20 minutes at 1.5 bar and 121°C) or by sterile filtration. The components can either be sterilized together or, if necessary, separately. All media components can be present at the beginning of growth, or they can optionally be added continuously or batchwise.

Culture conditions are defined separately for each experiment. The temperature should be in a range between 15°C and 45°C. The temperature can be kept constant or can be altered during the experiment. The pH of the medium should be in the range of 5 to 8.5, preferably around 7.0, and can be maintained by the addition of buffers to the media. An exemplary buffer for this purpose is a potassium phosphate buffer. Synthetic buffers such as MOPS, HEPES, ACES and others can alternatively or simultaneously be used. It is also possible to maintain a constant culture pH through the addition of NaOH or NH_4OH during growth. If complex medium components such as yeast extract are utilized, the necessity for additional buffers may be reduced, due to the fact that many complex compounds have high buffer capacities. If a fermentor is utilized for culturing the micro-organisms, the pH can also be controlled using gaseous ammonia.

The incubation time is usually in a range from several hours to several days. This time is selected in order to permit the maximal amount of product to accumulate in the broth. The disclosed growth experiments can be carried out in a variety of vessels, such as microtiter plates, glass tubes, glass flasks or glass or metal fermentors of different sizes. For screening a large number of clones, the microorganisms should be cultured in microtiter plates, glass tubes or shake flasks, either with or without baffles. Preferably 100 ml shake flasks are used, filled with 10% (by volume) of the required growth medium. The flasks should be shaken on a rotary shaker (amplitude 25 mm) using a speed-range of 100 – 300 rpm. Evaporation losses can be diminished by the maintenance of a humid atmosphere; alternatively, a mathematical correction for evaporation losses should be performed.

If genetically modified clones are tested, an unmodified control clone or a control clone containing the basic plasmid without any insert should also be tested. The medium is inoculated to an OD_{600} of O.5 – 1.5 using cells grown on agar plates, such as CM plates (10 g/l glucose, 2,5 g/l NaCl, 2 g/l urea, 10 g/l polypeptone, 5 g/l yeast extract, 5 g/l meat extract, 22 g/l NaCl, 2 g/l urea, 10 g/l polypeptone, 5 g/l yeast extract, 5 g/l meat extract, 22 g/l agar, pH 6.8 with 2M NaOH) that had been incubated at 30°C. Inoculation of the media is accomplished by either introduction of a saline suspension of *C. glutamicum* cells from CM plates or addition of a liquid preculture of this bacterium.

Example 8 – *In vitro* Analysis of the Function of Mutant Proteins

The determination of activities and kinetic parameters of enzymes is well established in the art. Experiments to determine the activity of any given altered enzyme must be tailored to the specific activity of the wild-type enzyme, which is well within the ability of one of ordinary skill in the art. Overviews about enzymes in general, as well as specific details concerning structure, kinetics, principles, methods, applications and examples for the determination of many enzyme activities may be found, for example, in the following references: Dixon, M., and Webb, E.C., (1979) Enzymes. Longmans: London; Fersht, (1985) Enzyme Structure and Mechanism. Freeman: New York; Walsh, (1979) Enzymatic Reaction Mechanisms. Freeman: San Francisco; Price, N.C., Stevens, L. (1982) Fundamentals of Enzymology. Oxford Univ. Press: Oxford; Boyer, P.D., ed. (1983) The Enzymes, 3rd ed. Academic Press: New York; Bisswanger, H., (1994) Enzymkinetik, 2nd ed. VCH: Weinheim (ISBN 3527300325); Bergmeyer, H.U., Bergmeyer, J., Graßl, M., eds. (1983-1986) Methods of Enzymatic Analysis, 3rd ed., vol. I-XII, Verlag Chemie: Weinheim; and Ullmann's Encyclopedia of Industrial Chemistry (1987) vol. A9, "Enzymes". VCH: Weinheim, p. 352-363.

The activity of proteins which bind to DNA can be measured by several well-established methods, such as DNA band-shift assays (also called gel retardation assays). The effect of such proteins on the expression of other molecules can be measured using reporter gene assays (such as that described in Kolmar, H. *et al.* (1995) *EMBO J.* 14: 3895-3904 and references cited therein). Reporter gene test systems are well known and established for applications in both pro- and eukaryotic cells, using enzymes such as beta-galactosidase, green fluorescent protein, and several others.

The determination of activity of membrane-transport proteins can be performed according to techniques such as those described in Gennis, R.B. (1989) "Pores, Channels and Transporters", in Biomembranes, Molecular Structure and Function, Springer: Heidelberg, p. 85-137; 199-234; and 270-322.

Example 9: Analysis of Impact of Mutant Protein on the Production of the Desired Product

The effect of the genetic modification in *C. glutamicum* on production of a desired compound (such as an amino acid) can be assessed by growing the modified microorganism under suitable conditions (such as those described above) and analyzing the medium and/or the cellular component for increased production of the desired product (*i.e.*, an amino acid). Such analysis techniques are well known to one of ordinary skill in the art, and include spectroscopy, thin layer chromatography, staining methods of various kinds, enzymatic and microbiological methods, and analytical chromatography such as high performance liquid chromatography (see, for example, Ullman, Encyclopedia of Industrial Chemistry, vol. A2, p. 89-90 and p. 443-613, VCH: Weinheim (1985); Fallon, A. *et al.*, (1987) "Applications of HPLC in Biochemistry" in: Laboratory Techniques in Biochemistry and Molecular Biology, vol. 17; Rehm *et al.* (1993) Biotechnology, vol. 3, Chapter III: "Product recovery and purification", page 469-714, VCH: Weinheim; Belter, P.A. *et al.* (1988) Bioseparations: downstream processing for biotechnology, John Wiley and Sons; Kennedy, J.F. and Cabral, J.M.S. (1992) Recovery processes for biological materials, John Wiley and Sons; Shaeiwitz, J.A. and Henry, J.D. (1988) Biochemical separations, in: Ulmann's Encyclopedia of Industrial Chemistry, vol. B3, Chapter 11, page 1-27, VCH: Weinheim; and Dechow, F.J. (1989) Separation and purification techniques in biotechnology, Noyes Publications.)

In addition to the measurement of the final product of fermentation, it is also possible to analyze other components of the metabolic pathways utilized for the production of the desired compound, such as intermediates and side-products, to determine the overall efficiency of production of the compound. Analysis methods

include measurements of nutrient levels in the medium (*e.g.*, sugars, hydrocarbons, nitrogen sources, phosphate, and other ions), measurements of biomass composition and growth, analysis of the production of common metabolites of biosynthetic pathways, and measurement of gasses produced during fermentation. Standard methods for these measurements are outlined in Applied Microbial Physiology, A Practical Approach, P.M. Rhodes and P.F. Stanbury, eds., IRL Press, p. 103-129; 131-163; and 165-192 (ISBN: 0199635773) and references cited therein.

Example 10: Purification of the Desired Product from *C. glutamicum* Culture

Recovery of the desired product from the *C. glutamicum* cells or supernatant of the above-described culture can be performed by various methods well known in the art. If the desired product is not secreted from the cells, the cells can be harvested from the culture by low-speed centrifugation, the cells can be lysed by standard techniques, such as mechanical force or sonication. The cellular debris is removed by centrifugation, and the supernatant fraction containing the soluble proteins is retained for further purification of the desired compound. If the product is secreted from the *C. glutamicum* cells, then the cells are removed from the culture by low-speed centrifugation, and the supernate fraction is retained for further purification.

The supernatant fraction from either purification method is subjected to chromatography with a suitable resin, in which the desired molecule is either retained on a chromatography resin while many of the impurities in the sample are not, or where the impurities are retained by the resin while the sample is not. Such chromatography steps may be repeated as necessary, using the same or different chromatography resins. One of ordinary skill in the art would be well-versed in the selection of appropriate chromatography resins and in their most efficacious application for a particular molecule to be purified. The purified product may be concentrated by filtration or ultrafiltration, and stored at a temperature at which the stability of the product is maximized.

There are a wide array of purification methods known to the art and the preceding method of purification is not meant to be limiting. Such purification techniques are described, for example, in Bailey, J.E. & Ollis, D.F. Biochemical Engineering Fundamentals, McGraw-Hill: New York (1986).

The identity and purity of the isolated compounds may be assessed by techniques standard in the art. These include high-performance liquid chromatography (HPLC), spectroscopic methods, staining methods, thin layer chromatography, NIRS, enzymatic assay, or microbiologically. Such analysis methods are reviewed in: Patek *et al.* (1994) *Appl. Environ. Microbiol.* 60: 133-140; Malakhova *et al.* (1996) *Biotekhnologiya* 11: 27-32; and Schmidt *et al.* (1998) *Bioprocess Engineer.* 19: 67-70. Ulmann's Encyclopedia

of Industrial Chemistry, (1996) vol. A27, VCH: Weinheim, p. 89-90, p. 521-540, p. 540-547, p. 559-566, 575-581 and p. 581-587; Michal, G. (1999) Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology, John Wiley and Sons; Fallon, A. *et al.* (1987) Applications of HPLC in Biochemistry in: Laboratory Techniques in Biochemistry and Molecular Biology, vol. 17.

Example 11: Analysis of the Gene Sequences of the Invention

The comparison of sequences and determination of percent homology between two sequences are art-known techniques, and can be accomplished using a mathematical algorithm, such as the algorithm of Karlin and Altschul (1990) *Proc. Natl. Acad. Sci.* USA 87:2264-68, modified as in Karlin and Altschul (1993) *Proc. Natl. Acad. Sci.* USA 90:5873-77. Such an algorithm is incorporated into the NBLAST and XBLAST programs (version 2.0) of Altschul, *et al.* (1990) *J. Mol. Biol.* 215:403-10. BLAST nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12 to obtain nucleotide sequences homologous to MCP nucleic acid molecules of the invention. BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to MCP protein molecules of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul *et al.*, (1997) *Nucleic Acids Res.* 25(17):3389-3402. When utilizing BLAST and Gapped BLAST programs, one of ordinary skill in the art will know how to optimize the parameters of the program (*e.g.*, XBLAST and NBLAST) for the specific sequence being analyzed.

Another example of a mathematical algorithm utilized for the comparison of sequences is the algorithm of Meyers and Miller ((1988) *Comput. Appl. Biosci.* 4: 11-17). Such an algorithm is incorporated into the ALIGN program (version 2.0) which is part of the GCG sequence alignment software package. When utilizing the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used. Additional algorithms for sequence analysis are known in the art, and include ADVANCE and ADAM. described in Torelli and Robotti (1994) *Comput. Appl. Biosci.* 10:3-5; and FASTA, described in Pearson and Lipman (1988) *P.N.A.S.* 85:2444-8.

The percent homology between two amino acid sequences can also be accomplished using the GAP program in the GCG software package (available at http://www.gcg.com), using either a Blosum 62 matrix or a PAM250 matrix, and a gap weight of 12, 10, 8, 6, or 4 and a length weight of 2, 3, or 4. The percent homology between two nucleic acid sequences can be accomplished using the GAP program in the

GCG software package, using standard parameters, such as a gap weight of 50 and a length weight of 3.

A comparative analysis of the gene sequences of the invention with those present in Genbank has been performed using techniques known in the art (see, *e.g.*, Bexevanis and Ouellette, eds. (1998) Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins. John Wiley and Sons: New York). The gene sequences of the invention were compared to genes present in Genbank in a three-step process. In a first step, a BLASTN analysis (*e.g.*, a local alignment analysis) was performed for each of the sequences of the invention against the nucleotide sequences present in Genbank, and the top 500 hits were retained for further analysis. A subsequent FASTA search (*e.g.*, a combined local and global alignment analysis, in which limited regions of the sequences are aligned) was performed on these 500 hits. Each gene sequence of the invention was subsequently globally aligned to each of the top three FASTA hits, using the GAP program in the GCG software package (using standard parameters). In order to obtain correct results, the length of the sequences extracted from Genbank were adjusted to the length of the query sequences by methods well-known in the art. The results of this analysis are set forth in Table 4. The resulting data is identical to that which would have been obtained had a GAP (global) analysis alone been performed on each of the genes of the invention in comparison with each of the references in Genbank, but required significantly reduced computational time as compared to such a database-wide GAP (global) analysis. Sequences of the invention for which no alignments above the cutoff values were obtained are indicated on Table 4 by the absence of alignment information. It will further be understood by one of ordinary skill in the art that the GAP alignment homology percentages set forth in Table 4 under the heading "% homology (GAP)" are listed in the European numerical format, wherein a ',' represents a decimal point. For example, a value of "40,345" in this column represents "40.345%".

Example 12: Construction and Operation of DNA Microarrays

The sequences of the invention may additionally be used in the construction and application of DNA microarrays (the design, methodology, and uses of DNA arrays are well known in the art, and are described, for example, in Schena, M. *et al.* (1995) *Science* 270: 467-470; Wodicka, L. *et al.* (1997) *Nature Biotechnology* 15: 1359-1367; DeSaizieu, A. *et al.* (1998) *Nature Biotechnology* 16: 45-48; and DeRisi, J.L. *et al.* (1997) *Science* 278: 680-686).

DNA microarrays are solid or flexible supports consisting of nitrocellulose, nylon, glass, silicone, or other materials. Nucleic acid molecules may be attached to the surface in an ordered manner. After appropriate labeling, other nucleic acids or nucleic

acid mixtures can be hybridized to the immobilized nucleic acid molecules, and the label may be used to monitor and measure the individual signal intensities of the hybridized molecules at defined regions. This methodology allows the simultaneous quantification of the relative or absolute amount of all or selected nucleic acids in the applied nucleic acid sample or mixture. DNA microarrays, therefore, permit an analysis of the expression of multiple (as many as 6800 or more) nucleic acids in parallel (see, *e.g.*, Schena, M. (1996) *BioEssays* 18(5): 427-431).

The sequences of the invention may be used to design oligonucleotide primers which are able to amplify defined regions of one or more *C. glutamicum* genes by a nucleic acid amplification reaction such as the polymerase chain reaction. The choice and design of the 5' or 3' oligonucleotide primers or of appropriate linkers allows the covalent attachment of the resulting PCR products to the surface of a support medium described above (and also described, for example, Schena, M. *et al.* (1995) *Science* 270: 467-470).

Nucleic acid microarrays may also be constructed by *in situ* oligonucleotide synthesis as described by Wodicka, L. *et al.* (1997) *Nature Biotechnology* 15: 1359-1367. By photolithographic methods, precisely defined regions of the matrix are exposed to light. Protective groups which are photolabile are thereby activated and undergo nucleotide addition, whereas regions that are masked from light do not undergo any modification. Subsequent cycles of protection and light activation permit the synthesis of different oligonucleotides at defined positions. Small, defined regions of the genes of the invention may be synthesized on microarrays by solid phase oligonucleotide synthesis.

The nucleic acid molecules of the invention present in a sample or mixture of nucleotides may be hybridized to the microarrays. These nucleic acid molecules can be labeled according to standard methods. In brief, nucleic acid molecules (*e.g.*, mRNA molecules or DNA molecules) are labeled by the incorporation of isotopically or fluorescently labeled nucleotides, *e.g.*, during reverse transcription or DNA synthesis. Hybridization of labeled nucleic acids to microarrays is described (*e.g.*, in Schena, M. *et al.* (1995) *supra*; Wodicka, L. *et al.* (1997), *supra*; and DeSaizieu A. *et al.* (1998), *supra*). The detection and quantification of the hybridized molecule are tailored to the specific incorporated label. Radioactive labels can be detected, for example, as described in Schena, M. *et al.* (1995) *supra*) and fluorescent labels may be detected, for example, by the method of Shalon *et al.* (1996) *Genome Research* 6: 639-645).

The application of the sequences of the invention to DNA microarray technology, as described above, permits comparative analyses of different strains of *C. glutamicum* or other Corynebacteria. For example, studies of inter-strain variations

based on individual transcript profiles and the identification of genes that are important for specific and/or desired strain properties such as pathogenicity, productivity and stress tolerance are facilitated by nucleic acid array methodologies. Also, comparisons of the profile of expression of genes of the invention during the course of a fermentation reaction are possible using nucleic acid array technology.

Example 13: Analysis of the Dynamics of Cellular Protein Populations (Proteomics)

The genes, compositions, and methods of the invention may be applied to study the interactions and dynamics of populations of proteins, termed 'proteomics'. Protein populations of interest include, but are not limited to, the total protein population of *C. glutamicum* (*e.g.*, in comparison with the protein populations of other organisms), those proteins which are active under specific environmental or metabolic conditions (*e.g.*, during fermentation, at high or low temperature, or at high or low pH), or those proteins which are active during specific phases of growth and development.

Protein populations can be analyzed by various well-known techniques, such as gel electrophoresis. Cellular proteins may be obtained, for example, by lysis or extraction, and may be separated from one another using a variety of electrophoretic techniques. Sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE) separates proteins largely on the basis of their molecular weight. Isoelectric focusing polyacrylamide gel electrophoresis (IEF-PAGE) separates proteins by their isoelectric point (which reflects not only the amino acid sequence but also posttranslational modifications of the protein). Another, more preferred method of protein analysis is the consecutive combination of both IEF-PAGE and SDS-PAGE, known as 2-D-gel electrophoresis (described, for example, in Hermann *et al.* (1998) *Electrophoresis* 19: 3217-3221; Fountoulakis *et al.* (1998) *Electrophoresis* 19: 1193-1202; Langen *et al.* (1997) *Electrophoresis* 18: 1184-1192; Antelmann *et al.* (1997) *Electrophoresis* 18: 1451-1463). Other separation techniques may also be utilized for protein separation, such as capillary gel electrophoresis; such techniques are well known in the art.

Proteins separated by these methodologies can be visualized by standard techniques, such as by staining or labeling. Suitable stains are known in the art, and include Coomassie Brilliant Blue, silver stain, or fluorescent dyes such as Sypro Ruby (Molecular Probes). The inclusion of radioactively labeled amino acids or other protein precursors (*e.g.*, ^{35}S-methionine, ^{35}S-cysteine, ^{14}C-labelled amino acids, ^{15}N-amino acids, $^{15}NO_3$ or $^{15}NH_4^+$ or ^{13}C-labelled amino acids) in the medium of *C. glutamicum* permits the labeling of proteins from these cells prior to their separation. Similarly,

fluorescent labels may be employed. These labeled proteins can be extracted, isolated and separated according to the previously described techniques.

Proteins visualized by these techniques can be further analyzed by measuring the amount of dye or label used. The amount of a given protein can be determined quantitatively using, for example, optical methods and can be compared to the amount of other proteins in the same gel or in other gels. Comparisons of proteins on gels can be made, for example, by optical comparison, by spectroscopy, by image scanning and analysis of gels, or through the use of photographic films and screens. Such techniques are well-known in the art.

To determine the identity of any given protein, direct sequencing or other standard techniques may be employed. For example, N- and/or C-terminal amino acid sequencing (such as Edman degradation) may be used, as may mass spectrometry (in particular MALDI or ESI techniques (see, *e.g.*, Langen.*et al.* (1997) *Electrophoresis* 18: 1184-1192)). The protein sequences provided herein can be used for the identification of *C. glutamicum* proteins by these techniques.

The information obtained by these methods can be used to compare patterns of protein presence, activity, or modification between different samples from various biological conditions (*e.g.*, different organisms, time points of fermentation, media conditions, or different biotopes, among others). Data obtained from such experiments alone, or in combination with other techniques, can be used for various applications, such as to compare the behavior of various organisms in a given (*e.g.*, metabolic) situation, to increase the productivity of strains which produce fine chemicals or to increase the efficiency of the production of fine chemicals.

Equivalents

Those of ordinary skill in the art will recognize, or will be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the following claims.

What is claimed:

1. An isolated nucleic acid molecule from *Corynebacterium glutamicum* encoding an MCP protein, or a portion thereof, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.

2. The isolated nucleic acid molecule of claim 1, wherein said nucleic acid molecule encodes an MCP protein involved in fine chemical production.

3. An isolated *Corynebacterium glutamicum* nucleic acid molecule selected from the group consisting of those sequences set forth in Appendix A, or a portion thereof, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.

4. An isolated nucleic acid molecule which encodes a polypeptide sequence selected from the group consisting of those sequences set forth in Appendix B, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.

5. An isolated nucleic acid molecule which encodes a naturally occurring allelic variant of a polypeptide selected from the group of amino acid sequences consisting of those sequences set forth in Appendix B, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.

6. An isolated nucleic acid molecule comprising a nucleotide sequence which is at least 50% homologous to a nucleotide sequence selected from the group consisting of those sequences set forth in Appendix A, or a portion thereof, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.

7. An isolated nucleic acid molecule comprising a fragment of at least 15 nucleotides of a nucleic acid comprising a nucleotide sequence selected from the group consisting of those sequences set forth in Appendix A, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.

8. An isolated nucleic acid molecule which hybridizes to the nucleic acid molecule of any one of claims 1-7 under stringent conditions.

9. An isolated nucleic acid molecule comprising the nucleic acid molecule of claim 1 or a portion thereof and a nucleotide sequence encoding a heterologous polypeptide.

10. A vector comprising the nucleic acid molecule of any one of claims 1-9.

11. The vector of claim 10, which is an expression vector.

12. A host cell transfected with the expression vector of claim 11.

13. The host cell of claim 12, wherein said cell is a microorganism.

14. The host cell of claim 13, wherein said cell belongs to the genus *Corynebacterium* or *Brevibacterium.*

15. The host cell of claim 12, wherein the expression of said nucleic acid molecule results in the modulation in production of a fine chemical from said cell.

16. The host cell of claim 15, wherein said fine chemical is selected from the group consisting of: organic acids, proteinogenic and nonproteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides, and enzymes.

17. A method of producing a polypeptide comprising culturing the host cell of claim 12 in an appropriate culture medium to, thereby, produce the polypeptide.

18. An isolated MCP polypeptide from *Corynebacterium glutamicum*, or a portion thereof.

19. The polypeptide of claim 18, wherein said polypeptide is involved in fine chemical production.

20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of those sequences set forth in Appendix B, provided that the amino acid sequence is not encoded by any of the F-designated genes set forth in Table 1.

21. An isolated polypeptide comprising a naturally occurring allelic variant of a polypeptide comprising an amino acid sequence selected from the group consisting of those sequences set forth in Appendix B, or a portion thereof, provided that the amino acid sequence is not encoded by any of the F-designated genes set forth in Table 1.

22. The isolated polypeptide of claim 18, further comprising heterologous amino acid sequences.

23. An isolated polypeptide which is encoded by a nucleic acid molecule comprising a nucleotide sequence which is at least 50% homologous to a nucleic acid selected from the group consisting of those sequences set forth in Appendix A, provided that the nucleic acid molecule does not consist of any of the F-designated nucleic acid molecules set forth in Table 1.

24. An isolated polypeptide comprising an amino acid sequence which is at least 50% homologous to an amino acid sequence selected from the group consisting of those sequences set forth in Appendix B, provided that the amino acid sequence is not encoded by any of the F-designated genes set forth in Table 1.

25. A method for producing a fine chemical, comprising culturing a cell containing a vector of claim 12 such that the fine chemical is produced.

26. The method of claim 25, wherein said method further comprises the step of recovering the fine chemical from said culture.

27. The method of claim 25, wherein said method further comprises the step of transfecting said cell with the vector of claim 11 to result in a cell containing said vector.

28. The method of claim 25, wherein said cell belongs to the genus *Corynebacterium* or *Brevibacterium.*

29. The method of claim 25, wherein said cell is selected from the group consisting of: *Corynebacterium glutamicum, Corynebacterium herculis, Corynebacterium, lilium, Corynebacterium acetoacidophilum, Corynebacterium acetoglutamicum, Corynebacterium acetophilum, Corynebacterium ammoniagenes, Corynebacterium fujiokense, Corynebacterium nitrilophilus, Brevibacterium ammoniagenes, Brevibacterium butanicum, Brevibacterium divaricatum, Brevibacterium flavum, Brevibacterium healii, Brevibacterium ketoglutamicum, Brevibacterium ketosoreductum, Brevibacterium lactofermentum, Brevibacterium linens, Brevibacterium paraffinolyticum,* and those strains set forth in Table 3.

30. The method of claim 25, wherein expression of the nucleic acid molecule from said vector results in modulation of production of said fine chemical.

31. The method of claim 25, wherein said fine chemical is selected from the group consisting of: organic acids, proteinogenic and nonproteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides, and enzymes.

32. The method of claim 25, wherein said fine chemical is an amino acid.

33. The method of claim 32, wherein said amino acid is drawn from the group consisting of: lysine, glutamate, glutamine, alanine, aspartate, glycine, serine, threonine, methionine, cysteine, valine, leucine, isoleucine, arginine, proline, histidine, tyrosine, phenylalanine, and tryptophan.

34. A method for producing a fine chemical, comprising culturing a cell whose genomic DNA has been altered by the inclusion of a nucleic acid molecule of any one of claims 1-9.

35. A method for diagnosing the presence or activity of Corynebacterium diphtheriae in a subject, comprising detecting the presence of one or more of the sequences set forth in Appendix A or Appendix B in the subject, provided that the sequences are not or are not encoded by any of the F-designated sequences set forth in Table 1, thereby diagnosing the presence or activity of Corynebacterium diphtheriae in the subject.

36. A host cell comprising a nucleic acid molecule selected from the group consisting of the nucleic acid molecules set forth in Appendix A, wherein the nucleic acid molecule is disrupted.

37. A host cell comprising a nucleic acid molecule selected from the group consisting of the nucleic acid molecules set forth in Appendix A, wherein the nucleic acid molecule comprises one or more nucleic acid modifications from the sequence set forth in Appendix A.

38. A host cell comprising a nucleic acid molecule selected from the group consisting of the nucleic acid molecules set forth in Appendix A, wherein the regulatory region of the nucleic acid molecule is modified relative to the wild-type regulatory region of the molecule.

CORYNEBACTERIUM GLUTAMICUM GENES ENCODING NOVEL PROTEINS

Abstract of the Disclosure

Isolated nucleic acid molecules, designated MCP nucleic acid molecules, which encode novel MCP proteins from *Corynebacterium glutamicum* are described. The invention also provides antisense nucleic acid molecules, recombinant expression vectors containing MCP nucleic acid molecules, and host cells into which the expression vectors have been introduced. The invention still further provides isolated MCP proteins, mutated MCP proteins, fusion proteins, antigenic peptides and methods for the improvement of production of a desired compound from *C. glutamicum* based on genetic engineering of MCP genes in this organism.

Customer Number: 000959

Attorney's
Docket No. BGI-129CP

DECLARATION, PETITION AND POWER OF ATTORNEY FOR PATENT APPLICATION

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name,

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled:

CORYNEBACTERIUM GLUTAMICUM GENES ENCODING NOVEL PROTEINS

the specification of which:

___X___ is attached hereto.

_____ was filed on _____ as Application Serial No._____

and was amended on _____.
(if applicable)

I do not know and do not believe that the subject matter of this application was known or used by others in the United States or patented or described in a printed publication in any country before my invention thereof, or patented or described in a printed publication in any country or in public use or on sale in the United States more than one year prior to the date of this application, or first patented or caused to be patented or made the subject of an inventor's certificate by me or my legal representatives or assigns in a country foreign to the United States prior to the date of this application on an application filed more than twelve months (six months if this application is for a design) before the filing of this application; and I acknowledge my duty to disclose information of which I am aware which is material to the examination of this application, that no application for patent or inventor's certificate on the subject matter of this application has been filed by me or my representatives or assigns in any country foreign to the United States, except those identified below, and that I have reviewed and understand the contents of the specification, including the claims as amended by any amendment referred to herein.

I acknowledge the duty to disclose to the Office all information known to me to be material to patentability as defined in Title 37, Code of Federal Regulations, §1.56.

CLAIM OF BENEFIT OF EARLIER FOREIGN APPLICATION(S)

I hereby claim priority benefits under Title 35, United States Code, §119 of any foreign application(s) for patent or inventor's certificate listed below, and have also identified below any foreign application(s) for patent or inventor's certificate filed by me on the same subject matter having a filing date before that of the application(s) from which priority is claimed.

Check one:

X no such applications have been filed.

__ such applications have been filed as follows

EARLIEST FOREIGN APPLICATION(S), IF ANY, FILED WITHIN 12 MONTHS (6 MONTHS FOR DESIGN) PRIOR TO THIS U.S. APPLICATION

Country	Application Number	Date of Filing (month,day,year)	Priority Claimed Under 35 USC 119
			_ Yes No _
			_ Yes No _
			_ Yes No _
			_ Yes No _
			_ Yes No _

ALL FOREIGN APPLICATION(S), IF ANY FILED MORE THAN 12 MONTHS (6 MONTHS FOR DESIGN) PRIOR TO THIS U.S. APPLICATION

CLAIM FOR BENEFIT OF U.S. PROVISIONAL APPLICATION(S)

I hereby claim the benefit under 35 U.S.C. §119(e) of any United States provisional application(s) listed below.

60/142,764	July 8, 1999
(Application Serial No.)	(Filing Date)
60/152,318	September 3, 1999
(Application Serial No.)	(Filing Date)

Express Mail Label No. EL 640 737 650 US

CLAIM FOR BENEFIT OF EARLIER U.S./PCT APPLICATION(S)

I hereby claim the benefit under Title 35, United States Code, §120 of any earlier United States application(s) or PCT international application(s) designating the United States listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the earlier application(s) in the manner provided by the first paragraph of Title 35, United States Code, §112, I acknowledge the duty to disclose to the Office all information known to me to be material to patentability as defined in Title 37, Code of Federal Regulations, §1.56 which became available between the filing date(s) of the earlier application(s) and the national or PCT international filing date of this application. As to subject matter of this application which is common to my earlier application(s), if any, described below, I do not know and do not believe that the same was known or used by others in the United States or patented or described in a printed publication in any country before my invention thereof, or patented or described in a printed publication in any country or in public use or on sale in the United States more than one year prior to the date(s) of said earlier application(s), or first patented or caused to be patented or made the subject of an inventor's certificate by me or my legal representatives or assigns in a country foreign to the United States prior to the date(s) of said earlier application(s) on an application filed more than twelve months (six months if this application is for a design) before the filing of said earlier application(s); and I acknowledge that no application for patent or inventor's certificate on said subject matter has been filed by me or my representatives or assigns in any country foreign to the United States except those identified herein.

(Application Serial No.)	(Filing Date)	(Status) (patented,pending,aband.)
(Application Serial No.)	(Filing Date)	(Status) (patented,pending,aband.)

POWER OF ATTORNEY: As a named inventor, I hereby appoint the following attorneys and/or agents to prosecute this application and transact all business in the Patent and Trademark Office connected therewith.

James E. Cockfield	Reg. No. 19,162	Megan E. Williams	Reg. No. 43,270
Thomas V. Smurzynski	Reg. No. 24,798	Nicholas P. Triano III	Reg. No. 36,397
Ralph A. Loren	Reg. No. 29,325	Peter C. Lauro	Reg. No. 32,360
Giulio A. DeConti, Jr.	Reg. No. 31,503	DeAnn F. Smith	Reg. No. 36,683
Ann Lamport Hammitte	Reg. No. 34,858	William D. DeVaul	Reg. No. 42,483
Elizabeth A. Hanley	Reg. No. 33,505	David J. Rikkers	Reg. No. 43,882
Amy E. Mandragouras	Reg. No. 36,207	Chi Suk Kim	Reg. No. 42,728
Anthony A. Laurentano	Reg. No. 38,220	Maria Laccotripe Zacharakis	Limited Recognition Under 37 C.F.R. § 10.9(b)
Jane E. Remillard	Reg. No. 38,872		
Jeremiah Lynch	Reg. No. 17,425	Debra J. Milasincic	Reg. No. P46,931
Kevin J. Canning	Reg. No. 35,470	David R. Burns	Reg. No. P46,590
David A. Lane, Jr.	Reg. No. 39,261		
Jeanne M. DiGiorgio	Reg. No. 41,710		

Send Correspondence to Giulio A. DeConti, Jr., Esq. at **Customer Number: 000959** whose address is:

Lahive & Cockfield, LLP, 28 State Street, Boston, MA 02109

Direct Telephone Calls to: (name and telephone number)

Giulio A. DeConti, Jr., Esq., (617) 227-7400

Wherefore I petition that letters patent be granted to me for the invention or discovery described and claimed in the attached specification and claims, and hereby subscribe my name to said specification and claims and to the foregoing declaration, power of attorney, and this petition.

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

Full name of sole or first inventor Markus Pompejus
Inventor's signature Date
Residence Wenjenstrasse 21, 67251 Freinsheim, Germany
Citizenship Germany
Post Office Address (if different)

Full name of second inventor, if any Burkhard Kröger	
Inventor's signature	Date
Residence Im Waldhof 1, 67117 Limburgerhof, Germany	
Citizenship Germany	
Post Office Address (if different)	

Full name of third inventor, if any Hartwig Schröder	
Inventor's signature	Date
Residence Goethestr. 5, 69226 Nussloch, Germany	
Citizenship Germany	
Post Office Address (if different)	

Full name of fourth inventor, if any Oskar Zelder	
Inventor's signature	Date
Residence Rossmarktstr. 27, 67346 Speyer, Germany	
Citizenship Germany	
Post Office Address (if different)	

Full name of fifth inventor, if any Gregor Haberhauer	
Inventor's signature	Date
Residence Moselstr. 42, 67117 Limburgerhof, Germany	
Citizenship Germany	
Post Office Address (if different)	

TABLE 1: GENES IN THE APPLICATION

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop
1	2	RXN01638	VV0005	54646	55545
3	4	F RXA01638	GR00456	825	436
5	6	F RXA01639	GR00456	1334	897
7	8	RXN01590	VV0015	66740	60294
9	10	F RXA01590	GR00445	1710	427
11	12	F RXA01542	GR00429	3	5063
13	14	RXN01539	VV0015	60006	57841
15	16	F RXA01539	GR00428	120	2042
17	18	RXN01422	VV0122	17001	16030
19	20	F RXA01422	GR00416	2003	1221
21	22	RXN01403	VV0126	4644	3997
23	24	F RXA01403	GR00409	4410	3997
25	26	RXN01326	VV0102	23923	24288
27	28	F RXA01326	GR00386	45	338
29	30	RXN01301	VV0068	8224	8748
31	32	F RXA01301	GR00375	1993	1589
33	34	RXN01276	VV0009	31190	31633
35	36	F RXA01276	GR00367	29993	30538
37	38	RXN01231	VV0020	30144	29902
39	40	F RXA01231	GR00356	1384	1887
41	42	RXN01210	VV0169	4230	5060
43	44	F RXA01210	GR00349	3	695
45	46	RXN01206	VV0268	303	4
47	48	F RXA01206	GR00346	593	853
49	50	RXN01121	VV0182	5808	6893
51	52	F RXA01121	GR00310	2479	3156
53	54	RXN01085	VV0093	16599	15721
55	56	F RXA01085	GR00303	960	4
57	58	RXN00022	VV0015	27262	28962
59	60	F RXA00022	GR00002	20563	21297
61	62	F RXA01921	GR00551	943	5
63	64	RXN00027	VV0127	60015	59650
65	66	F RXA00027	GR00003	5142	5507
67	68	RXN00028	VV0127	57099	59045
69	70	F RXA00028	GR00003	8058	6112
71	72	RXN00033	VV0127	51753	53087
73	74	RXN00056	VV0044	11980	12729
75	76	F RXA00056	GR00009	1463	714
77	78	RXN00067	VV0019	29740	29255
79	80	F RXA00067	GR00011	708	223
81	82	RXN00077	VV0154	4222	5583
83	84	F RXA00077	GR00012	4228	5589
85	86	RXN00080	VV0154	8446	6917
87	88	F RXA00080	GR00012	7342	6923
89	90	RXN00087	VV0048	204	731
91	92	F RXA00087	GR00013	3983	3456
93	94	RXN00096	VV0129	22302	22000
95	96	F RXA00096	GR00014	4746	5048
97	98	RXN00097	VV0129	21841	20666
99	100	F RXA00097	GR00014	5222	6382
101	102	RXN00114	VV0129	5849	6337
103	104	F RXA00114	GR00017	3420	3908

105	106	RXN00120	VV0142	2612	3451
107	108	F RXA00120	GR00019	2798	3451
109	110	RXN00128	VV0124	7960	9663
111	112	F RXA00128	GR00020	4709	3006
113	114	RXN00154	VV0167	3283	4125
115	116	F RXA00154	GR00023	8568	7726
117	118	RXN00162	VV0084	9489	9842
119	120	F RXA00162	GR00024	5438	5791
121	122	RXN00167	VV0232	4324	4821
123	124	F RXA00167	GR00025	4324	4584
125	126	RXN00171	VV0031	5311	5054
127	128	F RXA00171	GR00026	10316	10086
129	130	RXN00194	VV0115	4174	4614
131	132	F RXA00194	GR00030	290	6
133	134	RXN00197	VV0115	2733	1522
135	136	F RXA00197	GR00030	1731	2741
137	138	RXN00216	VV0096	16292	15303
139	140	RXN00222	VV0096	21079	22224
141	142	F RXA00222	GR00032	21073	22218
143	144	RXN00232	VV0214	601	92
145	146	F RXA00232	GR00035	527	18
147	148	RXN00236	VV0133	3300	2575
149	150	F RXA00236	GR00036	3300	2575
151	152	RXN00242	VV0133	7031	8308
153	154	F RXA00242	GR00036	7031	8233
155	156	RXN00247	VV0057	35082	34156
157	158	F RXA00247	GR00037	7097	6171
159	160	RXN00256	VV0015	3794	4564
161	162	F RXA00256	GR00039	968	1738
163	164	RXN00264	VV0123	14046	13669
165	166	F RXA00264	GR00040	2459	2836
167	168	RXN00267	VV0123	12366	12683
169	170	F RXA00267	GR00040	4091	3822
171	172	RXN00271	VV0019	4975	3986
173	174	F RXA00271	GR00041	3709	2720
175	176	RXN00272	VV0019	5686	6057
177	178	F RXA00272	GR00041	4420	4791
179	180	RXN00283	VV0127	33097	32066
181	182	F RXA00283	GR00045	142	1269
183	184	RXN00334	VV0197	3581	3246
185	186	F RXA00334	GR00057	16762	17097
187	188	RXN00338	VV0197	26797	25658
189	190	F RXA00338	GR00059	1	783
191	192	F RXA00318	GR00055	426	635
193	194	RXN00342	VV0049	1576	1148
195	196	F RXA00342	GR00061	73	501
197	198	RXN00344	VV0135	42719	43597
199	200	F RXA00344	GR00063	6	584
201	202	RXN00353	VV0135	32107	32799
203	204	F RXA00353	GR00068	988	1680
205	206	RXN00354	VV0135	33604	32792
207	208	RXN00362	VV0176	33334	34680
209	210	F RXA00362	GR00073	2	961
211	212	RXN00373	VV0226	6002	6340
213	214	F RXA00373	GR00079	342	4
215	216	RXN00390	VV0025	9834	9430
217	218	F RXA00390	GR00086	1437	1841

219	220	RXN00399	VV0025	13735	13421
221	222	F RXA00399	GR00087	830	1144
223	224	RXN00416	VV0181	1	
225	226	F RXA00416	GR00093	1	327
227	228	F RXA00418	GR00094	1	1065
229	230	RXN00422	VV0112	3820	4713
231	232	F RXA00422	GR00097	428	6
233	234	RXN00447	VV0112	23325	22906
235	236	F RXA00447	GR00108	518	817
237	238	RXN00455	VV0076	5523	4774
239	240	F RXA00455	GR00113	2	619
241	242	RXN00473	VV0086	31493	32281
243	244	F RXA00473	GR00119	5799	6563
245	246	RXN00485	VV0086	51200	48906
247	248	F RXA00485	GR00119	25230	23188
249	250	RXN00496	VV0086	17452	18477
251	252	F RXA00496	GR00123	1776	2177
253	254	RXN00503	VV0086	11688	13409
255	256	RXN00504	VV0086	13486	13905
257	258	F RXA00504	GR00125	5007	5252
259	260	RXN00505	VV0086	5810	6304
261	262	F RXA00505	GR00126	1	252
263	264	RXN00507	VV0086	4606	3752
265	266	F RXA00507	GR00127	1098	244
267	268	RXN00510	VV0086	1924	3432
269	270	F RXA00509	GR00128	316	140
271	272	F RXA00510	GR00128	384	914
273	274	RXN00515	VV0144	3289	2588
275	276	F RXA00515	GR00131	3	482
277	278	F RXA00520	GR00132	599	796
279	280	RXN00527	VV0079	23845	25608
281	282	F RXA00527	GR00136	3123	1360
283	284	RXN00547	VV0079	33886	35283
285	286	F RXA00547	GR00142	641	1054
287	288	F RXA00546	GR00142	1	690
289	290	RXN00552	VV0079	27617	28552
291	292	F RXA00552	GR00145	2	718
293	294	RXN00555	VV0079	30437	29499
295	296	F RXA00555	GR00145	2555	1665
297	298	RXN00560	VV0103	7606	7980
299	300	F RXA00560	GR00149	256	492
301	302	RXN00574	VV0323	16133	15255
303	304	F RXA00574	GR00156	767	1645
305	306	RXN00589	VV0323	2680	2231
307	308	F RXA00589	GR00156	14220	14582
309	310	RXN00616	VV0054	5670	5326
311	312	F RXA00616	GR00162	3574	3918
313	314	RXN00647	VV0109	12861	12229
315	316	F RXA00647	GR00169	641	1273
317	318	RXN00653	VV0109	6578	7342
319	320	F RXA00653	GR00169	6924	6160
321	322	RXN00662	VV0142	7711	8979
323	324	F RXA00662	GR00172	2671	1403
325	326	RXN00666	VV0109	1566	2480
327	328	F RXA00666	GR00175	390	4
329	330	RXN00704	VV0005	9240	9866
331	332	F RXA00704	GR00183	2972	3484

333	334	RXN00712	VV0005	1195	500
335	336	F RXA00712	GR00187	1048	500
337	338	RXN00720	VV0232	4899	5564
339	340	F RXA00720	GR00188	7665	7000
341	342	RXN00722	VV0052	2	
343	344	F RXA00722	GR00189	1015	512
345	346	RXN00729	VV0024	3903	2926
347	348	F RXA00729	GR00194	1	642
349	350	F RXA02867	GR10008	610	5
351	352	RXN00730	VV0024	2031	2837
353	354	F RXA00730	GR00194	1063	731
355	356	RXN00731	VV0133	8314	10809
357	358	F RXA00731	GR00195	2613	142
359	360	RXN00738	VV0254	3	
361	362	F RXA00738	GR00201	78	365
363	364	RXN00750	VV0010	30086	30523
365	366	F RXA00750	GR00202	18937	19374
367	368	RXN00762	VV0103	16953	17828
369	370	RXN00768	VV0103	12997	11879
371	372	F RXA00768	GR00204	5956	6399
373	374	F RXA00767	GR00204	5280	5993
375	376	RXN00769	VV0103	11654	11442
377	378	F RXA00769	GR00204	6624	6836
379	380	RXN00771	VV0103	26639	27457
381	382	F RXA00771	GR00205	857	180
383	384	RXN00785	VV0321	2	658
385	386	F RXA00785	GR00207	625	5
387	388	RXN00795	VV0321	6259	5732
389	390	F RXA00795	GR00211	4228	4755
391	392	RXN00831	VV0180	4205	4906
393	394	F RXA00831	GR00224	1662	961
395	396	RXN00835	VV0138	12068	13021
397	398	F RXA00835	GR00226	3	692
399	400	RXN00836	VV0138	13126	14841
401	402	F RXA00836	GR00226	797	2467
403	404	RXN00840	VV0138	6220	6933
405	406	F RXA00840	GR00228	742	1455
407	408	RXN00841	VV0138	6944	7480
409	410	F RXA00841	GR00228	1466	2002
411	412	RXN00846	VV0138	2367	1498
413	414	F RXA00846	GR00230	391	5
415	416	RXN00850	VV0067	4148	3321
417	418	RXN00854	VV0067	371	159
419	420	F RXA00854	GR00231	4708	4920
421	422	RXN00855	VV0255	735	1019
423	424	F RXA00855	GR00232	526	242
425	426	RXN00869	VV0127	5599	4679
427	428	F RXA00869	GR00239	1	792
429	430	RXN00915	VV0238	886	257
431	432	F RXA00915	GR00251	514	5
433	434	RXN00917	VV0238	7202	4524
435	436	F RXA00917	GR00251	5534	4152
437	438	RXN00921	VV0373	1	513
439	440	F RXA00921	GR00252	4750	2852
441	442	RXN00943	VV0116	11376	12287
443	444	F RXA00943	GR00258	3	509
445	446	F RXA02423	GR00706	221	6

447	448	RXN00945	VV0107	1876	2847
449	450	RXN00946	VV0107	3034	3807
451	452	F RXA00946	GR00259	3034	3807
453	454	RXN00953	VV0260	1834	1082
455	456	RXN00959	VV0208	402	857
457	458	F RXA00959	GR00265	402	728
459	460	RXN00963	VV0249	1816	2652
461	462	F RXA00963	GR00269	442	5
463	464	RXN00971	VV0149	14706	14389
465	466	F RXA00971	GR00273	1421	1149
467	468	RXN00991	VV0210	4424	3045
469	470	RXN01004	VV0210	3045	1984
471	472	RXN01016	VV0209	14476	15123
473	474	F RXA01016	GR00290	1141	494
475	476	RXN01023	VV0143	2343	3320
477	478	F RXA01023	GR00292	1817	867
479	480	RXN01028	VV0015	29000	31048
481	482	F RXA01028	GR00295	3	626
483	484	F RXA01812	GR00514	3	1232
485	486	RXN01069	VV0030	986	273
487	488	F RXA01069	GR00299	606	4
489	490	RXN01071	VV0030	4879	2816
491	492	F RXA02898	GR10040	1631	6
493	494	F RXA01071	GR00299	2822	2436
495	496	RXN01075	VV0084	42045	41635
497	498	F RXA01075	GR00300	3269	2859
499	500	RXN01128	VV0157	2427	3440
501	502	F RXA01128	GR00314	1325	312
503	504	RXN01134	VV0077	774	4
505	506	F RXA01134	GR00317	2	460
507	508	RXN01140	VV0077	1642	710
509	510	F RXA01140	GR00318	3272	4057
511	512	RXN01148	VV0136	3147	3746
513	514	F RXA01148	GR00323	1452	2051
515	516	RXN01153	VV0265	546	4
517	518	F RXA01153	GR00325	546	4
519	520	RXN01154	VV0266	644	6
521	522	F RXA01154	GR00326	608	6
523	524	RXN01155	VV0225	252	1721
525	526	F RXA01155	GR00327	1370	6
527	528	RXN01167	VV0117	12777	13172
529	530	F RXA01167	GR00333	3	323
531	532	RXN01169	VV0117	5804	6799
533	534	F RXA01169	GR00334	1	567
535	536	RXN01173	VV0117	11085	10471
537	538	F RXA01173	GR00334	4853	4239
539	540	RXN01174	VV0117	12236	11487
541	542	F RXA01174	GR00334	6004	5255
543	544	RXN01229	VV0020	32482	31205
545	546	F RXA01229	GR00355	2806	3498
547	548	RXN01246	VV0104	2815	3321
549	550	F RXA01246	GR00360	1824	2462
551	552	RXN01249	VV0271	1	
553	554	F RXA01249	GR00363	303	4
555	556	RXN01251	VV0219	13143	12835
557	558	F RXA01251	GR00365	228	536
559	560	RXN01263	VV0009	11816	12727

561	562	F RXA01263	GR00367	10720	11631
563	564	RXN01266	VV0009	15553	14519
565	566	F RXA01266	GR00367	14457	13423
567	568	RXN01275	VV0009	29514	30431
569	570	F RXA01275	GR00367	28418	29335
571	572	RXN01281	VV0212	4506	5267
573	574	F RXA01281	GR00369	3869	4630
575	576	RXN01296	VV0209	10462	9380
577	578	F RXA01296	GR00373	5836	4754
579	580	RXN01306	VV0148	8158	7151
581	582	F RXA01306	GR00376	5691	4684
583	584	RXN01324	VV0082	6588	6887
585	586	RXN01331	VV0005	39816	42212
587	588	F RXA01331	GR00387	1606	1031
589	590	F RXA00668	GR00176	797	6
591	592	F RXA00674	GR00177	755	6
593	594	RXN01337	VV0032	1925	3337
595	596	F RXA01337	GR00389	5065	3653
597	598	RXN01351	VV0123	2841	3425
599	600	RXN01362	VV0051	27040	23387
601	602	F RXA01362	GR00395	3	1397
603	604	F RXA01364	GR00396	1869	4
605	606	RXN01379	VV0091	10518	11459
607	608	F RXA01379	GR00402	926	6
609	610	RXN01390	VV0277	6654	7310
611	612	F RXA01390	GR00408	992	336
613	614	RXN01391	VV0277	5568	6257
615	616	F RXA01391	GR00408	2078	1389
617	618	RXN01400	VV0126	2988	1489
619	620	F RXA01400	GR00409	2988	1489
621	622	RXN01409	VV0278	5304	4483
623	624	F RXA01409	GR00410	5296	4481
625	626	RXN01434	VV0050	13792	10841
627	628	F RXA01434	GR00417	10228	9863
629	630	RXN01448	VV0089	9602	10768
631	632	F RXA01448	GR00418	19796	19017
633	634	RXN01459	VV0233	3311	4120
635	636	F RXA01459	GR00420	3311	4120
637	638	RXN01460	VV0233	4066	4359
639	640	F RXA01460	GR00420	4066	4359
641	642	RXN01471	VV0019	11467	10661
643	644	F RXA01471	GR00422	5243	4437
645	646	RXN01479	VV0019	18635	18874
647	648	F RXA01479	GR00422	12423	12650
649	650	RXN01484	VV0019	26292	25747
651	652	F RXA01484	GR00422	20068	19523
653	654	RXN01485	VV0019	26454	28505
655	656	F RXA01485	GR00422	20230	22281
657	658	RXN01492	VV0139	36004	36807
659	660	F RXA01492	GR00423	6133	5330
661	662	RXN01518	VV0008	23238	23711
663	664	F RXA01518	GR00424	23238	23711
665	666	RXN01549	VV0080	46	1704
667	668	F RXA01549	GR00430	8426	7566
669	670	F RXA02011	GR00603	46	363
671	672	RXN01557	VV0323	959	1774
673	674	F RXA01557	GR00433	959	1774

675	676	RXN01574	VV0009	48980	47946
677	678	F RXA01574	GR00438	6963	5929
679	680	RXN01589	VV0227	1216	197
681	682	RXN01592	VV0229	14706	13405
683	684	F RXA01592	GR00447	3	1295
685	686	RXN01597	VV0229	8480	7299
687	688	F RXA01597	GR00447	6220	7401
689	690	RXN01598	VV0229	7286	6324
691	692	F RXA01598	GR00447	7414	8376
693	694	RXN01618	VV0050	23629	23246
695	696	F RXA01618	GR00451	1387	1004
697	698	RXN01634	VV0050	43466	42915
699	700	F RXA01634	GR00454	4988	5539
701	702	RXN01635	VV0050	42879	42139
703	704	F RXA01635	GR00454	5575	6315
705	706	RXN01647	VV0005	43276	44445
707	708	F RXA01647	GR00456	12422	11535
709	710	RXN01658	VV0010	44183	42351
711	712	F RXA01658	GR00461	5	1489
713	714	RXN01659	VV0089	5059	5604
715	716	F RXA01659	GR00462	3	488
717	718	RXN01663	VV0089	4271	5128
719	720	F RXA01663	GR00463	438	4
721	722	RXN01669	VV0057	4529	5443
723	724	F RXA01669	GR00465	1002	271
725	726	RXN01672	VV0179	7849	8190
727	728	F RXA01672	GR00467	2	310
729	730	RXN01694	VV0139	13054	13953
731	732	F RXA01694	GR00474	3931	3032
733	734	RXN01696	VV0115	1381	203
735	736	F RXA01696	GR00475	799	203
737	738	RXN01697	VV0139	1581	625
739	740	F RXA01697	GR00476	761	1486
741	742	RXN01701	VV0162	375	4
743	744	F RXA01701	GR00478	196	528
745	746	RXN01703	VV0089	7108	8220
747	748	F RXA01703	GR00479	2118	1648
749	750	RXN01709	VV0022	847	416
751	752	F RXA01709	GR00483	745	416
753	754	RXN01711	VV0191	8153	6996
755	756	F RXA01711	GR00484	2007	850
757	758	RXN01721	VV0036	1026	4
759	760	RXN01734	VV0221	1251	1784
761	762	F RXA01734	GR00492	544	1077
763	764	RXN01742	VV0233	5246	4743
765	766	F RXA01742	GR00493	7614	8117
767	768	RXN01754	VV0127	38790	36850
769	770	F RXA01754	GR00497	4082	2142
771	772	RXN01761	VV0010	11968	7505
773	774	F RXA00739	GR00202	819	4
775	776	F RXA01587	GR00442	120	2102
777	778	F RXA01761	GR00499	7001	5484
779	780	RXN01765	VV0054	17190	18131
781	782	F RXA01765	GR00500	3144	4085
783	784	RXN01767	VV0015	55242	55706
785	786	F RXA01767	GR00501	341	6
787	788	RXN01769	VV0015	54296	54736

789	790	F RXA01769	GR00501	1275	847
791	792	RXN01771	VV0050	35063	35764
793	794	F RXA01771	GR00502	886	185
795	796	RXN01774	VV0015	1794	2519
797	798	F RXA01774	GR00503	634	1416
799	800	RXN01787	VV0039	256	948
801	802	F RXA01787	GR00506	2	355
803	804	RXN01796	VV0137	2070	2843
805	806	F RXA01796	GR00508	2	484
807	808	RXN01803	VV0216	3355	4314
809	810	F RXA01803	GR00509	5671	4712
811	812	RXN01809	VV0081	9171	10346
813	814	F RXA01062	GR00297	490	5
815	816	F RXA01809	GR00510	3	638
817	818	RXN01811	VV0146	1243	1923
819	820	RXN01813	VV0084	46618	45953
821	822	F RXA01813	GR00515	635	6
823	824	RXN01815	VV0084	49277	50068
825	826	F RXA01815	GR00515	3294	4085
827	828	RXN01825	VV0083	2847	2578
829	830	F RXA01825	GR00516	2847	2578
831	832	RXN01831	VV0083	10874	10413
833	834	F RXA01831	GR00516	10874	10413
835	836	RXN01834	VV0143	11244	11945
837	838	F RXA01834	GR00517	2478	1777
839	840	RXN01846	VV0010	287	6
841	842	F RXA01846	GR00523	261	4
843	844	RXN01847	VV0139	19018	18284
845	846	F RXA01847	GR00524	52	786
847	848	RXN01874	VV0248	352	5
849	850	F RXA01874	GR00535	2556	2903
851	852	RXN01875	VV0145	2894	2049
853	854	F RXA01875	GR00536	516	1313
855	856	F RXA02734	GR00762	6514	6897
857	858	RXN01877	VV0105	3493	2423
859	860	F RXA01877	GR00537	135	1199
861	862	RXN01879	VV0105	1505	573
863	864	F RXA01879	GR00537	2117	2704
865	866	F RXA01880	GR00537	2641	3048
867	868	RXN01896	VV0098	75888	76523
869	870	F RXA01896	GR00544	2	580
871	872	RXN01899	VV0098	77817	78602
873	874	F RXA01899	GR00544	1874	2659
875	876	RXN01902	VV0098	84095	83037
877	878	F RXA01902	GR00544	7957	7094
879	880	RXN01908	VV0187	4030	4875
881	882	F RXA01908	GR00545	4030	4512
883	884	RXN01909	VV0218	69	947
885	886	F RXA01909	GR00546	59	937
887	888	RXN01910	VV0218	1040	1885
889	890	F RXA01910	GR00546	1030	1875
891	892	RXN01911	VV0218	2209	3147
893	894	F RXA01911	GR00546	2199	3044
895	896	RXN01930	VV0127	46545	47495
897	898	F RXA01930	GR00555	3817	2867
899	900	RXN01944	VV0050	42128	41157
901	902	F RXA01944	GR00558	2	385

903	904	F RXA01636	GR00454	6326	6898
905	906	RXN01945	VV0050	41150	39159
907	908	F RXA01945	GR00558	392	1633
909	910	F RXA01627	GR00453	1	495
911	912	RXN01960	VV0200	2259	1942
913	914	F RXA01960	GR00565	187	504
915	916	RXN01985	VV0056	1331	282
917	918	RXN01987	VV0149	167	379
919	920	F RXA01987	GR00576	167	379
921	922	RXN01988	VV0149	887	462
923	924	F RXA01988	GR00576	779	462
925	926	RXN01991	VV0230	926	1798
927	928	F RXA01991	GR00581	926	1720
929	930	RXN01996	VV0174	28434	27898
931	932	F RXA01996	GR00585	88	624
933	934	RXN02007	VV0324	855	223
935	936	F RXA02007	GR00598	651	223
937	938	RXN02014	VV0137	8298	8804
939	940	F RXA02014	GR00607	935	540
941	942	RXN02019	VV0129	44705	44205
943	944	F RXA02019	GR00612	597	106
945	946	RXN02023	VV0160	3234	4001
947	948	F RXA02023	GR00613	3234	4001
949	950	RXN02032	VV0117	5181	5750
951	952	F RXA02032	GR00618	4160	4729
953	954	RXN02039	VV0190	1482	643
955	956	F RXA02039	GR00621	3	812
957	958	RXN02044	VV0025	17208	15826
959	960	RXN02045	VV0025	15823	15563
961	962	F RXA02045	GR00623	1913	2173
963	964	RXN02049	VV0009	35549	36157
965	966	F RXA02049	GR00624	1583	2029
967	968	RXN02050	VV0009	36003	36797
969	970	F RXA02050	GR00624	2462	2833
971	972	RXN02059	VV0222	10306	10800
973	974	F RXA02059	GR00625	4678	4184
975	976	RXN02066	VV0222	6187	6678
977	978	F RXA02066	GR00626	6187	6678
979	980	RXN02067	VV0222	6733	7188
981	982	F RXA02067	GR00626	6733	7188
983	984	RXN02075	VV0318	12990	13778
985	986	RXN02076	VV0318	13879	14412
987	988	F RXA02076	GR00628	6902	7435
989	990	RXN02094	VV0126	18268	18984
991	992	F RXA02094	GR00629	13282	13998
993	994	RXN02104	VV0318	7435	6314
995	996	F RXA02104	GR00631	5327	4908
997	998	F RXA02071	GR00628	458	6
999	1000	RXN02107	VV0123	21585	21244
1001	1002	F RXA02107	GR00632	1536	1877
1003	1004	RXN02108	VV0123	21217	20609
1005	1006	F RXA02108	GR00632	2077	2511
1007	1008	RXN02114	VV0180	3	
1009	1010	F RXA02114	GR00634	615	130
1011	1012	RXN02121	VV0102	12833	12129
1013	1014	F RXA02121	GR00636	5813	5109
1015	1016	RXN02138	VV0300	4409	4750

1017	1018	F RXA02138	GR00639	4409	4750
1019	1020	RXN02151	VV0300	19913	21100
1021	1022	F RXA02151	GR00639	19913	21100
1023	1024	RXN02169	VV0100	3172	4017
1025	1026	F RXA02169	GR00641	3172	4017
1027	1028	RXN02180	VV0100	16813	15356
1029	1030	F RXA02180	GR00641	16813	15356
1031	1032	RXN02185	VV0100	20185	20763
1033	1034	F RXA02185	GR00641	20185	20763
1035	1036	RXN02186	VV0100	21192	20995
1037	1038	F RXA02186	GR00641	21213	20995
1039	1040	RXN02207	VV0302	802	5
1041	1042	F RXA02207	GR00646	10909	11667
1043	1044	RXN02223	VV0308	2732	3232
1045	1046	F RXA02223	GR00652	425	6
1047	1048	RXN02226	VV0068	1059	4
1049	1050	F RXA02226	GR00653	1059	4
1051	1052	RXN02238	VV0204	1345	1629
1053	1054	F RXA02238	GR00654	5241	5525
1055	1056	RXN02254	VV0202	2	
1057	1058	F RXA02254	GR00654	21769	22449
1059	1060	RXN02271	VV0020	14281	14838
1061	1062	F RXA02271	GR00655	5406	5963
1063	1064	RXN02279	VV0020	236	1693
1065	1066	F RXA02279	GR00657	1	1404
1067	1068	RXN02296	VV0127	24138	24626
1069	1070	F RXA02296	GR00662	6978	7466
1071	1072	RXN02300	VV0127	28354	28022
1073	1074	F RXA02300	GR00662	11194	10862
1075	1076	RXN02301	VV0127	29070	28354
1077	1078	F RXA02301	GR00662	11910	11194
1079	1080	RXN02302	VV0127	29196	30074
1081	1082	F RXA02302	GR00662	12036	12800
1083	1084	RXN02303	VV0127	13326	14231
1085	1086	F RXA02303	GR00663	1	720
1087	1088	RXN02307	VV0127	12611	11991
1089	1090	F RXA02307	GR00664	395	6
1091	1092	RXN02314	VV0025	23092	23532
1093	1094	F RXA02314	GR00665	6379	5939
1095	1096	RXN02337	VV0141	4679	3357
1097	1098	F RXA02337	GR00672	2893	3816
1099	1100	RXN02339	VV0195	1	
1101	1102	F RXA02339	GR00674	1	492
1103	1104	RXN02340	VV0195	1640	576
1105	1106	F RXA02338	GR00673	484	5
1107	1108	F RXA02340	GR00674	1214	576
1109	1110	RXN02341	VV0078	4279	4764
1111	1112	F RXA02341	GR00675	415	5
1113	1114	RXN02360	VV0051	14638	12206
1115	1116	F RXA02360	GR00685	3644	6076
1117	1118	RXN02361	VV0051	12122	11472
1119	1120	F RXA02361	GR00685	6160	6810
1121	1122	RXN02367	VV0102	4639	5247
1123	1124	F RXA02367	GR00687	2162	1554
1125	1126	RXN02368	VV0102	3883	4557
1127	1128	F RXA02368	GR00687	2918	2244
1129	1130	RXN02381	VV0213	3765	2743

1131	1132	F RXA02381	GR00691	1792	770
1133	1134	RXN02383	VV0213	639	4
1135	1136	F RXA02383	GR00692	608	6
1137	1138	RXN02387	VV0176	2729	3490
1139	1140	F RXA02387	GR00694	683	6
1141	1142	RXN02398	VV0176	12750	11149
1143	1144	F RXA02398	GR00698	2841	4370
1145	1146	RXN02406	VV0084	22016	22564
1147	1148	F RXA02406	GR00701	1322	774
1149	1150	RXN02407	VV0084	21758	21387
1151	1152	F RXA02407	GR00701	1580	1885
1153	1154	RXN02408	VV0084	20832	19921
1155	1156	F RXA02408	GR00702	832	5
1157	1158	RXN02409	VV0084	21371	20835
1159	1160	F RXA02409	GR00702	1248	835
1161	1162	RXN02428	VV0110	4585	3452
1163	1164	F RXA02428	GR00707	4585	3452
1165	1166	RXN02454	VV0196	2810	1569
1167	1168	F RXA02454	GR00711	3	815
1169	1170	RXN02457	VV0124	19193	18084
1171	1172	F RXA02457	GR00712	1295	2404
1173	1174	RXN02460	VV0124	14649	15152
1175	1176	F RXA02460	GR00712	5839	5336
1177	1178	RXN02464	VV0211	1990	3189
1179	1180	F RXA02464	GR00713	1107	1613
1181	1182	RXN02465	VV0211	3590	3192
1183	1184	F RXA02465	GR00713	2014	1616
1185	1186	RXN02466	VV0211	92	6
1187	1188	F RXA02466	GR00714	92	6
1189	1190	RXN02505	VV0007	23969	24139
1191	1192	F RXA02505	GR00720	18423	18593
1193	1194	RXN02510	VV0171	17467	16832
1195	1196	F RXA02510	GR00721	1983	2618
1197	1198	RXN02519	VV0183	2709	4337
1199	1200	F RXA02519	GR00724	1933	128
1201	1202	RXN02520	VV0183	2243	1560
1203	1204	F RXA02520	GR00724	2222	2905
1205	1206	RXN02534	VV0057	11192	11995
1207	1208	F RXA02534	GR00726	5536	6339
1209	1210	RXN02537	VV0057	14617	15078
1211	1212	F RXA02537	GR00726	8961	9422
1213	1214	RXN02538	VV0057	15078	15749
1215	1216	F RXA02538	GR00726	9422	10093
1217	1218	RXN02555	VV0101	5340	4738
1219	1220	F RXA02555	GR00731	1757	1155
1221	1222	RXN02564	VV0154	10016	9015
1223	1224	F RXA02564	GR00732	2543	3217
1225	1226	RXN02568	VV0245	1657	5
1227	1228	F RXA02568	GR00735	1363	5
1229	1230	RXN02593	VV0098	11073	11669
1231	1232	F RXA02593	GR00741	18693	18481
1233	1234	F RXA02594	GR00741	19077	18754
1235	1236	RXN02606	VV0098	34557	35927
1237	1238	F RXA02606	GR00742	13514	12144
1239	1240	RXN02610	VV0098	31620	30694
1241	1242	F RXA02610	GR00742	16452	17378
1243	1244	RXN02624	VV0129	29202	30497

1245	1246	F RXA02624	GR00746	5602	4889
1247	1248	RXN02626	VV0314	2012	1008
1249	1250	RXN02656	VV0090	15756	14917
1251	1252	RXN02673	VV0315	14030	13398
1253	1254	F RXA02673	GR00753	14030	13398
1255	1256	RXN02680	VV0098	64917	66200
1257	1258	F RXA02680	GR00754	6392	5109
1259	1260	F RXA02679	GR00754	5268	5693
1261	1262	F RXA02681	GR00754	5751	6194
1263	1264	RXN02693	VV0098	74100	75875
1265	1266	F RXA02693	GR00755	1650	4
1267	1268	RXN02696	VV0017	7946	7491
1269	1270	F RXA02696	GR00756	742	287
1271	1272	RXN02697	VV0017	31257	32783
1273	1274	F RXA02697	GR00757	1	699
1275	1276	F RXA02719	GR00758	19598	20245
1277	1278	RXN02720	VV0017	8727	8026
1279	1280	F RXA02720	GR00759	631	5
1281	1282	RXN02744	VV0074	893	1696
1283	1284	F RXA02744	GR00763	14460	13657
1285	1286	RXN02770	VV0171	4202	2637
1287	1288	F RXA02770	GR00772	3	1322
1289	1290	RXN02781	VV0084	14566	13376
1291	1292	F RXA02781	GR00774	1345	155
1293	1294	RXN02782	VV0093	7148	8446
1295	1296	F RXA02782	GR00775	204	875
1297	1298	RXN02812	VV0210	342	4
1299	1300	F RXA02812	GR00793	2	568
1301	1302	RXN02817	VV0346	403	5
1303	1304	F RXA02817	GR00798	403	5
1305	1306	RXN02818	VV0347	611	6
1307	1308	F RXA02818	GR00799	611	6
1309	1310	RXN02825	VV0082	3589	1751
1311	1312	F RXA01322	GR00385	443	6
1313	1314	F RXA02824	GR00805	531	4
1315	1316	F RXA02825	GR00806	565	182
1317	1318	RXN02838	VV0161	1	
1319	1320	F RXA02838	GR00831	1	462
1321	1322	RXN02840	VV0365	488	339
1323	1324	F RXA02840	GR00835	488	339
1325	1326	RXN02841	VV0055	11788	12222
1327	1328	F RXA02841	GR00840	283	5
1329	1330	RXN02846	VV0127	30861	30112
1331	1332	F RXA02846	GR00845	578	6
1333	1334	RXN02847	VV0113	47	1135
1335	1336	F RXA02847	GR00847	598	5
1337	1338	RXN02849	VV0237	2	
1339	1340	F RXA02849	GR00849	2	283
1341	1342	RXN02911	VV0135	24643	25101
1343	1344	RXN02914	VV0127	17305	16763
1345	1346	RXN02921	VV0213	1871	1401
1347	1348	RXN02924	VV0088	4557	5105
1349	1350	RXN02927	VV0082	18836	19303
1351	1352	RXN02928	VV0082	19511	20203
1353	1354	RXN02931	VV0090	25420	25644
1355	1356	RXN02932	VV0176	23391	24362
1357	1358	RXN02934	VV0103	14533	14838

1359	1360	RXN02936	VV0197	24360	24557
1361	1362	RXN02939	VV0008	33988	32387
1363	1364	F RXA01383	GR00406	1147	5
1365	1366	RXN02950	VV0224	7629	7306
1367	1368	RXN02951	VV0176	5739	5131
1369	1370	RXN02957	VV0020	30448	30158
1371	1372	RXN02967	VV0318	6614	6931
1373	1374	RXN02971	VV0210	951	640
1375	1376	RXN02978	VV0010	2191	683
1377	1378	RXN02995	VV0069	348	1913
1379	1380	RXN02997	VV0069	3709	2981
1381	1382	RXN03001	VV0170	422	874
1383	1384	RXN03005	VV0237	1101	334
1385	1386	RXN03009	VV0238	353	6
1387	1388	RXN03010	VV0238	7435	7199
1389	1390	RXN03011	VV0098	2984	3184
1391	1392	RXN03012	VV0241	2	571
1393	1394	RXN03017	VV0218	5720	7258
1395	1396	F RXA02753	GR00765	2630	138
1397	1398	RXN03018	VV0218	7221	8213
1399	1400	RXN03024	VV0003	6315	7730
1401	1402	RXN03025	VV0003	8668	7796
1403	1404	RXN03027	VV0008	17	151
1405	1406	RXN03029	VV0009	95	607
1407	1408	RXN03031	VV0011	1	789
1409	1410	RXN03032	VV0012	3652	3936
1411	1412	RXN03034	VV0013	2	661
1413	1414	F RXA00063	GR00010	1658	1374
1415	1416	RXN03037	VV0015	5364	5549
1417	1418	RXN03041	VV0018	1770	1273
1419	1420	F RXA02892	GR10035	1171	668
1421	1422	RXN03045	VV0019	33044	34039
1423	1424	RXN03046	VV0020	1	336
1425	1426	RXN03047	VV0020	25070	26485
1427	1428	F RXA00036	GR00004	7204	8619
1429	1430	RXN03048	VV0020	27423	26551
1431	1432	F RXA00037	GR00004	9557	8685
1433	1434	RXN03050	VV0021	6368	7333
1435	1436	RXN03053	VV0026	12	1535
1437	1438	F RXA02885	GR10021	1	1536
1439	1440	RXN03055	VV0026	3519	3947
1441	1442	F RXA00261	GR00039	11693	11265
1443	1444	F RXA02888	GR10024	326	754
1445	1446	RXN03059	VV0030	5373	4894
1447	1448	F RXA02899	GR10040	2125	1646
1449	1450	RXN03062	VV0035	525	4
1451	1452	RXN03066	VV0038	7298	6636
1453	1454	F RXA02876	GR10016	405	1067
1455	1456	RXN03067	VV0038	7493	7323
1457	1458	RXN03068	VV0038	7648	7529
1459	1460	RXN03073	VV0042	1573	944
1461	1462	F RXA02905	GR10044	477	4
1463	1464	RXN03085	VV0048	4511	4161
1465	1466	RXN03089	VV0053	1183	26
1467	1468	F RXA00071	GR00011	4013	5464
1469	1470	RXN03098	VV0064	2100	2723
1471	1472	RXN03099	VV0064	5576	6250

1473	1474	RXN03104	VV0071	401	577
1475	1476	RXN03106	VV0074	15930	16121
1477	1478	RXN03107	VV0076	232	432
1479	1480	RXN03113	VV0086	6541	8139
1481	1482	F RXA00506	GR00126	489	1829
1483	1484	RXN03115	VV0089	148	546
1485	1486	RXN03122	VV0104	3329	3475
1487	1488	RXN03134	VV0127	65312	65662
1489	1490	RXN03135	VV0127	66674	67402
1491	1492	F RXA02285	GR00660	1544	2272
1493	1494	RXN03138	VV0129	21194	21664
1495	1496	RXN03140	VV0131	4550	4302
1497	1498	RXN03141	VV0135	31144	31473
1499	1500	RXN03146	VV0143	25998	26468
1501	1502	RXN03147	VV0144	2726	2977
1503	1504	RXN03149	VV0146	969	1235
1505	1506	RXN03152	VV0166	264	536
1507	1508	RXN03153	VV0176	46481	47044
1509	1510	RXN03154	VV0179	1328	2239
1511	1512	RXN03156	VV0187	4908	5087
1513	1514	F RXA00176	GR00027	3475	3317
1515	1516	RXN03162	VV0195	909	1304
1517	1518	RXN03167	VV0327	633	4
1519	1520	F RXA02862	GR10006	1695	2330
1521	1522	RXN03170	VV0328	457	209
1523	1524	F RXA02856	GR10003	459	211
1525	1526	RXN03172	VV0329	1392	367
1527	1528	F RXA02858	GR10004	1392	367
1529	1530	RXN03173	VV0330	1340	243
1531	1532	F RXA02874	GR10015	1348	869
1533	1534	RXN03174	VV0331	461	6
1535	1536	F RXA02884	GR10020	1695	2156
1537	1538	RXN03177	VV0333	816	151
1539	1540	F RXA02881	GR10019	94	759
1541	1542	RXN03182	VV0339	276	4
1543	1544	RXN03184	VV0374	517	20
1545	1546	RXN03185	VV0375	311	123
1547	1548	RXA00003	GR00001	2279	3019
1549	1550	RXA00008	GR00002	606	115
1551	1552	RXA00015	GR00002	5999	6307
1553	1554	RXA00018	GR00002	12979	14277
1555	1556	RXA00020	GR00002	17142	16363
1557	1558	RXA00021	GR00002	18766	20538
1559	1560	RXA00025	GR00003	2211	3647
1561	1562	RXA00031	GR00003	10383	9982
1563	1564	RXA00049	GR00008	2270	2956
1565	1566	RXA00052	GR00008	7957	7247
1567	1568	RXA00054	GR00008	8557	11469
1569	1570	RXA00058	GR00009	7394	6831
1571	1572	RXA00059	GR00009	8301	8020
1573	1574	RXA00065	GR00010	4140	4412
1575	1576	RXA00068	GR00011	1305	724
1577	1578	RXA00079	GR00012	6599	6820
1579	1580	RXA00082	GR00012	9019	8456
1581	1582	RXA00083	GR00013	771	1070
1583	1584	RXA00093	GR00014	204	2426
1585	1586	RXA00101	GR00014	10514	10107

1587	1588	RXA00108	GR00015	546	4
1589	1590	RXA00110	GR00016	364	912
1591	1592	RXA00117	GR00019	791	201
1593	1594	RXA00118	GR00019	918	1172
1595	1596	RXA00119	GR00019	1704	2462
1597	1598	RXA00121	GR00019	3473	4183
1599	1600	RXA00122	GR00019	4220	5842
1601	1602	RXA00127	GR00020	2871	2416
1603	1604	RXA00134	GR00021	1648	1079
1605	1606	RXA00140	GR00022	3841	3656
1607	1608	RXA00141	GR00022	4307	3846
1609	1610	RXA00142	GR00022	4776	4300
1611	1612	RXA00150	GR00023	4085	4858
1613	1614	RXA00151	GR00023	4956	5552
1615	1616	RXA00153	GR00023	7656	7231
1617	1618	RXA00155	GR00023	8615	9397
1619	1620	RXA00159	GR00024	3868	2687
1621	1622	RXA00161	GR00024	4893	5354
1623	1624	RXA00169	GR00026	5222	3150
1625	1626	RXA00170	GR00026	9914	8061
1627	1628	RXA00173	GR00027	1716	1384
1629	1630	RXA00174	GR00027	2079	1795
1631	1632	RXA00175	GR00027	2732	2103
1633	1634	RXA00179	GR00028	1714	1256
1635	1636	RXA00180	GR00028	2334	1795
1637	1638	RXA00183	GR00028	7344	8195
1639	1640	RXA00185	GR00028	9418	12045
1641	1642	RXA00199	GR00031	2172	754
1643	1644	RXA00200	GR00031	2837	2535
1645	1646	RXA00207	GR00032	6430	6747
1647	1648	RXA00211	GR00032	10120	10782
1649	1650	RXA00218	GR00032	18104	19243
1651	1652	RXA00220	GR00032	20666	20163
1653	1654	RXA00230	GR00034	746	27
1655	1656	RXA00233	GR00036	420	4
1657	1658	RXA00234	GR00036	998	459
1659	1660	RXA00237	GR00036	3668	4045
1661	1662	RXA00238	GR00036	4186	4554
1663	1664	RXA00239	GR00036	5118	4534
1665	1666	RXA00240	GR00036	5342	5133
1667	1668	RXA00244	GR00037	1565	930
1669	1670	RXA00245	GR00037	3049	1565
1671	1672	RXA00248	GR00037	7843	7121
1673	1674	RXA00250	GR00038	6	221
1675	1676	RXA00252	GR00038	485	727
1677	1678	RXA00257	GR00039	1760	2215
1679	1680	RXA00258	GR00039	3219	3890
1681	1682	RXA00260	GR00039	9234	10409
1683	1684	RXA00273	GR00042	185	1297
1685	1686	RXA00274	GR00042	1556	4165
1687	1688	RXA00275	GR00042	4696	4238
1689	1690	RXA00276	GR00042	5016	4675
1691	1692	RXA00279	GR00043	4001	2616
1693	1694	RXA00282	GR00044	793	5
1695	1696	RXA00285	GR00046	3	515
1697	1698	RXA00286	GR00046	579	1142
1699	1700	RXA00294	GR00047	2761	3189

1701	1702	RXA00297	GR00048	2861	3772
1703	1704	RXA00320	GR00057	358	537
1705	1706	RXA00321	GR00057	2411	597
1707	1708	RXA00322	GR00057	3658	2555
1709	1710	RXA00325	GR00057	8594	9238
1711	1712	RXA00326	GR00057	9378	9857
1713	1714	RXA00336	GR00057	19461	19931
1715	1716	RXA00337	GR00058	530	6
1717	1718	RXA00339	GR00059	817	1533
1719	1720	RXA00349	GR00066	3	1061
1721	1722	RXA00355	GR00069	635	510
1723	1724	RXA00375	GR00080	549	49
1725	1726	RXA00380	GR00082	836	216
1727	1728	RXA00387	GR00084	1403	591
1729	1730	RXA00392	GR00086	3890	3027
1731	1732	RXA00394	GR00086	5322	4990
1733	1734	RXA00395	GR00086	5417	5716
1735	1736	RXA00396	GR00086	6653	6183
1737	1738	RXA00397	GR00086	7206	6667
1739	1740	RXA00398	GR00087	1	681
1741	1742	RXA00408	GR00091	642	1088
1743	1744	RXA00409	GR00091	1088	2500
1745	1746	RXA00411	GR00092	1685	1011
1747	1748	RXA00423	GR00097	909	457
1749	1750	RXA00424	GR00097	1379	909
1751	1752	RXA00425	GR00097	1433	1657
1753	1754	RXA00428	GR00098	2657	2025
1755	1756	RXA00429	GR00098	3063	2662
1757	1758	RXA00430	GR00098	3473	3063
1759	1760	RXA00433	GR00100	1446	1970
1761	1762	RXA00451	GR00110	816	325
1763	1764	RXA00457	GR00114	1451	372
1765	1766	RXA00462	GR00116	3023	1644
1767	1768	RXA00463	GR00116	4209	3388
1769	1770	RXA00468	GR00118	1282	464
1771	1772	RXA00469	GR00119	1647	472
1773	1774	RXA00472	GR00119	5449	4589
1775	1776	RXA00474	GR00119	6575	8152
1777	1778	RXA00475	GR00119	8822	8163
1779	1780	RXA00476	GR00119	8961	9821
1781	1782	RXA00481	GR00119	17636	18220
1783	1784	RXA00486	GR00120	1	702
1785	1786	RXA00490	GR00121	2676	1774
1787	1788	RXA00491	GR00122	1057	638
1789	1790	RXA00493	GR00123	3	326
1791	1792	RXA00519	GR00132	4	516
1793	1794	RXA00528	GR00136	3562	4650
1795	1796	RXA00529	GR00136	5274	4732
1797	1798	RXA00530	GR00136	6837	5557
1799	1800	RXA00535	GR00137	5155	5871
1801	1802	RXA00540	GR00139	2027	2269
1803	1804	RXA00549	GR00143	502	897
1805	1806	RXA00550	GR00143	935	1255
1807	1808	RXA00553	GR00145	742	1062
1809	1810	RXA00554	GR00145	1606	1136
1811	1812	RXA00563	GR00151	1	2739
1813	1814	RXA00564	GR00151	3744	4148

1815	1816	RXA00573	GR00156	117	767
1817	1818	RXA00576	GR00156	2916	2245
1819	1820	RXA00577	GR00156	2980	3327
1821	1822	RXA00578	GR00156	4087	3365
1823	1824	RXA00582	GR00156	9442	8924
1825	1826	RXA00585	GR00156	11894	11577
1827	1828	RXA00586	GR00156	12818	11937
1829	1830	RXA00587	GR00156	13008	13490
1831	1832	RXA00595	GR00159	3	332
1833	1834	RXA00597	GR00159	797	1066
1835	1836	RXA00598	GR00159	1070	1387
1837	1838	RXA00601	GR00159	3459	3749
1839	1840	RXA00602	GR00159	4907	4155
1841	1842	RXA00604	GR00159	5489	5779
1843	1844	RXA00610	GR00161	1193	2056
1845	1846	RXA00611	GR00161	3640	2165
1847	1848	RXA00613	GR00162	1652	1200
1849	1850	RXA00614	GR00162	1680	2594
1851	1852	RXA00617	GR00162	4002	5084
1853	1854	RXA00628	GR00165	1284	877
1855	1856	RXA00631	GR00166	172	1626
1857	1858	RXA00637	GR00167	2002	2754
1859	1860	RXA00646	GR00169	446	6
1861	1862	RXA00649	GR00169	2823	3278
1863	1864	RXA00652	GR00169	5449	5997
1865	1866	RXA00654	GR00169	7213	8478
1867	1868	RXA00656	GR00169	9495	9235
1869	1870	RXA00657	GR00169	10882	9980
1871	1872	RXA00661	GR00172	664	1353
1873	1874	RXA00667	GR00175	593	1177
1875	1876	RXA00676	GR00178	647	1393
1877	1878	RXA00678	GR00179	1037	303
1879	1880	RXA00691	GR00181	2152	1223
1881	1882	RXA00692	GR00181	3450	2317
1883	1884	RXA00693	GR00181	4303	3821
1885	1886	RXA00701	GR00182	427	801
1887	1888	RXA00707	GR00185	377	1348
1889	1890	RXA00713	GR00188	71	1033
1891	1892	RXA00714	GR00188	1809	1249
1893	1894	RXA00716	GR00188	3002	3514
1895	1896	RXA00719	GR00188	5283	6911
1897	1898	RXA00724	GR00191	811	164
1899	1900	RXA00726	GR00192	841	701
1901	1902	RXA00740	GR00202	1646	1068
1903	1904	RXA00741	GR00202	2986	2054
1905	1906	RXA00742	GR00202	5517	3868
1907	1908	RXA00743	GR00202	6652	6230
1909	1910	RXA00745	GR00202	13874	13341
1911	1912	RXA00746	GR00202	13755	14945
1913	1914	RXA00747	GR00202	15067	15654
1915	1916	RXA00748	GR00202	15917	16360
1917	1918	RXA00749	GR00202	17240	16542
1919	1920	RXA00751	GR00202	20245	19418
1921	1922	RXA00752	GR00202	21847	21419
1923	1924	RXA00757	GR00203	3119	4372
1925	1926	RXA00763	GR00204	1384	2166
1927	1928	RXA00765	GR00204	3283	3969

1929	1930	RXA00781	GR00206	2682	2395
1931	1932	RXA00788	GR00209	910	686
1933	1934	RXA00804	GR00215	438	881
1935	1936	RXA00805	GR00215	2057	2938
1937	1938	RXA00808	GR00217	1029	352
1939	1940	RXA00812	GR00219	287	1345
1941	1942	RXA00814	GR00219	2463	3236
1943	1944	RXA00815	GR00219	3236	3808
1945	1946	RXA00816	GR00219	4382	4678
1947	1948	RXA00826	GR00223	567	37
1949	1950	RXA00830	GR00224	266	988
1951	1952	RXA00853	GR00231	3775	3173
1953	1954	RXA00861	GR00235	6	431
1955	1956	RXA00862	GR00236	580	17
1957	1958	RXA00874	GR00241	758	1846
1959	1960	RXA00876	GR00241	4208	2454
1961	1962	RXA00881	GR00242	8057	8434
1963	1964	RXA00882	GR00242	8788	9465
1965	1966	RXA00883	GR00242	10060	9542
1967	1968	RXA00887	GR00242	13544	14266
1969	1970	RXA00889	GR00242	15341	15928
1971	1972	RXA00893	GR00244	789	193
1973	1974	RXA00895	GR00244	2578	1988
1975	1976	RXA00904	GR00246	1457	702
1977	1978	RXA00908	GR00247	1611	2168
1979	1980	RXA00916	GR00251	4108	518
1981	1982	RXA00926	GR00253	466	104
1983	1984	RXA00930	GR00253	3841	3089
1985	1986	RXA00932	GR00253	5068	5541
1987	1988	RXA00933	GR00253	6047	5586
1989	1990	RXA00940	GR00257	129	524
1991	1992	RXA00949	GR00259	5400	6047
1993	1994	RXA00969	GR00273	1	147
1995	1996	RXA00973	GR00274	2272	1670
1997	1998	RXA00978	GR00276	217	831
1999	2000	RXA00986	GR00280	60	401
2001	2002	RXA00987	GR00280	875	411
2003	2004	RXA00988	GR00280	1371	949
2005	2006	RXA01005	GR00286	520	1365
2007	2008	RXA01007	GR00287	2572	866
2009	2010	RXA01008	GR00287	2719	4659
2011	2012	RXA01011	GR00288	2089	857
2013	2014	RXA01017	GR00290	2175	1567
2015	2016	RXA01021	GR00291	1759	2280
2017	2018	RXA01029	GR00295	1338	1826
2019	2020	RXA01031	GR00295	3182	3847
2021	2022	RXA01032	GR00295	3974	4348
2023	2024	RXA01033	GR00295	4363	4698
2025	2026	RXA01034	GR00295	5177	4824
2027	2028	RXA01035	GR00295	5818	6423
2029	2030	RXA01036	GR00295	6513	6965
2031	2032	RXA01037	GR00295	7000	7527
2033	2034	RXA01038	GR00295	7530	8276
2035	2036	RXA01039	GR00295	9540	8965
2037	2038	RXA01040	GR00295	9711	10613
2039	2040	RXA01041	GR00295	10780	10932
2041	2042	RXA01042	GR00295	11088	12365

2043	2044	RXA01043	GR00295	12774	13346
2045	2046	RXA01044	GR00295	14024	15280
2047	2048	RXA01045	GR00295	15407	17230
2049	2050	RXA01046	GR00295	17441	19219
2051	2052	RXA01047	GR00295	19244	19717
2053	2054	RXA01058	GR00296	8566	8246
2055	2056	RXA01063	GR00297	828	499
2057	2058	RXA01066	GR00298	605	1330
2059	2060	RXA01068	GR00298	2184	3254
2061	2062	RXA01074	GR00300	2811	2107
2063	2064	RXA01076	GR00300	4374	3355
2065	2066	RXA01078	GR00300	6043	6876
2067	2068	RXA01083	GR00302	1777	1502
2069	2070	RXA01088	GR00304	3083	1902
2071	2072	RXA01091	GR00305	546	76
2073	2074	RXA01092	GR00305	702	881
2075	2076	RXA01092	GR00305	702	881
2077	2078	RXA01096	GR00306	4341	3643
2079	2080	RXA01102	GR00306	10018	8774
2081	2082	RXA01103	GR00306	10316	10092
2083	2084	RXA01107	GR00306	13612	14811
2085	2086	RXA01108	GR00306	15562	14912
2087	2088	RXA01109	GR00306	16281	15640
2089	2090	RXA01119	GR00310	1068	139
2091	2092	RXA01122	GR00311	557	36
2093	2094	RXA01123	GR00311	1090	644
2095	2096	RXA01127	GR00314	2	280
2097	2098	RXA01129	GR00314	1461	3326
2099	2100	RXA01131	GR00315	445	1311
2101	2102	RXA01137	GR00318	1101	1460
2103	2104	RXA01156	GR00327	1588	1388
2105	2106	RXA01158	GR00328	2580	1639
2107	2108	RXA01159	GR00328	3089	2775
2109	2110	RXA01160	GR00328	4187	3213
2111	2112	RXA01163	GR00331	710	6
2113	2114	RXA01165	GR00332	2155	1583
2115	2116	RXA01166	GR00332	3005	2523
2117	2118	RXA01170	GR00334	638	1120
2119	2120	RXA01171	GR00334	1714	2406
2121	2122	RXA01176	GR00335	1980	1477
2123	2124	RXA01177	GR00335	2121	4106
2125	2126	RXA01178	GR00335	4106	4555
2127	2128	RXA01184	GR00338	1489	17
2129	2130	RXA01186	GR00338	3742	2645
2131	2132	RXA01186	GR00338	3742	2645
2133	2134	RXA01187	GR00338	3850	4308
2135	2136	RXA01195	GR00343	1413	1859
2137	2138	RXA01196	GR00343	1889	2578
2139	2140	RXA01197	GR00343	3333	2881
2141	2142	RXA01198	GR00343	3422	3724
2143	2144	RXA01207	GR00347	126	773
2145	2146	RXA01213	GR00351	1508	282
2147	2148	RXA01218	GR00353	1078	1506
2149	2150	RXA01234	GR00357	633	250
2151	2152	RXA01237	GR00358	2751	2311
2153	2154	RXA01267	GR00367	16799	15486
2155	2156	RXA01268	GR00367	19365	18526

2157	2158	RXA01271	GR00367	23467	21656
2159	2160	RXA01273	GR00367	26475	25042
2161	2162	RXA01282	GR00369	5444	4665
2163	2164	RXA01294	GR00373	3537	2872
2165	2166	RXA01295	GR00373	3764	4738
2167	2168	RXA01304	GR00376	1982	2467
2169	2170	RXA01310	GR00380	803	477
2171	2172	RXA01313	GR00381	1116	172
2173	2174	RXA01315	GR00382	1394	744
2175	2176	RXA01316	GR00382	1855	1553
2177	2178	RXA01317	GR00382	2296	1877
2179	2180	RXA01318	GR00382	3616	2315
2181	2182	RXA01330	GR00387	569	1024
2183	2184	RXA01333	GR00389	1231	227
2185	2186	RXA01336	GR00389	3640	3038
2187	2188	RXA01342	GR00389	11296	12807
2189	2190	RXA01348	GR00392	261	752
2191	2192	RXA01349	GR00392	1531	755
2193	2194	RXA01357	GR00393	4357	4659
2195	2196	RXA01359	GR00393	6857	8038
2197	2198	RXA01366	GR00397	1369	980
2199	2200	RXA01367	GR00397	1518	1919
2201	2202	RXA01370	GR00398	1875	2225
2203	2204	RXA01372	GR00399	1	591
2205	2206	RXA01378	GR00401	1281	4
2207	2208	RXA01380	GR00403	2	2017
2209	2210	RXA01384	GR00406	3238	1523
2211	2212	RXA01396	GR00408	6475	6218
2213	2214	RXA01397	GR00408	6894	6475
2215	2216	RXA01401	GR00409	3193	3453
2217	2218	RXA01402	GR00409	3508	3981
2219	2220	RXA01405	GR00410	1844	1389
2221	2222	RXA01413	GR00412	854	1453
2223	2224	RXA01414	GR00412	1628	2134
2225	2226	RXA01417	GR00414	645	49
2227	2228	RXA01421	GR00416	1215	829
2229	2230	RXA01425	GR00417	1701	2585
2231	2232	RXA01429	GR00417	5651	6268
2233	2234	RXA01439	GR00418	5949	6494
2235	2236	RXA01440	GR00418	7496	6489
2237	2238	RXA01441	GR00418	8542	7514
2239	2240	RXA01445	GR00418	15083	14091
2241	2242	RXA01447	GR00418	17885	18733
2243	2244	RXA01452	GR00419	2363	2641
2245	2246	RXA01456	GR00420	898	1419
2247	2248	RXA01457	GR00420	1499	2173
2249	2250	RXA01463	GR00421	2493	1330
2251	2252	RXA01469	GR00422	2091	3122
2253	2254	RXA01470	GR00422	4112	3687
2255	2256	RXA01472	GR00422	5783	5328
2257	2258	RXA01473	GR00422	6596	5832
2259	2260	RXA01474	GR00422	6678	7223
2261	2262	RXA01475	GR00422	7651	7226
2263	2264	RXA01476	GR00422	7847	8188
2265	2266	RXA01488	GR00423	2179	1349
2267	2268	RXA01494	GR00423	8515	7520
2269	2270	RXA01497	GR00424	262	1179

2271	2272	RXA01501	GR00424	8130	7843
2273	2274	RXA01504	GR00424	10710	11318
2275	2276	RXA01505	GR00424	11318	11815
2277	2278	RXA01506	GR00424	11815	12225
2279	2280	RXA01507	GR00424	12239	12661
2281	2282	RXA01519	GR00424	23725	24471
2283	2284	RXA01520	GR00424	24784	25167
2285	2286	RXA01523	GR00424	27951	28901
2287	2288	RXA01525	GR00424	32301	30580
2289	2290	RXA01527	GR00425	5126	2616
2291	2292	RXA01536	GR00427	4066	2825
2293	2294	RXA01540	GR00428	3083	2382
2295	2296	RXA01543	GR00430	2802	37
2297	2298	RXA01544	GR00430	3496	2897
2299	2300	RXA01545	GR00430	4838	3588
2301	2302	RXA01546	GR00430	5584	4889
2303	2304	RXA01547	GR00430	6371	5709
2305	2306	RXA01548	GR00430	7432	6425
2307	2308	RXA01552	GR00431	6122	5145
2309	2310	RXA01554	GR00432	3719	1578
2311	2312	RXA01560	GR00435	767	438
2313	2314	RXA01575	GR00438	8024	7005
2315	2316	RXA01577	GR00438	8811	9185
2317	2318	RXA01579	GR00439	671	1054
2319	2320	RXA01585	GR00441	1226	600
2321	2322	RXA01586	GR00441	1597	1229
2323	2324	RXA01595	GR00447	3326	4285
2325	2326	RXA01600	GR00447	10460	11128
2327	2328	RXA01602	GR00447	13591	12062
2329	2330	RXA01605	GR00448	960	2474
2331	2332	RXA01610	GR00449	4343	3615
2333	2334	RXA01611	GR00449	4832	4476
2335	2336	RXA01612	GR00449	5235	4891
2337	2338	RXA01619	GR00451	2407	1433
2339	2340	RXA01622	GR00452	1908	2510
2341	2342	RXA01623	GR00452	2514	3224
2343	2344	RXA01624	GR00452	3220	3564
2345	2346	RXA01628	GR00453	866	1879
2347	2348	RXA01630	GR00454	341	1417
2349	2350	RXA01641	GR00456	5182	6552
2351	2352	RXA01642	GR00456	6557	7798
2353	2354	RXA01643	GR00456	8374	7949
2355	2356	RXA01645	GR00456	10574	9969
2357	2358	RXA01646	GR00456	11513	10695
2359	2360	RXA01656	GR00460	1548	2444
2361	2362	RXA01665	GR00463	2152	1433
2363	2364	RXA01671	GR00466	854	1468
2365	2366	RXA01673	GR00467	1807	773
2367	2368	RXA01675	GR00467	2824	3234
2369	2370	RXA01676	GR00467	4179	3424
2371	2372	RXA01677	GR00467	5043	4300
2373	2374	RXA01681	GR00467	10681	11313
2375	2376	RXA01685	GR00470	1488	910
2377	2378	RXA01686	GR00470	2026	1586
2379	2380	RXA01693	GR00474	1553	2974
2381	2382	RXA01714	GR00485	985	371
2383	2384	RXA01715	GR00485	1267	1962

2385	2386	RXA01729	GR00489	2636	3154
2387	2388	RXA01731	GR00491	109	807
2389	2390	RXA01738	GR00493	3971	4684
2391	2392	RXA01741	GR00493	7535	6738
2393	2394	RXA01748	GR00495	3681	4460
2395	2396	RXA01749	GR00495	4633	6249
2397	2398	RXA01750	GR00496	1878	3518
2399	2400	RXA01752	GR00497	557	6
2401	2402	RXA01753	GR00497	2095	557
2403	2404	RXA01760	GR00498	5095	5376
2405	2406	RXA01768	GR00501	827	450
2407	2408	RXA01770	GR00501	5134	1370
2409	2410	RXA01773	GR00503	34	444
2411	2412	RXA01775	GR00504	178	741
2413	2414	RXA01776	GR00504	838	2289
2415	2416	RXA01777	GR00504	2319	2777
2417	2418	RXA01778	GR00504	2912	4048
2419	2420	RXA01779	GR00504	4246	5664
2421	2422	RXA01780	GR00504	5721	6095
2423	2424	RXA01781	GR00504	6052	6312
2425	2426	RXA01782	GR00504	6384	6779
2427	2428	RXA01783	GR00504	6842	7078
2429	2430	RXA01785	GR00505	729	1304
2431	2432	RXA01788	GR00506	361	801
2433	2434	RXA01789	GR00506	875	1516
2435	2436	RXA01790	GR00506	1672	1731
2437	2438	RXA01791	GR00506	1885	2247
2439	2440	RXA01792	GR00506	2310	2582
2441	2442	RXA01793	GR00506	2916	3149
2443	2444	RXA01794	GR00506	3194	3427
2445	2446	RXA01799	GR00509	377	1570
2447	2448	RXA01800	GR00509	2292	1573
2449	2450	RXA01804	GR00509	6117	5797
2451	2452	RXA01805	GR00509	6515	6186
2453	2454	RXA01806	GR00509	6595	7074
2455	2456	RXA01816	GR00515	4210	4941
2457	2458	RXA01817	GR00515	4941	5573
2459	2460	RXA01820	GR00515	8360	9733
2461	2462	RXA01842	GR00522	1397	480
2463	2464	RXA01844	GR00522	1950	1771
2465	2466	RXA01845	GR00522	1919	2326
2467	2468	RXA01856	GR00527	225	770
2469	2470	RXA01857	GR00527	939	1589
2471	2472	RXA01858	GR00529	578	6
2473	2474	RXA01870	GR00534	2123	2797
2475	2476	RXA01871	GR00534	2797	3759
2477	2478	RXA01903	GR00545	3	281
2479	2480	RXA01904	GR00545	762	340
2481	2482	RXA01905	GR00545	1074	1604
2483	2484	RXA01906	GR00545	2322	2786
2485	2486	RXA01907	GR00545	3176	3787
2487	2488	RXA01923	GR00552	1311	1739
2489	2490	RXA01931	GR00555	4913	5566
2491	2492	RXA01941	GR00557	995	1429
2493	2494	RXA01942	GR00557	3526	2927
2495	2496	RXA01957	GR00564	389	850
2497	2498	RXA01958	GR00564	910	1416

2499	2500	RXA01959	GR00564	1639	2019
2501	2502	RXA01961	GR00565	521	1000
2503	2504	RXA01962	GR00565	1022	1591
2505	2506	RXA01963	GR00565	1757	2440
2507	2508	RXA01964	GR00566	1329	4
2509	2510	RXA01965	GR00566	1935	1375
2511	2512	RXA01966	GR00567	47	703
2513	2514	RXA01968	GR00567	3295	2138
2515	2516	RXA01969	GR00567	5689	5216
2517	2518	RXA01973	GR00570	2	583
2519	2520	RXA01974	GR00570	658	2109
2521	2522	RXA01976	GR00571	3742	2222
2523	2524	RXA01977	GR00571	4547	3972
2525	2526	RXA01982	GR00573	3001	1844
2527	2528	RXA01990	GR00581	1	999
2529	2530	RXA01992	GR00583	709	260
2531	2532	RXA01999	GR00589	2384	2854
2533	2534	RXA02001	GR00590	700	152
2535	2536	RXA02004	GR00594	3	209
2537	2538	RXA02006	GR00597	498	4
2539	2540	RXA02009	GR00601	127	5
2541	2542	RXA02013	GR00607	553	5
2543	2544	RXA02021	GR00613	2008	1061
2545	2546	RXA02036	GR00619	3441	3821
2547	2548	RXA02040	GR00621	1452	925
2549	2550	RXA02046	GR00623	2680	2943
2551	2552	RXA02051	GR00624	3186	3683
2553	2554	RXA02053	GR00624	5484	6062
2555	2556	RXA02057	GR00625	2972	3502
2557	2558	RXA02058	GR00625	4051	3500
2559	2560	RXA02069	GR00627	1116	1694
2561	2562	RXA02070	GR00627	1733	2830
2563	2564	RXA02080	GR00628	11017	10211
2565	2566	RXA02081	GR00628	12307	13935
2567	2568	RXA02084	GR00629	2920	2576
2569	2570	RXA02089	GR00629	8431	8901
2571	2572	RXA02090	GR00629	9764	8964
2573	2574	RXA02091	GR00629	10512	9862
2575	2576	RXA02097	GR00630	184	3555
2577	2578	RXA02102	GR00631	4479	3322
2579	2580	RXA02103	GR00631	4510	4905
2581	2582	RXA02109	GR00632	3460	2540
2583	2584	RXA02117	GR00636	1056	1529
2585	2586	RXA02123	GR00636	6558	7928
2587	2588	RXA02124	GR00636	7956	9911
2589	2590	RXA02125	GR00637	739	1539
2591	2592	RXA02129	GR00637	5906	6139
2593	2594	RXA02132	GR00638	737	1375
2595	2596	RXA02137	GR00639	4166	3369
2597	2598	RXA02141	GR00639	8457	8864
2599	2600	RXA02146	GR00639	14742	15368
2601	2602	RXA02152	GR00640	237	638
2603	2604	RXA02163	GR00640	10072	10824
2605	2606	RXA02164	GR00640	10824	12398
2607	2608	RXA02165	GR00640	12388	12999
2609	2610	RXA02166	GR00640	13048	13224
2611	2612	RXA02168	GR00641	2894	81

2613	2614	RXA02170	GR00641	4798	4025
2615	2616	RXA02172	GR00641	6919	6581
2617	2618	RXA02177	GR00641	12683	13615
2619	2620	RXA02178	GR00641	13628	14497
2621	2622	RXA02181	GR00641	17168	17845
2623	2624	RXA02183	GR00641	18663	19187
2625	2626	RXA02187	GR00641	21249	23447
2627	2628	RXA02199	GR00646	2591	3160
2629	2630	RXA02203	GR00646	7469	7092
2631	2632	RXA02206	GR00646	9927	10862
2633	2634	RXA02211	GR00648	2537	2989
2635	2636	RXA02212	GR00649	964	467
2637	2638	RXA02216	GR00651	2	307
2639	2640	RXA02217	GR00651	968	306
2641	2642	RXA02218	GR00651	1299	1565
2643	2644	RXA02219	GR00651	1578	2963
2645	2646	RXA02221	GR00651	6720	8081
2647	2648	RXA02227	GR00653	1236	1853
2649	2650	RXA02230	GR00653	4156	3620
2651	2652	RXA02231	GR00653	5111	4356
2653	2654	RXA02244	GR00654	12058	13590
2655	2656	RXA02255	GR00654	22507	23442
2657	2658	RXA02266	GR00655	653	1165
2659	2660	RXA02267	GR00655	2053	1181
2661	2662	RXA02280	GR00658	2	754
2663	2664	RXA02286	GR00660	3285	3833
2665	2666	RXA02287	GR00660	4071	4622
2667	2668	RXA02294	GR00662	5992	5618
2669	2670	RXA02295	GR00662	6842	6063
2671	2672	RXA02297	GR00662	7502	8638
2673	2674	RXA02298	GR00662	10310	8652
2675	2676	RXA02304	GR00663	1613	723
2677	2678	RXA02308	GR00664	939	511
2679	2680	RXA02324	GR00668	1548	2633
2681	2682	RXA02325	GR00668	4314	3445
2683	2684	RXA02331	GR00671	396	761
2685	2686	RXA02336	GR00672	2731	2552
2687	2688	RXA02347	GR00677	509	189
2689	2690	RXA02349	GR00678	394	5
2691	2692	RXA02352	GR00681	2	556
2693	2694	RXA02356	GR00684	761	1756
2695	2696	RXA02358	GR00685	1239	1529
2697	2698	RXA02362	GR00685	7045	10743
2699	2700	RXA02374	GR00688	1626	2246
2701	2702	RXA02390	GR00695	1500	832
2703	2704	RXA02393	GR00697	168	449
2705	2706	RXA02395	GR00698	2	733
2707	2708	RXA02396	GR00698	1309	1031
2709	2710	RXA02403	GR00700	896	1660
2711	2712	RXA02412	GR00703	2043	2522
2713	2714	RXA02417	GR00705	4755	2632
2715	2716	RXA02421	GR00705	7237	6428
2717	2718	RXA02425	GR00707	1	630
2719	2720	RXA02427	GR00707	3447	3061
2721	2722	RXA02430	GR00707	7498	7683
2723	2724	RXA02433	GR00708	2981	3580
2725	2726	RXA02437	GR00709	1661	2470

2727	2728	RXA02443	GR00709	6818	7771
2729	2730	RXA02444	GR00709	7836	9113
2731	2732	RXA02452	GR00710	5271	5092
2733	2734	RXA02459	GR00712	4341	5075
2735	2736	RXA02461	GR00712	6252	5845
2737	2738	RXA02467	GR00714	643	419
2739	2740	RXA02472	GR00715	5435	5725
2741	2742	RXA02473	GR00715	6664	5924
2743	2744	RXA02475	GR00715	9595	8441
2745	2746	RXA02478	GR00716	1245	10
2747	2748	RXA02482	GR00718	914	105
2749	2750	RXA02483	GR00718	1813	1001
2751	2752	RXA02484	GR00718	2317	1817
2753	2754	RXA02486	GR00718	3441	4076
2755	2756	RXA02488	GR00719	1	369
2757	2758	RXA02489	GR00719	373	996
2759	2760	RXA02495	GR00720	9002	6435
2761	2762	RXA02496	GR00720	10025	9219
2763	2764	RXA02498	GR00720	11016	11819
2765	2766	RXA02500	GR00720	13460	13558
2767	2768	RXA02506	GR00720	19484	18603
2769	2770	RXA02514	GR00723	1	837
2771	2772	RXA02518	GR00723	3464	3874
2773	2774	RXA02521	GR00724	2924	4366
2775	2776	RXA02524	GR00725	2405	3094
2777	2778	RXA02525	GR00725	3113	3490
2779	2780	RXA02540	GR00726	12438	12001
2781	2782	RXA02544	GR00726	16715	18142
2783	2784	RXA02545	GR00726	18749	18192
2785	2786	RXA02546	GR00726	19927	18824
2787	2788	RXA02549	GR00728	1331	6
2789	2790	RXA02552	GR00730	924	130
2791	2792	RXA02554	GR00731	1050	427
2793	2794	RXA02569	GR00736	82	831
2795	2796	RXA02570	GR00736	837	1478
2797	2798	RXA02573	GR00739	594	151
2799	2800	RXA02575	GR00739	1907	3064
2801	2802	RXA02576	GR00740	1569	148
2803	2804	RXA02577	GR00740	2463	1579
2805	2806	RXA02584	GR00741	8925	8575
2807	2808	RXA02585	GR00741	9917	8937
2809	2810	RXA02588	GR00741	13037	12354
2811	2812	RXA02591	GR00741	15780	17609
2813	2814	RXA02598	GR00742	2576	3166
2815	2816	RXA02600	GR00742	5027	3630
2817	2818	RXA02601	GR00742	5258	7246
2819	2820	RXA02602	GR00742	7239	7742
2821	2822	RXA02604	GR00742	8800	10875
2823	2824	RXA02609	GR00742	16197	16445
2825	2826	RXA02617	GR00745	1404	1910
2827	2828	RXA02619	GR00746	204	1103
2829	2830	RXA02620	GR00746	1192	1845
2831	2832	RXA02639	GR00749	511	1344
2833	2834	RXA02647	GR00751	4155	4616
2835	2836	RXA02649	GR00752	1284	283
2837	2838	RXA02652	GR00752	2973	3551
2839	2840	RXA02655	GR00752	9313	8330

2841	2842	RXA02662	GR00753	1461	1724
2843	2844	RXA02665	GR00753	6497	6018
2845	2846	RXA02670	GR00753	10199	10780
2847	2848	RXA02672	GR00753	12303	13400
2849	2850	RXA02678	GR00754	3858	4775
2851	2852	RXA02683	GR00754	7742	7065
2853	2854	RXA02685	GR00754	10058	9402
2855	2856	RXA02688	GR00754	12256	12924
2857	2858	RXA02689	GR00754	13405	13064
2859	2860	RXA02690	GR00754	14502	13405
2861	2862	RXA02700	GR00757	3507	4742
2863	2864	RXA02701	GR00757	4838	6145
2865	2866	RXA02712	GR00758	13067	12273
2867	2868	RXA02714	GR00758	14754	14326
2869	2870	RXA02715	GR00758	15847	15458
2871	2872	RXA02721	GR00759	1373	636
2873	2874	RXA02725	GR00760	1478	867
2875	2876	RXA02727	GR00760	6287	5376
2877	2878	RXA02735	GR00763	777	73
2879	2880	RXA02736	GR00763	1753	797
2881	2882	RXA02751	GR00764	6393	5920
2883	2884	RXA02756	GR00766	3851	2961
2885	2886	RXA02757	GR00766	4475	3930
2887	2888	RXA02765	GR00769	3552	2794
2889	2890	RXA02766	GR00770	986	594
2891	2892	RXA02774	GR00773	3	473
2893	2894	RXA02775	GR00773	744	968
2895	2896	RXA02776	GR00773	1713	1372
2897	2898	RXA02777	GR00773	4626	5732
2899	2900	RXA02778	GR00773	10095	10319
2901	2902	RXA02779	GR00773	10617	10895
2903	2904	RXA02780	GR00773	10954	11280
2905	2906	RXA02783	GR00775	845	1393
2907	2908	RXA02784	GR00775	1751	1936
2909	2910	RXA02786	GR00777	2	808
2911	2912	RXA02789	GR00777	5237	5782
2913	2914	RXA02793	GR00777	9385	8684
2915	2916	RXA02796	GR00778	1648	1100
2917	2918	RXA02798	GR00778	2842	4266
2919	2920	RXA02799	GR00780	182	454
2921	2922	RXA02815	GR00796	3	554
2923	2924	RXA02823	GR00804	275	6
2925	2926	RXA02827	GR00812	428	6
2927	2928	RXA02842	GR00841	356	15
2929	2930	RXA02845	GR00844	2	616
2931	2932	RXA02848	GR00848	113	511

TABLE 2: GENES IDENTIFIED FROM GENBANK

GenBank™ Accession No.	Gene Name	Gene Function	Reference
A09073	ppg	Phosphoenol pyruvate carboxylase	Bachmann, B. et al. "DNA fragment coding for phosphoenolpyruvat corboxylase, recombinant DNA carrying said fragment, strains carrying the recombinant DNA and method for producing L-aminino acids using said strains," Patent: EP 0358940-A 3 03/21/90
A45579, A45581, A45583, A45585 A45587 ·		Threonine dehydratase	Moeckel, B. et al. "Production of L-isoleucine by means of recombinant micro-organisms with deregulated threonine dehydratase," Patent: WO 9519442-A 5 07/20/95
AB003132	murC; ftsQ; ftsZ		Kobayashi, M. et al. "Cloning, sequencing, and characterization of the ftsZ gene from coryneform bacteria," *Biochem. Biophys. Res. Commun.*, 236(2):383-388 (1997)
AB015023	murC; ftsQ		Wachi, M. et al. "A murC gene from Coryneform bacteria," *Appl. Microbiol. Biotechnol.*, 51(2):223-228 (1999)
AB018530	dtsR		Kimura, E. et al. "Molecular cloning of a novel gene, dtsR, which rescues the detergent sensitivity of a mutant derived from *Brevibacterium lactofermentum*," *Biosci. Biotechnol. Biochem.*, 60(10):1565-1570 (1996)
AB018531	dtsR1; dtsR2		
AB020624	murI	D-glutamate racemase	
AB023377	tkt	transketolase	
AB024708	gltB; gltD	Glutamine 2-oxoglutarate aminotransferase large and small subunits	
AB025424	acn	aconitase	
AB027714	rep	Replication protein	
AB027715	rep; aad	Replication protein; aminoglycoside adenyltransferase	
AF005242	argC	N-acetylglutamate-5-semialdehyde dehydrogenase	
AF005635	glnA	Glutamine synthetase	
AF030405	hisF	cyclase	
AF030520	argG	Argininosuccinate synthetase	
AF031518	argF	Ornithine carbamolytransferase	
AF036932	aroD	3-dehydroquinate dehydratase	

GenBank™ Accession No.	Gene Name	Gene Function	Reference
AF038548	pyc	Pyruvate carboxylase	
AF038651	dciAE; apt; rel	Dipeptide-binding protein; adenine phosphoribosyltransferase; GTP pyrophosphokinase	Wehmeier, L. et al. "The role of the Corynebacterium glutamicum rel gene in (p)ppGpp metabolism," *Microbiology,* 144:1853-1862 (1998)
AF041436	argR	Arginine repressor	
AF045998	impA	Inositol monophosphate phosphatase	
AF048764	argH	Argininosuccinate lyase	
AF049897	argC; argJ; argB; argD; argF; argR; argG; argH	N-acetylglutamylphosphate reductase; ornithine acetyltransferase; N-acetylglutamate kinase; acetylornithine transminase; ornithine carbamoyltransferase; arginine repressor; argininosuccinate synthase; argininosuccinate lyase	
AF050109	inhA	Enoyl-acyl carrier protein reductase	
AF050166	hisG	ATP phosphoribosyltransferase	
AF051846	hisA	Phosphoribosylformimino-5-amino-1-phosphoribosyl-4-imidazolecarboxamide isomerase	
AF052652	metA	Homoserine O-acetyltrånsferase	Park, S. et al. "Isolation and analysis of metA, a methionine biosynthetic gene encoding homoserine acetyltransferase in Corynebacterium glutamicum," *Mol. Cells.,* 8(3):286-294 (1998)
AF053071	aroB	Dehydroquinate synthetase	
AF060558	hisH	Glutamine amidotransferase	
AF086704	hisE	Phosphoribosyl-ATP-pyrophosphohydrolase	
AF114233	aroA	5-enolpyruvylshikimate 3-phosphate synthase	
AF116184	panD	L-aspartate-alpha-decarboxylase precursor	Dusch, N. et al. "Expression of the Corynebacterium glutamicum panD gene encoding L-aspartate-alpha-decarboxylase leads to pantothenate overproduction in Escherichia coli," *Appl. Environ. Microbiol.,* 65(4)1530-1539 (1999)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
AF124518	aroD; aroE	3-dehydroquinase; shikimate dehydrogenase	
AF124600	aroC; aroK; aroB; pepQ	Chorismate synthase; shikimate kinase; 3-dehydroquinate synthase; putative cytoplasmic peptidase	
AF145897	inhA		
AF145898	inhA		
AJ001436	ectP	Transport of ectoine, glycine betaine, proline	Peter, H. et al. "Corynebacterium glutamicum is equipped with four secondary carriers for compatible solutes: Identification, sequencing, and characterization of the proline/ectoine uptake system, ProP, and the ectoine/proline/glycine betaine carrier, EctP," *J. Bacteriol.*, 180(22):6005-6012 (1998)
AJ004934	dapD	Tetrahydrodipicolinate succinylase (incomplete[i])	Wehrmann, A. et al. "Different modes of diaminopimelate synthesis and their role in cell wall integrity: A study with Corynebacterium glutamicum," *J. Bacteriol.*, 180(12):3159-3165 (1998)
AJ007732	ppc; secG; amt; ocd; soxA	Phosphoenolpyruvate-carboxylase; ?; high affinity ammonium uptake protein; putative ornithine-cyclodecarboxylase; sarcosine oxidase	
AJ010319	ftsY, glnB, glnD; srp; amtP	Involved in cell division; PII protein; uridylyltransferase (uridylyl-removing enzmye); signal recognition particle; low affinity ammonium uptake protein	Jakoby, M. et al. "Nitrogen regulation in Corynebacterium glutamicum; Isolation of genes involved in biochemical characterization of corresponding proteins," *FEMS Microbiol.*, 173(2):303-310 (1999)
AJ132968	cat	Chloramphenicol aceteyl transferase	
AJ224946	mqo	L-malate: quinone oxidoreductase	Molenaar, D. et al. "Biochemical and genetic characterization of the membrane-associated malate dehydrogenase (acceptor) from Corynebacterium glutamicum," *Eur. J. Biochem.*, 254(2):395-403 (1998)
AJ238250	ndh	NADH dehydrogenase	
AJ238703	porA	Porin	Lichtinger, T. et al. "Biochemical and biophysical characterization of the cell wall porin of Corynebacterium glutamicum: The channel is formed by a low molecular mass polypeptide," *Biochemistry*, 37(43):15024-15032 (1998)
D17429		Transposable element IS31831	Vertes, A.A. et al. "Isolation and characterization of IS31831, a transposable element from Corynebacterium glutamicum," *Mol. Microbiol.*, 11(4):739-746 (1994)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
D84102	odhA	2-oxoglutarate dehydrogenase	Usuda, Y. et al. "Molecular cloning of the Corynebacterium glutamicum (Brevibacterium lactofermentum AJ12036) odhA gene encoding a novel type of 2-oxoglutarate dehydrogenase," *Microbiology,* 142:3347-3354 (1996)
E01358	hdh; hk	Homoserine dehydrogenase; homoserine kinase	Katsumata, R. et al. "Production of L-thereonine and L-isoleucine," Patent: JP 1987232392-A 1 10/12/87
E01359		Upstream of the start codon of homoserine kinase gene	Katsumata, R. et al. "Production of L-thereonine and L-isoleucine," Patent: JP 1987232392-A 2 10/12/87
E01375		Tryptophan operon	
E01376	trpL; trpE	Leader peptide; anthranilate synthase	Matsui, K. et al. "Tryptophan operon, peptide and protein coded thereby, utilization of tryptophan operon gene expression and production of tryptophan," Patent: JP 1987244382-A 1 10/24/87
E01377		Promoter and operator regions of tryptophan operon	Matsui, K. et al. "Tryptophan operon, peptide and protein coded thereby, utilization of tryptophan operon gene expression and production of tryptophan," Patent: JP 1987244382-A 1 10/24/87
E03937		Biotin-synthase	Hatakeyama, K. et al. "DNA fragment containing gene capable of coding biotin synthetase and its utilization," Patent: JP 1992278088-A 1 10/02/92
E04040		Diamino pelargonic acid aminotransferase	Kohama, K. et al. "Gene coding diaminopelargonic acid aminotransferase and desthiobiotin synthetase and its utilization," Patent: JP 1992330284-A 1 11/18/92
E04041		Desthiobiotinsynthetase	Kohama, K. et al. "Gene coding diaminopelargonic acid aminotransferase and desthiobiotin synthetase and its utilization," Patent: JP 1992330284-A 1 11/18/92
E04307		Flavum aspartase	Kurusu, Y. et al. "Gene DNA coding aspartase and utilization thereof," Patent: JP 1993030977-A 1 02/09/93
E04376		Isocitric acid lyase	Katsumata, R. et al. "Gene manifestation controlling DNA," Patent: JP 1993056782-A 3 03/09/93
E04377		Isocitric acid lyase N-terminal fragment	Katsumata, R. et al. "Gene manifestation controlling DNA," Patent: JP 1993056782-A 3 03/09/93
E04484		Prephenate dehydratase	Sotouchi, N. et al. "Production of L-phenylalanine by fermentation," Patent: JP 1993076352-A 2 03/30/93
E05108		Aspartokinase	Fugono, N. et al. "Gene DNA coding Aspartokinase and its use," Patent: JP 1993184366-A 1 07/27/93
E05112		Dihydro-dipichorinate synthetase	Hatakeyama, K. et al. "Gene DNA coding dihydrodipicolinic acid synthetase and its use," Patent: JP 1993184371-A 1 07/27/93

GenBank™ Accession No.	Gene Name	Gene Function	Reference
E05776		Diaminopimelic acid dehydrogenase	Kobayashi, M. et al. "Gene DNA coding Diaminopimelic acid dehydrogenase and its use," Patent: JP 1993284970-A 1 11/02/93
E05779		Threonine synthase	Kohama, K. et al. "Gene DNA coding threonine synthase and its use," Patent: JP 1993284972-A 1 11/02/93
E06110		Prephenate dehydratase	Kikuchi, T. et al. "Production of L-phenylalanine by fermentation method," Patent: JP 1993344881-A 1 12/27/93
E06111		Mutated Prephenate dehydratase	Kikuchi, T. et al. "Production of L-phenylalanine by fermentation method," Patent: JP 1993344881-A 1 12/27/93
E06146		Acetohydroxy acid synthetase	Inui, M. et al. "Gene capable of coding Acetohydroxy acid synthetase and its use," Patent: JP 1993344893-A 1 12/27/93
E06825		Aspartokinase	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E06826		Mutated aspartokinase alpha subunit	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E06827		Mutated aspartokinase alpha subunit	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E07701	secY		Honno, N. et al. "Gene DNA participating in integration of membraneous protein to membrane," Patent: JP 1994169780-A 1 06/21/94
E08177		Aspartokinase	Sato, Y. et al. "Genetic DNA capable of coding Aspartokinase released from feedback inhibition and its utilization," Patent: JP 1994261766-A 1 09/20/94
E08178, E08179, E08180, E08181, E08182		Feedback inhibition-released Aspartokinase	Sato, Y. et al. "Genetic DNA capable of coding Aspartokinase released from feedback inhibition and its utilization," Patent: JP 1994261766-A 1 09/20/94
E08232		Acetohydroxy-acid isomeroreductase	Inui, M. et al. "Gene DNA coding acetohydroxy acid isomeroreductase," Patent: JP 1994277067-A 1 10/04/94
E08234	secE		Asai, Y. et al. "Gene DNA coding for translocation machinery of protein," Patent: JP 1994277073-A 1 10/04/94
E08643		FT aminotransferase and desthiobiotin synthetase promoter region	Hatakeyama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031476-A 1 02/03/95
E08646		Biotin synthetase	Hatakeyama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031476-A 1 02/03/95

GenBank™ Accession No.	Gene Name	Gene Function	Reference
E08649		Aspartase	Kohama, K. et al "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031478-A 1 02/03/95
E08900		Dihydrodipicolinate reductase	Madori, M. et al. "DNA fragment containing gene coding Dihydrodipicolinate acid reductase and utilization thereof," Patent: JP 1995075578-A 1 03/20/95
E08901		Diaminopimelic acid decarboxylase	Madori, M. et al. "DNA fragment containing gene coding Diaminopimelic acid decarboxylase and utilization thereof," Patent: JP 1995075579-A 1 03/20/95
E12594		Serine hydroxymethyltransferase	Hatakeyama, K. et al. "Production of L-trypophan," Patent: JP 1997028391-A 1 02/04/97
E12760, E12759, E12758		transposase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12764		Arginyl-tRNA synthetase; diaminopimelic acid decarboxylase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12767		Dihydrodipicolinic acid synthetase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12770		aspartokinase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12773		Dihydrodipicolinic acid reductase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E13655		Glucose-6-phosphate dehydrogenase	Hatakeyama, K. et al. "Glucose-6-phosphate dehydrogenase and DNA capable of coding the same," Patent: JP 1997224661-A 1 09/02/97
L01508	IlvA	Threonine dehydratase	Moeckel, B. et al. "Functional and structural analysis of the threonine dehydratase of Corynebacterium glutamicum," *J. Bacteriol.*, 174:8065-8072 (1992)
L07603	EC 4.2.1.15	3-deoxy-D-arabinoheptulosonate-7-phosphate synthase	Chen, C. et al. "The cloning and nucleotide sequence of Corynebacterium glutamicum 3-deoxy-D-arabinoheptulosonate-7-phosphate synthase gene," *FEMS Microbiol. Lett.*, 107:223-230 (1993)
L09232	IlvB; ilvN; ilvC	Acetohydroxy acid synthase large subunit; Acetohydroxy acid synthase small subunit; Acetohydroxy acid isomeroreductase	Keilhauer, C. et al. "Isoleucine synthesis in Corynebacterium glutamicum: molecular analysis of the ilvB-ilvN-ilvC operon," *J. Bacteriol.*, 175(17):5595-5603 (1993)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
L18874	PtsM	Phosphoenolpyruvate sugar phosphotransferase	Fouet, A et al. "Bacillus subtilis sucrose-specific enzyme II of the phosphotransferase system: expression in Escherichia coli and homology to enzymes II from enteric bacteria," *PNAS USA,* 84(24):8773-8777 (1987); Lee, J.K. et al. "Nucleotide sequence of the gene encoding the Corynebacterium glutamicum mannose enzyme II and analyses of the deduced protein sequence," *FEMS Microbiol. Lett.,* 119(1-2):137-145 (1994)
L27123	aceB	Malate synthase	Lee, H-S. et al. "Molecular characterization of aceB, a gene encoding malate synthase in Corynebacterium glutamicum," *J. Microbiol. Biotechnol.,* 4(4):256-263 (1994)
L27126		Pyruvate kinase	Jetten, M. S. et al. "Structural and functional analysis of pyruvate kinase from Corynebacterium glutamicum," *Appl. Environ. Microbiol.,* 60(7):2501-2507 (1994)
L28760	aceA	Isocitrate lyase	
L35906	dtxr	Diphtheria toxin repressor	Oguiza, J.A. et al. "Molecular cloning, DNA sequence analysis, and characterization of the Corynebacterium diphtheriae dtxR from Brevibacterium lactofermentum," *J. Bacteriol.,* 177(2):465-467 (1995)
M13774		Prephenate dehydratase	Follettie, M.T. et al. "Molecular cloning and nucleotide sequence of the Corynebacterium glutamicum pheA gene," *J. Bacteriol.,* 167:695-702 (1986)
M16175	5S rRNA		Park, Y-H. et al. "Phylogenetic analysis of the coryneform bacteria by 56 rRNA sequences," *J. Bacteriol.,* 169:1801-1806 (1987)
M16663	trpE	Anthranilate synthase, 5' end	Sano, K. et al. "Structure and function of the trp operon control regions of Brevibacterium lactofermentum, a glutamic-acid-producing bacterium," *Gene,* 52:191-200 (1987)
M16664	trpA	Tryptophan synthase, 3'end	Sano, K. et al. "Structure and function of the trp operon control regions of Brevibacterium lactofermentum, a glutamic-acid-producing bacterium," *Gene,* 52:191-200 (1987)
M25819		Phosphoenolpyruvate carboxylase	O'Regan, M. et al. "Cloning and nucleotide sequence of the Phosphoenolpyruvate carboxylase-coding gene of Corynebacterium glutamicum ATCC13032," *Gene,* 77(2):237-251 (1989)
M85106		23S rRNA gene insertion sequence	Roller, C. et al. "Gram-positive bacteria with a high DNA G+C content are characterized by a common insertion within their 23S rRNA genes," *J. Gen. Microbiol.,* 138:1167-1175 (1992)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
M85107, M85108		23S rRNA gene insertion sequence	Roller, C. et al. "Gram-positive bacteria with a high DNA G+C content are characterized by a common insertion within their 23S rRNA genes," *J. Gen. Microbiol.*, 138:1167-1175 (1992)
M89931	aecD; brnQ; yhbw	Beta C-S lyase; branched-chain amino acid uptake carrier; hypothetical protein yhbw	Rossol, I. et al. "The Corynebacterium glutamicum aecD gene encodes a C-S lyase with alpha, beta-elimination activity that degrades aminoethylcysteine," *J. Bacteriol.*, 174(9):2968-2977 (1992); Tauch, A. et al. "Isoleucine uptake in Corynebacterium glutamicum ATCC 13032 is directed by the brnQ gene product," *Arch. Microbiol.*, 169(4):303-312 (1998)
S59299	trp	Leader gene (promoter)	Herry, D.M. et al. "Cloning of the trp gene cluster from a tryptophan-hyperproducing strain of Corynebacterium glutamicum: identification of a mutation in the trp leader sequence," *Appl. Environ. Microbiol.*, 59(3):791-799 (1993)
U11545	trpD	Anthranilate phosphoribosyltransferase	O'Gara, J.P. and Dunican, L.K. (1994) Complete nucleotide sequence of the Corynebacterium glutamicum ATCC 21850 tpD gene." Thesis, Microbiology Department, University College Galway, Ireland.
U13922	cglIM; cglIR; clgIIR	Putative type II 5-cytosoine methyltransferase; putative type II restriction endonuclease; putative type I or type III restriction endonuclease	Schafer, A. et al. "Cloning and characterization of a DNA region encoding a stress-sensitive restriction system from Corynebacterium glutamicum ATCC 13032 and analysis of its role in intergeneric conjugation with Escherichia coli," *J. Bacteriol.*, 176(23):7309-7319 (1994); Schafer, A. et al. "The Corynebacterium glutamicum cglIM gene encoding a 5-cytosine in an McrBC-deficient Escherichia coli strain," *Gene,* 203(2):95-101 (1997)
U14965	recA		
U31224	ppx		Ankri, S. et al. "Mutations in the Corynebacterium glutamicumproline biosynthetic pathway: A natural bypass of the proA step," *J. Bacteriol.*, 178(15):4412-4419 (1996)
U31225	proC	L-proline: NADP+ 5-oxidoreductase	Ankri, S. et al. "Mutations in the Corynebacterium glutamicumproline biosynthetic pathway: A natural bypass of the proA step," *J. Bacteriol.*, 178(15):4412-4419 (1996)
U31230	obg; proB; unkdh	?;gamma glutamyl kinase;similar to D-isomer specific 2-hydroxyacid dehydrogenases	Ankri, S. et al. "Mutations in the Corynebacterium glutamicumproline biosynthetic pathway: A natural bypass of the proA step," *J. Bacteriol.*, 178(15):4412-4419 (1996)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
U31281	bioB	Biotin synthase	Serebriiskii, I.G., "Two new members of the bio B superfamily: Cloning, sequencing and expression of bio B genes of Methylobacillus flagellatum and Corynebacterium glutamicum," *Gene,* 175:15-22 (1996)
U35023	thtR; accBC	Thiosulfate sulfurtransferase; acyl CoA carboxylase	Jager, W. et al. "A Corynebacterium glutamicum gene encoding a two-domain protein similar to biotin carboxylases and biotin-carboxyl-carrier proteins," *Arch. Microbiol.,* 166(2);76-82 (1996)
U43535	cmr	Multidrug resistance protein	Jager, W. et al. "A Corynebacterium glutamicum gene conferring multidrug resistance in the heterologous host Escherichia coli," *J. Bacteriol.,* 179(7):2449-2451 (1997)
U43536	clpB	Heat shock ATP-binding protein	
U53587	aphA-3	3'5''-aminoglycoside phosphotransferase	
U89648		Corynebacterium glutamicum unidentified sequence involved in histidine biosynthesis, partial sequence	
X04960	trpA; trpB; trpC; trpD; trpE; trpG; trpL	Tryptophan operon	Matsui, K. et al. "Complete nucleotide and deduced amino acid sequences of the Brevibacterium lactofermentum tryptophan operon," *Nucleic Acids Res.,* 14(24):10113-10114 (1986)
X07563	lys A	DAP decarboxylase (meso-diaminopimelate decarboxylase, EC 4.1.1.20)	Yeh, P. et al. "Nucleic sequence of the lysA gene of Corynebacterium glutamicum and possible mechanisms for modulation of its expression," *Mol. Gen. Genet.,* 212(1):112-119 (1988)
X14234	EC 4.1.1.31	Phosphoenolpyruvate carboxylase	Eikmanns, B.J. et al. "The Phosphoenolpyruvate carboxylase gene of Corynebacterium glutamicum: Molecular cloning, nucleotide sequence, and expression," *Mol. Gen. Genet.,* 218(2):330-339 (1989); Lepiniec, L. et al. "Sorghum Phosphoenolpyruvate carboxylase gene family: structure, function and molecular evolution," *Plant. Mol. Biol.,* 21 (3):487-502 (1993)
X17313	fda	Fructose-bisphosphate aldolase	Von der Osten, C.H. et al. "Molecular cloning, nucleotide sequence and fine-structural analysis of the Corynebacterium glutamicum fda gene: structural comparison of C. glutamicum fructose-1, 6-biphosphate aldolase to class I and class II aldolases," *Mol. Microbiol.,*
X53993	dapA	L-2, 3-dihydrodipicolinate synthetase (EC 4.2.1.52)	Bonnassie, S. et al. "Nucleic sequence of the dapA gene from Corynebacterium glutamicum," *Nucleic Acids Res.,* 18(21):6421 (1990)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X54223		AttB-related site	Cianciotto, N. et al. "DNA sequence homology between att B-related sites of Corynebacterium diphtheriae, Corynebacterium ulcerans, Corynebacterium glutamicum , and the attP site of lambdacorynephage," *FEMS. Microbiol, Lett.,* 66:299-302 (1990)
X54740	argS; lysA	Arginyl-tRNA synthetase; Diaminopimelate decarboxylase	Marcel, T. et al. "Nucleotide sequence and organization of the upstream region of the Corynebacterium glutamicum lysA gene," *Mol. Microbiol.,* 4(11):1819-1830 (1990)
X55994	trpL; trpE	Putative leader peptide; anthranilate synthase component 1	Heery, D.M. et al. "Nucleotide sequence of the Corynebacterium glutamicum trpE gene," *Nucleic Acids Res.,* 18(23):7138 (1990)
X56037	thrC	Threonine synthase	Han, K.S. et al. "The molecular structure of the Corynebacterium glutamicum threonine synthase gene," *Mol. Microbiol.,* 4(10):1693-1702 (1990)
X56075	attB-related site	Attachment site	Cianciotto, N. et al. "DNA sequence homology between att B-related sites of Corynebacterium diphtheriae, Corynebacterium ulcerans, Corynebacterium glutamicum , and the attP site of lambdacorynephage," *FEMS. Microbiol, Lett.,* 66:299-302 (1990)
X57226	lysC-alpha; lysC-beta; asd	Aspartokinase-alpha subunit; Aspartokinase-beta subunit; aspartate beta semialdehyde dehydrogenase	Kalinowski, J. et al. "Genetic and biochemical analysis of the Aspartokinase from Corynebacterium glutamicum," *Mol. Microbiol.,* 5(5):1197-1204 (1991); Kalinowski, J. et al. "Aspartokinase genes lysC alpha and lysC beta overlap and are adjacent to the aspertate beta-semialdehyde dehydrogenase gene asd in Corynebacterium glutamicum," *Mol. Gen. Genet.,* 224(3):317-324 (1990)
X59403	gap;pgk; tpi	Glyceraldehyde-3-phosphate; phosphoglycerate kinase; triosephosphate isomerase	Eikmanns, B.J. "Identification, sequence analysis, and expression of a Corynebacterium glutamicum gene cluster encoding the three glycolytic enzymes glyceraldehyde-3-phosphate dehydrogenase, 3-phosphoglycerate kinase, and triosephosphate isomeras," *J. Bacteriol.,* 174(19):6076-6086 (1992)
X59404	gdh	Glutamate dehydrogenase	Bormann, E.R. et al. "Molecular analysis of the Corynebacterium glutamicum gdh gene encoding glutamate dehydrogenase," *Mol. Microbiol.,* 6(3):317-326 (1992)
X60312	lysI	L-lysine permease	Seep-Feldhaus, A.H. et al. "Molecular analysis of the Corynebacterium glutamicum lysI gene involved in lysine uptake," *Mol. Microbiol.,* 5(12):2995-3005 (1991)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X66078	cop1	Ps1 protein	Joliff, G. et al. "Cloning and nucleotide sequence of the csp1 gene encoding PS1, one of the two major secreted proteins of Corynebacterium glutamicum: The deduced N-terminal region of PS1 is similar to the Mycobacterium antigen 85 complex," *Mol. Microbiol.,* 6(16):2349-2362 (1992)
X66112	glt	Citrate synthase	Eikmanns, B.J. et al. "Cloning sequence, expression and transcriptional analysis of the Corynebacterium glutamicum gltA gene encoding citrate synthase," *Microbiol.,* 140:1817-1828 (1994)
X67737	dapB	Dihydrodipicolinate reductase	
X69103	csp2	Surface layer protein PS2	Peyret, J.L. et al. "Characterization of the cspB gene encoding PS2, an ordered surface-layer protein in Corynebacterium glutamicum," *Mol. Microbiol.,* 9(1):97-109 (1993)
X69104		IS3 related insertion element	Bonamy, C. et al. "Identification of IS1206, a Corynebacterium glutamicum IS3-related insertion sequence and phylogenetic analysis," *Mol. Microbiol.,* 14(3):571-581 (1994)
X70959	leuA	Isopropylmalate synthase	Patek, M. et al. "Leucine synthesis in Corynebacterium glutamicum: enzyme activities, structure of leuA, and effect of leuA inactivation on lysine synthesis," *Appl. Environ. Microbiol.,* 60(1):133-140 (1994)
X71489	icd	Isocitrate dehydrogenase (NADP+)	Eikmanns, B.J. et al. "Cloning sequence analysis, expression, and inactivation of the Corynebacterium glutamicum icd gene encoding isocitrate dehydrogenase and biochemical characterization of the enzyme," *J. Bacteriol.,* 177(3):774-782 (1995)
X72855	GDHA	Glutamate dehydrogenase (NADP+)	
X75083, X70584	mtrA	5-methyltryptophan resistance	Heery, D.M. et al. "A sequence from a tryptophan-hyperproducing strain of Corynebacterium glutamicum encoding resistance to 5-methyltryptophan," *Biochem. Biophys. Res. Commun.,* 201(3):1255-1262 (1994)
X75085	recA		Fitzpatrick, R. et al. "Construction and characterization of recA mutant strains of Corynebacterium glutamicum and Brevibacterium lactofermentum," *Appl. Microbiol. Biotechnol.,* 42(4):575-580 (1994)
X75504	aceA; thiX	Partial Isocitrate lyase; ?	Reinscheid, D.J. et al. "Characterization of the isocitrate lyase gene from Corynebacterium glutamicum and biochemical analysis of the enzyme," *J. Bacteriol.,* 176(12):3474-3483 (1994)
X76875		ATPase beta-subunit	Ludwig, W. et al. "Phylogenetic relationships of bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit genes," *Antonie Van Leeuwenhoek,* 64:285-305 (1993)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X77034	tuf	Elongation factor Tu	Ludwig, W. et al. "Phylogenetic relationships of bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit genes," *Antonie Van Leeuwenhoek,* 64:285-305 (1993)
X77384	recA		Billman-Jacobe, H. "Nucleotide sequence of a recA gene from Corynebacterium glutamicum," *DNA Seq.,* 4(6):403-404 (1994)
X78491	aceB	Malate synthase	Reinscheid, D.J. et al. "Malate synthase from Corynebacterium glutamicum pta-ack operon encoding phosphotransacetylase: sequence analysis," *Microbiology,* 140:3099-3108 (1994)
X80629	16S rDNA	16S ribosomal RNA	Rainey, F.A. et al. "Phylogenetic analysis of the genera Rhodococcus and Norcardia and evidence for the evolutionary origin of the genus Norcardia from within the radiation of Rhodococcus species," *Microbiol.,* 141:523-528 (1995)
X81191	gluA; gluB; gluC; gluD	Glutamate uptake system	Kronemeyer, W. et al. "Structure of the gluABCD cluster encoding the glutamate uptake system of Corynebacterium glutamicum," *J. Bacteriol.*, 177(5):1152-1158 (1995)
X81379	dapE	Succinyldiaminopimelate desuccinylase	Wehrmann, A. et al. "Analysis of different DNA fragments of Corynebacterium glutamicum complementing dapE of Escherichia coli," *Microbiology*, 40:3349-56 (1994)
X82061	16S rDNA	16S ribosomal RNA	Ruimy, R. et al. "Phylogeny of the genus Corynebacterium deduced from analyses of small-subunit ribosomal DNA sequences," *Int. J. Syst. Bacteriol.,* 45(4):740-746 (1995)
X82928	asd; lysC	Aspartate-semialdehyde dehydrogenase; ?	Serebrijski, I. et al. "Multicopy suppression by asd gene and osmotic stress-dependent complementation by heterologous proA in proA mutants," *J. Bacteriol.,* 177(24):7255-7260 (1995)
X82929	proA	Gamma-glutamyl phosphate reductase	Serebrijski, I. et al. "Multicopy suppression by asd gene and osmotic stress-dependent complementation by heterologous proA in proA mutants," *J. Bacteriol.,* 177(24):7255-7260 (1995)
X84257	16S rDNA	16S ribosomal RNA	Pascual, C. et al. "Phylogenetic analysis of the genus Corynebacterium based on 16S rRNA gene sequences," *Int. J. Syst. Bacteriol.,* 45(4):724-728 (1995)
X85965	aroP; dapE	Aromatic amino acid permease; ?	Wehrmann, A. et al. "Functional analysis of sequences adjacent to dapE of Corynebacterium glutamicumproline reveals the presence of aroP, which encodes the aromatic amino acid transporter," *J. Bacteriol.,* 177(20):5991-5993 (1995)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X86157	argB; argC; argD; argF; argJ	Acetylglutamate kinase; N-acetyl-gamma-glutamyl-phosphate reductase; acetylornithine aminotransferase; ornithine carbamoyltransferase; glutamate N-acetyltransferase	Sakanyan, V. et al. "Genes and enzymes of the acetyl cycle of arginine biosynthesis in Corynebacterium glutamicum: enzyme evolution in the early steps of the arginine pathway," *Microbiology,* 142:99-108 (1996)
X89084	pta; ackA	Phosphate acetyltransferase; acetate kinase	Reinscheid, D.J. et al. "Cloning, sequence analysis, expression and inactivation of the Corynebacterium glutamicum pta-ack operon encoding phosphotransacetylase and acetate kinase," *Microbiology,* 145:503-513 (1999)
X89850	attB	Attachment site	Le Marrec, C. et al. "Genetic characterization of site-specific integration functions of phi AAU2 infecting "Arthrobacter aureus C70," *J. Bacteriol.,* 178(7):1996-2004 (1996)
X90356		Promoter fragment F1	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology,* 142:1297-1309 (1996)
X90357		Promoter fragment F2	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology,* 142:1297-1309 (1996)
X90358		Promoter fragment F10	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology,* 142:1297-1309 (1996)
X90359		Promoter fragment F13	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology,* 142:1297-1309 (1996)
X90360		Promoter fragment F22	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology,* 142:1297-1309 (1996)
X90361		Promoter fragment F34	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology,* 142:1297-1309 (1996)
X90362		Promoter fragment F37	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology,* 142:1297-1309 (1996)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X90363		Promoter fragment F45	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology,* 142:1297-1309 (1996)
X90364		Promoter fragment F64	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology,* 142:1297-1309 (1996)
X90365		Promoter fragment F75	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology,* 142:1297-1309 (1996)
X90366		Promoter fragment PF101	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology,* 142:1297-1309 (1996)
X90367		Promoter fragment PF104	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology,* 142:1297-1309 (1996)
X90368		Promoter fragment PF109	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology,* 142:1297-1309 (1996)
X93513	amt	Ammonium transport system	Siewe, R.M. et al. "Functional and genetic characterization of the (methyl) ammonium uptake carrier of Corynebacterium glutamicum," *J. Biol. Chem.,* 271(10):5398-5403 (1996)
X93514	betP	Glycine betaine transport system	Peter, H. et al. "Isolation, characterization, and expression of the Corynebacterium glutamicum betP gene, encoding the transport system for the compatible solute glycine betaine," *J. Bacteriol.,* 178(17):5229-5234 (1996)
X95649	orf4		Patek, M. et al. "Identification and transcriptional analysis of the dapB-ORF2-dapA-ORF4 operon of Corynebacterium glutamicum, encoding two enzymes involved in L-lysine synthesis," *Biotechnol. Lett.,* 19:1113-1117 (1997)
X96471	lysE; lysG	Lysine exporter protein; Lysine export regulator protein	Vrljic, M. et al. "A new type of transporter with a new type of cellular function: L-lysine export from Corynebacterium glutamicum," *Mol. Microbiol.,* 22(5):815-826 (1996)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X96580	panB; panC; xylB	3-methyl-2-oxobutanoate hydroxymethyltransferase; pantoate-beta-alanine ligase; xylulokinase	Sahm, H. et al. "D-pantothenate synthesis in Corynebacterium glutamicum and use of panBC and genes encoding L-valine synthesis for D-pantothenate overproduction," *Appl. Environ. Microbiol.*, 65(5):1973-1979 (1999)
X96962		Insertion sequence IS1207 and transposase	
X99289		Elongation factor P	Ramos, A. et al. "Cloning, sequencing and expression of the gene encoding elongation factor P in the amino-acid producer Brevibacterium lactofermentum (Corynebacterium glutamicum ATCC 13869)," *Gene,* 198:217-222 (1997)
Y00140	thrB	Homoserine kinase	Mateos, L.M. et al. "Nucleotide sequence of the homoserine kinase (thrB) gene of the Brevibacterium lactofermentum," *Nucleic Acids Res.*, 15(9):3922 (1987)
Y00151	ddh	Meso-diaminopimelate D-dehydrogenase (EC 1.4.1.16)	Ishino, S. et al. "Nucleotide sequence of the meso-diaminopimelate D-dehydrogenase gene from Corynebacterium glutamicum," *Nucleic Acids Res.*, 15(9):3917 (1987)
Y00476	thrA	Homoserine dehydrogenase	Mateos, L.M. et al. "Nucleotide sequence of the homoserine dehydrogenase (thrA) gene of the Brevibacterium lactofermentum," *Nucleic Acids Res.*, 15(24):10598 (1987)
Y00546	hom; thrB	Homoserine dehydrogenase; homoserine kinase	Peoples, O.P. et al. "Nucleotide sequence and fine structural analysis of the Corynebacterium glutamicum hom-thrB operon," *Mol. Microbiol.*, 2(1):63-72 (1988)
Y08964	murC; ftsQ/divD; ftsZ	UPD-N-acetylmuramate-alanine ligase; division initiation protein or cell division protein; cell division protein	Honrubia, M.P. et al. "Identification, characterization, and chromosomal organization of the ftsZ gene from Brevibacterium lactofermentum," *Mol. Gen. Genet.*, 259(1):97-104 (1998)
Y09163	putP	High affinity proline transport system	Peter, H. et al. "Isolation of the putP gene of Corynebacterium glutamicumproline and characterization of a low-affinity uptake system for compatible solutes," *Arch. Microbiol.*, 168(2):143-151 (1997)
Y09548	pyc	Pyruvate carboxylase	Peters-Wendisch, P.G. et al. "Pyruvate carboxylase from Corynebacterium glutamicum: characterization, expression and inactivation of the pyc gene," *Microbiology,* 144:915-927 (1998)
Y09578	leuB	3-isopropylmalate dehydrogenase	Patek, M. et al. "Analysis of the leuB gene from Corynebacterium glutamicum," *Appl. Microbiol. Biotechnol.*, 50(1):42-47 (1998)
Y12472		Attachment site bacteriophage Phi-16	Moreau, S. et al. "Site-specific integration of corynephage Phi-16: The construction of an integration vector," *Microbiol.*, 145:539-548 (1999)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
Y12537	proP	Proline/ectoine uptake system protein	Peter, H. et al. "Corynebacterium glutamicum is equipped with four secondary carriers for compatible solutes: Identification, sequencing, and characterization of the proline/ectoine uptake system, ProP, and the ectoine/proline/glycine betaine carrier, EctP," *J. Bacteriol.*, 180(22):6005-6012 (1998)
Y13221	glnA	Glutamine synthetase I	Jakoby, M. et al. "Isolation of Corynebacterium glutamicum glnA gene encoding glutamine synthetase I," *FEMS Microbiol. Lett.*, 154(1):81-88 (1997)
Y16642	lpd	Dihydrolipoamide dehydrogenase	
Y18059		Attachment site Corynephage 304L	Moreau, S. et al. "Analysis of the integration functions of φ304L: An integrase module among corynephages," *Virology*, 255(1):150-159 (1999)
Z21501	argS; lysA	Arginyl-tRNA synthetase; diaminopimelate decarboxylase (partial)	Oguiza, J.A. et al. "A gene encoding arginyl-tRNA synthetase is located in the upstream region of the lysA gene in Brevibacterium lactofermentum: Regulation of argS-lysA cluster expression by arginine," *J. Bacteriol.*,175(22):7356-7362 (1993)
Z21502	dapA; dapB	Dihydrodipicolinate synthase; dihydrodipicolinate reductase	Pisabarro, A. et al. "A cluster of three genes (dapA, orf2, and dapB) of Brevibacterium lactofermentum encodes dihydrodipicolinate reductase, and a third polypeptide of unknown function," *J. Bacteriol.*, 175(9):2743-2749 (1993)
Z29563	thrC	Threonine synthase	Malumbres, M. et al. "Analysis and expression of the thrC gene of the encoded threonine synthase," *Appl. Environ. Microbiol.*, 60(7)2209-2219 (1994)
Z46753	16S rDNA	Gene for 16S ribosomal RNA	
Z49822	sigA	SigA sigma factor	Oguiza, J.A. et al "Multiple sigma factor genes in Brevibacterium lactofermentum: Characterization of sigA and sigB," *J. Bacteriol.*, 178(2):550-553 (1996)
Z49823	galE; dtxR	Catalytic activity UDP-galactose 4-epimerase; diphtheria toxin regulatory protein	Oguiza, J.A. et al "The galE gene encoding the UDP-galactose 4-epimerase of Brevibacterium lactofermentum is coupled transcriptionally to the dmdR gene," *Gene*, 177:103-107 (1996)
Z49824	orf1; sigB	?; SigB sigma factor	Oguiza, J.A. et al "Multiple sigma factor genes in Brevibacterium lactofermentum: Characterization of sigA and sigB," *J. Bacteriol.*, 178(2):550-553 (1996)
Z66534		Transposase	Correia, A. et al. "Cloning and characterization of an IS-like element present in the genome of Brevibacterium lactofermentum ATCC 13869," *Gene*, 170(1):91-94 (1996)

[1] A sequence for this gene was published in the indicated reference. However, the sequence obtained by the inventors of the present application is significantly longer than the published version. It is believed that the published version relied on an incorrect start codon, and thus represents only a fragment of the actual coding region.

TABLE 3: Corynebacterium and Brevibacterium Strains Which May be Used in the Practice of the Invention

Genus	species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NCTC	DSMZ
Brevibacterium	ammoniagenes	21054							
Brevibacterium	ammoniagenes	19350							
Brevibacterium	ammoniagenes	19351							
Brevibacterium	ammoniagenes	19352							
Brevibacterium	ammoniagenes	19353							
Brevibacterium	ammoniagenes	19354							
Brevibacterium	ammoniagenes	19355							
Brevibacterium	ammoniagenes	19356							
Brevibacterium	ammoniagenes	21055							
Brevibacterium	ammoniagenes	21077							
Brevibacterium	ammoniagenes	21553							
Brevibacterium	ammoniagenes	21580							
Brevibacterium	ammoniagenes	39101							
Brevibacterium	butanicum	21196							
Brevibacterium	divaricatum	21792	P928						
Brevibacterium	flavum	21474							
Brevibacterium	flavum	21129							
Brevibacterium	flavum	21518							
Brevibacterium	flavum			B11474					
Brevibacterium	flavum			B11472					
Brevibacterium	flavum	21127							
Brevibacterium	flavum	21128							
Brevibacterium	flavum	21427							
Brevibacterium	flavum	21475							
Brevibacterium	flavum	21517							
Brevibacterium	flavum	21528							
Brevibacterium	flavum	21529							

Brevibacterium	flavum			B11477					
Brevibacterium	flavum			B11478					
Brevibacterium	flavum	21127							
Brevibacterium	flavum			B11474					
Brevibacterium	healii	15527							
Brevibacterium	ketoglutamicum	21004							
Brevibacterium	ketoglutamicum	21089							
Brevibacterium	ketosoreductum	21914							
Brevibacterium	lactofermentum				70				
Brevibacterium	lactofermentum				74				
Brevibacterium	lactofermentum				77				
Brevibacterium	lactofermentum	21798							
Brevibacterium	lactofermentum	21799							
Brevibacterium	lactofermentum	21800							
Brevibacterium	lactofermentum	21801							
Brevibacterium	lactofermentum			B11470					
Brevibacterium	lactofermentum			B11471					
Brevibacterium	lactofermentum	21086							
Brevibacterium	lactofermentum	21420							
Brevibacterium	lactofermentum	21086							
Brevibacterium	lactofermentum	31269							
Brevibacterium	linens	9174							
Brevibacterium	linens	19391							
Brevibacterium	linens	8377							
Brevibacterium	paraffinolyticum					11160			
Brevibacterium	spec.						717.73		
Brevibacterium	spec.						717.73		
Brevibacterium	spec.	14604							
Brevibacterium	spec.	21860							
Brevibacterium	spec.	21864							
Brevibacterium	spec.	21865							

Brevibacterium	spec.	21866							
Brevibacterium	spec.	19240							
Corynebacterium	acetoacidophilum	21476							
Corynebacterium	acetoacidophilum	13870							
Corynebacterium	acetoglutamicum			B11473					
Corynebacterium	acetoglutamicum			B11475					
Corynebacterium	acetoglutamicum	15806							
Corynebacterium	acetoglutamicum	21491							
Corynebacterium	acetoglutamicum	31270							
Corynebacterium	acetophilum			B3671					
Corynebacterium	ammoniagenes	6872						2399	
Corynebacterium	ammoniagenes	15511							
Corynebacterium	fujiokense	21496							
Corynebacterium	glutamicum	14067							
Corynebacterium	glutamicum	39137							
Corynebacterium	glutamicum	21254							
Corynebacterium	glutamicum	21255							
Corynebacterium	glutamicum	31830							
Corynebacterium	glutamicum	13032							
Corynebacterium	glutamicum	14305							
Corynebacterium	glutamicum	15455							
Corynebacterium	glutamicum	13058							
Corynebacterium	glutamicum	13059							
Corynebacterium	glutamicum	13060							
Corynebacterium	glutamicum	21492							
Corynebacterium	glutamicum	21513							
Corynebacterium	glutamicum	21526							
Corynebacterium	glutamicum	21543							
Corynebacterium	glutamicum	13287							
Corynebacterium	glutamicum	21851							
Corynebacterium	glutamicum	21253							

Corynebacterium	glutamicum	21514							
Corynebacterium	glutamicum	21516							
Corynebacterium	glutamicum	21299							
Corynebacterium	glutamicum	21300							
Corynebacterium	glutamicum	39684							
Corynebacterium	glutamicum	21488							
Corynebacterium	glutamicum	21649							
Corynebacterium	glutamicum	21650							
Corynebacterium	glutamicum	19223							
Corynebacterium	glutamicum	13869							
Corynebacterium	glutamicum	21157							
Corynebacterium	glutamicum	21158							
Corynebacterium	glutamicum	21159							
Corynebacterium	glutamicum	21355							
Corynebacterium	glutamicum	31808							
Corynebacterium	glutamicum	21674							
Corynebacterium	glutamicum	21562							
Corynebacterium	glutamicum	21563							
Corynebacterium	glutamicum	21564							
Corynebacterium	glutamicum	21565							
Corynebacterium	glutamicum	21566							
Corynebacterium	glutamicum	21567							
Corynebacterium	glutamicum	21568							
Corynebacterium	glutamicum	21569							
Corynebacterium	glutamicum	21570							
Corynebacterium	glutamicum	21571							
Corynebacterium	glutamicum	21572							
Corynebacterium	glutamicum	21573							
Corynebacterium	glutamicum	21579							
Corynebacterium	glutamicum	19049							
Corynebacterium	glutamicum	19050							

Corynebacterium	glutamicum	19051							
Corynebacterium	glutamicum	19052							
Corynebacterium	glutamicum	19053							
Corynebacterium	glutamicum	19054							
Corynebacterium	glutamicum	19055							
Corynebacterium	glutamicum	19056							
Corynebacterium	glutamicum	19057							
Corynebacterium	glutamicum	19058							
Corynebacterium	glutamicum	19059							
Corynebacterium	glutamicum	19060							
Corynebacterium	glutamicum	19185							
Corynebacterium	glutamicum	13286							
Corynebacterium	glutamicum	21515							
Corynebacterium	glutamicum	21527							
Corynebacterium	glutamicum	21544							
Corynebacterium	glutamicum	21492							
Corynebacterium	glutamicum			B8183					
Corynebacterium	glutamicum			B8182					
Corynebacterium	glutamicum			B12416					
Corynebacterium	glutamicum			B12417					
Corynebacterium	glutamicum			B12418					
Corynebacterium	glutamicum			B11476					
Corynebacterium	glutamicum	21608							
Corynebacterium	lilium		P973						
Corynebacterium	nitrilophilus	21419				11594			
Corynebacterium	spec.		P4445						
Corynebacterium	spec.		P4446						
Corynebacterium	spec.	31088							
Corynebacterium	spec.	31089							
Corynebacterium	spec.	31090							
Corynebacterium	spec.	31090							

Corynebacterium	spec.	31090							
Corynebacterium	spec.	15954							20145
Corynebacterium	spec.	21857							
Corynebacterium	spec.	21862							
Corynebacterium	spec.	21863							

ATCC: American Type Culture Collection, Rockville, MD, USA

FERM: Fermentation Research Institute, Chiba, Japan

NRRL: ARS Culture Collection, Northern Regional Research Laboratory, Peoria, IL, USA

CECT: Coleccion Espanola de Cultivos Tipo, Valencia, Spain

NCIMB: National Collection of Industrial and Marine Bacteria Ltd., Aberdeen, UK

CBS: Centraalbureau voor Schimmelcultures, Baarn, NL

NCTC: National Collection of Type Cultures, London, UK

DSMZ: Deutsche Sammlung von Mikroorganismen und Zellkulturen, Braunschweig, Germany

For reference see Sugawara, H. et al. (1993) World directory of collections of cultures of microorganisms: Bacteria, fungi and yeasts (4th edn), World federation for culture collections world data center on microorganisms, Saimata, Japen.

TABLE 4: ALIGNMENT RESULTS

ID #	length (NT)	Genbank Hit	Length	Accession	Name of Genbank Hit	Source of Genbank Hit	% homology (GAP)	Date of Deposit
rxa00003	864	GB_BA2.MPAE000013	10328	AE000013	Mycoplasma pneumoniae section 13 of 63 of the complete genome	Mycoplasma pneumoniae	37,409	18-Nov-96
		GB_BA2 MPAE000013	10328	AE000013	Mycoplasma pneumoniae section 13 of 63 of the complete genome	Mycoplasma pneumoniae	36,768	18-Nov-96
rxa00008	615	GB_HTG2 AC007356	185382	AC007356	Drosophila melanogaster chromosome 2 clone BACR24H09 (D595) RPCI-98 24.H 9 map 49A-49B strain y, cn bw sp, *** SEQUENCING IN PROGRESS ***, 13 unordered pieces.	Drosophila melanogaster	39,203	2-Aug-99
		GB_HTG2 AC007356	185382	AC007356	Drosophila melanogaster chromosome 2 clone BACR24H09 (D595) RPCI-98 24 H 9 map 49A-49B strain y, cn bw sp, *** SEQUENCING IN PROGRESS***, 13 unordered pieces	Drosophila melanogaster	39,203	2-Aug-99
		GB_EST36 AV194293	380	AV194293	AV194293 Yuji Kohara unpublished cDNA Strain N2 hermaphrodite embryo Caenorhabditis elegans cDNA clone yk627f12 5', mRNA sequence	Caenorhabditis elegans	38,947	22-Jul-99
rxa00015	432	GB_GSS4 AQ684785	671	AQ684785	HS_5481_B2_H06_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=1057 Col=12 Row=P, genomic survey sequence.	Homo sapiens	41,388	28-Jun-99
		GB_PR2.HS217O16	87552	AL031771	Human DNA sequence from clone 217O16 on chromosome 6q24 Contains GSS, complete sequence	Homo sapiens	37,471	23-Nov-99
		GB_EST15:AA528550	335	AA528550	nf01f01 s1 NCI_CGAP_Kid1 Homo sapiens cDNA clone IMAGE 912505, mRNA sequence	Homo sapiens	40,789	19-Aug-97
rxa00018	1422	GB_VI·HS5MCP	4320	M25411	Human cytomegalovirus major capsid protein (MCP) gene, complete cds	human herpesvirus 5	38,231	30-OCT-1994
		GB_BA2 AE001270	12448	AE001270	Treponema pallidum section 86 of 87 of the complete genome	Treponema pallidum	37,130	16-Jul-98
		GB_IN1 LMFL2385	22004	AL034389	Leishmania major Friedlin cosmid L2385, complete sequence	Leishmania major	37,518	15-MAR-1999
rxa00020	903	GB_PR4.AC006960	179757	AC006960	Homo sapiens clone UWGC djs58 from 7p14-15, complete sequence	Homo sapiens	36,618	05-MAR-1999
		GB_HTG3 AC008266	178972	AC008266	Homo sapiens clone DJ1145A24, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces	Homo sapiens	35,419	21-Aug-99
		GB_HTG3 AC008266	178972	AC008266	Homo sapiens clone DJ1145A24, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces	Homo sapiens	35,419	21-Aug-99
rxa00021	1896	GB_EST15·AA496164	429	AA496164	zu67e09 r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE 743080 5', mRNA sequence	Homo sapiens	35,526	11-Aug-97
		GB_EST30·AI660039	443	AI660039	we65d06 x1 Soares_thymus_NHFTh Homo sapiens cDNA clone IMAGE 2345963 3', mRNA sequence	Homo sapiens	42,574	10-MAY-1999
		GB_EST37 AI953059	522	AI953059	wq49g06 x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE 2474650 3', mRNA sequence	Homo sapiens	39,198	6-Sep-99
rxa00022	1824	GB_EST15 AA496164	429	AA496164	zu67e09 r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE 743080 5', mRNA sequence	Homo sapiens	41,141	11-Aug-97
		GB_PR3 AF022141	43473	AF022141	Homo sapiens chromosome 21q22 2 cosmid Q13F10, complete sequence	Homo sapiens	37,262	21-Jan-98
		GB_EST18.AA678649	538	AA678649	ah07c05 s1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE 1155944 3' similar to gb X16869 ELONGATION FACTOR 1-ALPHA 1 (HUMAN),, mRNA sequence	Homo sapiens	38,104	02-DEC-1997
rxa00025	1560	GB_PL2·AC009978	97554	AC009978	Genomic sequence for Arabidopsis thaliana BAC T23E18 from chromosome I, complete sequence	Arabidopsis thaliana	34,173	15-Nov-99
		GB_HTG2.AC005958	216706	AC005958	Homo sapiens, *** SEQUENCING IN PROGRESS ***, 40 unordered pieces	Homo sapiens	35,374	11-Nov-98
		GB_HTG2·AC005958	216706	AC005958	Homo sapiens, *** SEQUENCING IN PROGRESS ***, 40 unordered pieces	Homo sapiens	35,374	11-Nov-98
rxa00027	489	GB_PR3 HSDJ247C2	98358	AL049713	Human DNA sequence from clone 247C2 on chromosome 11p13, complete sequence	Homo sapiens	33,056	23-Nov-99
		GB_PR3 HSDJ247C2	98358	AL049713	Human DNA sequence from clone 247C2 on chromosome 11p13, complete sequence	Homo sapiens	37,988	23-Nov-99
rxa00028								
rxa00031	525	GB_PL1 SPBC725	37949	AL034352	S.pombe chromosome II cosmid c725	Schizosaccharomyces pombe	36,084	29-MAR-1999
		GB_EST5 N22565	435	N22565	yw30f05 s1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE·253761 3', mRNA sequence	Homo sapiens	41,570	20-DEC-1995
		GB_EST21 AA993042	464	AA993042	ot92f07 s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE 1624261 3', mRNA sequence	Homo sapiens	41,499	27-Aug-98
rxa00049	810	GB_HTG2 HSJ749H19	253387	AL117380	Homo sapiens chromosome 20 clone RP4-749H19 map q13 11-13 33, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Homo sapiens	37,132	03-DEC-1999

TABLE 4: ALIGNMENT RESULTS

		GB_HTG2:HSJ749H19	253387	AL117380	Homo sapiens chromosome 20 clone RP4-749H19 map q13.11-13.33, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	37,132	03-DEC-1999
		GB_HTG4 AC010137	155817	AC010137	Homo sapiens clone NH0169D01, *** SEQUENCING IN PROGRESS ***, 4 unordered pieces	Homo sapiens	40,052	17-OCT-1999
rxa00052	834	GB_EST37:AI962012	382	AI962012	wt41e06 x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2510050 3' similar to SW ALC2_HUMAN P01877 IG ALPHA-2 CHAIN C REGION. ;, mRNA sequence	Homo sapiens	40,486	20-Aug-99
		GB_GSS13 AQ454792	450	AQ454792	HS_5195_B2_H04_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=771 Col=8 Row=P, genomic survey sequence.	Homo sapiens	40,991	21-Apr-99
		GB_GSS13 AQ454792	450	AQ454792	HS_5195_B2_H04_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=771 Col=8 Row=P, genomic survey sequence	Homo sapiens	40,278	21-Apr-99
rxa00054	3036	GB_GSS5 AQ773786	459	AQ773786	HS_2222_A1_E07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2222 Col=13 Row=I, genomic survey sequence	Homo sapiens	40,087	29-Jul-99
		GB_GSS5 AQ773786	459	AQ773786	HS_2222_A1_E07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2222 Col=13 Row=I, genomic survey sequence	Homo sapiens	40,087	29-Jul-99
rxa00056	873	GB_IN1 CEF56H9	28291	Z74473	Caenorhabditis elegans cosmid F56H9, complete sequence	Caenorhabditis elegans	35,301	23-Nov-98
		GB_IN1:CEF56H9	28291	Z74473	Caenorhabditis elegans cosmid F56H9, complete sequence	Caenorhabditis elegans	38,941	23-Nov-98
rxa00058	687	GB_HTG6 AC011647	141830	AC011647	Homo sapiens clone RP11-15D18, *** SEQUENCING IN PROGRESS ***, 29 unordered pieces	Homo sapiens	39,939	04-DEC-1999
		GB_HTG6 AC011647	141830	AC011647	Homo sapiens clone RP11-15D18, *** SEQUENCING IN PROGRESS ***, 29 unordered pieces	Homo sapiens	37,537	04-DEC-1999
rxa00059	405	GB_GSS6 AQ825754	463	AQ825754	HS_5441_A2_G02_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=1017 Col=4 Row=M, genomic survey sequence	Homo sapiens	34,444	27-Aug-99
		GB_PAT:I32939	30001	I32939	Sequence 1 from patent US 5589385.	Unknown.	42,049	6-Feb-97
		GB_PAT.AR031772	30001	AR031772	Sequence 1 from patent US 5866410	Unknown.	42,049	29-Sep-99
rxa00065	396	GB_PAT E16763	2517	E16763	gDNA encoding aspartate transferase (AAT)	Corynebacterium glutamicum	98,765	28-Jul-99
		GB_EST32 AU050556	813	AU050556	AU050556 Paralichthys olivaceus library (Aoki T) Paralichthys olivaceus cDNA clone WF7-19, mRNA sequence.	Paralichthys olivaceus	35,638	8-Jun-99
		GB_EST32 AU050215	733	AU050215	AU050215 Paralichthys olivaceus library (Aoki T) Paralichthys olivaceus cDNA clone WB1-12, mRNA sequence	Paralichthys olivaceus	35,638	8-Jun-99
rxa00067	609	GB_HTG3.AC008289	115120	AC008289	Drosophila melanogaster chromosome 2 clone BACR04E05 (D1055) RPCI-98 04 E 5 map 57B-57B strain y, cn bw sp, *** SEQUENCING IN PROGRESS ***, 100 unordered pieces.	Drosophila melanogaster	30,397	17-Aug-99
		GB_IN2:AC004433	85862	AC004433	Drosophila melanogaster, chromosome 2R, region 57B1-57B6, P1 clone DS03659, complete sequence.	Drosophila melanogaster	35,501	01-DEC-1998
		GB_HTG3.AC008289	115120	AC008289	Drosophila melanogaster chromosome 2 clone BACR04E05 (D1055) RPCI-98 04 E.5 map 57B-57B strain y, cn bw sp, *** SEQUENCING IN PROGRESS ***, 100 unordered pieces	Drosophila melanogaster	30,397	17-Aug-99
rxa00068	705	GB_PL2 ATAC006201	87947	AC006201	Arabidopsis thaliana chromosome II BAC T27K22 genomic sequence, complete sequence	Arabidopsis thaliana	39,099	12-MAR-1999
		GB_HTG5 AC010146	271437	AC010146	Homo sapiens clone NH0355I13, WORKING DRAFT SEQUENCE, 1 unordered pieces	Homo sapiens	34,237	12-Nov-99
		GB_GSS3 B85079	307	B85079	RPCI11-29O9 TP RPCI-11 Homo sapiens genomic clone RPCI-11-29O9, genomic survey sequence.	Homo sapiens	39,560	9-Apr-99
rxa00077	1485	GB_PR4 AC007157	152937	AC007157	Homo sapiens, clone hRPK 78_A_1, complete sequence	Homo sapiens	37,661	27-Apr-99
		GB_HTG1 CEY43C5	149571	AL021449	Caenorhabditis elegans chromosome IV clone Y43C5, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Caenorhabditis elegans	25,242	23-Jan-98
		GB_HTG1 CEY43C5	149571	AL021449	Caenorhabditis elegans chromosome IV clone Y43C5, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Caenorhabditis elegans	38,258	23-Jan-98
rxa00079	345	GB_IN1 CTAJ2763	1097	AJ002763	Chironomus tentans mRNA for P23 protein (23 kDa)	Chironomus tentans	36,176	26-Jan-98
		GB_IN1 CTHRP23	752	AJ003820	Chironomus tentans mRNA for hnRNP protein, hrp23	Chironomus tentans	36,176	02-DEC-1998
		GB_EST17 AA650674	540	AA650674	30788 Lambda-PRL2 Arabidopsis thaliana cDNA clone 277G7T7, mRNA sequence	Arabidopsis thaliana	36,965	31-OCT-1997
rxa00080	1653	GB_EST38 AW039986	564	AW039986	EST282477 tomato mixed elicitor, BTI Lycopersicon esculentum cDNA clone cLET19F23, mRNA sequence.	Lycopersicon esculentum	38,078	18-OCT-1999

TABLE 4: ALIGNMENT RESULTS

		GB_EST33:AI778332	378	AI778332	EST259211 tomato susceptible, Cornell Lycopersicon esculentum cDNA clone cLES5A13, mRNA sequence.	Lycopersicon esculentum	38,298	29-Jun-99
		GB_EST38 AW039988	564	AW039988	EST282479 tomato mixed elicitor, BTI Lycopersicon esculentum cDNA clone cLET19F23, mRNA sequence	Lycopersicon esculentum	38,078	18-OCT-1999
rxa00082	687	GB_PR1 HSS171	333303	AJ011930	Homo sapiens chromosome 21q22 3, PAC clones 314N7, 225L15, BAC clone 7B7, complete sequence bases 1. .333303	Homo sapiens	36,111	10-Nov-98
		GB_PR1 HSS171	333303	AJ011930	Homo sapiens chromosome 21q22 3, PAC clones 314N7, 225L15, BAC clone 7B7, complete sequence bases 1 .333303	Homo sapiens	35,432	10-Nov-98
		GB_PR3:AC004000	128117	AC004000	Human PAC clone DJ404F18 from Xq23, complete sequence	Homo sapiens	38,750	15-Jan-98
rxa00083	423	GB_HTG1 CNS018OY	168868	AL109769	Homo sapiens chromosome 14 clone R-501E21, *** SEQUENCING IN PROGRESS ***, in ordered pieces	Homo sapiens	33,806	15-OCT-1999
		GB_HTG1 CNS018OY	168868	AL109769	Homo sapiens chromosome 14 clone R-501E21, *** SEQUENCING IN PROGRESS ***, in ordered pieces.	Homo sapiens	33,806	15-OCT-1999
		GB_PR3.HS516C23	116685	Z93021	Human DNA sequence from clone 516C23 on chromosome 6q12 Contains CA repeat (D6S402) and GSSs, complete sequence	Homo sapiens	36,562	23-Nov-99
rxa00087	651	GB_BA1 PSEBPHABC	6780	M83673	P pseudoalcaligenes dioxygenase (bphABC) gene cluster, complete cds	Pseudomonas pseudoalcaligenes	39,564	26-Apr-93
		GB_BA1 PSEBPHA	5700	M86348	Pseudomonas sp LB400 biphenyl dioxygenase (bphA), biphenyl dioxygenase (bphE), biphenyl dioxygenase (bphF) and biphenyl dioxygenase (bphG)s, complete cds, and dihydrodiol dehydrogenase (bphB), partial cds	Burkholderia sp LB400	39,564	18-Jul-97
		GB_PAT E04215	4721	E04215	Benzene dioxygenase gene.	Pseudomonas aeruginosa	45,814	29-Sep-97
rxa00093	2346	GB_HTG2 AC007361	36465	AC007361	Homo sapiens clone NH0144P23, *** SEQUENCING IN PROGRESS ***, 1 unordered pieces	Homo sapiens	37,179	23-Apr-99
		GB_PR4 AC006043	189036	AC006043	Homo sapiens BAC clone NH0538D15 from 7q11 23-q21 1, complete sequence	Homo sapiens	37,060	20-Feb-99
		GB_HTG2 AC007361	36465	AC007361	Homo sapiens clone NH0144P23, *** SEQUENCING IN PROGRESS ***, 1 unordered pieces	Homo sapiens	37,179	23-Apr-99
rxa00096	426	GB_EST15 AA533064	534	AA533064	nj60d06.s1 NCI_CGAP_Pr9 Homo sapiens cDNA clone IMAGE:996875, mRNA sequence	Homo sapiens	39,024	21-Aug-97
		GB_IN1.CELF01G12	34671	U53342	Caenorhabditis elegans cosmid F01G12.	Caenorhabditis elegans	38,060	5-Apr-96
		GB_PR3 AC004511	45005	AC004511	Homo sapiens chromosome 5, P1 clone 792C12 (LBNL H22), complete sequence	Homo sapiens	39,163	31-MAR-1998
rxa00097	1299	GB_OM CFU60590	6726	U60590	Canis familiaris TTX-resistant sodium channel mRNA, complete cds	Canis familiaris	39,528	8-Jan-98
		GB_GSS15 AQ664394	485	AQ664394	HS_5480_B1_B02_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=1056 Col=3 Row=D, genomic survey sequence	Homo sapiens	39,666	23-Jun-99
		GB_BA2 RSAF000233	5984	AF000233	Rhodobacter sphaeroides nitric oxide reductase operon norC, norB, norQ, norD, nnrT and nnrU genes, complete cds	Rhodobacter sphaeroides	37,500	6-Jun-97
rxa00101								
rxa00108	643	GB_PR4 AC007115	180821	AC007115	Homo sapiens chromosome 12 clone 917O5, complete sequence	Homo sapiens	35,165	17-Aug-99
		GB_PR3 AC004080	129354	AC004080	Homo sapiens PAC clone DJ0170O19 from 7p15-p21, complete sequence	Homo sapiens	38,560	29-Jan-98
		GB_HTG1 HSAJ9613	45302	AJ009613	Homo sapiens chromosome 17 clone cosmid 5L5 map p11, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Homo sapiens	39,274	11-Nov-98
rxa00110	672	GB_PL1:MIATGENB	166924	Y08502	A thaliana mitochondrial genome, part B	Mitochondrion Arabidopsis thaliana	36,391	13-Nov-98
		GB_PL2:AC010718	87684	AC010718	Arabidopsis thaliana chromosome I BAC F28O16 genomic sequence, complete sequence	Arabidopsis thaliana	36,622	30-OCT-1999
		GB_PL2:AC007729	106639	AC007729	Arabidopsis thaliana chromosome II BAC T18C6 genomic sequence, complete sequence	Arabidopsis thaliana	35,053	5-Jun-99
rxa00114	612	GB_OM BTMICSD1	362	Z27071	B.taurus (cos1E3) microsatellite DNA (362bp)	Bos taurus	37,117	10-Aug-95
		GB_OM BTMICSD1	362	Z27071	B taurus (cos1E3) microsatellite DNA (362bp)	Bos taurus	36,486	10-Aug-95
rxa00117	714	GB_PL2:AF080249	3194	AF080249	Arabidopsis thaliana kinesin-like heavy chain (KATD) mRNA, complete cds	Arabidopsis thaliana	37,846	14-Apr-99
		GB_PL2:IG002P16	110946	AF007270	Arabidopsis thaliana BAC IG002P16.	Arabidopsis thaliana	37,110	12-Jun-97
		GB_PL2:AF080249	3194	AF080249	Arabidopsis thaliana kinesin-like heavy chain (KATD) mRNA, complete cds	Arabidopsis thaliana	36,506	14-Apr-99
rxa00118	378	GB_HTG2 AC008043	124844	AC008043	Drosophila melanogaster chromosome 3 clone BACR05A08 (D750) RPCI-98 05 A 8 map 94A-94A strain y, cn bw sp, *** SEQUENCING IN PROGRESS ***, 86 unordered pieces.	Drosophila melanogaster	33,780	2-Aug-99

TABLE 4: ALIGNMENT RESULTS

		GB_HTG2:AC008043	124844	AC008043	Drosophila melanogaster chromosome 3 clone BACR05A08 (D750) RPCI-98 05.A.8 map 94A-94A strain y, cn bw sp, *** SEQUENCING IN PROGRESS***, 86 unordered pieces	Drosophila melanogaster	33,780	2-Aug-99
		GB_PR3 AC004827	129690	AC004827	Homo sapiens PAC clone DJ044L15 from Xq23, complete sequence	Homo sapiens	32,320	17-OCT-1998
rxa00119	882	GB_PR4 HSU34879	46610	U34879	Human 17-beta-hydroxysteroid dehydrogenase (EDH17B2) gene, complete cds	Homo sapiens	36,671	14-Jan-99
		GB_PR4.HSU34879	46610	U34879	Human 17-beta-hydroxysteroid dehydrogenase (EDH17B2) gene, complete cds	Homo sapiens	38,345	14-Jan-99
		GB_EST37:AW005997	702	AW005997	wz91c01 x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2566176 3' similar to TR O08609 O08609 TRANSCRIPTION FACTOR-LIKE PROTEIN 4 ,, mRNA sequence	Homo sapiens	40,774	10-Sep-99
rxa00120	963	GB_BA1:TRU80216	1936	U80216	Thermomicrobium roseum 70 kDa heat shock protein Hsp70 (DnaK) gene, complete cds	Thermomicrobium roseum	38,000	1-Feb-97
		GB_HTG1 HS791K14	155318	AL035685	Homo sapiens chromosome 20 clone RP4-791K14, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Homo sapiens	37,277	23-Nov-99
		GB_HTG1 HS791K14	155318	AL035685	Homo sapiens chromosome 20 clone RP4-791K14, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Homo sapiens	37,277	23-Nov-99
rxa00121	834	GB_HTG1 HSBA298O6	198847	AL118525	Homo sapiens chromosome 20 clone RP11-298O6, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Homo sapiens	36,199	24-Nov-99
		GB_HTG1 HS791K14	155318	AL035685	Homo sapiens chromosome 20 clone RP4-791K14, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Homo sapiens	36,983	23-Nov-99
		GB_HTG1 HS791K14	155318	AL035685	Homo sapiens chromosome 20 clone RP4-791K14, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Homo sapiens	36,983	23-Nov-99
rxa00122	1746	GB_PL1:MZECPN60A	6575	L21007	Corn nuclear-encoded mitochondrial chaperonin 60 (cpn60I) gene, complete cds	Zea mays	36,098	26-Jul-93
		GB_PL1:ZMCPNAGA	2247	Z12114	Z mays CPNA gene encoding mitochondrial chaperonin-60	Zea mays	37,702	01-OCT-1992
		GB_PL1 ZMCHHSP60	2138	Z11546	Z mays mRNA for mitochondrial chaperonin hsp60	Zea mays	37,721	11-Jun-92
rxa00127	588	GB_PR4:AC005193	108400	AC005193	Homo sapiens clone DJ0655N24, complete sequence	Homo sapiens	37,500	1-Jul-99
		GB_PR4 AC005193	108400	AC005193	Homo sapiens clone DJ0655N24, complete sequence	Homo sapiens	36,796	1-Jul-99
rxa00128	1827	GB_GSS11 AQ299024	449	AQ299024	HS_3178_B1_B06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3178 Col=11 Row=D, genomic survey sequence	Homo sapiens	40,757	15-DEC-1998
		GB_GSS11 AQ299024	449	AQ299024	HS_3178_B1_B06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3178 Col=11 Row=D, genomic survey sequence	Homo sapiens	40,443	15-DEC-1998
rxa00134	693	GB_GSS10 AQ177172	393	AQ177172	HS_3225_A2_E10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3225 Col=20 Row=I, genomic survey sequence	Homo sapiens	50,000	17-OCT-1998
		GB_PR3 AC005726	185215	AC005726	Homo sapiens chromosome 17, clone hRPK 192_H_23, complete sequence	Homo sapiens	37,778	30-OCT-1998
		GB_PR3 AC005726	185215	AC005726	Homo sapiens chromosome 17, clone hRPK 192_H_23, complete sequence	Homo sapiens	38,710	30-OCT-1998
rxa00140	309	GB_VI OPU75930	131993	U75930	Orgyia pseudotsugata nuclear polyhedrosis virus complete genome.	Orgyia pseudotsugata nuclear polyhedrosis virus	39,007	06-MAR-1998
		GB_HTG2 AC006319	156299	AC006319	Homo sapiens clone DJ0837C09, *** SEQUENCING IN PROGRESS ***, 1 unordered pieces	Homo sapiens	31,773	23-Apr-99
		GB_HTG2 AC006319	156299	AC006319	Homo sapiens clone DJ0837C09, *** SEQUENCING IN PROGRESS ***, 1 unordered pieces	Homo sapiens	31,773	23-Apr-99
rxa00141	585	GB_VI:OPU75930	131993	U75930	Orgyia pseudotsugata nuclear polyhedrosis virus complete genome	Orgyia pseudotsugata nuclear polyhedrosis virus	38,079	06-MAR-1998
		GB_PR4.AC004526	297898	AC004526	Homo sapiens chromosome 17, Neurofibromatosis 1 locus, complete sequence	Homo sapiens	37,336	25-Feb-99
		GB_PR2.HUMNEUROF	100849	L05367	Human oligodendrocyte myelin glycoprotein (OMG) exons 1-2, neurofibromatosis 1 (NF1) exons 28-49, ecotropic viral integration site 2B (EVI2B) exons 1-2, ecotropic viral integration site 2A (EVI2A) exons 1-2; adenylate kinase (AK3) exons 1-2	Homo sapiens	37,336	20-Sep-95
rxa00142	600	GB_PR4 HUAC002331	139480	AC002331	Homo sapiens Chromosome 16 BAC clone CIT987SK-A-A-218C7, complete sequence.	Homo sapiens	38,898	23-Nov-99
		GB_PR3:AF064861	133965	AF064861	Homo sapiens PAC 128M19 derived from chromosome 21q22 3, containing the HMG-14 and CHD5 genes, complete cds, complete sequence.	Homo sapiens	37,182	2-Jun-98
		GB_HTG3 AC009451	165302	AC009451	Homo sapiens chromosome 17 clone 2286_H_12 map 17, *** SEQUENCING IN PROGRESS ***, 26 unordered pieces.	Homo sapiens	33,167	22-Aug-99
rxa00150	897	GB_PR4 AF130343	292721	AF130343	Homo sapiens chromosome 8 clone PAC 87 2 map 8q24 1, complete sequence.	Homo sapiens	36,032	9-Jul-99
		GB_HTG4 AC008578	98891	AC008578	Homo sapiens chromosome 5 clone CIT-HSPC_558D4, *** SEQUENCING IN PROGRESS ***, 143 unordered pieces	Homo sapiens	38,129	31-OCT-1999

TABLE 4: ALIGNMENT RESULTS

		GB_HTG4:AC008578	98891	AC008578	Homo sapiens chromosome 5 clone CIT-HSPC_558D4, *** SEQUENCING IN PROGRESS ***, 143 unordered pieces	Homo sapiens	38,129	31-OCT-1999
rxa00151	720	GB_PL2 AF058914	111767	AF058914	Arabidopsis thaliana BAC F21E10.	Arabidopsis thaliana	36,068	15-Apr-98
		GB_PR1:AB019440	200000	AB019440	Homo sapiens DNA for immunoglobulin heavy-chain variable region, complete sequence, 4 of 5	Homo sapiens	36,517	24-Feb-99
		GB_PR2 AP000098	100000	AP000098	Homo sapiens genomic DNA of 21q22 1, GART and AML related, Q78C10-149C3 region, segment 1/20, complete sequence	Homo sapiens	39,224	25-Sep-99
rxa00153	549	GB_PR4 AC006265	177707	AC006265	Homo sapiens chromosome 17, clone hRPK 566_B_16, complete sequence	Homo sapiens	34,862	28-Jan-99
		GB_HTG2 AC007389	207188	AC007389	Homo sapiens clone NH0418H16, *** SEQUENCING IN PROGRESS ***, 6 unordered pieces	Homo sapiens	36,044	5-Jun-99
		GB_HTG2 AC007389	207188	AC007389	Homo sapiens clone NH0418H16, *** SEQUENCING IN PROGRESS ***, 6 unordered pieces	Homo sapiens	36,044	5-Jun-99
rxa00154								
rxa00155	906	GB_BA2 AE001707	19518	AE001707	Thermotoga maritima section 19 of 136 of the complete genome	Thermotoga maritima	36,854	2-Jun-99
		GB_PR2 HS1126I14	19544	AL078589	Human DNA sequence from clone 1126I14 on chromosome 6q16 1-16 3 Contains an STS and GSSs, complete sequence	Homo sapiens	36,723	23-Nov-99
		GB_BA1 MTCY01B2	35938	Z95554	Mycobacterium tuberculosis H37Rv complete genome, segment 72/162	Mycobacterium tuberculosis	40,435	17-Jun-98
rxa00159	1305	GB_EST38 AW048718	475	AW048718	UI-M-BH1-amy-d-01-0-UI s1 NIH_BMAP_M_S2 Mus musculus cDNA clone UI-M-BH1-amy-d-01-0-UI 3', mRNA sequence	Mus musculus	39,789	18-Sep-99
		GB_EST21:AA993450	381	AA993450	ot32h09 s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE 1618529 3', mRNA sequence	Homo sapiens	38,684	27-Aug-98
		GB_BA1.AB007009	363	AB007009	Cytophaga sp 16S rRNA gene, partial sequence.	Cytophaga sp	39,039	13-OCT-1997
rxa00161	585	GB_HTG3:AC009708	25123	AC009708	Homo sapiens chromosome 8 clone 318_G_5 map 8, LOW-PASS SEQUENCE SAMPLING	Homo sapiens	37,108	28-Aug-99
		GB_HTG3.AC009708	25123	AC009708	Homo sapiens chromosome 8 clone 318_G_5 map 8, LOW-PASS SEQUENCE SAMPLING	Homo sapiens	37,108	28-Aug-99
		GB_PR3 HSN104C4	40203	Z83855	Human DNA sequence from clone N104C4 on chromosome 22 Contains GSSs, complete sequence	Homo sapiens	37,634	23-Nov-99
rxa00162	477	GB_HTG1 CEY94A7	41009	Z99294	Caenorhabditis elegans chromosome V clone Y94A7, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Caenorhabditis elegans	41,502	18-Sep-97
		GB_HTG1.CEY94A7	41009	Z99294	Caenorhabditis elegans chromosome V clone Y94A7, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Caenorhabditis elegans	41,502	18-Sep-97
		GB_BA2 AE001182	11228	AE001182	Borrelia burgdorferi (section 68 of 70) of the complete genome.	Borrelia burgdorferi	39,655	15-DEC-1997
rxa00167	621	GB_HTG7.AC007937	206265	AC007937	Mus musculus chromosome 10 clone RP21-536F4 map 10, *** SEQUENCING IN PROGRESS ***, 6 unordered pieces	Mus musculus	37,092	09-DEC-1999
		GB_RO:MMU6590	6429	AJ006590	Mus musculus mRNA for GANP protein	Mus musculus	38,678	2-Jun-99
		GB_HTG3 AC008852	116219	AC008852	Homo sapiens chromosome 5 clone CITB-H1_2176I21, *** SEQUENCING IN PROGRESS ***, 13 unordered pieces	Homo sapiens	35,691	3-Aug-99
rxa00169	2196	GB_GSS3.B11032	896	B11032	T17F10-T7 TAMU Arabidopsis thaliana genomic clone T17F10, genomic survey sequence	Arabidopsis thaliana	42,024	14-MAY-1997
		GB_GSS3 B10120	909	B10120	T27N10-Sp6 1 TAMU Arabidopsis thaliana genomic clone T27N10, genomic survey sequence	Arabidopsis thaliana	41,581	14-MAY-1997
		GB_GSS3 B09409	916	B09409	T27M2-Sp6 TAMU Arabidopsis thaliana genomic clone T27M2, genomic survey sequence	Arabidopsis thaliana	41,356	14-MAY-1997
rxa00170	1977	GB_GSS8 AQ027582	456	AQ027582	CIT-HSP-2325M20.TR CIT-HSP Homo sapiens genomic clone 2325M20, genomic survey sequence.	Homo sapiens	40,749	30-Jun-98
		GB_GSS6 AQ833529	484	AQ833529	HS_5304_B2_C02_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=880 Col=4 Row=F, genomic survey sequence	Homo sapiens	38,017	27-Aug-99
		GB_PR2 HSM800174	2326	AL049389	Homo sapiens mRNA, cDNA DKFZp586O0118 (from clone DKFZp586O0118)	Homo sapiens	37,556	21-MAY-1999
rxa00171	281	GB_EST38 AL118463	279	AL118463	w9112a43 Beddington mouse dissected endoderm Mus musculus cDNA clone 528_12E22 5', mRNA sequence.	Mus musculus	50,000	23-Sep-99
		GB_EST15 AA499834	419	AA499834	vg05e06 r1 Soares mouse NbMH Mus musculus cDNA clone IMAGE 860482 5', mRNA sequence.	Mus musculus	39,801	1-Jul-97
		GB_EST24:AI211527	431	AI211527	p0h01a1 r1 Aspergillus nidulans 24hr asexual developmental and vegetative cDNA lambda zap library Emericella nidulans cDNA clone p0h01a1 5', mRNA sequence.	Emericella nidulans	41,584	19-OCT-1998
rxa00173	456	GB_PR3 AC004400	33367	AC004400	Homo sapiens chromosome 19, cosmid F24069, complete sequence.	Homo sapiens	38,902	12-MAR-1998

TABLE 4: ALIGNMENT RESULTS

		GB_PL1:VFU14956	1474	U14956	Vicia faba ferredoxin NADP+ reductase precursor (fnr) mRNA, complete cds.	Vicia faba	38,753	28-Sep-94
		GB_PR3 AC004400	33367	AC004400	Homo sapiens chromosome 19, cosmid F24069, complete sequence	Homo sapiens	40,515	12-MAR-1998
rxa00174	408	GB_PL2 AF075293	4332	AF075293	Candida albicans strain 1161 agglutinin-like protein 6 (ALS6) gene, complete cds	Candida albicans	41,235	2-Jul-99
		GB_PL2 JSPCHS1	1525	X94995	Juglans nigra x Juglans regia mRNA for chalcone synthase (CHS1)	Juglans nigra x Juglans regia	39,558	19-Nov-99
		GB_PL2 JSPCHS2	1534	X94706	Juglans nigra x Juglans regia mRNA for chalcone synthase (CHS2).	Juglans nigra x Juglans regia	38,821	19-Nov-99
rxa00175								
rxa00179	582	GB_BA1 CGPUTP	3791	Y09163	C.glutamicum putP gene	Corynebacterium glutamicum	100,000	8-Sep-97
		GB_IN2:L76038	2421	L76038	Anopheles gambiae prophenoloxidase mRNA, complete cds	Anopheles gambiae	35,751	23-Jul-98
		GB_IN2:AF031626	8486	AF031626	Anopheles gambiae prophenoloxidase (AgProPO) gene, complete cds	Anopheles gambiae	36,395	5-Jan-99
rxa00180	663	GB_BA1 CGPUTP	3791	Y09163	C glutamicum putP gene	Corynebacterium glutamicum	100,000	8-Sep-97
		GB_HTG1 HS120G22	57021	AL031847	Homo sapiens chromosome 1 clone RP1-120G22, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	35,976	23-Nov-99
		GB_HTG1 HS120G22	57021	AL031847	Homo sapiens chromosome 1 clone RP1-120G22, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Homo sapiens	35,976	23-Nov-99
rxa00183	975	GB_IN2 AF049132	16005	AF049132	Florometra serratissima mitochondrion, complete genome	Mitochondrion Florometra serratissima	33,710	15-Jan-99
		GB_IN1 MTCE	13794	X54252	C. elegans complete mitochondrial genome	Mitochondrion Caenorhabditis elegans	35,036	30-Nov-97
		GB_IN2 AF049132	16005	AF049132	Florometra serratissima mitochondrion, complete genome	Mitochondrion Florometra serratissima	36,021	15-Jan-99
rxa00185	2751	GB_EST31 AI693167	500	AI693167	wd68c11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE 2336756 3' similar to SW HIOM_BOVIN P10950 HYDROXYINDOLE O-METHYLTRANSFERASE;, mRNA sequence	Homo sapiens	37,800	2-Jun-99
		GB_GSS1 CNS010IZ	1000	AL099029	Drosophila melanogaster genome survey sequence SP6 end of BAC BACN04K17 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence	Drosophila melanogaster	35,158	26-Jul-99
		GB_EST31 AI693167	500	AI693167	wd68c11 x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2336756 3' similar to SW:HIOM_BOVIN P10950 HYDROXYINDOLE O-METHYLTRANSFERASE;, mRNA sequence	Homo sapiens	39,052	2-Jun-99
rxa00194	564	GB_GSS10 AQ192671	396	AQ192671	HS_2251_B2_A04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2251 Col=8 Row=B, genomic survey sequence	Homo sapiens	44,240	4-Nov-98
		GB_GSS8.AQ044307	644	AQ044307	CIT-HSP-2331N9.TR CIT-HSP Homo sapiens genomic clone 2331N9, genomic survey sequence	Homo sapiens	36,150	14-Jul-98
		GB_EST36 AI925874	564	AI925874	wo20d11.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2455893 3' similar to TR O67849 O67849 GTP-BINDING PROTEIN. ,, mRNA sequence	Homo sapiens	45,588	2-Sep-99
rxa00197	1335	GB_GSS12 AQ399208	436	AQ399208	mgxb0001M23f CUGI Rice Blast BAC Library Magnaporthe grisea genomic clone mgxb0001M23f, genomic survey sequence	Magnaporthe grisea	63,529	06-MAR-1999
		GB_GSS12:AQ398449	472	AQ398449	mgxb0001P11f CUGI Rice Blast BAC Library Magnaporthe grisea genomic clone mgxb0001P11f, genomic survey sequence.	Magnaporthe grisea	49,580	06-MAR-1999
		GB_OM BTMMP9	2350	X78324	B.taurus bmmp9 mRNA for matrix metalloproteinase	Bos taurus	40,440	30-MAR-1995
rxa00199	1542	GB_BA1 AB024708	8734	AB024708	Corynebacterium glutamicum gltB and gltD genes for glutamine 2-oxoglutarate aminotransferase large and small subunits, complete cds	Corynebacterium glutamicum	36,237	13-MAR-1999
		GB_HTG2 AC007837	103949	AC007837	Drosophila melanogaster chromosome 2 clone BACR04I07 (D644) RPCI-98 04 I 7 map 57B2-B3 strain y, cn bw sp, *** SEQUENCING IN PROGRESS***, 49 unordered pieces	Drosophila melanogaster	36,045	2-Aug-99
		GB_HTG2 AC007837	103949	AC007837	Drosophila melanogaster chromosome 2 clone BACR04I07 (D644) RPCI-98 04 I 7 map 57B2-B3 strain y, cn bw sp, *** SEQUENCING IN PROGRESS***, 49 unordered pieces	Drosophila melanogaster	36,045	2-Aug-99

TABLE 4: ALIGNMENT RESULTS

rxa00200	3561	GB_BA2:MSU46844	16951	U46844	Mycobacterium smegmatis catalase-peroxidase (katG), putative arabinosyl transferase (embC, embA, embB), genes complete cds and putative propionyl-coA carboxylase beta chain (pccB) genes, partial cds	Mycobacterium smegmatis	53,937	12-MAY-1997
		GB_BA2 MAU66560	7853	U66560	Mycobacterium avium EmbR (embR), EmbA (embA) and EmbB (embB) genes, complete cds	Mycobacterium avium	52,241	8-Nov-96
		GB_BA1 MTY13D12	37085	Z80343	Mycobacterium tuberculosis H37Rv complete genome; segment 156/162	Mycobacterium tuberculosis	52,812	17-Jun-98
rxa00207	441	GB_PR3:HTCRBCHR9	216293	AF029308	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families.	Homo sapiens	39,286	13-Apr-98
		GB_PR3 HTCRBCHR9	216293	AF029308	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families.	Homo sapiens	37,116	13-Apr-98
rxa00211	786	GB_PR2 HSU81831	38674	U81831	Human cosmid LL12NCO1-67C6, ETV6 gene, intron 1A, partial sequence	Homo sapiens	35,509	3-Jan-97
		GB_RO MUSKROX2S2	2868	M28845	Mus musculus zinc finger protein (Krox-24) gene, exon 2	Mus musculus	40,566	21-MAY-1996
		GB_HTG2.AC007440	120642	AC007440	Drosophila melanogaster chromosome 2 clone BACR37I09 (D593) RPCI-98 37 I 9 map 49A-49B strain y, cn bw sp, *** SEQUENCING IN PROGRESS ***, 103 unordered pieces.	Drosophila melanogaster	36,753	2-Aug-99
rxa00218								
rxa00220	627	GB_BA1 ASU04436	4668	U04436	Anabaena sp PCC 7120 putative polyketide synthase gene, complete cds	Anabaena sp	33,766	21-DEC-1993
		GB_RO AF068199	3490	AF068199	Mus musculus D-dopachrome tautomerase gene, complete cds	Mus musculus	38,833	26-Aug-98
		GB_RO AF068199	3490	AF068199	Mus musculus D-dopachrome tautomerase gene, complete cds	Mus musculus	34,776	26-Aug-98
rxa00222	1269	GB_PL1 AB011477	78181	AB011477	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone MHK7, complete sequence	Arabidopsis thaliana	36,766	20-Nov-99
		GB_EST17 AA615900	427	AA615900	vo91b05 r1 Barstead mouse irradiated colon MPLRB7 Mus musculus cDNA clone IMAGE.1066449 5' similar to SW MUCL_RAT P98089 INTESTINAL MUCIN-LIKE PROTEIN ,, mRNA sequence	Mus musculus	39,782	07-OCT-1997
		GB_EST38:AW039188	486	AW039188	EST281423 tomato mixed elicitor, BTI Lycopersicon esculentum cDNA clone cLET9F17, mRNA sequence	Lycopersicon esculentum	41,286	18-OCT-1999
rxa00230	843	GB_PR3.AC005255	94343	AC005255	Homo sapiens chromosome 19, CIT-HSP-146e8, complete sequence	Homo sapiens	35,990	6-Jul-98
		GB_PR3 AC005255	94343	AC005255	Homo sapiens chromosome 19, CIT-HSP-146e8, complete sequence	Homo sapiens	38,175	6-Jul-98
rxa00232	633	GB_HTG2.AC007118	200000	AC007118	Homo sapiens chromosome 4, *** SEQUENCING IN PROGRESS ***, 45 unordered pieces	Homo sapiens	36,772	19-MAR-1999
		GB_HTG2 AC007118	200000	AC007118	Homo sapiens chromosome 4, *** SEQUENCING IN PROGRESS ***, 45 unordered pieces	Homo sapiens	36,772	19-MAR-1999
		GB_GSS1:CNS004WZ	978	AL055537	Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR11G02 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence	Drosophila melanogaster	34,518	3-Jun-99
rxa00233	517	GB_BA1.AB006206	7443	AB006206	Streptomyces griseus AmfR, AmfA and AmfB genes and 4 ORFs, complete cds	Streptomyces griseus	38,690	5-Feb-99
		GB_PR4 AC006999	112878	AC006999	Homo sapiens clone NH0462A19, complete sequence.	Homo sapiens	40,244	17-Jul-99
		GB_HTG2 AC007042	132400	AC007042	Homo sapiens clone NH0399H17, *** SEQUENCING IN PROGRESS ***, 5 unordered pieces	Homo sapiens	40,244	06-MAR-1999
rxa00234	663	GB_PAT E13059	3480	E13059	gDNA encoding cytochrome b5	unidentified	40,091	24-Jun-98
		GB_PL1 AB022444	2104	AB022444	Mortierella alpina gene for cytochrome b5, complete cds	Mortierella alpina	42,314	14-Jul-99
		GB_GSS9 AQ112619	443	AQ112619	CIT-HSP-2371D11 TR CIT-HSP Homo sapiens genomic clone 2371D11, genomic survey sequence.	Homo sapiens	39,623	29-Aug-98
rxa00236	849	GB_BA1 CGPROMF34	60	X90361	C glutamicum DNA for promoter fragment F34	Corynebacterium glutamicum	98,333	4-Nov-96
		GB_IN1 CEF56G4	38062	Z81552	Caenorhabditis elegans cosmid F56G4, complete sequence.	Caenorhabditis elegans	36,190	08-OCT-1999
		GB_EST16:C51159	370	C51159	C51159 Yuji Kohara unpublished cDNA Strain N2 hermaphrodite embryo Caenorhabditis elegans cDNA clone yk491h3 5', mRNA sequence	Caenorhabditis elegans	41,096	18-OCT-1999
rxa00237	501	GB_GSS9 AQ148605	511	AQ148605	HS_3137_B2_A11_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3137 Col=22 Row=B, genomic survey sequence	Homo sapiens	37,959	08-OCT-1998
		GB_GSS11 AQ274889	622	AQ274889	RPCI-5-1111N8T7 RPCI-5 Homo sapiens genomic clone RPCI-5-1111N8T7, genomic survey sequence	Homo sapiens	44,628	10-Nov-98

TABLE 4: ALIGNMENT RESULTS

		GB_GSS11:AQ274889	622	AQ274889	RPCI-5-1111N8T7 RPCI-5 Homo sapiens genomic clone RPCI-5-1111N8T7, genomic survey sequence.	Homo sapiens	37,321	10-Nov-98
rxa00238	492	GB_PL2 PBU91560	2605	U91560	Paracoccidioides brasiliensis heat shock protein 70 (Hsp70) gene, complete cds	Paracoccidioides brasiliensis	37,137	12-MAR-1999
		GB_HTG6 AC007957	212658	AC007957	Homo sapiens, *** SEQUENCING IN PROGRESS ***, 2 ordered pieces.	Homo sapiens	38,285	26-Nov-99
		GB_PR4:AC009288	140876	AC009288	Homo sapiens, complete sequence	Homo sapiens	36,575	19-Nov-99
rxa00239	708	GB_PL2 PBU91560	2605	U91560	Paracoccidioides brasiliensis heat shock protein 70 (Hsp70) gene, complete cds	Paracoccidioides brasiliensis	45,545	12-MAR-1999
		GB_BA2 CJU96452	1450	U96452	Campylobacter jejuni major outer membrane porin gene, complete cds	Campylobacter jejuni	37,197	02-DEC-1998
		GB_RO RATPF4	1675	M15254	Rat platelet factor 4 (PF4) gene	Rattus norvegicus	35,014	27-Apr-93
rxa00240	333	GB_BA1 CGLYSI	4232	X60312	C glutamicum lysI gene for L-lysine permease	Corynebacterium glutamicum	46,207	30-Jan-92
		GB_PR3 AC005358	184886	AC005358	Homo sapiens chromosome 17, clone hRPK 746_E_8, complete sequence	Homo sapiens	35,843	29-Aug-98
		GB_BA1 CGLYSI	4232	X60312	C glutamicum lysI gene for L-lysine permease	Corynebacterium glutamicum	42,025	30-Jan-92
rxa00242	1401	GB_BA1 CGLYSI	4232	X60312	C glutamicum lysI gene for L-lysine permease	Corynebacterium glutamicum	100,000	30-Jan-92
		GB_PR3 HSJ514B11	100494	AL049554	Human DNA sequence from clone 514B11 on chromosome 6q16 1-21 Contains an EST, STSs and GSSs, complete sequence	Homo sapiens	37,010	23-Nov-99
		GB_HTG3 AC009393	137353	AC009393	Drosophila melanogaster chromosome 3 clone BACR17F05 (D977) RPCI-98 17.F 5 map 87D-87D strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 111 unordered pieces	Drosophila melanogaster	39,600	27-Aug-99
rxa00244	759	GB_HTG4:AC011290	148409	AC011290	Homo sapiens clone NH0064I02, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces	Homo sapiens	38,102	15-OCT-1999
		GB_HTG4.AC011290	148409	AC011290	Homo sapiens clone NH0064I02, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces	Homo sapiens	38,102	15-OCT-1999
		GB_EST23 AI077162	527	AI077162	TENU3384 T cruzi epimastigote normalized cDNA Library Trypanosoma cruzi cDNA clone 28o6 5' similar to TRANSPLANTATION ANTIGEN P35B sp|P23591|TUM3_MOUSE, mRNA sequence	Trypanosoma cruzi	38,847	10-Aug-98
rxa00245	1608	GB_HTG2 AC007644	141048	AC007644	Homo sapiens chromosome 17 clone hRPK 19_F_16 map 17, *** SEQUENCING IN PROGRESS ***, 17 unordered pieces	Homo sapiens	36,929	23-MAY-1999
		GB_HTG2:AC007644	141048	AC007644	Homo sapiens chromosome 17 clone hRPK 19_F_16 map 17, *** SEQUENCING IN PROGRESS ***, 17 unordered pieces.	Homo sapiens	36,929	23-MAY-1999
		GB_HTG2 AC007644	141048	AC007644	Homo sapiens chromosome 17 clone hRPK 19_F_16 map 17, *** SEQUENCING IN PROGRESS ***, 17 unordered pieces	Homo sapiens	34,025	23-MAY-1999
rxa00247	1050	GB_PR2 AP000119	100000	AP000119	Homo sapiens genomic DNA of 21q22 1, GART and AML related, SLC5A3-f4A4 region, segment 2/8, complete sequence	Homo sapiens	36,187	25-Sep-99
		GB_PR2 AP000051	100000	AP000051	Homo sapiens genomic DNA, chromosome 21q22 1, segment 22/28, complete sequence	Homo sapiens	36,187	20-Nov-99
		GB_PR2 AP000166	100000	AP000166	Homo sapiens genomic DNA, chromosome 21q22 1, D21S226-AML region, clone B2344F14-f50E8, segment 2/9, complete sequence	Homo sapiens	37,942	20-Nov-99
rxa00248	846	GB_PR4 AC006464	99908	AC006464	Homo sapiens BAC clone NH0436C12 from 2, complete sequence	Homo sapiens	36,797	22-OCT-1999
		GB_PR4 AC006238	211945	AC006238	Homo sapiens chromosome 18, clone hRPK 474_N_24, complete sequence	Homo sapiens	32,896	31-Jan-99
		GB_PR4 AC006238	211945	AC006238	Homo sapiens chromosome 18, clone hRPK 474_N_24, complete sequence	Homo sapiens	34,438	31-Jan-99
rxa00250	870	GB_GSS10.AQ244736	469	AQ244736	HS_2056_B1_F03_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2056 Col=5 Row=L, genomic survey sequence	Homo sapiens	36,310	03-OCT-1998
		GB_PAT.I07323	340	I07323	Sequence 5 from Patent EP 0331961	Unknown	38,125	02-DEC-1994
		GB_PR1:HS11Q13RP	10777	Y12377	H sapiens FGF/int-2 gene upstream flanking region	Homo sapiens	36,155	17-Apr-97
rxa00252	366	GB_BA1 MTCY20G9	37218	Z77162	Mycobacterium tuberculosis H37Rv complete genome, segment 25/162	Mycobacterium tuberculosis	39,554	17-Jun-98
		GB_BA1 MTV004	69350	AL009198	Mycobacterium tuberculosis H37Rv complete genome, segment 144/162	Mycobacterium tuberculosis	40,443	18-Jun-98
		GB_BA1 MTV004	69350	AL009198	Mycobacterium tuberculosis H37Rv complete genome, segment 144/162	Mycobacterium tuberculosis	41,803	18-Jun-98

TABLE 4: ALIGNMENT RESULTS

rxa00256	894	GB_PR4:AC005343	137213	AC005343	Homo sapiens Chromosome 12p13.3 BAC RPCI11-21K20 (Roswell Park Cancer Institute Human BAC Library) complete sequence.	Homo sapiens	36,436	2-Apr-99
		GB_PR3 AC003005	45084	AC003005	Human DNA from chromosome 19-specific cosmid F25419 containing ZNF gene family members, genomic sequence, complete sequence	Homo sapiens	36,395	22-OCT-1997
		GB_HTG3:AC007930	67668	AC007930	Drosophila melanogaster chromosome 2 clone BACR49A06 (D772) RPCI-98 49 A 6 map 43B-43B strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 40 unordered pieces	Drosophila melanogaster	32,503	20-Sep-99
rxa00257	579	GB_PR4.AC005343	137213	AC005343	Homo sapiens Chromosome 12p13 3 BAC RPCI11-21K20 (Roswell Park Cancer Institute Human BAC Library) complete sequence	Homo sapiens	37,063	2-Apr-99
		GB_HTG1 HS1096J16	194423	AL121721	Homo sapiens chromosome 20 clone RP5-1096J16, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Homo sapiens	37,217	23-Nov-99
		GB_HTG1.HS1096J16	194423	AL121721	Homo sapiens chromosome 20 clone RP5-1096J16, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Homo sapiens	37,217	23-Nov-99
rxa00258	795	GB_PR3 HSJ747H23	114201	AL049699	Human DNA sequence from clone 747H23 on chromosome 6q13-15 Contains the 3' part of the ME1 gene for malic enzyme 1, soluble (NADP-dependent malic enzyme, malate oxidoreductase, EC 1.1 1 40), a novel gene and the 5' part of the gene for N-acetylglucosamine-phosphate mutase Contains ESTs, STSs, GSSs and two putative CpG islands, complete sequence	Homo sapiens	36,469	23-Nov-99
		GB_HTG2:HSJ202D23	175496	AL121716	Homo sapiens chromosome 6 clone RP1-202D23 map q14 1-15, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Homo sapiens	36,469	03-DEC-1999
		GB_HTG2 HSJ202D23	175496	AL121716	Homo sapiens chromosome 6 clone RP1-202D23 map q14 1-15, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Homo sapiens	36,469	03-DEC-1999
rxa00260	1299	GB_PR3 HS360B4	23388	AL031716	Human DNA sequence from clone 360B4 on chromosome 16 Contains part of a gene for a PUTATIVE novel protein similar to predicted bacterial and worm proteins and ESTs, complete sequence	Homo sapiens	36,145	23-Nov-99
		GB_EST19 AA741904	423	AA741904	LmLv39p3/71A Leishmania major promastigote full length cDNA library from early logarithmic stage (day 3) Leishmania major cDNA clone 71A 5', mRNA sequence	Leishmania major	39,192	10-DEC-1998
		GB_PR3.HS360B4	23388	AL031716	Human DNA sequence from clone 360B4 on chromosome 16 Contains part of a gene for a PUTATIVE novel protein similar to predicted bacterial and worm proteins and ESTs, complete sequence	Homo sapiens	39,494	23-Nov-99
rxa00264								
rxa00267	441	GB_GSS10 AQ258013	761	AQ258013	nbxb0019H05f CUGI Rice BAC Library Oryza sativa genomic clone nbxb0019H05f, genomic survey sequence.	Oryza sativa	52,033	23-OCT-1998
		GB_EST10 AA167894	552	AA167894	CpEST.021 uniZAPCpIOWAsporoLib1 Cryptosporidium parvum cDNA 5' similar to lactate dehydrogenase, mRNA sequence	Cryptosporidium parvum	40,462	19-DEC-1996
		GB_HTG3:AC011591	129431	AC011591	Homo sapiens chromosome 17 clone 118_B_18 map 17, *** SEQUENCING IN PROGRESS ***, 25 unordered pieces.	Homo sapiens	35,469	07-OCT-1999
rxa00271	1113	GB_PL1 CHTRP1	3480	X70035	C.heterostrophus gene for trifunctional tryptophan synthase	Cochliobolus heterostrophus	41,636	31-OCT-1996
		GB_VI FLU47643	1492	U47643	Feline leukemia virus Notch2 gene, clone FeLV/Notch2-AP (subgenomic), partial cds	Feline leukemia virus	37,869	25-OCT-1996
		GB_VI.FLU47644	1641	U47644	Feline leukemia virus Notch2 gene, clone FeLV/Notch2-B, partial cds	Feline leukemia virus	36,441	25-OCT-1996
rxa00272	495	GB_GSS8:AQ041841	373	AQ041841	CIT-HSP-2335L1 TR CIT-HSP Homo sapiens genomic clone 2335L1, genomic survey sequence	Homo sapiens	45,455	14-Jul-98
		GB_GSS13 AQ429301	591	AQ429301	CITBI-E1-2562H16 TR CITBI-E1 Homo sapiens genomic clone 2562H16, genomic survey sequence.	Homo sapiens	63,636	24-MAR-1999
		GB_GSS10 AQ237541	667	AQ237541	RPCI11-61O21 TJB 1 RPCI-11 Homo sapiens genomic clone RPCI-11-61O21, genomic survey sequence	Homo sapiens	62,222	21-Apr-99
rxa00273	1236	GB_BA1 CGBETPGEN	2339	X93514	C glutamicum betP gene.	Corynebacterium glutamicum	44,056	8-Sep-97

TABLE 4: ALIGNMENT RESULTS

		GB_PR2:HS142F18	141672	AL031073	Human DNA sequence from clone 142F18 on chromosome Xq26.3-27.2 Contains part of a gene similar to melanoma-associated antigen, EST, GSS and an inverted repeat, complete sequence	Homo sapiens	44,643	23-Nov-99
		GB_IN2.AC007177	101320	AC007177	Drosophila melanogaster, chromosome 2R, region 59C1-59C5, P1 clones DS06621 and DS02186, complete sequence	Drosophila melanogaster	36,721	27-MAR-1999
rxa00274	2733	GB_HTG3:AC011675	98026	AC011675	Homo sapiens clone 10_J_17, LOW-PASS SEQUENCE SAMPLING	Homo sapiens	35,405	10-OCT-1999
		GB_HTG3 AC011675	98026	AC011675	Homo sapiens clone 10_J_17, LOW-PASS SEQUENCE SAMPLING	Homo sapiens	35,405	10-OCT-1999
		GB_HTG3:AC010598	174019	AC010598	Homo sapiens chromosome 5 clone CIT-HSPC_560O9, *** SEQUENCING IN PROGRESS ***, 50 unordered pieces	Homo sapiens	36,908	16-Sep-99
rxa00275	582	GB_GSS14.AQ574926	666	AQ574926	nbxb0086K14f CUGI Rice BAC Library Oryza sativa genomic clone nbxb0086K14f, genomic survey sequence	Oryza sativa	33,830	2-Jun-99
		GB_HTG2 AC004396	43686	AC004396	Homo sapiens, *** SEQUENCING IN PROGRESS ***, 2 unordered pieces	Homo sapiens	38,298	19-Jul-99
		GB_HTG2 AC004396	43686	AC004396	Homo sapiens, *** SEQUENCING IN PROGRESS ***, 2 unordered pieces	Homo sapiens	38,298	19-Jul-99
rxa00276	465	GB_PL1 SC9952X	29286	Z49212	S cerevisiae chromosome XIII cosmid 9952	Saccharomyces cerevisiae	37,118	11-Aug-97
		GB_PL1 S45357	4017	S45357	PSE-1=protein secretion enhancer [Saccharomyces cerevisiae, Genomic, 4017 nt]	Saccharomyces cerevisiae	41,394	08-MAY-1993
		GB_PL1 SCPSE1G	4017	Z11538	S.cerevisiae PSE-1 gene.	Saccharomyces cerevisiae	41,394	13-Aug-96
rxa00279	1509	GB_HTG3 AC009911	99707	AC009911	Drosophila melanogaster chromosome 2 clone BACR01N17 (D1036) RPCI-98 01 N 17 map 38A-38A strain y, cn bw sp, *** SEQUENCING IN PROGRESS ***, 69 unordered pieces	Drosophila melanogaster	33,023	05-OCT-1999
		GB_HTG3 AC009911	99707	AC009911	Drosophila melanogaster chromosome 2 clone BACR01N17 (D1036) RPCI-98 01 N 17 map 38A-38A strain y, cn bw sp, *** SEQUENCING IN PROGRESS ***, 69 unordered pieces	Drosophila melanogaster	33,023	05-OCT-1999
		GB_HTG4 AC008397	230451	AC008397	Homo sapiens chromosome 19 clone CIT-HSPC_251H24, *** SEQUENCING IN PROGRESS ***, 81 unordered pieces.	Homo sapiens	37,432	31-OCT-1999
rxa00282	889	GB_PR3 HSB11B7	37290	Z82171	Human DNA sequence from cosmid B11B7 on chromosome 22 contains ESTs.	Homo sapiens	35,845	23-Nov-99
		GB_PR3.HSB11B7	37290	Z82171	Human DNA sequence from cosmid B11B7 on chromosome 22 contains ESTs	Homo sapiens	37,126	23-Nov-99
		GB_RO RATMTA	4197	L39264	Rattus norvegicus beta-2 adrenergic receptor gene, complete cds and promoter region	Rattus norvegicus	41,259	23-Feb-96
rxa00283	1155	GB_GSS8 AQ030327	411	AQ030327	HS_2177_B1_H06_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2177 Col=11 Row=P, genomic survey sequence	Homo sapiens	37,656	1-Jul-98
		GB_PR3.HSL118GB	27858	Z68883	Human DNA sequence from cosmid L118G10, Huntington's Disease Region, chromosome 4p16 3	Homo sapiens	37,412	23-Nov-99
		GB_PR3 HSJ513G18	110770	AL109760	Human DNA sequence from clone 513G18 on chromosome 4, complete sequence.	Homo sapiens	37,412	23-Nov-99
rxa00286	687	GB_EST10 AA157040	414	AA157040	zo51c05 r1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone IMAGE 590408 5' similar to gb M84711 40S RIBOSOMAL PROTEIN S3A (HUMAN),, mRNA sequence	Homo sapiens	37,136	11-DEC-1996
		GB_EST11 AA213935	629	AA213935	zn57a04 r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:562254 5' similar to gb M84711 40S RIBOSOMAL PROTEIN S3A (HUMAN),, mRNA sequence	Homo sapiens	34,219	1-Aug-97
		GB_STS.BLYBG	459	L43987	Hordeum vulgare (clone ABG380) chromosome 4H,6H,7H STS mRNA, sequence tagged site	Hordeum vulgare	37,786	27-Jul-95
rxa00294	552	GB_PR2 HSAC000121	93163	AC000121	Human BAC clone RG249A12 from 7q22, complete sequence.	Homo sapiens	36,735	31-Jan-97
		GB_BA2 CGU31281	1614	U31281	Corynebacterium glutamicum biotin synthase (bioB) gene, complete cds	Corynebacterium glutamicum	100,000	21-Nov-96
		GB_PR2 HSAC000121	93163	AC000121	Human BAC clone RG249A12 from 7q22, complete sequence	Homo sapiens	37,662	31-Jan-97
rxa00297	1035	GB_HTG2 AC006938	82665	AC006938	Drosophila melanogaster chromosome 2 clone DS01630 (D506) map 60C7-60C8 strain y, cn bw sp, *** SEQUENCING IN PROGRESS ***, 9 unordered pieces	Drosophila melanogaster	37,241	2-Aug-99
		GB_HTG2 AC007116	25478	AC007116	Drosophila melanogaster chromosome 2 clone DS04467 (D447) map 60C6-60C8 strain y, cn bw sp, *** SEQUENCING IN PROGRESS ***, 5 unordered pieces	Drosophila melanogaster	38,630	30-Jul-99
		GB_HTG2 AC006938	82665	AC006938	Drosophila melanogaster chromosome 2 clone DS01630 (D506) map 60C7-60C8 strain y, cn bw sp, *** SEQUENCING IN PROGRESS ***, 9 unordered pieces.	Drosophila melanogaster	37,241	2-Aug-99
rxa00320	303	GB_GSS14.AQ585202	564	AQ585202	RPCI-11-451L11 TJ RPCI-11 Homo sapiens genomic clone RPCI-11-451L11, genomic survey sequence	Homo sapiens	37,319	7-Jun-99
		GB_BA1 NGPILC1	3144	Y13022	N.gonorrhoeae pilC1 gene, strain 640	Neisseria gonorrhoeae	38,667	07-OCT-1997

TABLE 4: ALIGNMENT RESULTS

		GB_BA1:NGPILC1	3144	Y13022	N.gonorrhoeae pilC1 gene, strain 640.	Neisseria gonorrhoeae	36,000	07-OCT-1997
rxa00321								
rxa00322	1227	GB_HTG2 AC007533	153053	AC007533	Homo sapiens chromosome 16 clone 474B12, *** SEQUENCING IN PROGRESS ***, 5 ordered pieces	Homo sapiens	39,469	12-MAY-1999
		GB_HTG2:AC007533	153053	AC007533	Homo sapiens chromosome 16 clone 474B12, *** SEQUENCING IN PROGRESS ***, 5 ordered pieces	Homo sapiens	39,469	12-MAY-1999
		GB_PR2 HUM133K23	82512	AC000061	Human BAC clone 133K23 from 7q31 2, complete sequence	Homo sapiens	38,950	14-Nov-96
rxa00325	768	GB_BA2 CDU73860	1273	U73860	Corynebacterium diphtheriae heme oxygenase homolog (hmuO) gene, complete cds	Corynebacterium diphtheriae	52,604	7-Feb-97
		GB_BA1:AB019621	652	AB019621	Corynebacterium diphtheriae mRNA for Heme oxygenase, complete cds	Corynebacterium diphtheriae	55,675	31-Jul-99
		GB_EST23 AI096171	554	AI096171	28 EcoRI Rice Etiolated Leaf cDNA Library Oryza sativa cDNA clone RZ513, mRNA sequence.	Oryza sativa	38,536	19-Aug-98
rxa00326	603	GB_PH MYP4CG	11624	X51522	Bacteriophage P4 complete DNA genome.	Bacteriophage P4	40,577	17-Feb-97
		GB_PH MYP4ALPH	3063	X05623	Bacteriophage P4 alpha gene and cis replication region crr	Bacteriophage P4	38,640	12-Sep-93
		GB_IN1.CEF22B3	30480	Z68336	Caenorhabditis elegans cosmid F22B3, complete sequence	Caenorhabditis elegans	39,012	2-Sep-99
rxa00334	459	GB_BA1 CGGLNA	3686	Y13221	Corynebacterium glutamicum glnA gene.	Corynebacterium glutamicum	37,640	28-Aug-97
		GB_GSS10 AQ248516	259	AQ248516	T5J22-Sp6 TAMU Arabidopsis thaliana genomic clone T5J22, genomic survey sequence	Arabidopsis thaliana	38,525	06-OCT-1998
		GB_BA1 CGGLNA	3686	Y13221	Corynebacterium glutamicum glnA gene	Corynebacterium glutamicum	40,487	28-Aug-97
rxa00336	594	GB_BA1 CGGLNA	3686	Y13221	Corynebacterium glutamicum glnA gene	Corynebacterium glutamicum	34,797	28-Aug-97
		GB_OV XLFIMB1GN	7026	X95549	X.laevis FIM-B 1 gene.	Xenopus laevis	33,217	13-Feb-97
		GB_BA1.CGGLNA	3686	Y13221	Corynebacterium glutamicum glnA gene	Corynebacterium glutamicum	37,371	28-Aug-97
rxa00337	1173	GB_BA1 CGU43536	3464	U43536	Corynebacterium glutamicum heat shock, ATP-binding protein (clpB) gene, complete cds.	Corynebacterium glutamicum	36,406	13-MAR-1997
		GB_BA1 CGAJ4934	1160	AJ004934	Corynebacterium glutamicum dapD gene, complete CDS	Corynebacterium glutamicum	39,734	17-Jun-98
		GB_EST37 AI944838	396	AI944838	bs06a08 y1 Drosophila melanogaster adult testis library Drosophila melanogaster cDNA clone bs06a08 5', mRNA sequence.	Drosophila melanogaster	37,626	17-Aug-99
rxa00338	1263	GB_BA1 BLTRP	7725	X04960	Brevibacterium lactofermentum tryptophan operon	Corynebacterium glutamicum	39,790	10-Feb-99
		GB_PAT E01688	7725	E01688	Genomic DNA of trp operon of prepibacterium latophelmentamn	unidentified	39,871	29-Sep-97
		GB_PAT E01375	7726	E01375	DNA sequence of tryptophan operon	Corynebacterium glutamicum	39,871	29-Sep-97
rxa00339	840	GB_VI OPU75930	131993	U75930	Orgyia pseudotsugata nuclear polyhedrosis virus complete genome	Orgyia pseudotsugata nuclear polyhedrosis virus	38,264	06-MAR-1998
		GB_VI OPU75930	131993	U75930	Orgyia pseudotsugata nuclear polyhedrosis virus complete genome.	Orgyia pseudotsugata nuclear polyhedrosis virus	38,620	06-MAR-1998
		GB_HTG3 AC008340	126593	AC008340	Drosophila melanogaster chromosome 2 clone BACR07J20 (D918) RPCI-98 07 J 20 map 42D-42E strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 92 unordered pieces	Drosophila melanogaster	38,193	6-Aug-99
rxa00342	552	GB_EST34:AI794353	636	AI794353	fc43d12.y1 Zebrafish WashU MPIMG EST Danio rerio cDNA 5' similar to TR Q62868 Q62868 ROK-ALPHA. ,, mRNA sequence	Danio rerio	40,283	2-Jul-99
		GB_PR2 U73635	33676	U73635	Human Chromosome 11 Cosmid cSRL156b6, complete sequence	Homo sapiens	39,366	25-Jul-97
		GB_PR2 U73635	33676	U73635	Human Chromosome 11 Cosmid cSRL156b6, complete sequence	Homo sapiens	37,970	25-Jul-97
rxa00344	1002	GB_HTG2 HS312E8	33595	AL032819	Homo sapiens chromosome 16 clone LA16-312E8, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Homo sapiens	40,415	03-DEC-1999

TABLE 4: ALIGNMENT RESULTS

		GB_HTG2:HS312E8	33595	AL032819	Homo sapiens chromosome 16 clone LA16-312E8, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Homo sapiens	40,415	03-DEC-1999
		GB_OM BOVINOPHOS	1573	M55916	Bovine inositol polyphosphate 1-phosphatase (inositol polyphosphate 1-phosphatase gene) mRNA, complete cds.	Bos taurus	38,420	27-Apr-93
rxa00349	1590	GB_PR3 HS353E16	189765	AL031591	Human DNA sequence from clone 353E16 on chromosome 22q11.22-12 3, complete sequence	Homo sapiens	34,766	23-Nov-99
		GB_HTG2 AC005059	170128	AC005059	Homo sapiens clone RG074A24, *** SEQUENCING IN PROGRESS ***, 25 unordered pieces	Homo sapiens	37,011	13-MAR-1999
		GB_HTG2:AC005059	170128	AC005059	Homo sapiens clone RG074A24, *** SEQUENCING IN PROGRESS ***, 25 unordered pieces	Homo sapiens	37,011	13-MAR-1999
rxa00353	816	GB_BA1 D87976	2352	D87976	Brevibacterium lactofermentum DNA for D-2-hydroxyisocaproate dehydrogenase (ddh), complete cds.	Corynebacterium glutamicum	39,290	7-Feb-99
		GB_BA1 CGDDH	1829	Y00151	Corynebacterium glutamicum ddh gene for meso-diaminopimelate D-dehydrogenase (EC 1 4 1 16)	Corynebacterium glutamicum	39,342	12-Sep-93
		GB_BA1 CGDDH	1829	Y00151	Corynebacterium glutamicum ddh gene for meso-diaminopimelate D-dehydrogenase (EC 1 4.1 16)	Corynebacterium glutamicum	38,624	12-Sep-93
rxa00355	1143	GB_BA1.CGDDH	1829	Y00151	Corynebacterium glutamicum ddh gene for meso-diaminopimelate D-dehydrogenase (EC 1 4 1 16)	Corynebacterium glutamicum	100,000	12-Sep-93
		GB_BA1 D87976	2352	D87976	Brevibacterium lactofermentum DNA for D-2-hydroxyisocaproate dehydrogenase (ddh), complete cds	Corynebacterium glutamicum	98,411	7-Feb-99
		GB_PAT E14511	1034	E14511	DNA encoding Brevibacterium diaminopimelic acid dehydrogenase	Corynebacterium glutamicum	100,000	28-Jul-99
rxa00362	1470	GB_HTG4 AC009043	170748	AC009043	Homo sapiens chromosome 16 clone RPCI-11_184F14, *** SEQUENCING IN PROGRESS ***, 122 unordered pieces.	Homo sapiens	37,337	31-OCT-1999
		GB_HTG4 AC009043	170748	AC009043	Homo sapiens chromosome 16 clone RPCI-11_184F14, *** SEQUENCING IN PROGRESS ***, 122 unordered pieces.	Homo sapiens	37,337	31-OCT-1999
		GB_PR4 HSZO2TJP09	811	AF177521	Homo sapiens tight junction protein ZO-2 (TJP2) gene, exons 8 and 9	Homo sapiens	40,758	28-Sep-99
rxa00373	439	GB_PAT AR004983	2277	AR004983	Sequence 5 from patent US 5747317	Unknown	41,638	04-DEC-1998
		GB_EST37:AI967505	380	AI967505	Ljirnpest03-215-c10 Ljirnp Lambda HybriZap two-hybrid library Lotus japonicus cDNA clone LP215-03-c10 5' similar to 60S ribosomal protein L39, mRNA sequence	Lotus japonicus	45,882	24-Aug-99
		GB_EST27 AI399460	670	AI399460	NCSP4F6T7 Subtracted Perithecial Neurospora crassa cDNA clone SP4F6 3', mRNA sequence	Neurospora crassa	38,571	8-Feb-99
rxa00375	624	GB_IN2:AC004445	61852	AC004445	Drosophila melanogaster DNA sequence (P1 DS00445 (D93)), complete sequence.	Drosophila melanogaster	37,236	01-MAY-1998
		GB_HTG6 AC011694	160557	AC011694	Homo sapiens clone RP11-19D19, *** SEQUENCING IN PROGRESS ***, 33 unordered pieces	Homo sapiens	34,087	03-DEC-1999
		GB_HTG6 AC011694	160557	AC011694	Homo sapiens clone RP11-19D19, *** SEQUENCING IN PROGRESS ***, 33 unordered pieces	Homo sapiens	40,523	03-DEC-1999
rxa00380	744	GB_BA1:COXHSPAB	2302	M20482	C burnetii heat shock operon encoding two heat shock proteins (htpA and htpB), complete cds	Coxiella burnetii	37,788	26-Apr-93
		GB_RO:CBGPIMR	1735	Z37977	C barabensis (griseus) mRNA for glucose phosphate isomerase	Cricetulus griseus	37,823	14-Sep-95
		GB_GSS10 AQ172617	505	AQ172617	HS_3197_A2_G09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3197 Col=18 Row=M, genomic survey sequence	Homo sapiens	37,580	17-OCT-1998
rxa00387	978	GB_BA1 MTY25D10	40838	Z95558	Mycobacterium tuberculosis H37Rv complete genome, segment 28/162	Mycobacterium tuberculosis	60,477	17-Jun-98
		GB_BA1 MSGY224	40051	AD000004	Mycobacterium tuberculosis sequence from clone y224	Mycobacterium tuberculosis	60,270	03-DEC-1996
		GB_BA1 U00018	42991	U00018	Mycobacterium leprae cosmid B2168.	Mycobacterium leprae	37,913	01-MAR-1994
rxa00390	528	GB_IN1 DMU29153	8230	U29153	Drosophila melanogaster nudel (ndl) mRNA, complete cds	Drosophila melanogaster	36,190	08-DEC-1995
		GB_IN1 DMU29153	8230	U29153	Drosophila melanogaster nudel (ndl) mRNA, complete cds	Drosophila melanogaster	37,202	08-DEC-1995
rxa00392	987	GB_IN2.AE001274	268984	AE001274	Leishmania major chromosome 1, complete sequence	Leishmania major	37,885	24-MAR-1999
		GB_EST11 AA270543	516	AA270543	va68h06 r1 Soares mouse 3NME12 5 Mus musculus cDNA clone IMAGE 736571 5', mRNA sequence.	Mus musculus	40,546	26-MAR-1997
		GB_IN2 AE001274	268984	AE001274	Leishmania major chromosome 1, complete sequence	Leishmania major	36,103	24-MAR-1999
rxa00394	456	GB_GSS9 AQ158990	728	AQ158990	nbxb0012L11r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0012L11r, genomic survey sequence.	Oryza sativa	41,463	12-Sep-98

TABLE 4: ALIGNMENT RESULTS

		GB_GSS12:AQ342952	761	AQ342952	RPCI11-122O15.TV RPCI-11 Homo sapiens genomic clone RPCI-11-122O15, genomic survey sequence	Homo sapiens	37,556	07-MAY-1999
		GB_GSS9 AQ158990	728	AQ158990	nbxb0012L11r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0012L11r, genomic survey sequence.	Oryza sativa	37,923	12-Sep-98
rxa00395	423	GB_PR2 HS1052M9	134245	AL022718	Human DNA sequence from clone 1052M9 on chromosome Xq25 Contains the SH2D1A gene for SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome) (DSHP), part of a 60S Acidic Ribosomal protein 1 (RPLP1) LIKE gene and part of a mouse DOC4 LIKE gene Contains ESTs and GSSs, complete sequence	Homo sapiens	43,564	23-Nov-99
		GB_BA2 RCPHSYNG	45959	Z11165	R capsulatus complete photosynthesis gene cluster.	Rhodobacter capsulatus	36,930	2-Sep-99
		GB_PR2 HS1052M9	134245	AL022718	Human DNA sequence from clone 1052M9 on chromosome Xq25 Contains the SH2D1A gene for SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome) (DSHP), part of a 60S Acidic Ribosomal protein 1 (RPLP1) LIKE gene and part of a mouse DOC4 LIKE gene Contains ESTs and GSSs, complete sequence	Homo sapiens	33,981	23-Nov-99
rxa00396	594	GB_PL2 AC002311	85855	AC002311	Arabidopsis thaliana chromosome I BAC T26J12 genomic sequence, complete sequence	Arabidopsis thaliana	38,957	4-Feb-98
		GB_PL2 AC002311	85855	AC002311	Arabidopsis thaliana chromosome I BAC T26J12 genomic sequence, complete sequence	Arabidopsis thaliana	36,300	4-Feb-98
rxa00397	924	GB_PL1 HASMT	27694	D31785	Hansenula wingei mitochondrial DNA, complete sequence	Mitochondrion Pichia canadensis	33,985	10-Jun-99
		GB_PL1 HASMT	27694	D31785	Hansenula wingei mitochondrial DNA, complete sequence	Mitochondrion Pichia canadensis	33,775	10-Jun-99
rxa00398	873	GB_HTG1 CNS01DRT	222150	AL118557	Homo sapiens chromosome 14 clone R-1033H12, *** SEQUENCING IN PROGRESS ***, in ordered pieces.	Homo sapiens	35,417	25-Sep-99
		GB_HTG1 CNS01DRT	222150	AL118557	Homo sapiens chromosome 14 clone R-1033H12, *** SEQUENCING IN PROGRESS ***, in ordered pieces	Homo sapiens	35,417	25-Sep-99
		GB_HTG1 CNS01DRT	222150	AL118557	Homo sapiens chromosome 14 clone R-1033H12, *** SEQUENCING IN PROGRESS ***, in ordered pieces.	Homo sapiens	38,005	25-Sep-99
rxa00399	438	GB_IN1 CELC32B5	42545	U80843	Caenorhabditis elegans cosmid C32B5.	Caenorhabditis elegans	36,468	05-DEC-1996
		GB_IN1 CELC32B5	42545	U80843	Caenorhabditis elegans cosmid C32B5	Caenorhabditis elegans	40,000	05-DEC-1996
rxa00408	570	GB_PR4 AC005940	158414	AC005940	Homo sapiens chromosome 17, clone hRPK 167_N_20, complete sequence	Homo sapiens	35,219	18-MAR-1999
		GB_PR1 HSSERCA11	3050	Y15726	Homo sapiens SERCA3 gene, exons 11-14.	Homo sapiens	35,036	30-Jun-98
		GB_PR4 AC005940	158414	AC005940	Homo sapiens chromosome 17, clone hRPK 167_N_20, complete sequence	Homo sapiens	36,926	18-MAR-1999
rxa00409	1536	GB_PR1 HSSERCA11	3050	Y15726	Homo sapiens SERCA3 gene, exons 11-14	Homo sapiens	38,555	30-Jun-98
		GB_PR4 AC005940	158414	AC005940	Homo sapiens chromosome 17, clone hRPK 167_N_20, complete sequence	Homo sapiens	36,370	18-MAR-1999
		GB_PR3 HS591B8	142552	AL035410	Human DNA sequence from clone 591B8 on chromosome 1p13 1, complete sequence	Homo sapiens	35,891	23-Nov-99
rxa00411	798	GB_BA1 AP000003	233000	AP000003	Pyrococcus horikoshii OT3 genomic DNA, 544001-777000 nt position (3/7)	Pyrococcus horikoshii	36,849	8-Feb-99
		GB_PL2 F25A4	115721	AC008263	Arabidopsis thaliana chromosome 1 BAC F25A4 sequence, complete sequence	Arabidopsis thaliana	37,628	15-Sep-99
		GB_PR3 HS413H6	142599	AL022724	Human DNA sequence from clone 413H6 on chromosome 6p22 3-24 3 Contains a hamster Androgen-dependent Expressed Protein like protein gene, ESTs and GSSs, complete sequence	Homo sapiens	36,755	23-Nov-99
rxa00416	1673	GB_EST8 C10137	360	C10137	C10137 Yuji Kohara unpublished cDNA Strain N2 hermaphrodite embryo Caenorhabditis elegans cDNA clone yk188a1 5', mRNA sequence	Caenorhabditis elegans	35,574	18-OCT-1999
		GB_EST36:AV186952	376	AV186952	AV186952 Yuji Kohara unpublished cDNA Strain N2 hermaphrodite embryo Caenorhabditis elegans cDNA clone yk506a5 5', mRNA sequence	Caenorhabditis elegans	36,702	22-Jul-99
		GB_EST16 C48235	383	C48235	C48235 Yuji Kohara unpublished cDNA.Strain N2 hermaphrodite embryo Caenorhabditis elegans cDNA clone yk459h10 5', mRNA sequence	Caenorhabditis elegans	42,440	18-OCT-1999
rxa00422	1017	GB_BA1 MTCY227	35946	Z77724	Mycobacterium tuberculosis H37Rv complete genome, segment 114/162	Mycobacterium tuberculosis	39,822	17-Jun-98
		GB_BA1 MTV023	47852	AL022022	Mycobacterium tuberculosis H37Rv complete genome, segment 148/162	Mycobacterium tuberculosis	39,841	17-Jun-98

TABLE 4: ALIGNMENT RESULTS

		GB_PR3:AC003091	137817	AC003091	Human BAC clone RG326G04 from 7p21, complete sequence.	Homo sapiens	36,653	6-Nov-97
rxa00423	576	GB_BA1 AP000063	185300	AP000063	Aeropyrum pernix genomic DNA, section 6/7	Aeropyrum pernix	38,908	22-Jun-99
		GB_IN1.LDHSP100	7726	Z94053	L.donovani hsp100 gene	Leishmania donovani	39,646	28-Apr-97
		GB_GSS11 AQ274393	572	AQ274393	nbxb0035G12r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0035G12r, genomic survey sequence.	Oryza sativa	35,714	3-Nov-98
rxa00424	594	GB_BA1 AP000063	185300	AP000063	Aeropyrum pernix genomic DNA, section 6/7	Aeropyrum pernix	38,225	22-Jun-99
		GB_BA1 AP000063	185300	AP000063	Aeropyrum pernix genomic DNA, section 6/7	Aeropyrum pernix	36,735	22-Jun-99
		GB_IN1.LDHSP100	7726	Z94053	L.donovani hsp100 gene	Leishmania donovani	35,125	28-Apr-97
rxa00425	348	GB_EST30 AV021214	281	AV021214	AV021214 Mus musculus 18-day embryo C57BL/6J Mus musculus cDNA clone 1190021P08, mRNA sequence	Mus musculus	35,849	28-Aug-99
		GB_HTG3:AC009278	164119	AC009278	Homo sapiens clone 44_J_4, *** SEQUENCING IN PROGRESS ***, 14 unordered pieces	Homo sapiens	36,705	12-Aug-99
		GB_HTG3 AC009278	164119	AC009278	Homo sapiens clone 44_J_4, *** SEQUENCING IN PROGRESS ***, 14 unordered pieces	Homo sapiens	36,705	12-Aug-99
rxa00428	756	GB_BA2 AF127082	10847	AF127082	Myxococcus xanthus ATP-dependent protease proteolytic subunit ClpP (clpP), ATP-dependent protease ATPase subunit ClpX (clpX), prolyl endopeptidase precursor Pep (pep), ATP-dependent protease LonV(lonV), oligopeptide permease homolog OppA (oppA), oligopeptide permease homolog OppB (oppB), and oligopeptide permease homolog OppC (oppC) genes, complete cds	Myxococcus xanthus	40,995	18-MAY-1999
		GB_PL1:AB017080	653	AB017080	Porphyra sp DNA, internal transcribed spacer 1 (ITS1)	Porphyra sp	38,491	10-Sep-99
		GB_EST27:AI442425	541	AI442425	sa26g05.y1 Gm-c1004 Glycine max cDNA clone GENOME SYSTEMS CLONE ID Gm-c1004-465 5' similar to SW NDC1_RABIT Q28615 RENAL SODIUM/DICARBOXYLATE COTRANSPORTER ,, mRNA sequence	Glycine max	40,000	01-DEC-1999
rxa00429	525	GB_EST3 R33129	440	R33129	yh81c08 s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE 136142 3' similar to gb X53742_rna1 FIBULIN 1, ISOFORM B PRECURSOR (HUMAN),, mRNA sequence	Homo sapiens	37,216	28-Apr-95
		GB_PH AF115103	40739	AF115103	Streptococcus thermophilus bacteriophage Sfi21, complete genome	Streptococcus thermophilus bacteriophage Sfi21	36,069	18-Jul-99
		GB_PH AF115102	37370	AF115102	Streptococcus thermophilus bacteriophage Sfi19, complete genome	Streptococcus thermophilus bacteriophage Sfi19	36,260	18-Jul-99
rxa00430	534	GB_BA1 MSGY126	37164	AD000012	Mycobacterium tuberculosis sequence from clone y126	Mycobacterium tuberculosis	55,491	10-DEC-1996
		GB_BA1 MTY13D12	37085	Z80343	Mycobacterium tuberculosis H37Rv complete genome; segment 156/162	Mycobacterium tuberculosis	55,491	17-Jun-98
		GB_BA1:MSGB971CS	37566	L78821	Mycobacterium leprae cosmid B971 DNA sequence	Mycobacterium leprae	36,905	15-Jun-96
rxa00433	648	GB_PR2 AP000073	100000	AP000073	Homo sapiens genomic DNA, chromosome 8p11 2, senescence gene region, section 9/19, complete sequence	Homo sapiens	38,043	20-Nov-99
		GB_IN1 CELF29G9	42751	AF016440	Caenorhabditis elegans cosmid F29G9	Caenorhabditis elegans	35,474	7-Aug-97
		GB_BA1.MSGY414A	40121	AD000007	Mycobacterium tuberculosis sequence from clone y414a	Mycobacterium tuberculosis	36,809	03-DEC-1996
rxa00447								
rxa00451	615	GB_EST26 AI389267	643	AI389267	GH20396.5prime GH Drosophila melanogaster head pOT2 Drosophila melanogaster cDNA clone GH20396 5prime, mRNA sequence	Drosophila melanogaster	41,085	28-Jan-99
		GB_EST37 AI945493	574	AI945493	bs13e05 y1 Drosophila melanogaster adult testis library Drosophila melanogaster cDNA clone bs13e05 5', mRNA sequence	Drosophila melanogaster	44,040	17-Aug-99
		GB_GSS11 AQ288118	630	AQ288118	nbxb0032I18r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0032I18r, genomic survey sequence.	Oryza sativa	37,885	03-DEC-1998
rxa00455	873	GB_IN1 DMOVO	6655	X59772	D melanogaster ovo gene required for female germ line development	Drosophila melanogaster	35,104	24-Feb-99
		GB_EST14 AA390588	513	AA390588	LD09657.5prime LD Drosophila melanogaster embryo BlueScript Drosophila melanogaster cDNA clone LD09657 5prime, mRNA sequence	Drosophila melanogaster	39,759	28-Nov-98

TABLE 4: ALIGNMENT RESULTS

		GB_EST19:AA801874	621	AA801874	GM03519.5prime GM Drosophila melanogaster ovary BlueScript Drosophila melanogaster cDNA clone GM03519 5prime similar to U11383 ovo FBgn0003028 PID g520527 SWISS-PROT:P51521, mRNA sequence	Drosophila melanogaster	35,437	25-Nov-98
rxa00457	1203	GB_GSS8:AQ000125	398	AQ000125	CIT-HSP-2282P3 TF CIT-HSP Homo sapiens genomic clone 2282P3, genomic survey sequence	Homo sapiens	41,730	26-Jun-98
		GB_IN1:DROADDLIKE	4209	L14330	Drosophila melanogaster adducin-like protein, complete cds	Drosophila melanogaster	37,795	11-Jun-93
		GB_IN1:DROHTSC	3922	L05016	Drosophila melanogaster hu-li tai shao (hts) mRNA, complete cds	Drosophila melanogaster	37,081	26-Apr-93
rxa00462	1503	GB_HTG3 AC009210	103814	AC009210	Drosophila melanogaster chromosome 2 clone BACR01I06 (D1054) RPCI-98 01 I 6 map 55D-55D strain y, cn bw sp, *** SEQUENCING IN PROGRESS ***, 86 unordered pieces	Drosophila melanogaster	33,356	20-Aug-99
		GB_HTG3 AC009210	103814	AC009210	Drosophila melanogaster chromosome 2 clone BACR01I06 (D1054) RPCI-98 01 I 6 map 55D-55D strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 86 unordered pieces	Drosophila melanogaster	33,356	20-Aug-99
		GB_BA1:SCE9	37730	AL049841	Streptomyces coelicolor cosmid E9	Streptomyces coelicolor	37,308	19-MAY-1999
rxa00463	945	GB_BA2 AF052652	2096	AF052652	Corynebacterium glutamicum homoserine O-acetyltransferase (metA) gene, complete cds	Corynebacterium glutamicum	99,481	19-MAR-1998
		GB_GSS12 AQ407770	500	AQ407770	HS_5069_B1_F03_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=645 Col=5 Row=L, genomic survey sequence	Homo sapiens	40,081	17-MAR-1999
		GB_GSS15.AQ596209	358	AQ596209	HS_5482_A2_H10_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=1058 Col=20 Row=O, genomic survey sequence	Homo sapiens	40,000	8-Jun-99
rxa00468	942	GB_EST32.AI763196	341	AI763196	wi65h04 x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE 2398231 3', mRNA sequence	Homo sapiens	38,824	24-Jun-99
		GB_EST17 AA652964	329	AA652964	ns62e02 s1 NCI_CGAP_Pr22 Homo sapiens cDNA clone IMAGE 1188218 3', mRNA sequence	Homo sapiens	41,104	13-Nov-97
		GB_EST20 AA864303	411	AA864303	oh54d02.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE 1470435 3', mRNA sequence	Homo sapiens	41,422	13-MAY-1998
rxa00469	1299	GB_PR4:AC005988	173126	AC005988	Homo sapiens chromosome 17, clone hRPK 299_G_24, complete sequence	Homo sapiens	34,699	15-Jan-99
		GB_PR4 AC005988	173126	AC005988	Homo sapiens chromosome 17, clone hRPK 299_G_24, complete sequence	Homo sapiens	35,725	15-Jan-99
		GB_HTG3 AC009116	186292	AC009116	Homo sapiens chromosome 16 clone RPCI-11_477D3, *** SEQUENCING IN PROGRESS ***, 47 unordered pieces	Homo sapiens	36,222	3-Aug-99
rxa00472	942	GB_HTG3 AC007882	214882	AC007882	Homo sapiens clone NH0499D05, *** SEQUENCING IN PROGRESS ***, 2 unordered pieces	Homo sapiens	38,245	8-Sep-99
		GB_HTG3 AC007882	214882	AC007882	Homo sapiens clone NH0499D05, *** SEQUENCING IN PROGRESS ***, 2 unordered pieces	Homo sapiens	38,245	8-Sep-99
		GB_PR2 HUAC002038	161973	AC002038	Homo sapiens chromosome 2 clone 101B6 map 2p11, complete sequence	Homo sapiens	37,961	30-Jun-97
rxa00473	912	GB_HTG3.AC011445	144370	AC011445	Homo sapiens chromosome 19 clone CIT-HSPC_246B18, *** SEQUENCING IN PROGRESS ***, 31 unordered pieces	Homo sapiens	38,470	07-OCT-1999
		GB_HTG3.AC011445	144370	AC011445	Homo sapiens chromosome 19 clone CIT-HSPC_246B18, *** SEQUENCING IN PROGRESS ***, 31 unordered pieces	Homo sapiens	38,470	07-OCT-1999
		GB_RO:AB026437	2097	AB026437	Mus musculus DNA, 5' flanking region of interleukin 12 receptor beta 1	Mus musculus	40,000	02-OCT-1999
rxa00474	1701	GB_GSS10 AQ223838	543	AQ223838	HS_2218_A1_H03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2218 Col=5 Row=O, genomic survey sequence	Homo sapiens	40,189	20-Sep-98
		GB_GSS10 AQ223838	543	AQ223838	HS_2218_A1_H03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2218 Col=5 Row=O, genomic survey sequence	Homo sapiens	37,944	20-Sep-98
rxa00475	783	GB_PL2.GMAKHSDH2	10535	AF049708	Glycine max aspartokinase-homoserine dehydrogenase (AK-HSDH) gene, partial cds	Glycine max	36,446	7-Jul-99
		GB_EST14.AA386651	351	AA386651	vb54b04 r1 Ko mouse embryo 11 5dpc Mus musculus cDNA clone IMAGE:760783 5', mRNA sequence	Mus musculus	41,311	23-Apr-97
		GB_EST14.AA386603	498	AA386603	vb53c02 r1 Ko mouse embryo 11 5dpc Mus musculus cDNA clone IMAGE 760706 5' similar to TR G56689 G56689 DIMETHYLGLYCINE DEHYDROGENASE ;, mRNA sequence.	Mus musculus	40,644	23-Apr-97
rxa00476	984	GB_GSS5 AQ770769	554	AQ770769	HS_5357_B2_H01_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=933 Col=2 Row=P, genomic survey sequence.	Homo sapiens	35,560	28-Jul-99
		GB_IN1 CEM162	39977	Z82278	Caenorhabditis elegans cosmid M162, complete sequence	Caenorhabditis elegans	34,224	19-Nov-99
		GB_IN1:CEM162	39977	Z82278	Caenorhabditis elegans cosmid M162, complete sequence	Caenorhabditis elegans	33,777	19-Nov-99
rxa00481	708	GB_PR4 AC005013	195910	AC005013	Homo sapiens BAC clone GS165L15 from 7p15, complete sequence	Homo sapiens	35,755	28-Nov-98
		GB_HTG1 PFMAL4P4	224448	AL035477	Plasmodium falciparum chromosome 4 strain 3D7, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Plasmodium falciparum	37,213	11-Aug-99

TABLE 4: ALIGNMENT RESULTS

		GB_HTG1:PFMAL4P4	224448	AL035477	Plasmodium falciparum chromosome 4 strain 3D7, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Plasmodium falciparum	37,213	11-Aug-99
rxa00485	2418	GB_EST30 AV017239	238	AV017239	AV017239 Mus musculus 18-day embryo C57BL/6J Mus musculus cDNA clone 1110069G23, mRNA sequence	Mus musculus	39,916	28-Aug-99
		GB_EST33 AV093875	254	AV093875	AV093875 Mus musculus C57BL/6J ES cell Mus musculus cDNA clone 2400006D21, mRNA sequence	Mus musculus	38,189	22-Nov-99
		GB_EST33 AV084536	287	AV084536	AV084536 Mus musculus tongue C57BL/6J adult Mus musculus cDNA clone 2310007K01, mRNA sequence	Mus musculus	37,282	25-Jun-99
rxa00486	1032	GB_RO MUSP3VPR2	1089	AF098867	Mus sp 129SV V3/V1b vasopressin receptor gene, exon 2 and complete cds	Mus musculus	38,163	28-Apr-99
		GB_GSS9 AQ166448	407	AQ166448	HS_3137_B2_A06_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3137 Col=12 Row=B, genomic survey sequence	Homo sapiens	40,250	16-OCT-1998
		GB_GSS15 AQ614261	505	AQ614261	HS_5123_B1_F11_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=699 Col=21 Row=L, genomic survey sequence	Homo sapiens	37,905	15-Jun-99
rxa00490	1026	GB_EST15 AA463205	282	AA463205	zx71c06 s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE 796906 3', mRNA sequence.	Homo sapiens	39,502	10-Jun-97
		GB_BA1 SLLINC	36270	X79146	S lincolnensis (78-11) Lincomycin production genes.	Streptomyces lincolnensis	37,278	15-MAY-1996
		GB_GSS3 B10984	646	B10984	F22I8-Sp6 IGF Arabidopsis thaliana genomic clone F22I8, genomic survey sequence.	Arabidopsis thaliana	39,205	14-MAY-1997
rxa00491	543	GB_HTG1 CEY87G2	330612	AL022597	Caenorhabditis elegans chromosome I clone Y87G2, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Caenorhabditis elegans	37,405	26-OCT-1999
		GB_HTG1 CEY87G2	330612	AL022597	Caenorhabditis elegans chromosome I clone Y87G2, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Caenorhabditis elegans	37,405	26-OCT-1999
		GB_HTG1:CEY6B3	253516	Z92865	Caenorhabditis elegans chromosome I clone Y6B3, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Caenorhabditis elegans	38,213	30-Jul-98
rxa00493	1737	GB_BA1:SC6G4	41055	AL031317	Streptomyces coelicolor cosmid 6G4	Streptomyces coelicolor	61,649	20-Aug-98
		GB_BA2:U00015	42325	U00015	Mycobacterium leprae cosmid B1620.	Mycobacterium leprae	38,567	01-MAR-1994
		GB_BA1 U00020	36947	U00020	Mycobacterium leprae cosmid B229	Mycobacterium leprae	38,567	01-MAR-1994
rxa00496	1149	GB_VI:TVRNAP	6404	X68414	Toscana Virus genomic RNA for RNA-dependent RNA polymerase	Toscana virus	35,428	27-OCT-1992
		GB_IN2 DMU09808	9239	U09808	Drosophila melanogaster twisted gastrulation (tsg) and serine protease (gd) genes, complete cds	Drosophila melanogaster	36,837	25-Jun-98
		GB_IN2 DMU09808	9239	U09808	Drosophila melanogaster twisted gastrulation (tsg) and serine protease (gd) genes, complete cds	Drosophila melanogaster	37,782	25-Jun-98
rxa00504	543	GB_BA1:MTCY159	33818	Z83863	Mycobacterium tuberculosis H37Rv complete genome, segment 111/162	Mycobacterium tuberculosis	36,961	17-Jun-98
		GB_PR1 HUMHM145	2214	D10925	Human mRNA for HM145	Homo sapiens	36,066	3-Feb-99
		GB_EST14 AA415083	332	AA415083	Mg0017 RCW Lambda Zap Express Library Pyricularia grisea cDNA clone RCW17 5', mRNA sequence	Pyricularia grisea	40,181	09-DEC-1999
rxa00505	618	GB_PAT I92047	551	I92047	Sequence 14 from patent US 5726299	Unknown	46,250	01-DEC-1998
		GB_PAT I78759	549	I78759	Sequence 15 from patent US 5693781	Unknown	44,813	3-Apr-98
		GB_PAT:I92048	549	I92048	Sequence 15 from patent US 5726299	Unknown	44,813	01-DEC-1998
rxa00507	978	GB_PR2 HS1063B2	114596	AL035683	Human DNA sequence from clone 1063B2 on chromosome 20q13 1-13 2 Contains the 3' part of the gene for Beta-1,4-galactosyltransferase, ESTs, STSs and GSSs, complete sequence	Homo sapiens	36,449	23-Nov-99
		GB_HTG2 AC007225	218892	AC007225	Homo sapiens chromosome 16 clone 480G7, *** SEQUENCING IN PROGRESS ***, 38 unordered pieces	Homo sapiens	36,646	6-Apr-99
		GB_HTG2 AC007225	218892	AC007225	Homo sapiens chromosome 16 clone 480G7, *** SEQUENCING IN PROGRESS ***, 38 unordered pieces	Homo sapiens	36,646	6-Apr-99
rxa00510	1632	GB_GSS4 AQ707590	499	AQ707590	HS_5560_B1_H02_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=1136 Col=3 Row=P, genomic survey sequence	Homo sapiens	37,275	7-Jul-99
		GB_GSS4 AQ707590	499	AQ707590	HS_5560_B1_H02_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=1136 Col=3 Row=P, genomic survey sequence	Homo sapiens	37,275	7-Jul-99

TABLE 4: ALIGNMENT RESULTS

rxa00515	825	GB_BA1:CGICD	3595	X71489	C.glutamicum icd gene for monomeric isocitrate dehydrogenase.	Corynebacterium glutamicum	100,000	17-Feb-95
		GB_BA1.CGICD	3595	X71489	C glutamicum icd gene for monomeric isocitrate dehydrogenase	Corynebacterium glutamicum	38,150	17-Feb-95
		GB_GSS13 AQ451896	509	AQ451896	HS_5184_B1_C03_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=760 Col=5 Row=F, genomic survey sequence	Homo sapiens	36,638	21-Apr-99
rxa00519	2337	GB_BA1 CGICD	3595	X71489	C glutamicum icd gene for monomeric isocitrate dehydrogenase	Corynebacterium glutamicum	100,000	17-Feb-95
		GB_BA2 AF127018	2560	AF127018	Streptomyces coelicolor isocitrate dehydrogenase (idh) gene, idh-B allele, complete cds	Streptomyces coelicolor	66,667	1-Jun-99
		GB_BA1.AVIICD	3550	D73443	Azotobacter vinelandii icd gene for isocitrate dehydrogenase, complete cds	Azotobacter vinelandii	63,652	4-Feb-99
rxa00527	1887	GB_PAT I92049	2248	I92049	Sequence 16 from patent US 5726299	Unknown.	39,250	01-DEC-1998
		GB_PAT.I92053	2213	I92053	Sequence 20 from patent US 5726299	Unknown	70,635	01-DEC-1998
		GB_BA1 MTCY98	31225	Z83860	Mycobacterium tuberculosis H37Rv complete genome, segment 103/162	Mycobacterium tuberculosis	37,741	17-Jun-98
rxa00528	1212	GB_BA1 MSGY219	38721	AD000013	Mycobacterium tuberculosis sequence from clone y219	Mycobacterium tuberculosis	68,672	10-DEC-1996
		GB_BA1:MTCY21D4	20760	Z80775	Mycobacterium tuberculosis H37Rv complete genome, segment 3/262	Mycobacterium tuberculosis	39,762	24-Jun-99
		GB_BA1:SCH24	41625	AL049826	Streptomyces coelicolor cosmid H24	Streptomyces coelicolor	40,411	11-MAY-1999
rxa00529	666	GB_PR2:HSAC000109	41122	AC000109	Human Cosmid g0771a222 from 7q31 3, complete sequence	Homo sapiens	37,462	11-Sep-97
		GB_PR2:HSAC000110	45508	AC000110	Human Cosmid g0771a233, complete sequence	Homo sapiens	37,462	30-Jan-97
		GB_PR2:HSAC000109	41122	AC000109	Human Cosmid g0771a222 from 7q31 3, complete sequence	Homo sapiens	39,724	11-Sep-97
rxa00530	1404	GB_PR3 HS435C23	151798	Z92844	Human DNA sequence from PAC 435C23 on chromosome X Contains ESTs	Homo sapiens	36,482	23-Nov-99
		GB_PR3 HS435C23	151798	Z92844	Human DNA sequence from PAC 435C23 on chromosome X Contains ESTs	Homo sapiens	37,918	23-Nov-99
		GB_PL1 YSCADE3	4883	M12878	Saccharomyces cerevisiae C-1-tetrahydrofolate synthase (ADE3) gene, complete cds.	Saccharomyces cerevisiae	37,034	11-MAY-1995
rxa00535	840	GB_BA1 CGLEUA	3492	X70959	C glutamicum gene leuA for isopropylmalate synthase	Corynebacterium glutamicum	100,000	10-Feb-99
		GB_BA1 CORASKD	2957	L16848	Corynebacterium flavum aspartokinase (ask), and aspartate-semialdehyde dehydrogenase (asd) genes, complete cds	Corynebacterium flavescens	43,750	11-Jun-93
		GB_GSS10 AQ193141	515	AQ193141	HS_3060_B1_F11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3060 Col=21 Row=L, genomic survey sequence	Homo sapiens	44,773	4-Nov-98
rxa00540	366	GB_PAT I92052	2115	I92052	Sequence 19 from patent US 5726299	Unknown	74,795	01-DEC-1998
		GB_HTG2.AC008095	126322	AC008095	Drosophila melanogaster chromosome 2 clone BACR11H16 (D932) RPCI-98 11 H 16 map 52A-52A strain y, cn bw sp, *** SEQUENCING IN PROGRESS ***, 95 unordered pieces	Drosophila melanogaster	41,899	2-Aug-99
		GB_HTG2 AC008095	126322	AC008095	Drosophila melanogaster chromosome 2 clone BACR11H16 (D932) RPCI-98 11 H 16 map 52A-52A strain y, cn bw sp, *** SEQUENCING IN PROGRESS***, 95 unordered pieces	Drosophila melanogaster	41,899	2-Aug-99
rxa00547	1521	GB_BA1 MSGY219	38721	AD000013	Mycobacterium tuberculosis sequence from clone y219	Mycobacterium tuberculosis	36,910	10-DEC-1996
		GB_BA1 MTCY21D4	20760	Z80775	Mycobacterium tuberculosis H37Rv complete genome, segment 3/262	Mycobacterium tuberculosis	51,125	24-Jun-99
		GB_EST27 AI415174	292	AI415174	mc05c02 x1 Soares mouse p3NMF19 5 Mus musculus cDNA clone IMAGE:338018 3', mRNA sequence	Mus musculus	39,384	9-Feb-99
rxa00549	1797	GB_PL2 ATAC007135	27313	AC007135	Arabidopsis thaliana chromosome II BAC F9C22 genomic sequence, complete sequence	Arabidopsis thaliana	35,584	26-MAY-1999
		GB_PL2 ATAC006921	76042	AC006921	Arabidopsis thaliana chromosome II BAC F2H17 genomic sequence, complete sequence	Arabidopsis thaliana	36,581	23-MAR-1999
		GB_PL2 ATAC007135	27313	AC007135	Arabidopsis thaliana chromosome II BAC F9C22 genomic sequence, complete sequence	Arabidopsis thaliana	35,827	26-MAY-1999
rxa00550								
rxa00552	1059	GB_BA1 D90742	19201	D90742	Escherichia coli genomic DNA (23 8 - 24 2 min)	Escherichia coli	46,072	7-Feb-99
		GB_BA1:ECHTRB	3129	X61000	E coli K12 HtrB gene	Escherichia coli	39,164	30-Jun-93

TABLE 4: ALIGNMENT RESULTS

		GB_BA2:AE000207	11148	AE000207	Escherichia coli K-12 MG1655 section 97 of 400 of the complete genome.	Escherichia coli	46,072	12-Nov-98
rxa00553	444	GB_EST18:AB009093	479	AB009093	AB009093 Chlamydomonas W80 lambda ZAP II Chlamydomonas sp cDNA similar to photosystem II 10 kDa protein, mRNA sequence.	Chlamydomonas sp	41,808	05-DEC-1997
		GB_EST30.AI640954	641	AI640954	AEMTAP02 Aedes aegypti MT pSPORT Library Aedes aegypti cDNA clone AP02 5', mRNA sequence	Aedes aegypti	38,991	28-Apr-99
		GB_GSS13 AQ467517	206	AQ467517	HS_5219_A2_F02_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=795 Col=4 Row=K, genomic survey sequence	Homo sapiens	45,255	23-Apr-99
rxa00554	594	GB_EST6.W04418	364	W04418	za43c06 r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE 295306 5', mRNA sequence	Homo sapiens	39,688	22-Apr-96
		GB_EST35 AL041829	564	AL041829	DKFZp434C0318_s1 434 (synonym htes3) Homo sapiens cDNA clone DKFZp434C0318 3', mRNA sequence.	Homo sapiens	40,433	29-Sep-99
		GB_EST35 AL041828	386	AL041828	DKFZp434C0318_r1 434 (synonym htes3) Homo sapiens cDNA clone DKFZp434C0318 5', mRNA sequence	Homo sapiens	39,688	29-Sep-99
rxa00555								
rxa00560	498	GB_BA1 MTCY7H7A	10451	Z95618	Mycobacterium tuberculosis H37Rv complete genome, segment 39/162.	Mycobacterium tuberculosis	52,727	17-Jun-98
		GB_BA1 BAPURF	1885	X91252	B ammoniagenes purF gene	Corynebacterium ammoniagenes	61,092	5-Jun-97
		GB_PL1:YSCMET10A	3650	L26504	Saccharomyces carlsbergensis assimilatory sulfite reductase (MET10) gene, complete cds	Saccharomyces pastorianus	41,273	7-Feb-95
rxa00563	2762	GB_BA1 BAFASAA	10549	X64795	B ammoniagenes FAS gene	Corynebacterium ammoniagenes	66,910	14-OCT-1997
		GB_BA1:MTCY159	33818	Z83863	Mycobacterium tuberculosis H37Rv complete genome, segment 111/162	Mycobacterium tuberculosis	40,066	17-Jun-98
		GB_BA1 MBU36763	8391	U36763	Mycobacterium bovis fatty acid synthase gene, complete cds	Mycobacterium bovis	61,178	15-Jul-96
rxa00564	528	GB_PR3 HS833B7	86574	AL008637	Human DNA sequence from clone 833B7 on chromosome 22q12 3-13 2 Contains genes for NCF4 (P40PHOX) protein,cytokine receptor common beta chain precursor CSF2RB (partial), ESTs, CA repeat, STS, GSS, complete sequence	Homo sapiens	39,015	23-Nov-99
		GB_HTG3 AC008543	278334	AC008543	Homo sapiens chromosome 19 clone CIT-HSPC_499B15, *** SEQUENCING IN PROGRESS ***, 134 unordered pieces	Homo sapiens	36,328	2-Sep-99
		GB_HTG3 AC008543	278334	AC008543	Homo sapiens chromosome 19 clone CIT-HSPC_499B15, *** SEQUENCING IN PROGRESS ***, 134 unordered pieces	Homo sapiens	36,328	2-Sep-99
rxa00573								
rxa00574	1002	GB_GSS11 AQ301816	481	AQ301816	HS_3174_A1_B04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3174 Col=7 Row=C, genomic survey sequence	Homo sapiens	43,137	16-DEC-1998
		GB_PR3 AC004537	88872	AC004537	Homo sapiens PAC clone DJ0872F07 from 7q31, complete sequence	Homo sapiens	34,712	9-Apr-98
		GB_EST29 AI563059	339	AI563059	EST00183 watermelon lambda zap library Citrullus lanatus cDNA clone WMLS355 5' similar to unknown protein, mRNA sequence	Citrullus lanatus	37,758	26-MAR-1999
rxa00576	795	GB_EST37 AI947508	533	AI947508	603022E09 x1 603 - stressed root cDNA library from Wang/Bohnert lab Zea mays cDNA, mRNA sequence	Zea mays	38,728	19-Aug-99
		GB_GSS11:AQ296770	347	AQ296770	HS_3087_A2_B12_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3087 Col=24 Row=C, genomic survey sequence	Homo sapiens	40,058	15-DEC-1998
		GB_GSS13 AQ503769	589	AQ503769	RPCI-11-282O13 TV RPCI-11 Homo sapiens genomic clone RPCI-11-282O13, genomic survey sequence	Homo sapiens	37,993	29-Apr-99
rxa00577	471	GB_GSS14 AQ533027	638	AQ533027	RPCI-11-351M24 TJ RPCI-11 Homo sapiens genomic clone RPCI-11-351M24, genomic survey sequence	Homo sapiens	34,944	18-MAY-1999

TABLE 4: ALIGNMENT RESULTS

		GB_PR3:HS440B3	28047	AL022331	Homo sapiens DNA sequence from clone 440B3 on chromosome 22q12.1-3 Contains a pseudogene similar to 60S Ribosomal protein L17 Contains ESTs and an STS (genomic marker D22S1176), complete sequence	Homo sapiens	33,626	23-Nov-99
		GB_PL2 ZEU19267	1230	U19267	Zinnia elegans cysteine proteinase mRNA, complete cds	Zinnia elegans	35,456	26-Aug-96
rxa00578								
rxa00582	642	GB_BA1.CORAHPS	2570	L07603	Corynebacterium glutamicum 3-deoxy-D-arabinoheptulosonate-7-phosphate synthase gene, complete cds	Corynebacterium glutamicum	98,901	26-Apr-93
		GB_PR3 AC005389	120359	AC005389	Homo sapiens chromosome 17, clone hRPK 601_N_13, complete sequence	Homo sapiens	38,315	14-Aug-98
		GB_HTG6 AC008002	126629	AC008002	Drosophila melanogaster chromosome 2 clone BACR48E08 (D843) RPCI-98 48 E 8 map 21D-21E strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 85 unordered pieces	Drosophila melanogaster	32,437	07-DEC-1999
rxa00585	441	GB_BA1 CORAHPS	2570	L07603	Corynebacterium glutamicum 3-deoxy-D-arabinoheptulosonate-7-phosphate synthase gene, complete cds.	Corynebacterium glutamicum	98,039	26-Apr-93
		GB_PR4 AC004970	149951	AC004970	Homo sapiens BAC clone DJ1122F04 from 7q11 23-q21 2, complete sequence	Homo sapiens	39,900	27-Aug-99
		GB_PR2 HS102G20	99207	Z99127	Human DNA sequence from PAC 102G20 on chromosome 1q24-q25 Contains ESTS, STSs and a predicted CpG island	Homo sapiens	41,509	23-Nov-99
rxa00586	1005	GB_BA1 MTV017	67200	AL021897	Mycobacterium tuberculosis H37Rv complete genome; segment 48/162	Mycobacterium tuberculosis	56,219	24-Jun-99
		GB_BA1.MLU15183	36800	U15183	Mycobacterium leprae cosmid B1740	Mycobacterium leprae	55,622	09-MAR-1995
		GB_BA1 MTV017	67200	AL021897	Mycobacterium tuberculosis H37Rv complete genome, segment 48/162	Mycobacterium tuberculosis	37,838	24-Jun-99
rxa00587	459	GB_EST37 AI993539	514	AI993539	701496589 A thaliana, Ohio State clone set Arabidopsis thaliana cDNA clone 701496589, mRNA sequence	Arabidopsis thaliana	40,153	8-Sep-99
		GB_GSS10:AQ224941	511	AQ224941	HS_2009_B1_B06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2009 Col=11 Row=D, genomic survey sequence	Homo sapiens	43,750	20-Sep-98
		GB_EST23:AI099719	475	AI099719	33872 Lambda-PRL2 Arabidopsis thaliana cDNA clone 120M10XP 3', mRNA sequence	Arabidopsis thaliana	36,752	21-Aug-98
rxa00589	573	GB_PL2 ATAC003673	70575	AC003673	Arabidopsis thaliana chromosome II BAC F19F24 genomic sequence, complete sequence	Arabidopsis thaliana	39,785	1-Apr-98
		GB_PR3.HS427A4	149466	Z98049	Human DNA sequence from PAC 427A4 on chromosome 6q26-q27 Contains ribosomal protein S6 kinase, RSK3, ESTs, CpG island	Homo sapiens	35,145	23-Nov-99
		GB_PL2 ATAC005724	86671	AC005724	Arabidopsis thaliana chromosome II P1 MSF3 genomic sequence, complete sequence	Arabidopsis thaliana	39,785	24-Jan-99
rxa00595								
rxa00597	393	GB_PR3 AC004659	129577	AC004659	Homo sapiens chromosome 19, CIT-HSP-87m17 BAC clone, complete sequence	Homo sapiens	39,459	02-MAY-1998
		GB_GSS14 AQ575039	927	AQ575039	nbxb0086L01r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0086L01r, genomic survey sequence	Oryza sativa	37,786	2-Jun-99
		GB_BA1:NMRRNA	5209	X72495	N magadii rRNA operon	Natrialba magadii	39,788	10-Feb-95
rxa00598								
rxa00601	414	GB_BA2 AF175719	1368	AF175719	Porphyromonas gingivalis strain W50 immunoreactive 51kD antigen PG52 gene, complete cds.	Porphyromonas gingivalis	35,331	23-Aug-99
		GB_GSS9 AQ140775	464	AQ140775	HS_3128_A1_B11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3128 Col=21 Row=C, genomic survey sequence	Homo sapiens	40,431	24-Sep-98
		GB_EST8.AA018824	542	AA018824	ze57e09 s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE 363112 3', mRNA sequence	Homo sapiens	40,590	30-Jan-97
rxa00602	876	GB_EST30 AI642687	479	AI642687	vw02h03 x1 Soares mouse mammary gland NbMMG Mus musculus cDNA clone IMAGE:1230773 3', mRNA sequence.	Mus musculus	40,042	29-Apr-99
		GB_EST20.AA879989	412	AA879989	vw03a05 r1 Soares mouse mammary gland NbMMG Mus musculus cDNA clone IMAGE 1230800 5', mRNA sequence	Mus musculus	39,948	26-MAR-1998

TABLE 4: ALIGNMENT RESULTS

		GB_EST28:AI481047	438	AI481047	vf91a05.x1 Soares mouse mammary gland NbMMG Mus musculus cDNA clone IMAGE 851120 3', mRNA sequence	Mus musculus	38,128	09-MAR-1999
rxa00604	414	GB_HTG2:AC008205	131658	AC008205	Drosophila melanogaster chromosome 3 clone BACR33F18 (D764) RPCI-98 33 F 18 map 96A-96B strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 118 unordered pieces	Drosophila melanogaster	33,907	2-Aug-99
		GB_HTG2:AC008205	131658	AC008205	Drosophila melanogaster chromosome 3 clone BACR33F18 (D764) RPCI-98 33 F 18 map 96A-96B strain y, cn bw sp, *** SEQUENCING IN PROGRESS***, 118 unordered pieces	Drosophila melanogaster	33,907	2-Aug-99
		GB_IN1 DMBR7C10	56820	AL121804	Drosophila melanogaster clone BACR7C10	Drosophila melanogaster	44,267	10-OCT-1999
rxa00610	987	GB_BA1.SME242575	1403	AJ242575	Sinorhizobium meliloti partial oxi1 and dehydrogenase genes, isolate lpu119	Sinorhizobium meliloti	41,760	26-MAY-1999
		GB_PR3 AC004655	134929	AC004655	Homo sapiens Xp22-140-141 BAC GSHB-128G5 (Genome Systems Human BAC library) complete sequence	Homo sapiens	38,422	17-Sep-98
		GB_PR3 HS598F2	99886	AL021579	Human DNA sequence from clone 598F2 on chromosome 1q23 1-24 3 Contains ESTs, STS and GSS, complete sequence	Homo sapiens	38,351	23-Nov-99
rxa00611	1599	GB_HTG2 AC007108	190000	AC007108	Homo sapiens chromosome 4, *** SEQUENCING IN PROGRESS ***, 24 unordered pieces	Homo sapiens	17,451	17-MAR-1999
		GB_HTG2 AC007108	190000	AC007108	Homo sapiens chromosome 4, *** SEQUENCING IN PROGRESS ***, 24 unordered pieces.	Homo sapiens	17,451	17-MAR-1999
		GB_HTG4 AC010893	176178	AC010893	Homo sapiens chromosome unknown clone NH0480A20, WORKING DRAFT SEQUENCE, in unordered pieces	Homo sapiens	35,819	29-OCT-1999
rxa00613	576	GB_IN2 AC004361	87747	AC004361	Drosophila melanogaster DNA sequence (P1 DS07851 (D49)), complete sequence.	Drosophila melanogaster	35,081	29-MAY-1998
		GB_PL2 AC006268	105420	AC006268	Arabidopsis thaliana BAC T24G23 from chromosome IV near 21 cM, complete sequence	Arabidopsis thaliana	43,682	1-Jan-99
		GB_BA1 MLCB596	38426	AL035472	Mycobacterium leprae cosmid B596	Mycobacterium leprae	35,026	27-Aug-99
rxa00614	1038	GB_BA1 MTV025	121125	AL022121	Mycobacterium tuberculosis H37Rv complete genome; segment 155/162	Mycobacterium tuberculosis	53,061	24-Jun-99
		GB_BA1 SCH66	9153	AL049731	Streptomyces coelicolor cosmid H66	Streptomyces coelicolor	52,817	29-Apr-99
		GB_EST14 AA446728	411	AA446728	zw84f03.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE 783677 5', mRNA sequence	Homo sapiens	36,548	3-Jun-97
rxa00616								
rxa00617	351	GB_PL1 AB009030	2589	AB009030	Panax ginseng OSCPNY1 mRNA for beta-Amyrin Synthase, complete cds	Panax ginseng	39,048	03-OCT-1998
		GB_PR3 HS905G11	122469	AL035045	Human DNA sequence from clone 905G11 on chromosome 20p11.2-12.1 Contains STSs, GSSs and genomic marker D20S182, complete sequence.	Homo sapiens	39,255	23-Nov-99
		GB_RO.MMT1CPS	8147	X15147	Mouse Tla region T1c pseudogene for class I antigen major histocompatibility complex	Mus musculus	36,311	19-Feb-90
rxa00628	531	GB_HTG5:AC010674	220575	AC010674	Homo sapiens chromosome 15 clone RP11-430B1 map 15q21, *** SEQUENCING IN PROGRESS ***, 46 ordered pieces	Homo sapiens	37,714	5-Nov-99
		GB_HTG5:AC010674	220575	AC010674	Homo sapiens chromosome 15 clone RP11-430B1 map 15q21, *** SEQUENCING IN PROGRESS ***, 46 ordered pieces	Homo sapiens	39,293	5-Nov-99
rxa00631	1578	GB_BA1 BRLBIOAD	2272	D14083	Brevibacterium flavum genes for 7,8-diaminopelargonic acid aminotransferase and dethiobiotin synthetase, complete cds	Corynebacterium glutamicum	47,368	3-Feb-99
		GB_PAT:E04041	675	E04041	DNA sequence coding for desthiobiotinsynthetase	Corynebacterium glutamicum	46,552	29-Sep-97
		GB_EST20 AA820386	453	AA820386	LD23968.5prime LD Drosophila melanogaster embryo pOT2 Drosophila melanogaster cDNA clone LD23968 5prime, mRNA sequence	Drosophila melanogaster	45,679	25-Feb-99
rxa00637	876	GB_HTG2 AC007589	134659	AC007589	Drosophila melanogaster chromosome 3 clone BACR20D10 (D667) RPCI-98 20 D 10 map 82D-82E strain y, cn bw sp, *** SEQUENCING IN PROGRESS ***, 73 unordered pieces	Drosophila melanogaster	32,102	2-Aug-99
		GB_HTG2 AC007589	134659	AC007589	Drosophila melanogaster chromosome 3 clone BACR20D10 (D667) RPCI-98 20 D 10 map 82D-82E strain y, cn bw sp, *** SEQUENCING IN PROGRESS ***, 73 unordered pieces	Drosophila melanogaster	32,102	2-Aug-99
		GB_HTG3 AC009212	125452	AC009212	Drosophila melanogaster chromosome 3 clone BACR01A18 (D669) RPCI-98 01 A 18 map 82E-82F strain y, cn bw sp, *** SEQUENCING IN PROGRESS***, 119 unordered pieces	Drosophila melanogaster	37,126	23-Aug-99
rxa00646	541	GB_HTG1 AP000488	123363	AP000488	Homo sapiens chromosome 11 clone B759H8 map 11q23, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Homo sapiens	38,264	13-Sep-99

TABLE 4: ALIGNMENT RESULTS

		GB_HTG1:AP000488	123363	AP000488	Homo sapiens chromosome 11 clone B759H8 map 11q23, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Homo sapiens	38,264	13-Sep-99
		GB_HTG1 AP000488	123363	AP000488	Homo sapiens chromosome 11 clone B759H8 map 11q23, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Homo sapiens	36,484	13-Sep-99
rxa00647	756	GB_GSS13 AQ431426	536	AQ431426	HS_5140_A2_E01_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=716 Col=2 Row=I, genomic survey sequence	Homo sapiens	35,635	31-MAR-1999
		GB_OV CHKP4HA	3149	M26217	Chicken prolyl 4-hydroxylase alpha subunit gene, 3' end	Gallus gallus	40,655	28-Apr-93
		GB_HTG2 AC008271	168302	AC008271	Homo sapiens clone NH0123E16, *** SEQUENCING IN PROGRESS ***, 2 unordered pieces	Homo sapiens	37,417	31-Jul-99
rxa00649	579	GB_PR2 AC002563	136436	AC002563	Human PAC clone 127H14 from 12q, complete sequence	Homo sapiens	37,937	26-Sep-97
		GB_HTG3:AC011466	165953	AC011466	Homo sapiens chromosome 19 clone CIT-HSPC_453G23, *** SEQUENCING IN PROGRESS ***, 74 unordered pieces.	Homo sapiens	38,179	07-OCT-1999
		GB_HTG3 AC011466	165953	AC011466	Homo sapiens chromosome 19 clone CIT-HSPC_453G23, *** SEQUENCING IN PROGRESS ***, 74 unordered pieces	Homo sapiens	38,179	07-OCT-1999
rxa00652								
rxa00653								
rxa00654	1389	GB_EST1:Z34080	271	Z34080	ATTS3128 Grenoble-B Arabidopsis thaliana cDNA clone GBGe328 5', mRNA sequence	Arabidopsis thaliana	40,370	6-Jun-94
		GB_PR3 AC004460	113803	AC004460	Homo sapiens PAC clone DJ1086D14, complete sequence	Homo sapiens	36,150	24-MAR-1998
		GB_GSS6 AQ835185	571	AQ835185	HS_4832_A1_E02_T7A CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=4832 Col=3 Row=I, genomic survey sequence	Homo sapiens	39,429	27-Aug-99
rxa00656	384	GB_HTG3:AC009948	172463	AC009948	Homo sapiens clone NH0065L03, *** SEQUENCING IN PROGRESS ***, 2 unordered pieces	Homo sapiens	43,164	25-Sep-99
		GB_HTG3:AC009948	172463	AC009948	Homo sapiens clone NH0065L03, *** SEQUENCING IN PROGRESS ***, 2 unordered pieces	Homo sapiens	43,164	25-Sep-99
		GB_GSS13 AQ462899	522	AQ462899	HS_5212_A1_C09_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=788 Col=17 Row=E, genomic survey sequence	Homo sapiens	42,529	23-Apr-99
rxa00657	1026	GB_BA2 AF064700	3481	AF064700	Rhodococcus sp NO1-1 CprS and CprR genes, complete cds	Rhodococcus sp NO1-1	40,558	15-Jul-98
		GB_PR3 AC005346	38849	AC005346	Homo sapiens chromosome 16, cosmid clone 2H2 (LANL), complete sequence	Homo sapiens	35,553	31-Jul-98
		GB_HTG3 AC008905	129915	AC008905	Homo sapiens chromosome 5 clone CITB-H1_2259I14, *** SEQUENCING IN PROGRESS ***, 40 unordered pieces	Homo sapiens	37,179	3-Aug-99
rxa00661	813	GB_PL2:AC006193	118335	AC006193	Arabidopsis thaliana chromosome I BAC F13O11 genomic sequence, complete sequence	Arabidopsis thaliana	35,513	11-Jun-99
		GB_RO MMFABPE	6593	AJ223066	Mus musculus Fabpe gene	Mus musculus	37,500	27-Jul-98
		GB_PL2 AC006193	118335	AC006193	Arabidopsis thaliana chromosome I BAC F13O11 genomic sequence, complete sequence	Arabidopsis thaliana	33,552	11-Jun-99
rxa00662	1392	GB_EST29 AI551960	718	AI551960	vi48d09 y1 Beddington mouse embryonic region Mus musculus cDNA clone IMAGE 907025 5' similar to gb D10576 Mouse mRNA for ubiquitin activating enzyme E1 (MOUSE),, mRNA sequence	Mus musculus	39,972	23-MAR-1999
		GB_BA2 AE000633	19734	AE000633	Helicobacter pylori 26695 section 111 of 134 of the complete genome	Helicobacter pylori 26695	36,606	6-Apr-99
		GB_GSS10 AQ216730	529	AQ216730	HS_2262_A1_G06_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2262 Col=11 Row=M, genomic survey sequence	Homo sapiens	32,703	19-Sep-98
rxa00666	1038	GB_HTG3 AC009205	113482	AC009205	Drosophila melanogaster chromosome 2 clone BACR04C20 (D1035) RPCI-98 04 C 20 map 36E-37C strain y, cn bw sp, *** SEQUENCING IN PROGRESS ***, 101 unordered pieces	Drosophila melanogaster	36,713	17-Sep-99
		GB_EST25 AI259480	626	AI259480	LP02903.5prime LP Drosophila melanogaster larval-early pupal pOT2 Drosophila melanogaster cDNA clone LP02903 5prime, mRNA sequence	Drosophila melanogaster	37,173	17-Nov-98
		GB_HTG3 AC009205	113482	AC009205	Drosophila melanogaster chromosome 2 clone BACR04C20 (D1035) RPCI-98 04 C 20 map 36E-37C strain y, cn bw sp, *** SEQUENCING IN PROGRESS ***, 101 unordered pieces	Drosophila melanogaster	36,713	17-Sep-99
rxa00667	1137	GB_PAT AR048317	2627	AR048317	Sequence 3 from patent US 5821090	Unknown	39,805	29-Sep-99
		GB_PAT A46560	2627	A46560	Sequence 3 from Patent WO9526406	Eremothecium gossypii	39,805	07-MAR-1997
		GB_VI HEHCMVCG	229354	X17403	Human cytomegalovirus strain AD169 complete genome	human herpesvirus 5	39,854	10-Feb-99
rxa00676	870	GB_HTG1 CEY38F1	178443	Z98861	Caenorhabditis elegans chromosome II clone Y38F1, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Caenorhabditis elegans	35,880	03-DEC-1998

TABLE 4: ALIGNMENT RESULTS

		GB_HTG1:CEY38F1	178443	Z98861	Caenorhabditis elegans chromosome II clone Y38F1, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Caenorhabditis elegans	35,880	03-DEC-1998
		GB_PR3 HS934G17	107603	AL021155	Homo sapiens DNA sequence from PAC 934G17 on chromosome 1p36 21 Contains the alternatively spliced CLCN6 gene for chloride chanel proteins CLC-6A (KIAA0046) -B, -C and -D, the alternatively spliced NPPA gene coding for Atrial Natriuretic Factor ANF precursor (Atrial Natriuretic peptide ANP, Prepronatriodilatin), the NPPB gene for Brain Natriuretic Protein BNP, and a pseudogene similar to SBF1 (and other Myotubularin-related protein genes) Contains ESTs, STSs and the genomic marker D1S2740, complete sequence	Homo sapiens	38,489	23-Nov-99
rxa00678	858	GB_PR2 CNS00004	205573	AL049778	Human chromosome 14 DNA sequence *** IN PROGRESS *** BAC R-643C12 of RPCI-11 library from chromosome 14 of Homo sapiens (Human), complete sequence	Homo sapiens	33,138	17-Jun-99
		GB_GSS1 AG000894	723	AG000894	Homo sapiens genomic DNA, 21q region, clone 64E11X19, genomic survey sequence.	Homo sapiens	37,391	6-Feb-99
		GB_IN1 TSMIEXRNA	481	X90847	Trypanosoma simiae mini-exon DNA.	Trypanosoma simiae	35,135	15-Feb-99
rxa00691	1053	GB_EST26.AA899042	505	AA899042	UI-R-E0-bz-a-06-0-UI s2 UI-R-E0 Rattus norvegicus cDNA clone UI-R-E0-bz-a-06-0-UI 3' similar to gi|485266|gb|U09256|RNU09256 Rattus norvegicus Sprague-Dawley transketolase mRNA, complete cds, mRNA sequence	Rattus norvegicus	41,400	4-Jul-99
		GB_RO.RNU09256	2098	U09256	Rattus norvegicus Sprague-Dawley transketolase mRNA, complete cds	Rattus norvegicus	39,652	11-MAY-1994
		GB_EST29 AI599628	510	AI599628	EST251331 Normalized rat embryo, Bento Soares Rattus sp. cDNA clone REMEH65 3' end, mRNA sequence	Rattus sp	39,096	21-Apr-99
rxa00692	1257	GB_PL2 SPU66305	8226	U66305	Schizosaccharomyces pombe ABC transporter (mam1) gene, complete cds	Schizosaccharomyces pombe	36,842	30-Jul-97
		GB_PL1 SPBC25B2	26016	AL031853	S.pombe chromosome II cosmid c25B2	Schizosaccharomyces pombe	36,803	09-OCT-1998
		GB_PL1 SPBC2G5	23645	AL033385	S pombe chromosome II cosmid c2G5	Schizosaccharomyces pombe	36,803	04-DEC-1998
rxa00693	606	GB_BA2:RRU65510	16259	U65510	Rhodospirillum rubrum CO-induced hydrogenase operon (cooM, cooK, cooL, cooX, cooU, cooH) genes, iron sulfur protein (cooF) gene, carbon monoxide dehydrogenase (cooS) gene, carbon monoxide dehydrogenase accessory proteins (cooC, cooT, cooJ) genes, putative transcriptional activator (cooA) gene, nicotinate-nucleotide pyrophosphorylase (nadC) gene, complete cds, L-aspartate oxidase (nadB) gene, and alkyl hydroperoxide reductase (ahpC) gene, partial cds	Rhodospirillum rubrum	41,970	9-Apr-97
		GB_PL1 LETHM27	1152	X95296	L esculentum mRNA for THM27 protein	Lycopersicon esculentum	38,919	10-Jun-96
		GB_EST38 AW033855	646	AW033855	EST277426 tomato callus, TAMU Lycopersicon esculentum cDNA clone cLEC29F6 similar to transcription factor, myb-related, mRNA sequence.	Lycopersicon esculentum	35,945	15-Sep-99
rxa00701	498	GB_EST34 AI785570	454	AI785570	uj44d03 x1 Sugano mouse liver mlia Mus musculus cDNA clone IMAGE 1922789 3' similar to gb Z28407 60S RIBOSOMAL PROTEIN L8 (HUMAN),, mRNA sequence	Mus musculus	37,565	2-Jul-99
		GB_EST25 AI256147	684	AI256147	ui95e12.x1 Sugano mouse liver mlia Mus musculus cDNA clone IMAGE 1890190 3' similar to gb Z28407 60S RIBOSOMAL PROTEIN L8 (HUMAN);, mRNA sequence	Mus musculus	41,232	12-Nov-98
		GB_BA1 CARCG12	2079	X14979	C aurantiacus reaction center genes 1 and 2	Chloroflexus aurantiacus	36,943	23-Apr-91
rxa00704	750	GB_EST15 AA497266	456	AA497266	fa04f08 s1 Zebrafish ICRFzfls Danio rerio cDNA clone 3A13 3', mRNA sequence.	Danio rerio	38,631	30-Jun-97
		GB_EST36 AI884217	515	AI884217	fc75e10 x1 Zebrafish WashU MPIMG EST Danio rerio cDNA 3', mRNA sequence.	Danio rerio	38,012	26-Jul-99
		GB_HTG1 CEY43F8_1	110000	Z95393	Caenorhabditis elegans chromosome V clone Y43F8, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Caenorhabditis elegans	37,889	Z95393
rxa00707	906	GB_GSS8 AQ013755	715	AQ013755	RPCI11-23F24 TKBF RPCI-11 Homo sapiens genomic clone RPCI-11-23F24, genomic survey sequence.	Homo sapiens	41,724	14-Apr-99
		GB_GSS3 B86449	434	B86449	RPCI11-23F24 TV RPCI-11 Homo sapiens genomic clone RPCI-11-23F24, genomic survey sequence.	Homo sapiens	42,936	9-Apr-99
		GB_GSS5 AQ797072	449	AQ797072	nbxb0071D10f CUGI Rice BAC Library Oryza sativa genomic clone nbxb0071D10f, genomic survey sequence.	Oryza sativa	39,101	4-Aug-99
rxa00712	819	GB_BA2 AF011544	7527	AF011544	Bacillus subtilis phosphoribosylaminoimidazole-carboxamide formyltransferase (purH-J) gene, partial cds, phosphoribosylglycinamide synthetase (purD), YecA (yecA), putative adenine deaminase (yecB), YecC (yecC), and YecD (yecD) genes, complete cds, and putative glutamate synthase (yecE) gene, partial cds	Bacillus subtilis	36,927	06-OCT-1997

TABLE 4: ALIGNMENT RESULTS

		GB_BA2:AF011544	7527	AF011544	Bacillus subtilis phosphoribosylaminoimidazole-carboxamide formyltransferase (purH-J) gene, partial cds, phosphoribosylglycinamide synthetase (purD), YecA (yecA), putative adenine deaminase (yecB), YecC (yecC), and YecD (yecD) genes, complete cds, and putative glutamate synthase (yecE) gene, partial cds	Bacillus subtilis	39,752	06-OCT-1997
rxa00713	1056	GB_PAT I92037	241	I92037	Sequence 4 from patent US 5726299	Unknown	99,048	01-DEC-1998
		GB_PAT I78748	241	I78748	Sequence 4 from patent US 5693781	Unknown	99,048	3-Apr-98
		GB_HTG3 AC009281	221178	AC009281	Homo sapiens chromosome 15 clone 8_C_22 map 15, *** SEQUENCING IN PROGRESS ***, 49 unordered pieces	Homo sapiens	36,255	12-Aug-99
rxa00714	684	GB_PL1 CCR5839	871	AJ005839	Cyclotella cryptica mRNA for fucoxanthin chlorophyll a/c binding protein, fcp12	Cyclotella cryptica	36,364	30-Jul-98
		GB_PR2:HS1002M8	111768	AL035454	Human DNA sequence from clone 1002M8 on chromosome 20p11 21-11 23, complete sequence	Homo sapiens	36,444	23-Nov-99
		GB_PR2 HS1002M8	111768	AL035454	Human DNA sequence from clone 1002M8 on chromosome 20p11 21-11 23, complete sequence	Homo sapiens	34,894	23-Nov-99
rxa00716	636	GB_PAT I78753	1187	I78753	Sequence 9 from patent US 5693781	Unknown	36,022	3-Apr-98
		GB_PAT I92042	1187	I92042	Sequence 9 from patent US 5726299	Unknown	36,022	01-DEC-1998
		GB_HTG3:AC005769	200000	AC005769	Homo sapiens chromosome 4, *** SEQUENCING IN PROGRESS ***, 5 unordered pieces	Homo sapiens	36,745	21-Aug-99
rxa00719	1752	GB_BA2 U32687	11847	U32687	Haemophilus influenzae Rd section 2 of 163 of the complete genome	Haemophilus influenzae Rd	36,937	29-MAY-1998
		GB_EST13 AA333602	357	AA333602	EST37710 Embryo, 8 week I Homo sapiens cDNA 5' end similar to guanine nucleotide-binding protein rap2, ras-oncogene related, mRNA sequence.	Homo sapiens	45,938	21-Apr-97
		GB_BA2 U32687	11847	U32687	Haemophilus influenzae Rd section 2 of 163 of the complete genome	Haemophilus influenzae Rd	36,390	29-MAY-1998
rxa00720	789	GB_EST1 M61974	437	M61974	EST00024 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBA87, mRNA sequence.	Homo sapiens	40,138	26-MAY-1992
		GB_EST3:R73776	389	R73776	yi55h07.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE 143197 5', mRNA sequence	Homo sapiens	41,818	5-Jun-95
		GB_EST35 AL043192	793	AL043192	DKFZp434G0723_r1 434 (synonym htes3) Homo sapiens cDNA clone DKFZp434G0723 5', mRNA sequence	Homo sapiens	38,571	29-Sep-99
rxa00722	1088	GB_HTG3 AC008573	205755	AC008573	Homo sapiens chromosome 5 clone CIT-HSPC_551I11, *** SEQUENCING IN PROGRESS ***, 95 unordered pieces	Homo sapiens	38,506	3-Aug-99
		GB_HTG3 AC008573	205755	AC008573	Homo sapiens chromosome 5 clone CIT-HSPC_551I11, *** SEQUENCING IN PROGRESS ***, 95 unordered pieces	Homo sapiens	38,506	3-Aug-99
		GB_BA1 MTV014	58280	AL021646	Mycobacterium tuberculosis H37Rv complete genome, segment 137/162	Mycobacterium tuberculosis	41,392	18-Jun-98
rxa00724	2100	GB_BA1 SC7A1	32039	AL034447	Streptomyces coelicolor cosmid 7A1	Streptomyces coelicolor	54,858	15-DEC-1998
		GB_BA1 BSY13937	27779	Y13937	Bacillus subtilis genomic DNA from the spoVM region	Bacillus subtilis	47,010	30-MAR-1998
		GB_BA2 L78127	1225	L78127	Enterococcus faecium genomic DNA fragment	Enterococcus faecium	36,880	18-Aug-99
rxa00726	614	GB_BA1 BACJH642	282700	D84432	Bacillus subtilis DNA, 283 Kb region containing skin element.	Bacillus subtilis	56,694	6-Feb-99
		GB_BA1 BSUB0013	218470	Z99116	Bacillus subtilis complete genome (section 13 of 21) from 2395261 to 2613730	Bacillus subtilis	36,513	26-Nov-97
		GB_BA1 SC4H8	15560	AL020958	Streptomyces coelicolor cosmid 4H8	Streptomyces coelicolor	35,073	10-DEC-1997
rxa00729								
rxa00730	930	GB_HTG3 AC010758	145821	AC010758	Homo sapiens clone 1_B_18, *** SEQUENCING IN PROGRESS ***, 20 unordered pieces	Homo sapiens	35,738	22-Sep-99
		GB_HTG3 AC010758	145821	AC010758	Homo sapiens clone 1_B_18, *** SEQUENCING IN PROGRESS ***, 20 unordered pieces	Homo sapiens	35,738	22-Sep-99
		GB_GSS13:AQ469090	414	AQ469090	CITBI-E1-2596D12.TF CITBI-E1 Homo sapiens genomic clone 2596D12, genomic survey sequence	Homo sapiens	36,842	23-Apr-99
rxa00731	2619	GB_BA1 CGLYSI	4232	X60312	C glutamicum lysI gene for L-lysine permease	Corynebacterium glutamicum	100,000	30-Jan-92

TABLE 4: ALIGNMENT RESULTS

		GB_BA1:CGLYSI	4232	X60312	C.glutamicum lysI gene for L-lysine permease.	Corynebacterium glutamicum	37,645	30-Jan-92
rxa00738	386	GB_BA1 MTCY10G2	38970	Z92539	Mycobacterium tuberculosis H37Rv complete genome, segment 47/162	Mycobacterium tuberculosis	54,427	17-Jun-98
		GB_HTG1 HSJ564F22	106277	AL080249	Homo sapiens chromosome 20 clone RP4-564F22, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Homo sapiens	44,000	23-Nov-99
		GB_HTG1 HSJ564F22	106277	AL080249	Homo sapiens chromosome 20 clone RP4-564F22, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Homo sapiens	44,000	23-Nov-99
rxa00740	702	GB_PL2 AF100167	1557	AF100167	Glycine max unknown mRNA	Glycine max	35,823	4-Nov-98
		GB_EST28 AI465702	268	AI465702	vw83g01 y1 Stratagene mouse skin (#937313) Mus musculus cDNA clone IMAGE 1261584 5', mRNA sequence	Mus musculus	43,226	09-MAR-1999
		GB_EST20 AA856157	359	AA856157	vw83g01 r1 Stratagene mouse skin (#937313) Mus musculus cDNA clone IMAGE 1261584 5', mRNA sequence	Mus musculus	43,226	06-MAR-1998
rxa00741	1056	GB_HTG2 AC007185	199340	AC007185	Drosophila melanogaster chromosome 2 clone BACR44N04 (D545) RPCI-98 44.N 4 map 36A-36A strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 50 unordered pieces	Drosophila melanogaster	39,583	2-Aug-99
		GB_HTG2 AC007185	199340	AC007185	Drosophila melanogaster chromosome 2 clone BACR44N04 (D545) RPCI-98 44 N 4 map 36A-36A strain y, cn bw sp, *** SEQUENCING IN PROGRESS***, 50 unordered pieces	Drosophila melanogaster	39,583	2-Aug-99
		GB_PL2:F17I23	134784	AF160182	Arabidopsis thaliana BAC F17I23.	Arabidopsis thaliana	37,788	20-Jun-99
rxa00742	1773	GB_IN1 CEC05C10	26263	Z48178	Caenorhabditis elegans cosmid C05C10, complete sequence	Caenorhabditis elegans	39,243	2-Sep-99
		GB_IN1 CEC05C10	26263	Z48178	Caenorhabditis elegans cosmid C05C10, complete sequence	Caenorhabditis elegans	38,041	2-Sep-99
rxa00743	546	GB_GSS9 AQ093649	320	AQ093649	HS_3022_A1_E06_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3022 Col=11 Row=I, genomic survey sequence	Homo sapiens	34,277	27-Aug-98
		GB_GSS9 AQ093649	320	AQ093649	HS_3022_A1_E06_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3022 Col=11 Row=I, genomic survey sequence	Homo sapiens	34,277	27-Aug-98
rxa00745	657	GB_HTG2 AC008195	130309	AC008195	Drosophila melanogaster chromosome 3 clone BACR42I20 (D748) RPCI-98 42 I 20 map 93F-93F strain y, cn bw sp, *** SEQUENCING IN PROGRESS ***, 77 unordered pieces.	Drosophila melanogaster	38,095	2-Aug-99
		GB_IN2:DMU53190	3477	U53190	Drosophila melanogaster Camguk (cmg) mRNA, complete cds	Drosophila melanogaster	39,623	30-Nov-98
		GB_HTG2 AC008195	130309	AC008195	Drosophila melanogaster chromosome 3 clone BACR42I20 (D748) RPCI-98 42 I 20 map 93F-93F strain y, cn bw sp, *** SEQUENCING IN PROGRESS ***, 77 unordered pieces	Drosophila melanogaster	38,095	2-Aug-99
rxa00746	1314	GB_HTG3 AC010076	148614	AC010076	Homo sapiens chromosome 15 clone BAC 64K10 map 14q25, LOW-PASS SEQUENCE SAMPLING	Homo sapiens	36,336	11-Sep-99
		GB_HTG3 AC010076	148614	AC010076	Homo sapiens chromosome 15 clone BAC 64K10 map 14q25, LOW-PASS SEQUENCE SAMPLING	Homo sapiens	36,336	11-Sep-99
		GB_PR3 HS402G11	177241	AL022328	Human DNA sequence from clone 402G11 on chromosome 22q13 31-13 33 Contains genes for SAPK3 (stress-activated protein kinase 3), PRKM11 (protein kinase mitogen-activated 11), KIAA0315, ESTs, GSSs and CpG islands, complete sequence.	Homo sapiens	38,752	23-Nov-99
rxa00747	711	GB_HTG4 AC010081	176777	AC010081	Homo sapiens clone NH0065E07, *** SEQUENCING IN PROGRESS ***, 1 unordered pieces	Homo sapiens	37,016	29-OCT-1999
		GB_HTG4 AC010081	176777	AC010081	Homo sapiens clone NH0065E07, *** SEQUENCING IN PROGRESS ***, 1 unordered pieces	Homo sapiens	37,016	29-OCT-1999
		GB_HTG3 AC011194	196098	AC011194	Mus musculus chromosome 11 clone 196_F_5 map 11, *** SEQUENCING IN PROGRESS ***, 32 unordered pieces.	Mus musculus	38,735	01-OCT-1999
rxa00748	567	GB_GSS13 AQ457887	478	AQ457887	HS_5189_B2_B06_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=765 Col=12 Row=D, genomic survey sequence	Homo sapiens	37,844	23-Apr-99
		GB_IN1 EHEXRIDRI	170	X58630	E.histolytica extrachromosomal ribosomal DNA for DRA I repeat unit	Entamoeba histolytica	42,353	13-Aug-91
		GB_IN1 EHEXRDNA	3699	X61182	E histolytica extrachromosomal ribosomal DNA downstream of rRNA genes	Entamoeba histolytica	38,905	2-Sep-96
rxa00749	822	GB_BA1 BSUB0003	209100	Z99106	Bacillus subtilis complete genome (section 3 of 21) from 402751 to 611850.	Bacillus subtilis	37,238	26-Nov-97
		GB_BA1 AB001488	148068	AB001488	Bacillus subtilis genome sequence, 148 kb sequence of the region between 35 and 47 degree	Bacillus subtilis	37,238	13-Feb-99
		GB_HTG3 AC008060	161486	AC008060	Homo sapiens clone DJ0912I13, *** SEQUENCING IN PROGRESS ***, 4 unordered pieces	Homo sapiens	39,474	13-Aug-99
rxa00750								

TABLE 4: ALIGNMENT RESULTS

rxa00751	951	GB_PR4 AC006449	286758	AC006449	Homo sapiens chromosome 17, clone hCIT 58_E_17, complete sequence	Homo sapiens	38,223	23-OCT-1999
		GB_HTG2 AC002118	170891	AC002118	Homo sapiens chromosome 17 clone 303_E_14, *** SEQUENCING IN PROGRESS ***, 20 unordered pieces.	Homo sapiens	37,112	13-Feb-98
		GB_HTG2 AC002118	170891	AC002118	Homo sapiens chromosome 17 clone 303_E_14, *** SEQUENCING IN PROGRESS ***, 20 unordered pieces.	Homo sapiens	37,112	13-Feb-98
rxa00752	552	GB_PL2 F5K24	109786	AF128395	Arabidopsis thaliana BAC F5K24	Arabidopsis thaliana	38,899	03-MAR-1999
		GB_BA1 MBHRDED	6300	Y09870	M barkeri hdrE & hdrD genes, ORF1, ORF2, ORF3 & ORF4	Methanosarcina barkeri	40,609	04-DEC-1998
		GB_PL1:SC9920	23498	Z48639	S cerevisiae chromosome XIII cosmid 9920.	Saccharomyces cerevisiae	35,754	11-Aug-97
rxa00757	1377	GB_PAT.E13655	2260	E13655	gDNA encoding glucose-6-phosphate dehydrogenase	Corynebacterium glutamicum	46,045	24-Jun-98
		GB_GSS9 AQ103710	369	AQ103710	HS_3092_B1_C01_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3092 Col=1 Row=F, genomic survey sequence	Homo sapiens	36,339	27-Aug-98
		GB_HTG3 AC009305	167705	AC009305	Homo sapiens clone NH0153B21, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces	Homo sapiens	36,691	13-Aug-99
rxa00763	906	GB_BA1 SC7B7	13800	AL009199	Streptomyces coelicolor cosmid 7B7	Streptomyces coelicolor	39,013	02-DEC-1997
		GB_HTG2 HSJ473J16	203460	AL109942	Homo sapiens chromosome 6 clone RP3-473J16 map q25 3-26, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Homo sapiens	38,192	03-DEC-1999
		GB_HTG2.HSJ473J16	203460	AL109942	Homo sapiens chromosome 6 clone RP3-473J16 map q25 3-26, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Homo sapiens	38,192	03-DEC-1999
rxa00765	810	GB_BA1.MTV043	68848	AL022004	Mycobacterium tuberculosis H37Rv complete genome; segment 40/162	Mycobacterium tuberculosis	38,568	24-Jun-99
		GB_BA2:PAU93274	8008	U93274	Pseudomonas aeruginosa YafE (yafE), LeuB (leuB), Asd (asd), FimV (fimV), and HisT (hisT) genes, complete cds, TrpF (trpF) gene, partial cds, and unknown gene.	Pseudomonas aeruginosa	37,656	23-Jun-98
		GB_BA1 MTCY31	37630	Z73101	Mycobacterium tuberculosis H37Rv complete genome; segment 41/162	Mycobacterium tuberculosis	38,209	17-Jun-98
rxa00768	1242	GB_HTG5 AC008194	194555	AC008194	Drosophila melanogaster chromosome X clone BACR49A05 (D745) RPCI-98 49 A 5 map 18A-18A strain y, cn bw sp, *** SEQUENCING IN PROGRESS ***, 90 unordered pieces	Drosophila melanogaster	34,078	15-Nov-99
		GB_HTG5 AC008194	194555	AC008194	Drosophila melanogaster chromosome X clone BACR49A05 (D745) RPCI-98 49 A 5 map 18A-18A strain y, cn bw sp, *** SEQUENCING IN PROGRESS ***, 90 unordered pieces	Drosophila melanogaster	31,194	15-Nov-99
		GB_BA2 AF044495	9599	AF044495	Agrobacterium tumefaciens chemotaxis operon, complete sequence	Agrobacterium tumefaciens	40,165	2-Jul-98
rxa00769	336	GB_PR3 AC003068	42184	AC003068	Human Cosmid g5129z059 from 7q31 3, complete sequence	Homo sapiens	35,152	6-Nov-97
		GB_PR2 HSAC000374	41585	AC000374	Human cosmid g1980a170, complete sequence	Homo sapiens	35,152	12-MAR-1997
		GB_PR3 AC003068	42184	AC003068	Human Cosmid g5129z059 from 7q31.3, complete sequence	Homo sapiens	37,309	6-Nov-97
rxa00771	942	GB_PR2:HS172K2	131234	Z84814	Human DNA sequence from PAC 172K2 on chromosome 6 contains HLA CLASS II DRA pseudogene, DRB3*01012 genes, DRB9 pseudogene butyrophilin precursor and ESTs	Homo sapiens	34,719	23-Nov-99
		GB_HTG1:HSA555E18	1177	AL121780	Homo sapiens chromosome 20 clone RP11-555E18, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	41,450	23-Nov-99
		GB_HTG1 HSA555E18	1177	AL121780	Homo sapiens chromosome 20 clone RP11-555E18, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Homo sapiens	41,450	23-Nov-99
rxa00781	411	GB_PR3.HS48A11	129294	AL031132	Human DNA sequence from clone 48A11 on chromosome 20p12 Contains EST, STS, GSS, complete sequence	Homo sapiens	37,284	23-Nov-99
		GB_IN1 CELC03B1	42297	U40952	Caenorhabditis elegans cosmid C03B1	Caenorhabditis elegans	38,177	25-Nov-95
		GB_PR3 HS48A11	129294	AL031132	Human DNA sequence from clone 48A11 on chromosome 20p12 Contains EST, STS, GSS, complete sequence	Homo sapiens	35,162	23-Nov-99
rxa00785	680	GB_EST11 AA223451	349	AA223451	zr06d01.r1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE 650689 5', mRNA sequence	Homo sapiens	38,682	19-Feb-97
		GB_EST9 AA081255	446	AA081255	zn33d08 r1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone IMAGE.549231 5', mRNA sequence	Homo sapiens	40,271	21-OCT-1996

TABLE 4: ALIGNMENT RESULTS

		GB_EST9:C16722	314	C16722	C16722 Clontech human aorta polyA+ mRNA (#6572) Homo sapiens cDNA clone GEN-522C02 5', mRNA sequence.	Homo sapiens	44,013	30-Sep-96
rxa00788	348	GB_PL2 UMU62738	13812	U62738	Ustilago maydis ferrichrome siderophore peptide synthetase (sid2) gene, complete cds.	Ustilago maydis	31,792	30-DEC-1997
		GB_PR1:AB012723	40850	AB012723	Homo sapiens gene for kinesin-like protein, complete cds	Homo sapiens	35,398	8-Jan-99
		GB_HTG3:AC008625	16830	AC008625	Homo sapiens chromosome 5 clone CIT978SKB_157D17, *** SEQUENCING IN PROGRESS ***, 19 unordered pieces	Homo sapiens	42,560	3-Aug-99
rxa00795	651	GB_IN2 AC003120	59991	AC003120	Drosophila melanogaster DNA sequence (P1 DS01523 (D34)), complete sequence	Drosophila melanogaster	39,252	17-Jul-98
		GB_EST19 AA802212	574	AA802212	GM04027 5prime GM Drosophila melanogaster ovary BlueScript Drosophila melanogaster cDNA clone GM04027 5prime, mRNA sequence	Drosophila melanogaster	37,828	25-Nov-98
		GB_IN2 AF168467	4652	AF168467	Drosophila melanogaster dual specificity kinase DYRK2 mRNA, complete cds	Drosophila melanogaster	36,933	5-Aug-99
rxa00804	567	GB_GSS12:AQ356039	499	AQ356039	CITBI-E1-2535P11 TR CITBI-E1 Homo sapiens genomic clone 2535P11, genomic survey sequence	Homo sapiens	40,569	24-Jan-99
		GB_PR4 AC005037	190508	AC005037	Homo sapiens clone NH0469M07, complete sequence.	Homo sapiens	41,209	14-MAY-1999
		GB_HTG5 AC007272	175463	AC007272	Homo sapiens clone NH0013J08, *** SEQUENCING IN PROGRESS ***, 5 unordered pieces	Homo sapiens	41,209	2-Nov-99
rxa00805	1005	GB_GSS1:CNS00U61	320	AL090583	Arabidopsis thaliana genome survey sequence SP6 end of BAC T6D17 of TAMU library from strain Columbia of Arabidopsis thaliana, genomic survey sequence.	Arabidopsis thaliana	36,364	28-Jun-99
		GB_PL1.AB026639	63921	AB026639	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21L13, complete sequence.	Arabidopsis thaliana	38,485	07-MAY-1999
		GB_PL1 AB026639	63921	AB026639	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone K21L13, complete sequence	Arabidopsis thaliana	35,451	07-MAY-1999
rxa00808	1581	GB_BA1 MLCB2548	38916	AL023093	Mycobacterium leprae cosmid B2548	Mycobacterium leprae	50,854	27-Aug-99
		GB_BA1:MLCL373	37304	AL035500	Mycobacterium leprae cosmid L373	Mycobacterium leprae	40,295	27-Aug-99
		GB_PL2 SCE9781	68302	U18916	Saccharomyces cerevisiae chromosome V cosmids 9781, 8198, 9115, 9981, and lambda clones 3955 and 6052	Saccharomyces cerevisiae	37,677	1-Aug-97
rxa00812	1182	GB_HTG2 AC006003	114949	AC006003	Homo sapiens clone DJ0782K24, *** SEQUENCING IN PROGRESS ***, 16 unordered pieces	Homo sapiens	35,284	22-Nov-98
		GB_HTG2:AC006003	114949	AC006003	Homo sapiens clone DJ0782K24, *** SEQUENCING IN PROGRESS ***, 16 unordered pieces	Homo sapiens	35,284	22-Nov-98
		GB_GSS9 AQ090529	323	AQ090529	HS_3007_B1_E09_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3007 Col=17 Row=J, genomic survey sequence	Homo sapiens	41,176	26-Aug-98
rxa00814	897	GB_VI:EHVU20824	184427	U20824	Equine herpesvirus 2, complete genome	Equine herpesvirus 2	35,274	2-Feb-96
		GB_VI:EHVU20824	184427	U20824	Equine herpesvirus 2, complete genome	Equine herpesvirus 2	38,808	2-Feb-96
		GB_PR3 HS466N1	79528	Z97630	Human DNA sequence from clone 466N1 on chromosome 22q12-13 Contains H1F0(H1 histone family, member 0) gene, 2-amino-3-ketobutyrate -CoA ligase(nuclear gene encoding mitochondrial protein), GALR3 (galanin receptor) gene, ESTs, GSSs and CpG islands, complete sequence	Homo sapiens	38,496	23-Nov-99
rxa00815	696	GB_PR3.CNS01DRL	174928	AL117355	Human chromosome 14 DNA sequence *** IN PROGRESS *** BAC R-354E14 of RPCI-11 library from chromosome 14 of Homo sapiens (Human), complete sequence	Homo sapiens	36,578	26-Nov-99
		GB_PR4 AC007283	127361	AC007283	Homo sapiens clone NH0536I18, complete sequence.	Homo sapiens	37,609	28-Sep-99
		GB_EST14 AA406984	477	AA406984	MBAFCZ7H08T3 Brugia malayi adult female cDNA (SAW96MLW-BmAF) Brugia malayi cDNA clone AFCZ7H08 5', mRNA sequence	Brugia malayi	41,919	01-MAY-1997
rxa00816	420	GB_EST27 AI414036	467	AI414036	ma03e08 x1 Soares mouse p3NMF19 5 Mus musculus cDNA clone IMAGE 303494 3' similar to TR Q85299 Q85299 HOMOLOGUE OF RETROVIRAL PSEUDOPROTEASE ;, mRNA sequence	Mus musculus	40,176	9-Feb-99
		GB_GSS15:AQ642295	501	AQ642295	RPCI93-DpnII-28G21 TV RPCI93-DpnII Trypanosoma brucei genomic clone RPCI93-DpnII-28G21, genomic survey sequence	Trypanosoma brucei	37,540	8-Jul-99
		GB_PL2 ZMU82481	2750	U82481	Zea mays KI domain interacting kinase 1 (KIK1) mRNA, complete cds	Zea mays	41,783	1-Jan-98
rxa00826	654	GB_PR4:AC008179	181745	AC008179	Homo sapiens clone NH0576F01, complete sequence.	Homo sapiens	35,736	28-Sep-99
		GB_HTG1 AC002413	63369	AC002413	Homo sapiens chromosome X clone bWXD111, *** SEQUENCING IN PROGRESS ***, 2 unordered pieces	Homo sapiens	37,600	12-Aug-97
		GB_HTG1:AC002413	63369	AC002413	Homo sapiens chromosome X clone bWXD111, *** SEQUENCING IN PROGRESS ***, 2 unordered pieces	Homo sapiens	37,600	12-Aug-97
rxa00830	846	GB_GSS6 AQ823465	535	AQ823465	HS_3217_A1_D08_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3217 Col=15 Row=G, genomic survey sequence	Homo sapiens	40,417	26-Aug-99

TABLE 4: ALIGNMENT RESULTS

		GB_GSS6:AQ825402	381	AQ825402	HS_5498_A1_G01_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=1074 Col=1 Row=M, genomic survey sequence	Homo sapiens	43,068	26-Aug-99
		GB_HTG1 HSU242F8	92944	AL022167	Homo sapiens chromosome X clone LL0XNC01-242F8, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Homo sapiens	38,321	23-Nov-99
rxa00831								
rxa00835	1077	GB_EST35 AI864917	468	AI864917	wj66f11 x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2407821 3' similar to WP F01F1 9 CE01235 VACUOLAR AMINOPEPTIDASE ,, mRNA sequence	Homo sapiens	37,607	30-Aug-99
		GB_EST35 AI864917	468	AI864917	wj66f11 x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE 2407821 3' similar to WP F01F1 9 CE01235 VACUOLAR AMINOPEPTIDASE ,, mRNA sequence	Homo sapiens	38,444	30-Aug-99
rxa00836	1816	GB_EST11 AA212728	424	AA212728	mw81g02 r1 Soares mouse NML Mus musculus cDNA clone IMAGE 677138 5', mRNA sequence	Mus musculus	40,284	18-Feb-97
		GB_EST26 AI390258	557	AI390258	mw81g02 y1 Soares mouse NML Mus musculus cDNA clone IMAGE 677138 5', mRNA sequence	Mus musculus	41,261	2-Feb-99
		GB_PR3 AC003669	159446	AC003669	Homo sapiens Xp22 BAC GS-594A7 (Genome Systems Human BAC library) contains Bmx gene, complete sequence	Homo sapiens	34,914	24-MAR-1998
rxa00840								
rxa00841								
rxa00846	993	GB_BA1 U00017	42157	U00017	Mycobacterium leprae cosmid B2126	Mycobacterium leprae	35,635	01-MAR-1994
		GB_BA1:MLCB2533	40245	AL035310	Mycobacterium leprae cosmid B2533	Mycobacterium leprae	38,280	27-Aug-99
		GB_RO:AB022047S7	18721	AB022053	Mus musculus gene for prolyl oligopeptidase, exon 11, 12, 13, 14, 15 and complete cds	Mus musculus	36,633	20-Aug-99
rxa00853	726	GB_PR3 HS531H16	155116	AL031664	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 531H16, complete sequence	Homo sapiens	41,110	23-Nov-99
		GB_PR3:HS531H16	155116	AL031664	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 531H16, complete sequence	Homo sapiens	37,343	23-Nov-99
		GB_HTG3 AC010264	81671	AC010264	Homo sapiens chromosome 5 clone CIT-HSPC_468K18, *** SEQUENCING IN PROGRESS ***, 66 unordered pieces.	Homo sapiens	38,776	15-Sep-99
rxa00854	336	GB_IN1:CELM04G7	41778	AF036700	Caenorhabditis elegans cosmid M04G7	Caenorhabditis elegans	37,349	05-DEC-1997
		GB_EST20 AA850405	451	AA850405	EST193172 Normalized rat ovary, Bento Soares Rattus sp cDNA clone ROVAF27 3' end, mRNA sequence.	Rattus sp	40,789	30-Apr-98
		GB_HTG2 AF165144	110891	AF165144	Homo sapiens chromosome 8 clone BAC 393A07 map 8q, *** SEQUENCING IN PROGRESS ***, in ordered pieces	Homo sapiens	34,234	16-Jul-99
rxa00855	408	GB_HTG2:AC007173	140775	AC007173	Drosophila melanogaster chromosome 2 clone BACR01A03 (D538) RPCI-98 01 A 3 map 36E-36E strain y, cn bw sp, *** SEQUENCING IN PROGRESS ***, 36 unordered pieces	Drosophila melanogaster	36,341	2-Aug-99
		GB_HTG2 AC007173	140775	AC007173	Drosophila melanogaster chromosome 2 clone BACR01A03 (D538) RPCI-98 01 A 3 map 36E-36E strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 36 unordered pieces	Drosophila melanogaster	36,341	2-Aug-99
		GB_PL2 YSCH8179	44113	U00062	Saccharomyces cerevisiae chromosome VIII cosmid 8179	Saccharomyces cerevisiae	38,560	4-Sep-97
rxa00861	426	GB_BA1 CGORF4GEN	2398	X95649	C glutamicum ORF4 gene	Corynebacterium glutamicum	100,000	10-MAR-1998
		GB_BA1 SC9A10	9000	AL031260	Streptomyces coelicolor cosmid 9A10	Streptomyces coelicolor	63,830	11-Aug-98
		GB_BA2:AF039028	2475	AF039028	Streptomyces toyocaensis D-ala-D-ala dipeptidase (vanXst) gene, complete cds, and unknown gene	Streptomyces toyocaensis	61,939	5-Jan-99
rxa00862	682	GB_PAT E14520	2001	E14520	DNA encoding Brevibacterium dihydrodipicolinic acid synthase	Corynebacterium glutamicum	36,154	28-Jul-99

TABLE 4: ALIGNMENT RESULTS

		GB_PAT:E12773	2001	E12773	DNA encoding Brevibacterium dihydrodipicolinic acid reductase.	Corynebacterium glutamicum	36,154	24-Jun-98
		GB_PAT E16749	2001	E16749	gDNA encoding dihydrodipicolinate synthase (DDPS)	Corynebacterium glutamicum	36,154	28-Jul-99
rxa00869	1044	GB_EST24 AI166579	645	AI166579	xylem est 398 Poplar xylem Lambda ZAPII library Populus balsamifera subsp trichocarpa cDNA 5', mRNA sequence	Populus balsamifera subsp trichocarpa	39,854	03-DEC-1998
		GB_BA1 MTCY06H11	38000	Z85982	Mycobacterium tuberculosis H37Rv complete genome, segment 73/162	Mycobacterium tuberculosis	42,801	17-Jun-98
		GB_EST34 AV153098	283	AV153098	AV153098 Mus musculus hippocampus C57BL/6J adult Mus musculus cDNA clone 2900052L10, mRNA sequence	Mus musculus	39,576	7-Jul-99
rxa00874	1212	GB_HTG2 AC007885	108561	AC007885	Drosophila melanogaster chromosome 2 clone BACR02G15 (D643) RPCI-98 02 G 15 map 60F-60F strain y, cn bw sp, *** SEQUENCING IN PROGRESS ***, 65 unordered pieces	Drosophila melanogaster	38,276	2-Aug-99
		GB_HTG2:AC007582	127205	AC007582	Drosophila melanogaster chromosome 2 clone BACR17E16 (D642) RPCI-98 17 E 16 map 60F-60F strain y, cn bw sp, *** SEQUENCING IN PROGRESS ***, 81 unordered pieces	Drosophila melanogaster	36,246	2-Aug-99
		GB_HTG2 AC007885	108561	AC007885	Drosophila melanogaster chromosome 2 clone BACR02G15 (D643) RPCI-98 02 G 15 map 60F-60F strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 65 unordered pieces	Drosophila melanogaster	38,276	2-Aug-99
rxa00876	1878	GB_EST10:AA144736	479	AA144736	mr72d08.r1 Stratagene mouse testis (#937308) Mus musculus cDNA clone IMAGE 602991 5', mRNA sequence	Mus musculus	41,474	11-Feb-97
		GB_EST32 AU069076	316	AU069076	AU069076 Rice callus Oryza sativa cDNA clone C51993_1A, mRNA sequence	Oryza sativa	46,330	7-Jun-99
		GB_EST10.AA144736	479	AA144736	mr72d08 r1 Stratagene mouse testis (#937308) Mus musculus cDNA clone IMAGE 602991 5', mRNA sequence.	Mus musculus	43,243	11-Feb-97
rxa00881	501	GB_HTG4 AC010103	192320	AC010103	Homo sapiens chromosome unknown clone NH0508H21, WORKING DRAFT SEQUENCE, in unordered pieces.	Homo sapiens	36,620	29-OCT-1999
		GB_HTG4 AC010103	192320	AC010103	Homo sapiens chromosome unknown clone NH0508H21, WORKING DRAFT SEQUENCE, in unordered pieces	Homo sapiens	36,620	29-OCT-1999
		GB_HTG4:AC010103	192320	AC010103	Homo sapiens chromosome unknown clone NH0508H21, WORKING DRAFT SEQUENCE, in unordered pieces	Homo sapiens	34,280	29-OCT-1999
rxa00882	801	GB_BA1:MTCY48	35377	Z74020	Mycobacterium tuberculosis H37Rv complete genome, segment 69/162	Mycobacterium tuberculosis	37,927	17-Jun-98
		GB_PAT.AR005211	3453	AR005211	Sequence 1 from patent US 5747651	Unknown	39,620	04-DEC-1998
		GB_PAT I40600	3453	I40600	Sequence 1 from patent US 5621090	Unknown	39,620	13-MAY-1997
rxa00883	642	GB_PR2 HS217O16	87552	AL031771	Human DNA sequence from clone 217O16 on chromosome 6q24 Contains GSS, complete sequence	Homo sapiens	33,866	23-Nov-99
		GB_PR2 HS217O16	87552	AL031771	Human DNA sequence from clone 217O16 on chromosome 6q24 Contains GSS, complete sequence	Homo sapiens	35,479	23-Nov-99
rxa00887								
rxa00889	711	GB_BA1.MTCY27	27548	Z95208	Mycobacterium tuberculosis H37Rv complete genome, segment 104/162	Mycobacterium tuberculosis	36,978	17-Jun-98
		GB_BA1 U00016	42931	U00016	Mycobacterium leprae cosmid B1937	Mycobacterium leprae	55,651	01-MAR-1994
		GB_PR4 AC007326	102898	AC007326	Homo sapiens, complete sequence	Homo sapiens	40,205	2-Nov-99
rxa00893	720	GB_PL1 HVCPMII	6225	Y09602	H vulgare gene encoding serine carboxypeptidase II, CP-MII	Hordeum vulgare	35,704	10-MAR-1997
		GB_EST35 AI814621	441	AI814621	wj75d04 x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE 2408647 3' similar to TR O00578 O00578 KIAA0167 [1] ;, mRNA sequence	Homo sapiens	37,788	24-Aug-99
		GB_EST3 R51723	376	R51723	yg77h06 r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE 39671 5' similar to gb M77016 TROPOMODULIN (HUMAN),, mRNA sequence.	Homo sapiens	41,489	18-MAY-1995
rxa00895	714	GB_HTG3 AC009414	188673	AC009414	Homo sapiens clone NH0490M08, *** SEQUENCING IN PROGRESS ***, 5 unordered pieces	Homo sapiens	36,775	17-Sep-99
		GB_HTG3 AC009414	188673	AC009414	Homo sapiens clone NH0490M08, *** SEQUENCING IN PROGRESS ***, 5 unordered pieces	Homo sapiens	36,775	17-Sep-99
		GB_PR3 HSJ824F16	139330	AL050325	Human DNA sequence from clone 824F16 on chromosome 20, complete sequence	Homo sapiens	37,286	23-Nov-99

TABLE 4: ALIGNMENT RESULTS

rxa00904	815	GB_HTG5:AC006447	141662	AC006447	Mus musculus, *** SEQUENCING IN PROGRESS ***, 2 unordered pieces.	Mus musculus	35,945	17-Nov-99
		GB_HTG5 AC011064	233428	AC011064	Drosophila melanogaster chromosome X clone BACN05G06 (D1107) RPCI-98 05 G 6 map 12F-13A strain y, cn bw sp, *** SEQUENCING IN PROGRESS ***, 220 unordered pieces	Drosophila melanogaster	37,783	16-Nov-99
		GB_HTG6 AC008334	154566	AC008334	Drosophila melanogaster chromosome X clone BACR08K05 (D885) RPCI-98 08 K 5 map 12F-12F strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 84 unordered pieces	Drosophila melanogaster	37,783	02-DEC-1999
rxa00908	681	GB_GSS12.AQ409791	561	AQ409791	HS_5090_B2_B12_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=666 Col=24 Row=D, genomic survey sequence	Homo sapiens	39,711	17-MAR-1999
		GB_GSS3 B83773	535	B83773	CpG0110A CpIOWAgDNA1 Cryptosporidium parvum genomic, genomic survey sequence	Cryptosporidium parvum	44,615	06-MAY-1999
		GB_GSS12 AQ409791	561	AQ409791	HS_5090_B2_B12_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=666 Col=24 Row=D, genomic survey sequence	Homo sapiens	41,333	17-MAR-1999
rxa00915	753	GB_HTG2 HS1118M15	190466	AL109964	Homo sapiens chromosome 20 clone RP5-1118M15, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Homo sapiens	40,027	30-Nov-99
		GB_HTG2 HS1057B20	204291	AL109823	Homo sapiens chromosome 20 clone RP5-1057B20 map q11 21-12, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Homo sapiens	38,535	30-Nov-99
		GB_HTG2 HS1118M15	190466	AL109964	Homo sapiens chromosome 20 clone RP5-1118M15, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Homo sapiens	40,027	30-Nov-99
rxa00916	3714	GB_EST28 AI543268	568	AI543268	SD09973 5prime SD Drosophila melanogaster Schneider L2 cell culture pOT2 Drosophila melanogaster cDNA clone SD09973 5prime, mRNA sequence	Drosophila melanogaster	40,426	22-MAR-1999
		GB_IN2:AC004301	68620	AC004301	Drosophila melanogaster DNA sequence (P1 DS07134 (D192)), complete sequence	Drosophila melanogaster	37,696	29-MAY-1998
		GB_EST37 AI994315	524	AI994315	701502677 A thaliana, Ohio State clone set Arabidopsis thaliana cDNA clone 701502677, mRNA sequence	Arabidopsis thaliana	40,076	8-Sep-99
rxa00917	2802	GB_BA1:SYCSLRB	146271	D64000	Synechocystis sp. PCC6803 complete genome, 19/27, 2392729-2538999	Synechocystis sp	38,447	13-Feb-99
		GB_HTG1 CEY39E4_2	110000	Z94158	Caenorhabditis elegans chromosome III clone Y39E4, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Caenorhabditis elegans	38,218	Z94158
		GB_HTG1 CEY39E4_2	110000	Z94158	Caenorhabditis elegans chromosome III clone Y39E4, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Caenorhabditis elegans	38,218	Z94158
rxa00921								
rxa00926	486	GB_OM SSU75316	5996	U75316	Sus scrofa beta-myosin heavy chain mRNA, complete cds	Sus scrofa	38,958	03-DEC-1996
		GB_EST21 AA970971	371	AA970971	op10b11 s1 NCI_CGAP_Kid6 Homo sapiens cDNA clone IMAGE 1575261 3', mRNA sequence	Homo sapiens	40,841	13-Apr-99
		GB_OM SSU75316	5996	U75316	Sus scrofa beta-myosin heavy chain mRNA, complete cds	Sus scrofa	38,578	03-DEC-1996
rxa00930	876	GB_BA1 MTCI270A	1670	Z98045	Mycobacterium tuberculosis H37Rv complete genome, segment 116/162	Mycobacterium tuberculosis	37,927	17-Jun-98
		GB_BA1 U00011	40429	U00011	Mycobacterium leprae cosmid B1177	Mycobacterium leprae	38,623	01-MAR-1994
		GB_RO S58745	817	S58745	thyrotroph embryonic factor=leucine zipper transcription factor [rats, pituitary, mRNA, 817 nt]	Rattus sp	41,483	07-MAY-1993
rxa00932	597	GB_PR4:AC009509	192690	AC009509	Homo sapiens 12p11-37.2-54 4 BAC RP11-1060J15 (Roswell Park Cancer Institute Human BAC Library) complete sequence	Homo sapiens	38,776	01-DEC-1999
		GB_PR3.AC004072	170658	AC004072	Human Chromosome X clone bWXD342, complete sequence	Homo sapiens	35,000	08-MAR-1998
		GB_PR4 AC004617	176552	AC004617	Homo sapiens chromosome Y, clone 264,M,20, complete sequence	Homo sapiens	35,702	13-OCT-1999
rxa00933	585	GB_PL1.MGNGAGPOLH	5638	L35053	Transposon MAGGY gag and pol gene homologues, partial cds's	Magnaporthe grisea	40,283	4-Aug-94
		GB_PL1 MGNGAGPOLH	5638	L35053	Transposon MAGGY gag and pol gene homologues, partial cds's	Magnaporthe grisea	37,739	4-Aug-94
rxa00940	519	GB_PR2 HS179N16	172048	Z95152	Homo sapiens DNA sequence from PAC 179N16 on chromosome 6p21 1-21 33 Contains the SAPK4 (MAPK p38delta) gene, and the alternatively spliced SAPK2 gene coding for CSaids binding protein CSBP2 and a MAPK p38beta LIKE protein Contains ESTs, STSs and two predicted CpG islands, complete sequence.	Homo sapiens	38,252	23-Nov-99
		GB_EST26:AU001018	304	AU001018	AU001018 Bombyx mori p50(Daizo) Bombyx mori cDNA clone fbf0932f, mRNA sequence	Bombyx mori	45,745	15-Jan-99
		GB_EST26:AU001019	304	AU001019	AU001019 Bombyx mori p50(Daizo) Bombyx mori cDNA clone fbf0934f, mRNA sequence	Bombyx mori	45,745	15-Jan-99
rxa00943	1035	GB_BA2 AF079317	184457	AF079317	Sphingomonas aromaticivorans plasmid pNL1, complete plasmid sequence	Sphingomonas aromaticivorans	38,151	12-Jan-99

TABLE 4: ALIGNMENT RESULTS

		GB_HTG3:AC008329	114408	AC008329	Drosophila melanogaster chromosome 2 clone BACR31D05 (D861) RPCI-98 31.D.5 map 28C-28D strain y, cn bw sp, *** SEQUENCING IN PROGRESS ***, 105 unordered pieces	Drosophila melanogaster	34,317	17-Aug-99
		GB_HTG3 AC008329	114408	AC008329	Drosophila melanogaster chromosome 2 clone BACR31D05 (D861) RPCI-98 31 D 5 map 28C-28D strain y, cn bw sp, *** SEQUENCING IN PROGRESS ***, 105 unordered pieces.	Drosophila melanogaster	34,317	17-Aug-99
rxa00946	897	GB_BA1 MTV008	63033	AL021246	Mycobacterium tuberculosis H37Rv complete genome, segment 108/162	Mycobacterium tuberculosis	36,045	17-Jun-98
		GB_GSS14 AQ571765	526	AQ571765	HS_2094_A2_B09_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2094 Col=18 Row=C, genomic survey sequence.	Homo sapiens	38,021	1-Jun-99
		GB_RO RRFE65G	2464	X60468	R rattus FE65 gene for adaptor protein interacting with the beta-amyloid precursor protein intracellular domain	Rattus rattus	38,417	1-Feb-96
rxa00949	771	GB_VI PPCCGAAA	5366	M26281	Hamster papovavirus complete genome	Hamster papovavirus	36,579	22-MAY-1995
		GB_VI.HAPVXX	5366	X02449	Hamster Papovavirus (HapV) genome	Hamster papovavirus	36,579	22-OCT-1999
		GB_BA2 AE000878	15432	AE000878	Methanobacterium thermoautotrophicum from bases 976801 to 992232 (section 84 of 148) of the complete genome	Methanobacterium thermoautotrophicum	36,856	15-Nov-97
rxa00959	579	GB_BA1 CGMTRAR	951	X75083	C.glutamicum mtrA gene locus with 5-methyltryptophan resistance	Corynebacterium glutamicum	99,133	18-Aug-94
		GB_BA1 CGMTRA	587	X75084	C glutamicum sequence corresponding to mtrA locus	Corynebacterium glutamicum	99,216	18-Aug-94
		GB_BA1 BLTRP	7725	X04960	Brevibacterium lactofermentum tryptophan operon	Corynebacterium glutamicum	96,800	10-Feb-99
rxa00963	960	GB_EST15 AA484511	504	AA484511	nf08f07 s1 NCI_CGAP_Li1 Homo sapiens cDNA clone IMAGE.913189 similar to gb Y00764 UBIQUINOL-CYTOCHROME C REDUCTASE 11 KD PROTEIN (HUMAN),, mRNA sequence	Homo sapiens	43,750	18-Aug-97
		GB_EST20 AA894481	544	AA894481	nw76b10 s1 NCI_CGAP_Pr12 Homo sapiens cDNA clone IMAGE 1252507 similar to gb Y00764 UBIQUINOL-CYTOCHROME C REDUCTASE 11 KD PROTEIN (HUMAN),, mRNA sequence	Homo sapiens	37,500	6-Apr-98
		GB_EST15 AA526497	582	AA526497	ni96d07 s1 NCI_CGAP_Pr21 Homo sapiens cDNA clone IMAGE 984685 3' similar to gb Y00764 UBIQUINOL-CYTOCHROME C REDUCTASE 11 KD PROTEIN (HUMAN),, mRNA sequence	Homo sapiens	38,554	5-Aug-97
rxa00969	1458	GB_BA1 CGHOMTHR	3685	Y00546	Corynebacterium glutamicum hom-thrB genes for homoserine dehydrogenase and homoserine kinase	Corynebacterium glutamicum	99,588	12-Sep-93
		GB_PAT.I09077	3685	I09077	Sequence 1 from Patent WO 8809819	Unknown.	99,246	02-DEC-1994
		GB_BA1:BLTHRA	1483	Y00476	B. lactofermentum thr A gene	Corynebacterium glutamicum	99,378	05-MAY-1993
rxa00971	341	GB_BA1 CGHOMTHR	3685	Y00546	Corynebacterium glutamicum hom-thrB genes for homoserine dehydrogenase and homoserine kinase	Corynebacterium glutamicum	35,435	12-Sep-93
		GB_PAT I09077	3685	I09077	Sequence 1 from Patent WO 8809819	Unknown	35,435	02-DEC-1994
		GB_BA1 BLTHRB	1139	Y00140	Brevibacterium lactofermentum thrB gene for homoserine kinase	Corynebacterium glutamicum	40,964	12-Sep-93
rxa00973	726	GB_BA1 CGHOMTHR	3685	Y00546	Corynebacterium glutamicum hom-thrB genes for homoserine dehydrogenase and homoserine kinase.	Corynebacterium glutamicum	41,797	12-Sep-93
		GB_PAT.I09077	3685	I09077	Sequence 1 from Patent WO 8809819	Unknown	41,797	02-DEC-1994
		GB_IN2 AC006574	127035	AC006574	Drosophila melanogaster, chromosome 2R, region 39A3-39B1, P1 clones DS02919 and DS05130, complete sequence	Drosophila melanogaster	37,355	16-Feb-99
rxa00978	738	GB_PR2:HSAC000372	41730	AC000372	Human cosmid g1980a186, complete sequence	Homo sapiens	34,674	12-MAR-1997
		GB_PR3 AC005503	40998	AC005503	Homo sapiens clone UWGC g5129s003 from 7q31, complete sequence	Homo sapiens	34,674	20-Aug-98
		GB_PR2:HSAC000372	41730	AC000372	Human cosmid g1980a186, complete sequence	Homo sapiens	38,881	12-MAR-1997
rxa00986	465	GB_GSS10 AQ258013	761	AQ258013	nbxb0019H05f CUGI Rice BAC Library Oryza sativa genomic clone nbxb0019H05f, genomic survey sequence	Oryza sativa	31,533	23-OCT-1998
		GB_PR3 HS83L6	61187	Z99130	Human DNA sequence from PAC 83L6 on chromosome Xp11 1-11 22 Contains ZXDA (ZFPA) zinc finger gene, ESTs and STSs, complete sequence	Homo sapiens	38,395	23-Nov-99
		GB_PR3 HS598A24	96558	AL031115	Human DNA sequence from clone 598A24 on chromosome Xp11 1-11 23 Contains zinc finger X-linked proteins ZXDA, ZXDB ESTs and STS, complete sequence	Homo sapiens	37,333	23-Nov-99

TABLE 4: ALIGNMENT RESULTS

rxa00987	588	GB_HTG1:HS24A17	2000	AL035452	Homo sapiens chromosome X clone RP6-24A17, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Homo sapiens	38,821	23-Nov-99
		GB_HTG1:HS24A17	2000	AL035452	Homo sapiens chromosome X clone RP6-24A17, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Homo sapiens	38,821	23-Nov-99
		GB_PR2 HS1156N12	146360	AL009047	Human DNA sequence from clone 1156N12 on chromosome X Contains an STS and GSSs, complete sequence	Homo sapiens	38,821	23-Nov-99
rxa00988	546	GB_IN1:CELZC328	30350	AF000194	Caenorhabditis elegans cosmid ZC328	Caenorhabditis elegans	36,122	23-Apr-97
		GB_IN1 CELZC328	30350	AF000194	Caenorhabditis elegans cosmid ZC328	Caenorhabditis elegans	37,959	23-Apr-97
rxa01005	969	GB_BA1 FVBPOAD2A	45519	D26094	Flavobacterium sp plasmid pOAD2 DNA, whole sequence	Flavobacterium sp	37,998	6-Feb-99
		GB_GSS1 CNS00UGV	472	AL090973	Arabidopsis thaliana genome survey sequence SP6 end of BAC T6P9 of TAMU library from strain Columbia of Arabidopsis thaliana, genomic survey sequence	Arabidopsis thaliana	39,024	28-Jun-99
		GB_GSS1 CNS00S69	512	AL087999	Arabidopsis thaliana genome survey sequence SP6 end of BAC T1C4 of TAMU library from strain Columbia of Arabidopsis thaliana, genomic survey sequence	Arabidopsis thaliana	35,938	28-Jun-99
rxa01007								
rxa01008								
rxa01011	1356	GB_EST38 AW039107	598	AW039107	EST281080 tomato mixed elicitor, BTI Lycopersicon esculentum cDNA clone cLET12F19, mRNA sequence.	Lycopersicon esculentum	39,724	18-OCT-1999
		GB_BA1 MTY13E12	43401	Z95390	Mycobacterium tuberculosis H37Rv complete genome, segment 147/162	Mycobacterium tuberculosis	38,618	17-Jun-98
		GB_BA1 MBU15140	2136	U15140	Mycobacterium bovis ribosomal proteins IF-1 (infA), L36 (rpmJ), S13 (rpsM) and S11 (rpsK) genes, complete cds, and S4 (rpsD) gene, partial cds	Mycobacterium bovis	37,070	28-OCT-1996
rxa01016	771	GB_BA1 CGBPHI16	962	Y12472	C glutamicum DNA, attachment site bacteriophage Phi-16	Corynebacterium glutamicum	45,098	05-MAR-1999
		GB_BA1 CGBPHI16	962	Y12472	C.glutamicum DNA, attachment site bacteriophage Phi-16	Corynebacterium glutamicum	37,251	05-MAR-1999
rxa01017	732	GB_BA1 CGBPHI16	962	Y12472	C glutamicum DNA, attachment site bacteriophage Phi-16	Corynebacterium glutamicum	39,245	05-MAR-1999
		GB_BA2 AF099014	2500	AF099014	Streptomyces coelicolor strain A3(2) transposase (tnpA) and Fe-containing superoxide dismutase I (sodF1) genes, complete cds	Streptomyces coelicolor	38,036	1-Jun-99
		GB_HTG3 AC009249	119461	AC009249	Drosophila melanogaster chromosome 3 clone BACR02M06 (D1003) RPCI-98 02 M 6 map 98B-98B strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 97 unordered pieces	Drosophila melanogaster	37,853	27-Aug-99
rxa01021	622	GB_BA2 U39718	8603	U39718	Mycoplasma genitalium section 40 of 51 of the complete genome	Mycoplasma genitalium	39,348	5-Nov-98
		GB_GSS3:B46221	457	B46221	HS-1063-A2-D06-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 796 Col=12 Row=G, genomic survey sequence	Homo sapiens	39,933	21-OCT-1997
		GB_OV AF035529	848	AF035529	Xenopus laevis Smad6 mRNA, partial cds	Xenopus laevis	37,203	1-Jan-98
rxa01023	1101	GB_HTG2 HSJ435K13	151301	AL109941	Homo sapiens chromosome 6 clone RP3-435K13 map q14 1-16 1, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Homo sapiens	34,405	03-DEC-1999
		GB_HTG2 HSJ435K13	151301	AL109941	Homo sapiens chromosome 6 clone RP3-435K13 map q14 1-16 1, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Homo sapiens	34,405	03-DEC-1999
		GB_BA1 RCU57682	86896	U57682	Rhodobacter capsulatus cosmids 143-147, complete sequence	Rhodobacter capsulatus	39,022	7-Feb-97
rxa01028	2172	GB_IN1 CBU55260	2518	U55260	Caenorhabditis briggsae beta tubulin (mec-7) gene, complete cds.	Caenorhabditis briggsae	39,467	5-Jun-96
		GB_HTG1 CEY1A5	196643	AL008872	Caenorhabditis elegans chromosome III clone Y1A5, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Caenorhabditis elegans	38,168	9-Nov-97
		GB_HTG1 CEY1A5	196643	AL008872	Caenorhabditis elegans chromosome III clone Y1A5, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Caenorhabditis elegans	38,168	9-Nov-97

TABLE 4: ALIGNMENT RESULTS

rxa01029	612	GB_PR3:HS466P17	149963	AL023806	Human DNA sequence from clone 466P17 on chromosome 6q24. Contains a putative novel gene, the 5' part of the EPM2A (Laforin) gene, ESTs STSs, GSSs, genomic marker D6S1703 and D6S1443, a putative CpG island and a ca repeat polymorphism, complete sequence	Homo sapiens	38,330	23-Nov-99
		GB_PR3:HS466P17	149963	AL023806	Human DNA sequence from clone 466P17 on chromosome 6q24. Contains a putative novel gene, the 5' part of the EPM2A (Laforin) gene, ESTs STSs, GSSs, genomic marker D6S1703 and D6S1443, a putative CpG island and a ca repeat polymorphism, complete sequence	Homo sapiens	39,262	23-Nov-99
		GB_RO D78344	59641	D78344	Mouse DNA for Ig gamma-chains, partial cds	Mus musculus	35,472	5-Feb-99
rxa01031	789	GB_PR4:AC006948	168558	AC006948	Homo sapiens chromosome 17, clone hRPK 334_M_10, complete sequence	Homo sapiens	44,005	27-Apr-99
		GB_PL2:AC011665	101845	AC011665	Arabidopsis thaliana chromosome I BAC T6L1 genomic sequence, complete sequence	Arabidopsis thaliana	38,170	11-Nov-99
		GB_RO:MMU19724	5523	U19724	Mus musculus MMTV integration locus, aromatase gene, 3'UTR.	Mus musculus	35,256	17-Feb-96
rxa01032	498	GB_EST9 AA118349	576	AA118349	ml56b06 r1 Stratagene mouse testis (#937308) Mus musculus cDNA clone IMAGE 515987 5' similar to gb L04852 Mouse (MOUSE),, mRNA sequence	Mus musculus	43,056	19-Nov-96
		GB_EST9 AA118349	576	AA118349	ml56b06 r1 Stratagene mouse testis (#937308) Mus musculus cDNA clone IMAGE 515987 5' similar to gb L04852 Mouse (MOUSE),, mRNA sequence	Mus musculus	42,273	19-Nov-96
rxa01033	459	GB_GSS13.AQ434868	520	AQ434868	HS_5117_B1_D07_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=693 Col=13 Row=H, genomic survey sequence	Homo sapiens	38,608	31-MAR-1999
		GB_HTG2 HSDJ794I6	137124	AL109976	Homo sapiens chromosome 20 clone RP4-794I6, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Homo sapiens	28,929	27-Nov-99
		GB_HTG2:HSDJ794I6	137124	AL109976	Homo sapiens chromosome 20 clone RP4-794I6, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Homo sapiens	28,929	27-Nov-99
rxa01034	477	GB_PL2:ATT29H11	87011	AL049659	Arabidopsis thaliana DNA chromosome 3, BAC clone T29H11	Arabidopsis thaliana	32,495	9-Jun-99
		GB_PL2.ATT29H11	87011	AL049659	Arabidopsis thaliana DNA chromosome 3, BAC clone T29H11	Arabidopsis thaliana	40,042	9-Jun-99
		GB_EST25:AU045739	436	AU045739	AU045739 Mouse sixteen-cell-embryo cDNA Mus musculus cDNA clone J0940F02 3', mRNA sequence	Mus musculus	35,435	09-DEC-1998
rxa01035	729	GB_GSS1 CNS00QD8	526	AL085658	Arabidopsis thaliana genome survey sequence SP6 end of BAC F11C22 of IGF library from strain Columbia of Arabidopsis thaliana, genomic survey sequence.	Arabidopsis thaliana	36,466	28-Jun-99
		GB_GSS13 AQ447948	515	AQ447948	mgxb0015A01r CUGI Rice Blast BAC Library Magnaporthe grisea genomic clone mgxb0015A01r, genomic survey sequence	Magnaporthe grisea	45,833	8-Apr-99
		GB_GSS1 CNS00QD8	526	AL085658	Arabidopsis thaliana genome survey sequence SP6 end of BAC F11C22 of IGF library from strain Columbia of Arabidopsis thaliana, genomic survey sequence.	Arabidopsis thaliana	37,500	28-Jun-99
rxa01036	576	GB_HTG2:AC004846	143577	AC004846	Homo sapiens clone DJ0647C14, *** SEQUENCING IN PROGRESS ***, 21 unordered pieces	Homo sapiens	38,137	12-Jun-98
		GB_EST19 AA804532	427	AA804532	ns28c05.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE 1184936 3' similar to contains element MER40 repetitive element ;, mRNA sequence	Homo sapiens	33,582	18-Feb-98
		GB_HTG2 AC006342	201618	AC006342	Homo sapiens clone DJ0054D12, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces.	Homo sapiens	38,137	11-Jan-99
rxa01037	651	GB_PR4 AC004812	138532	AC004812	Homo sapiens PAC clone 267D11 from 12, complete sequence	Homo sapiens	39,750	05-DEC-1998
		GB_HTG2 AC006342	201618	AC006342	Homo sapiens clone DJ0054D12, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces	Homo sapiens	41,214	11-Jan-99
		GB_HTG2 AC004846	143577	AC004846	Homo sapiens clone DJ0647C14, *** SEQUENCING IN PROGRESS ***, 21 unordered pieces	Homo sapiens	41,214	12-Jun-98
rxa01038								
rxa01039	699	GB_PR4 HUAC004682	189134	AC004682	Homo sapiens Chromosome 16 BAC clone CIT987SK-A-259H10, complete sequence	Homo sapiens	36,192	23-Nov-99
		GB_HTG2 HS500L14	164856	AL023583	Homo sapiens chromosome 6 clone RP3-500L14 map p23-24 3, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Homo sapiens	34,632	30-Nov-99
		GB_HTG2 HS500L14	164856	AL023583	Homo sapiens chromosome 6 clone RP3-500L14 map p23-24 3, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Homo sapiens	34,632	30-Nov-99
rxa01040	1026	GB_EST24 AI193549	479	AI193549	qe70e06 x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1744354 3', mRNA sequence	Homo sapiens	40,126	29-OCT-1998
		GB_PR2 HSU38545	3609	U38545	Human ARF-activated phosphatidylcholine-specific phospholipase D1a (hPLD1) mRNA, complete cds	Homo sapiens	38,652	10-MAR-1997
		GB_PR2 AC002481	28244	AC002481	Human cosmid clone LUCA12 from 3p21 3, complete sequence	Homo sapiens	39,643	21-Aug-97

TABLE 4: ALIGNMENT RESULTS

rxa01041	276	GB_HTG6:AC007957	212658	AC007957	Homo sapiens, *** SEQUENCING IN PROGRESS ***, 2 ordered pieces.	Homo sapiens	40,809	26-Nov-99
		GB_PR2.AP000552	157086	AP000552	Homo sapiens genomic DNA, chromosome 22q11.2, BCRL2 region, clone.KB1183D5	Homo sapiens	40,809	01-OCT-1999
		GB_PR3.HS57A13	169693	Z83848	Human DNA sequence from PAC 57A13 between markers DXS6791 and DXS8038 on chromosome X contains glutamate receptor subunit GluRC, ESTs, STS and polymorphic CA repeat	Homo sapiens	37,647	23-Nov-99
rxa01042	1401	GB_BA1 MTCY10G2	38970	Z92539	Mycobacterium tuberculosis H37Rv complete genome, segment 47/162.	Mycobacterium tuberculosis	36,023	17-Jun-98
		GB_BA1 MTCY10G2	38970	Z92539	Mycobacterium tuberculosis H37Rv complete genome, segment 47/162	Mycobacterium tuberculosis	37,010	17-Jun-98
		GB_EST29 AI551042	538	AI551042	vx33d11 x1 Stratagene mouse lung 937302 Mus musculus cDNA clone IMAGE:1277013 3', mRNA sequence.	Mus musculus	38,806	23-MAR-1999
rxa01043	696	GB_BA1 AF006658	2500	AF006658	Bacteroides fragilis beta-glucosidase gene, complete cds	Bacteroides fragilis	39,156	12-Jul-97
		GB_BA1 MLB1790G	37617	Z14314	M leprae genes rplL, rpoB, rpoC, end, rpsL, rpsG, efg, tuf, rpsJ, rplC for ribosomal protein L7, RNA polymerase beta subunit, RNA polymerase beta' subunit, endonuclease, ribosomal protein S7, ribosomal protein S12, elongation factor G, elongation factor Tu, ribosomal protein S10, ribosomal protein L3 and mkl gene	Mycobacterium leprae	39,970	11-Feb-93
		GB_BA1 AF006658	2500	AF006658	Bacteroides fragilis beta-glucosidase gene, complete cds	Bacteroides fragilis	36,472	12-Jul-97
rxa01044	1380	GB_HTG6 AC010998	144338	AC010998	Homo sapiens clone RP11-95I16, *** SEQUENCING IN PROGRESS ***, 17 unordered pieces	Homo sapiens	37,630	08-DEC-1999
		GB_HTG6.AC010998	144338	AC010998	Homo sapiens clone RP11-95I16, *** SEQUENCING IN PROGRESS ***, 17 unordered pieces	Homo sapiens	37,864	08-DEC-1999
		GB_BA2 AE000939	10599	AE000939	Methanobacterium thermoautotrophicum from bases 1698671 to 1709269 (section 145 of 148) of the complete genome.	Methanobacterium thermoautotrophicum	34,480	15-Nov-97
rxa01045	1947	GB_VI:FCVF6A	8440	M18247	Feline leukemia virus, subgroup A (FeLV-FAIDS), complete nucleotide sequence	Feline leukemia virus	37,617	29-MAR-1996
		GB_OM.CATFLVPOL	3639	L06140	Felis catus endogenous FeLV proviral polyprotein (protease (PRO), reverse transcriptase (RT), integrase/endonuclease (INT)) and pol pseudogene, 3' end	Felis catus	41,966	21-Aug-95
		GB_VI CEAVCG	9189	M33677	Caprine arthritis encephalitis virus, complete proviral genome	Caprine arthritis-encephalitis virus	36,297	04-MAR-1996
rxa01046	1902	GB_HTG3 AC008423	177734	AC008423	Homo sapiens chromosome 5 clone CIT-HSPC_298N6, *** SEQUENCING IN PROGRESS ***, 56 unordered pieces	Homo sapiens	38,720	3-Aug-99
		GB_HTG3 AC008423	177734	AC008423	Homo sapiens chromosome 5 clone CIT-HSPC_298N6, *** SEQUENCING IN PROGRESS ***, 56 unordered pieces	Homo sapiens	38,720	3-Aug-99
		GB_HTG3 AC008423	177734	AC008423	Homo sapiens chromosome 5 clone CIT-HSPC_298N6, *** SEQUENCING IN PROGRESS ***, 56 unordered pieces.	Homo sapiens	35,882	3-Aug-99
rxa01047	597	GB_EST20 AA842685	510	AA842685	MBAFCZ9C11T3 Brugia malayi adult female cDNA (SAW96MLW-BmAF) Brugia malayi cDNA clone AFCZ9C11 5', mRNA sequence	Brugia malayi	37,965	02-MAR-1998
		GB_EST20 AA842685	510	AA842685	MBAFCZ9C11T3 Brugia malayi adult female cDNA (SAW96MLW-BmAF) Brugia malayi cDNA clone AFCZ9C11 5', mRNA sequence	Brugia malayi	41,697	02-MAR-1998
rxa01058	444	GB_GSS9 AQ160800	745	AQ160800	nbxb0006C07r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0006C07r, genomic survey sequence	Oryza sativa	38,242	12-Sep-98
		GB_GSS3 B10162	1102	B10162	F11B10-Sp6 IGF Arabidopsis thaliana genomic clone F11B10, genomic survey sequence	Arabidopsis thaliana	42,263	14-MAY-1997
		GB_BA1 AB032799	9077	AB032799	Chromobacterium violaceum violacein biosynthetic gene cluster (vioA, vio B, vio C, vio D), complete cds	Chromobacterium violaceum	34,475	02-OCT-1999
rxa01063	453	GB_GSS4 AQ707752	510	AQ707752	HS_5560_A2_G07_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=1136 Col=14 Row=M, genomic survey sequence	Homo sapiens	36,932	7-Jul-99
		GB_GSS4 AQ707752	510	AQ707752	HS_5560_A2_G07_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=1136 Col=14 Row=M, genomic survey sequence	Homo sapiens	35,885	7-Jul-99
rxa01066	849	GB_BA2 U32709	10010	U32709	Haemophilus influenzae Rd section 24 of 163 of the complete genome	Haemophilus influenzae Rd	36,158	29-MAY-1998
		GB_RO AB009615	1515	AB009615	Mus musculus mRNA for type II phosphatidylinositolphosphate kinase-alpha, complete cds	Mus musculus	37,861	13-Feb-99

TABLE 4: ALIGNMENT RESULTS

		GB_RO:AB032899	1914	AB032899	Rattus norvegicus PIPK2 alpha mRNA for phosphatidylinositol 5-phosphate 4-kinase alpha, complete cds	Rattus norvegicus	38,480	07-OCT-1999
rxa01068	1194	GB_HTG4 AC006091	176878	AC006091	Drosophila melanogaster chromosome 3 clone BACR48G05 (D475) RPCI-98 48.G 5 map 91F1-91F13 strain y, cn bw sp, *** SEQUENCING IN PROGRESS ***, 4 unordered pieces	Drosophila melanogaster	35,539	27-OCT-1999
		GB_HTG4 AC006091	176878	AC006091	Drosophila melanogaster chromosome 3 clone BACR48G05 (D475) RPCI-98 48.G 5 map 91F1-91F13 strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 4 unordered pieces	Drosophila melanogaster	35,539	27-OCT-1999
		GB_HTG2 AC008141	100729	AC008141	Drosophila melanogaster chromosome 3 clone BACR17F04 (D988) RPCI-98 17.F 4 map 91F-91F strain y, cn bw sp, *** SEQUENCING IN PROGRESS ***, 69 unordered pieces	Drosophila melanogaster	34,415	2-Aug-99
rxa01069	837	GB_EST15 AA531901	524	AA531901	TgESTzz32g09 r1 TgME49 invivo Bradyzoite cDNA size selected Toxoplasma gondii cDNA clone tgzz32g09 r1 5', mRNA sequence.	Toxoplasma gondii	43,005	22-Jul-97
		GB_EST15 AA520183	527	AA520183	TgESTzz39d01.s1 TgME49 invivo Bradyzoite cDNA size selected Toxoplasma gondii cDNA clone tgzz39d01 s1 3', mRNA sequence	Toxoplasma gondii	40,664	16-Jul-97
		GB_HTG6 AC010846	187611	AC010846	Drosophila melanogaster chromosome X clone BACR13G13 (D894) RPCI-98 13.G 13 map 14B-14C strain y, cn bw sp, *** SEQUENCING IN PROGRESS ***, 97 unordered pieces	Drosophila melanogaster	36,679	03-DEC-1999
rxa01071	2187	GB_EST20 AA880319	450	AA880319	vx39h01.r1 Stratagene mouse lung 937302 Mus musculus cDNA clone IMAGE:1277617 5', mRNA sequence	Mus musculus	40,724	26-MAR-1998
		GB_GSS14 AQ558382	435	AQ558382	HS_2068_B1_F06_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2068 Col=11 Row=L, genomic survey sequence	Homo sapiens	36,882	29-MAY-1999
		GB_GSS15 AQ600385	483	AQ600385	HS_5357_B2_C05_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=933 Col=10 Row=F, genomic survey sequence	Homo sapiens	40,476	10-Jun-99
rxa01074	828	GB_BA1 PSEHEDDH	3060	M74256	Pseudomonas aeruginosa 6-phosphogluconate dehydratase (edd) gene, and glyceraldehyde-3-phosphate dehydrogenase (gap) gene, complete cds	Pseudomonas aeruginosa	39,657	30-Nov-93
		GB_BA1 CGL007732	4460	AJ007732	Corynebacterium glutamicum 3' ppc gene, secG gene, amt gene, ocd gene and 5' soxA gene	Corynebacterium glutamicum	39,168	7-Jan-99
		GB_EST9 AA066016	406	AA066016	ml52f12 r1 Stratagene mouse testis (#937308) Mus musculus cDNA clone IMAGE 515663 5', mRNA sequence	Mus musculus	43,382	3-Feb-97
rxa01075	534	GB_EST21 AA986543	445	AA986543	ue14f08.x1 Sugano mouse embryo mewa Mus musculus cDNA clone IMAGE 1480359 3', mRNA sequence	Mus musculus	31,236	28-MAY-1998
		GB_EST22 AI035794	509	AI035794	ue17d01 y1 Sugano mouse embryo mewa Mus musculus cDNA clone IMAGE 1480609 5', mRNA sequence	Mus musculus	42,264	26-Jun-98
		GB_EST22 AI006506	384	AI006506	ue14f08 y1 Sugano mouse embryo mewa Mus musculus cDNA clone IMAGE:1480359 5', mRNA sequence.	Mus musculus	46,637	12-Jun-98
rxa01076	1143	GB_HTG2 AC007741	162450	AC007741	Homo sapiens clone NH0340F16, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces.	Homo sapiens	38,209	5-Jun-99
		GB_HTG2 AC007741	162450	AC007741	Homo sapiens clone NH0340F16, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces	Homo sapiens	38,209	5-Jun-99
		GB_EST33 AV072325	317	AV072325	AV072325 Mus musculus stomach C57BL/6J adult Mus musculus cDNA clone 2200003E03, mRNA sequence	Mus musculus	48,485	24-Jun-99
rxa01078	957	GB_BA2 RCPHSYNG	45959	Z11165	R capsulatus complete photosynthesis gene cluster	Rhodobacter capsulatus	36,603	2-Sep-99
		GB_BA2:RCPHSYNG	45959	Z11165	R capsulatus complete photosynthesis gene cluster	Rhodobacter capsulatus	37,989	2-Sep-99
		GB_PR4:AF073931	7898	AF073931	Homo sapiens low-voltage activated calcium channel alpha 1H mRNA, complete cds	Homo sapiens	37,953	04-MAR-1999
rxa01083	399	GB_BA2 AF112535	4363	AF112535	Corynebacterium glutamicum putative glutaredoxin NrdH (nrdH), NrdI (nrdI), and ribonucleotide reductase alpha-chain (nrdE) genes, complete cds	Corynebacterium glutamicum	99,499	5-Aug-99
		GB_PR3 HSH3D2	1789	AF053138	Homo sapiens histone deacetylase 3 gene, exons 11, 12, 13 and partial cds	Homo sapiens	33,512	28-MAR-1998
		GB_PR4:AF059650	16015	AF059650	Homo sapiens histone deacetylase 3 (HDAC3) gene, complete cds.	Homo sapiens	38,814	03-MAR-1999
rxa01085	902	GB_EST4 H55032	951	H55032	HHU58a Sorghum bicolor cv. TX430 Sorghum bicolor cDNA clone HHU58 5' similar to transketolase, chloroplast (TKLC1), mRNA sequence	Sorghum bicolor	41,111	27-Sep-99
		GB_HTG2.HSBA27F12	123489	AL109914	Homo sapiens chromosome 6 clone RP11-27F12 map p22 3-24, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Homo sapiens	35,156	30-Nov-99
		GB_HTG2 HSBA27F12	123489	AL109914	Homo sapiens chromosome 6 clone RP11-27F12 map p22 3-24, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Homo sapiens	35,156	30-Nov-99
rxa01088	1305	GB_HTG5 AC010202	170004	AC010202	Homo sapiens chromosome 12q seeders clone RP11-210L7, *** SEQUENCING IN PROGRESS ***, 40 unordered pieces	Homo sapiens	37,313	6-Nov-99

TABLE 4: ALIGNMENT RESULTS

		GB_HTG5:AC010202	170004	AC010202	Homo sapiens chromosome 12q seeders clone RP11-210L7, *** SEQUENCING IN PROGRESS ***, 40 unordered pieces.	Homo sapiens	37,422	6-Nov-99
		GB_PR1:HSIGFACI	7260	X57025	Human IGF-I mRNA for insulin-like growth factor I	Homo sapiens	38,043	17-Feb-92
rxa01091	664	GB_BA1 ECORELA	4034	J04039	E coli relA gene encoding ATP GTP 3'-pyrophosphotransferase, complete cds	Escherichia coli	54,711	16-Nov-93
		GB_BA2 ECU29580	13234	U29580	Escherichia coli K-12 genome, approximately 62 minute region	Escherichia coli	37,327	5-Apr-99
		GB_BA2.AE000362	12595	AE000362	Escherichia coli K-12 MG1655 section 252 of 400 of the complete genome	Escherichia coli	37,327	12-Nov-98
rxa01096	547	GB_PL1 PCX24CRY	357	Z34459	P cryptogea X24 gene for cryptogein	Phytophthora cryptogea	43,310	19-Sep-96
		GB_EST24 AI244520	414	AI244520	qk14c08.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE 1868942 3', mRNA sequence	Homo sapiens	33,528	28-Jan-99
		GB_RO:MM26SPROT	1479	Y13071	Mus musculus mRNA for 26S proteasome non-ATPase subunit	Mus musculus	37,941	10-Sep-98
rxa01102	1368	GB_HTG3 AC009219	127519	AC009219	Drosophila melanogaster chromosome 3 clone BACR32N16 (D973) RPCI-98 32 N 16 map 86C-86C strain y, cn bw sp, *** SEQUENCING IN PROGRESS***, 74 unordered pieces.	Drosophila melanogaster	35,080	20-Aug-99
		GB_HTG3:AC009219	127519	AC009219	Drosophila melanogaster chromosome 3 clone BACR32N16 (D973) RPCI-98 32 N 16 map 86C-86C strain y, cn bw sp, *** SEQUENCING IN PROGRESS ***, 74 unordered pieces	Drosophila melanogaster	35,080	20-Aug-99
		GB_PR4:AC006065	191134	AC006065	Homo sapiens 12q24 2 BAC RPCI11-407A16 (Roswell Park Cancer Institute Human BAC Library) complete sequence	Homo sapiens	37,453	27-Feb-99
rxa01103	348	GB_EST13 AA340958	338	AA340958	EST46332 Fetal kidney II Homo sapiens cDNA 5' end, mRNA sequence	Homo sapiens	36,596	21-Apr-97
		GB_RO.MUSBCL22	5806	L31532	Mus musculus bcl-2 alpha gene, exon 2	Mus musculus	33,913	5-Apr-94
		GB_BA2 AE001165	13021	AE001165	Borrelia burgdorferi (section 51 of 70) of the complete genome	Borrelia burgdorferi	31,412	15-DEC-1997
rxa01107	1323	GB_HTG1 HS1030M6	173804	AL035089	Homo sapiens chromosome 20 clone RP5-1030M6, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Homo sapiens	34,935	23-Nov-99
		GB_HTG1 HS1030M6	173804	AL035089	Homo sapiens chromosome 20 clone RP5-1030M6, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	34,935	23-Nov-99
		GB_HTG2 AC005057	99370	AC005057	Homo sapiens clone RG052H06, *** SEQUENCING IN PROGRESS ***, 11 unordered pieces	Homo sapiens	35,897	12-Jun-98
rxa01108	774	GB_PR2 HSJ193N13	122961	AL078600	Human DNA sequence from clone RP1-193N13 on chromosome 6q21-22 31, complete sequence	Homo sapiens	37,115	22-Nov-99
		GB_EST34 AV139054	287	AV139054	AV139054 Mus musculus C57BL/6J 10-11 day embryo Mus musculus cDNA clone 2810048D09, mRNA sequence	Mus musculus	35,540	1-Jul-99
		GB_PL1:GTU21246	926	U21246	Gracilariopsis tenuifrons internal transcribed spacer region of the ribosomal repeat, ITS1, 5 8S rRNA gene and ITS2, complete sequence	Gracilariopsis tenuifrons	37,200	12-MAR-1995
rxa01109	765	GB_BA1 AB003332	1424	AB003332	Anabaena variabilis rbpF gene for RNA binding protein, complete cds	Anabaena variabilis	35,958	21-MAY-1999
		GB_BA1 BPETOXOP	9342	L10720	Bordetella pertussis toxin liberation operon	Bordetella pertussis	40,107	9-Jul-93
		GB_PAT I50844	951	I50844	Sequence 12 from patent US 5643747	Unknown	39,973	07-OCT-1997
rxa01119	1053	GB_GSS3 B36708	438	B36708	HS-1041-B1-C05-MF abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 823 Col=9 Row=F, genomic survey sequence	Homo sapiens	37,300	17-OCT-1997
		GB_PL2:F11A17	102077	AC007932	Arabidopsis thaliana chromosome 1 BAC F11A17 sequence, complete sequence	Arabidopsis thaliana	37,488	16-Aug-99
		GB_EST22.AI043264	283	AI043264	TENU0904 T. cruzi epimastigote normalized cDNA Library Trypanosoma cruzi cDNA clone 2i14 3', mRNA sequence	Trypanosoma cruzi	40,989	1-Jul-98
rxa01121	1209	GB_PAT:I78756	737	I78756	Sequence 12 from patent US 5693781	Unknown	40,975	3-Apr-98
		GB_PAT.I92045	737	I92045	Sequence 12 from patent US 5726299	Unknown.	40,975	01-DEC-1998
		GB_PL1:MTPACG	100314	X55026	P anserina complete mitochondrial genome	Mitochondrion Podospora anserina	34,477	08-DEC-1997
rxa01122	645	GB_HTG4 AC010148	228794	AC010148	Homo sapiens chromosome unknown clone NH0367B19, WORKING DRAFT SEQUENCE, in unordered pieces	Homo sapiens	42,130	29-OCT-1999
		GB_HTG4 AC010148	228794	AC010148	Homo sapiens chromosome unknown clone NH0367B19, WORKING DRAFT SEQUENCE, in unordered pieces	Homo sapiens	42,130	29-OCT-1999
		GB_HTG4 AC010148	228794	AC010148	Homo sapiens chromosome unknown clone NH0367B19, WORKING DRAFT SEQUENCE, in unordered pieces.	Homo sapiens	37,559	29-OCT-1999
rxa01123	570	GB_EST33 AV090612	274	AV090612	AV090612 Mus musculus tongue C57BL/6J adult Mus musculus cDNA clone 2310051C21, mRNA sequence	Mus musculus	33,212	28-Jun-99
		GB_EST33 AV090612	274	AV090612	AV090612 Mus musculus tongue C57BL/6J adult Mus musculus cDNA clone 2310051C21, mRNA sequence	Mus musculus	34,529	28-Jun-99

TABLE 4: ALIGNMENT RESULTS

rxa01127	1143	GB_BA1:CGLEUB	2042	Y09578	C glutamicum leuB gene.	Corynebacterium glutamicum	99,913	02-MAR-1999
		GB_BA1 MTV012	70287	AL021287	Mycobacterium tuberculosis H37Rv complete genome, segment 132/162	Mycobacterium tuberculosis	39,295	23-Jun-99
		GB_BA1 SC1C2	42210	AL031124	Streptomyces coelicolor cosmid 1C2	Streptomyces coelicolor	62,456	15-Jan-99
rxa01128	1137	GB_BA1 CGLEUB	2042	Y09578	C glutamicum leuB gene	Corynebacterium glutamicum	38,515	02-MAR-1999
		GB_GSS8 AQ066341	241	AQ066341	HS_2243_B1_A02_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2243 Col=3 Row=B, genomic survey sequence	Homo sapiens	39,004	4-Aug-98
		GB_EST24 AI168493	459	AI168493	ou64g08 s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE 1632638 3' similar to gb D90209 DNA-BINDING PROTEIN TAXREB67 (HUMAN),, mRNA sequence	Homo sapiens	42,117	23-OCT-1998
rxa01129	1989	GB_BA1:MTCI28	36300	Z97050	Mycobacterium tuberculosis H37Rv complete genome; segment 10/162	Mycobacterium tuberculosis	38,159	23-Jun-98
		GB_HTG1 LMFL6852	37286	AL034359	Leishmania major chromosome 4 clone L6852 strain Friedlin, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Leishmania major	38,485	29-Apr-99
		GB_HTG1 LMFL6852	37286	AL034359	Leishmania major chromosome 4 clone L6852 strain Friedlin, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Leishmania major	38,485	29-Apr-99
rxa01131	990	GB_BA1 CGLEUB	2042	Y09578	C glutamicum leuB gene	Corynebacterium glutamicum	99,313	02-MAR-1999
		GB_PR4 AC007253	225699	AC007253	Homo sapiens BAC clone NH0454P05 from 2, complete sequence	Homo sapiens	35,421	22-OCT-1999
		GB_HTG3:AC011305	171067	AC011305	Homo sapiens clone NH0390E09, *** SEQUENCING IN PROGRESS ***, 1 unordered pieces	Homo sapiens	35,955	05-OCT-1999
rxa01134	871	GB_HTG4:AC009375	137069	AC009375	Drosophila melanogaster chromosome 3L/75A1 clone RPCI98-44L18, *** SEQUENCING IN PROGRESS ***, 59 unordered pieces	Drosophila melanogaster	37,380	16-OCT-1999
		GB_HTG4 AC009375	137069	AC009375	Drosophila melanogaster chromosome 3L/75A1 clone RPCI98-44L18, *** SEQUENCING IN PROGRESS ***, 59 unordered pieces	Drosophila melanogaster	37,380	16-OCT-1999
		GB_HTG4 AC009375	137069	AC009375	Drosophila melanogaster chromosome 3L/75A1 clone RPCI98-44L18, *** SEQUENCING IN PROGRESS ***, 59 unordered pieces	Drosophila melanogaster	38,489	16-OCT-1999
rxa01137	483	GB_IN2 AC005421	69992	AC005421	Drosophila melanogaster, chromosome 2L, region 22A1-22A1, P1 clone DS03601, complete sequence.	Drosophila melanogaster	37,367	31-OCT-1998
		GB_GSS1 CNS00KX9	1101	AL078350	Drosophila melanogaster genome survey sequence TET3 end of BAC BACR23A23 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence	Drosophila melanogaster	30,670	3-Jun-99
		GB_IN2 AC005421	69992	AC005421	Drosophila melanogaster, chromosome 2L, region 22A1-22A1, P1 clone DS03601, complete sequence	Drosophila melanogaster	33,333	31-OCT-1998
rxa01140	1056	GB_PR4 AC007948	99904	AC007948	Genomic sequence of Homo sapiens clone R417F14A from chromosome 18, complete sequence	Homo sapiens	36,249	6-Nov-99
		GB_HTG3 AC006278	140290	AC006278	Plasmodium falciparum chromosome 12 clone 3D7, *** SEQUENCING IN PROGRESS ***, 18 unordered pieces.	Plasmodium falciparum	36,592	23-Sep-99
		GB_HTG3 AC006278	140290	AC006278	Plasmodium falciparum chromosome 12 clone 3D7, *** SEQUENCING IN PROGRESS ***, 18 unordered pieces	Plasmodium falciparum	36,592	23-Sep-99
rxa01148	723	GB_BA1:MTCY261	27322	Z97559	Mycobacterium tuberculosis H37Rv complete genome, segment 95/162	Mycobacterium tuberculosis	50,139	17-Jun-98
		GB_EST15 AA501229	548	AA501229	vh62g12.r1 Knowles Solter mouse 11 5day limb bud Mus musculus cDNA clone IMAGE 891622 5' similar to TR G762951 G762951 PRPL-2 PROTEIN,, mRNA sequence.	Mus musculus	36,250	1-Jul-97
		GB_PR4 AF106062	1306	AF106062	Homo sapiens Wiskott-Aldrich syndrome protein interacting protein (WASPIP) mRNA, partial cds	Homo sapiens	43,205	31-Jul-99
rxa01153	543	GB_BA1:MTCY261	27322	Z97559	Mycobacterium tuberculosis H37Rv complete genome, segment 95/162	Mycobacterium tuberculosis	40,000	17-Jun-98
		GB_BA1 MLCB2533	40245	AL035310	Mycobacterium leprae cosmid B2533	Mycobacterium leprae	61,765	27-Aug-99
		GB_BA1 U00017	42157	U00017	Mycobacterium leprae cosmid B2126	Mycobacterium leprae	39,615	01-MAR-1994

TABLE 4: ALIGNMENT RESULTS

rxa01154	677	GB_BA1:MTCY49	39430	Z73966	Mycobacterium tuberculosis H37Rv complete genome; segment 93/162.	Mycobacterium tuberculosis	37,615	24-Jun-99
		GB_BA1:U00017	42157	U00017	Mycobacterium leprae cosmid B2126	Mycobacterium leprae	36,957	01-MAR-1994
		GB_BA2:AF086832	10612	AF086832	Streptomyces coelicolor putative ferredoxin, ARC (arc), 20S proteasome beta-subunit precursor (prcB), 20S proteasome alpha-subunit (prcA), putative LacI family repressor, and putative transporter genes, complete cds, and unknown genes	Streptomyces coelicolor	53,354	30-Jun-99
rxa01155	1570	GB_BA1 MTCY49	39430	Z73966	Mycobacterium tuberculosis H37Rv complete genome, segment 93/162	Mycobacterium tuberculosis	37,025	24-Jun-99
		GB_BA1 REZ82005	3301	Z82005	R erythropolis DNA, 20S proteasome structural genes region (3301 bp)	Rhodococcus erythropolis	54,128	8-Nov-97
		GB_BA2 RSU26422	3554	U26422	Rhodococcus erythropolis ORF6(2), ORF7(2), proteasome beta-type subunit 2 (prcB(2)), and proteasome alpha-type subunit 2 (prcA(2))genes, complete cds	Rhodococcus erythropolis	45,951	08-OCT-1997
rxa01156	257	GB_BA2 RSU26422	3554	U26422	Rhodococcus erythropolis ORF6(2), ORF7(2), proteasome beta-type subunit 2 (prcB(2)), and proteasome alpha-type subunit 2 (prcA(2)) genes, complete cds	Rhodococcus erythropolis	54,724	08-OCT-1997
		GB_HTG6 AC009218	126649	AC009218	Drosophila melanogaster chromosome 2 clone BACR33D17 (D945) RPCI-98 33 D 17 map 57B-57B strain y, cn bw sp, *** SEQUENCING IN PROGRESS ***, 76 unordered pieces	Drosophila melanogaster	42,570	02-DEC-1999
		GB_OV.QULNFLW	7933	D13223	Japanese quail genomic DNA for neurofilament-L (NF-L)	Coturnix coturnix	44,758	3-Feb-99
rxa01158	1065	GB_HTG3 AC011401	321277	AC011401	Homo sapiens chromosome 5 clone CIT978SKB_35K5, *** SEQUENCING IN PROGRESS ***, 65 unordered pieces	Homo sapiens	35,048	06-OCT-1999
		GB_HTG3 AC011401	321277	AC011401	Homo sapiens chromosome 5 clone CIT978SKB_35K5, *** SEQUENCING IN PROGRESS ***, 65 unordered pieces	Homo sapiens	35,048	06-OCT-1999
		GB_PR3:AC004386	172657	AC004386	Homo Sapiens Chromosome X clone bWXD691, complete sequence	Homo sapiens	37,223	10-Apr-98
rxa01159	438	GB_PAT I92035	413	I92035	Sequence 2 from patent US 5726299.	Unknown	78,169	01-DEC-1998
		GB_PAT I78746	413	I78746	Sequence 2 from patent US 5693781.	Unknown	78,169	3-Apr-98
		GB_HTG3 AC009209	108370	AC009209	Drosophila melanogaster chromosome 2 clone BACR24G16 (D1051) RPCI-98 24 G 16 map 47D-47D strain y, cn bw sp, *** SEQUENCING IN PROGRESS ***, 93 unordered pieces	Drosophila melanogaster	43,590	20-Aug-99
rxa01160	998	GB_PAT I78746	413	I78746	Sequence 2 from patent US 5693781	Unknown	96,032	3-Apr-98
		GB_PAT:I92035	413	I92035	Sequence 2 from patent US 5726299	Unknown	96,032	01-DEC-1998
		GB_BA2:AF014804	6449	AF014804	Neisseria meningitidis PglB (pglB), PglC (pglC), PglD (pglD), and AvtA (avtA) genes, complete cds	Neisseria meningitidis	37,977	3-Sep-99
rxa01165	696	GB_HTG2 AC007851	128979	AC007851	Drosophila melanogaster chromosome 2 clone BACR06M19 (D615) RPCI-98 06 M 19 map 50C-50D strain y, cn bw sp, *** SEQUENCING IN PROGRESS ***, 86 unordered pieces	Drosophila melanogaster	37,900	2-Aug-99
		GB_HTG2 AC007851	128979	AC007851	Drosophila melanogaster chromosome 2 clone BACR06M19 (D615) RPCI-98 06.M 19 map 50C-50D strain y, cn bw sp, *** SEQUENCING IN PROGRESS ***, 86 unordered pieces	Drosophila melanogaster	37,900	2-Aug-99
		GB_HTG2 AC007851	128979	AC007851	Drosophila melanogaster chromosome 2 clone BACR06M19 (D615) RPCI-98 06 M 19 map 50C-50D strain y, cn bw sp, *** SEQUENCING IN PROGRESS***, 86 unordered pieces	Drosophila melanogaster	34,114	2-Aug-99
rxa01166	1428	GB_BA1.LEUG6PD	1957	M64446	L mesenteroides glucose-6-phosphate dehydrogenase gene, complete cds	Leuconostoc mesenteroides	41,259	26-Apr-93
		GB_HTG3 AF188026	101456	AF188026	Homo sapiens chromosome 8 clone BAC 2379L20 map 8q24, *** SEQUENCING IN PROGRESS ***, in ordered pieces	Homo sapiens	35,535	08-OCT-1999
		GB_HTG3 AF188026	101456	AF188026	Homo sapiens chromosome 8 clone BAC 2379L20 map 8q24, *** SEQUENCING IN PROGRESS ***, in ordered pieces	Homo sapiens	35,535	08-OCT-1999
rxa01167	519	GB_PR2.HS1026E2	100418	AL022143	Human DNA sequence from clone 1026E2 on chromosome 1q24 1-25 3 EST, CA repeat, STS, GSS, complete sequence.	Homo sapiens	38,281	23-Nov-99
		GB_EST36 AI900015	496	AI900015	sb97f05 y1 Gm-c1012 Glycine max cDNA clone GENOME SYSTEMS CLONE ID Gm-c1012-634 5' similar to WP.T11G6 8 CE06432 RNA RECOGNITION MOTIF ,, mRNA sequence	Glycine max	42,045	06-DEC-1999
		GB_PR2.HS1026E2	100418	AL022143	Human DNA sequence from clone 1026E2 on chromosome 1q24 1-25 3 EST, CA repeat, STS, GSS, complete sequence	Homo sapiens	40,990	23-Nov-99
rxa01169	1119	GB_HTG2 AC005978	92586	AC005978	Drosophila melanogaster chromosome 2 clone DS00678 (D449) map 59D3-59D4 strain y, cn bw sp, *** SEQUENCING IN PROGRESS ***, 6 unordered pieces	Drosophila melanogaster	34,266	30-Jul-99
		GB_HTG2 AC005978	92586	AC005978	Drosophila melanogaster chromosome 2 clone DS00678 (D449) map 59D3-59D4 strain y, cn bw sp, *** SEQUENCING IN PROGRESS ***, 6 unordered pieces	Drosophila melanogaster	34,266	30-Jul-99

TABLE 4: ALIGNMENT RESULTS

		GB_HTG3:AC008304	91552	AC008304	Drosophila melanogaster chromosome 2 clone BACR04G19 (D646) RPCI-98 04.G.19 map 59D2-59D3 strain y, cn bw sp, *** SEQUENCING IN PROGRESS ***, 90 unordered pieces	Drosophila melanogaster	31,278	20-Sep-99
rxa01170	606	GB_PR1:AB014524	6542	AB014524	Homo sapiens mRNA for KIAA0624 protein, partial cds	Homo sapiens	43,478	6-Feb-99
		GB_EST38 AW016078	496	AW016078	UI-H-BI0p-abf-h-01-0-UI s1 NCI_CGAP_Sub2 Homo sapiens cDNA clone IMAGE 2711665 3', mRNA sequence	Homo sapiens	36,667	10-Sep-99
		GB_EST24 AI193238	323	AI193238	qe56c06.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE 1742986 3', mRNA sequence	Homo sapiens	37,427	29-OCT-1998
rxa01171	816	GB_HTG2 AC007548	110249	AC007548	Drosophila melanogaster chromosome 2 clone BACR48M17 (D614) RPCI-98 48.M 17 map 41C-41D strain y, cn bw sp, *** SEQUENCING IN PROGRESS ***, 66 unordered pieces	Drosophila melanogaster	35,634	2-Aug-99
		GB_PR3 HS273F20	111253	AL034371	Human DNA sequence from clone 273F20 on chromosome 6q16 1-16 3 Contains ESTs, STSs and GSSs, complete sequence	Homo sapiens	34,582	23-Nov-99
		GB_HTG2 AC007548	110249	AC007548	Drosophila melanogaster chromosome 2 clone BACR48M17 (D614) RPCI-98 48 M 17 map 41C-41D strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 66 unordered pieces	Drosophila melanogaster	35,634	2-Aug-99
rxa01173	738	GB_GSS8 B93272	338	B93272	CIT-HSP-2171E14 TF CIT-HSP Homo sapiens genomic clone 2171E14, genomic survey sequence	Homo sapiens	42,012	25-Jun-98
		GB_EST35 AV156265	282	AV156265	AV156265 Mus musculus head C57BL/6J 12-day embryo Mus musculus cDNA clone 3000001I03, mRNA sequence	Mus musculus	41,350	7-Jul-99
		GB_RO AF035777	2154	AF035777	Mus musculus somatostatin receptor subtype 5 (sst5) gene, complete cds	Mus musculus	38,928	05-DEC-1997
rxa01174	873	GB_HTG1 CEY51A2_3	110000	Z99275	Caenorhabditis elegans chromosome V clone Y51A2, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Caenorhabditis elegans	38,045	3-Dec-98
		GB_IN1.CEY51A2D	139259	AL021497	Caenorhabditis elegans cosmid Y51A2D, complete sequence	Caenorhabditis elegans	38,045	2-Sep-99
		GB_HTG1 CEY51A2_3	110000	Z99275	Caenorhabditis elegans chromosome V clone Y51A2, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Caenorhabditis elegans	38,045	3-Dec-98
rxa01176	627	GB_BA1 MTV021	23400	AL021957	Mycobacterium tuberculosis H37Rv complete genome, segment 97/162	Mycobacterium tuberculosis	39,159	18-Jun-98
		GB_BA1 MSGB1551CS	36548	L78813	Mycobacterium leprae cosmid B1551 DNA sequence	Mycobacterium leprae	53,215	15-Jun-96
		GB_BA1 MSGB1554CS	36548	L78814	Mycobacterium leprae cosmid B1554 DNA sequence	Mycobacterium leprae	53,215	15-Jun-96
rxa01177								
rxa01178	573	GB_PR4:AC006126	46100	AC006126	Homo sapiens chromosome 19, cosmid F18718, complete sequence	Homo sapiens	36,832	17-DEC-1998
		GB_PR4:AC006126	46100	AC006126	Homo sapiens chromosome 19, cosmid F18718, complete sequence	Homo sapiens	40,463	17-DEC-1998
		GB_EST23 AI128078	443	AI128078	qc47d10 x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE 1712755 3' similar to SW IF16_HUMAN Q16666 GAMMA-INTERFERON-INDUCIBLE PROTEIN IFI-16 ;, mRNA sequence	Homo sapiens	38,318	27-OCT-1998
rxa01184	1596	GB_HTG2 HSG248A21	96783	AL118512	Homo sapiens chromosome 1 clone GS1-248A21, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Homo sapiens	36,994	30-Nov-99
		GB_HTG2 HSG248A21	96783	AL118512	Homo sapiens chromosome 1 clone GS1-248A21, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Homo sapiens	36,994	30-Nov-99
		GB_PR3 AC004237	38715	AC004237	Homo sapiens chromosome 5, P1 clone 565a12 (LBNL H23), complete sequence.	Homo sapiens	36,514	27-Feb-98
rxa01186	1221	GB_BA1 MTCY274	39991	Z74024	Mycobacterium tuberculosis H37Rv complete genome, segment 126/162	Mycobacterium tuberculosis	34,758	19-Jun-98
		GB_BA1 SC6A9	39461	AL031035	Streptomyces coelicolor cosmid 6A9	Streptomyces coelicolor	38,500	24-Jul-98
		GB_BA2 AE000689	14698	AE000689	Aquifex aeolicus section 21 of 109 of the complete genome	Aquifex aeolicus	45,379	25-MAR-1998
rxa01187	573	GB_EST5 H60943	361	H60943	yr14g08 r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE 205310 5', mRNA sequence	Homo sapiens	39,205	06-OCT-1995
		GB_GSS1 AG018858	570	AG018858	Homo sapiens genomic DNA, 21q region, clone B125C11 SpN045(-21), genomic survey sequence	Homo sapiens	41,423	10-OCT-1999
		GB_GSS13 AQ454839	505	AQ454839	HS_5218_A1_E03_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=794 Col=5 Row=I, genomic survey sequence	Homo sapiens	34,599	21-Apr-99
rxa01195	570	GB_PR3 AF022813	1358	AF022813	Homo sapiens tetraspan (NAG-2) mRNA, complete cds	Homo sapiens	40,614	18-Nov-97

TABLE 4: ALIGNMENT RESULTS

		GB_EST34:AI798721	765	AI798721	we91g10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2348514 3' similar to SW NAG2_HUMAN O14817 NOVEL ANTIGEN 2 ,, mRNA sequence	Homo sapiens	35,256	6-Jul-99
		GB_EST34 AI808898	696	AI808898	wf66d02 x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE 2360547 3' similar to SW NAG2_HUMAN O14817 NOVEL ANTIGEN 2 ,, mRNA sequence	Homo sapiens	35,354	7-Jul-99
rxa01196	813	GB_BA1 MSGY151	37036	AD000018	Mycobacterium tuberculosis sequence from clone y151	Mycobacterium tuberculosis	36,634	10-DEC-1996
		GB_BA1 MTCY130	32514	Z73902	Mycobacterium tuberculosis H37Rv complete genome, segment 59/162	Mycobacterium tuberculosis	59,596	17-Jun-98
		GB_BA1 MSGY151	37036	AD000018	Mycobacterium tuberculosis sequence from clone y151	Mycobacterium tuberculosis	39,567	10-DEC-1996
rxa01197	576	GB_EST18 AA676822	524	AA676822	zj65c11 s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE 455156 3', mRNA sequence	Homo sapiens	40,741	19-DEC-1997
		GB_EST18 AA676822	524	AA676822	zj65c11 s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE 455156 3', mRNA sequence	Homo sapiens	40,331	19-DEC-1997
rxa01198	426	GB_HTG4.AC010195	164935	AC010195	Homo sapiens chromosome 10 clone RPCI11-587C2, *** SEQUENCING IN PROGRESS ***, 61 unordered pieces	Homo sapiens	36,058	21-OCT-1999
		GB_HTG4 AC010195	164935	AC010195	Homo sapiens chromosome 10 clone RPCI11-587C2, *** SEQUENCING IN PROGRESS ***, 61 unordered pieces	Homo sapiens	36,058	21-OCT-1999
		GB_HTG1 CEY44A6	326074	Z98863	Caenorhabditis elegans chromosome V clone Y44A6, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Caenorhabditis elegans	39,151	03-DEC-1998
rxa01206	400	GB_HTG1 CER08A5	51920	Z82281	Caenorhabditis elegans chromosome V clone R08A5, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Caenorhabditis elegans	43,557	14-OCT-1998
		GB_HTG1 CER08A5	51920	Z82281	Caenorhabditis elegans chromosome V clone R08A5, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Caenorhabditis elegans	43,557	14-OCT-1998
		GB_HTG1 CER08A5	51920	Z82281	Caenorhabditis elegans chromosome V clone R08A5, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Caenorhabditis elegans	34,987	14-OCT-1998
rxa01207	771	GB_PL2.SPBC8D2	43757	AL022072	S.pombe chromosome II cosmid c8D2	Schizosaccharomyces pombe	36,566	24-Nov-99
		GB_PL1 AB004538	38911	AB004538	Schizosaccharomyces pombe 39 kb genomic DNA, clone c568	Schizosaccharomyces pombe	36,148	15-Jul-97
		GB_HTG6:AC009220	110000	AC009220	Homo sapiens chromosome 7, *** SEQUENCING IN PROGRESS ***, 191 unordered pieces	Homo sapiens	33,940	15-Sep-99
rxa01210	954	GB_GSS4 AQ694235	530	AQ694235	HS_5496_A1_D03_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=1072 Col=5 Row=G, genomic survey sequence	Homo sapiens	37,259	6-Jul-99
		GB_GSS11 AQ322059	519	AQ322059	RPCI11-100G10 TV RPCI-11 Homo sapiens genomic clone RPCI-11-100G10, genomic survey sequence	Homo sapiens	37,229	06-MAY-1999
		GB_BA1:SCH24	41625	AL049826	Streptomyces coelicolor cosmid H24	Streptomyces coelicolor	38,126	11-MAY-1999
rxa01213	1350	GB_PR3 HS356B7	20733	AL031714	Human DNA sequence from clone 356B7 on chromosome 16 Contains the UBE21 gene for ubiquitin-conjugating enzyme E2I (homologous to yeast UBC9), and an RPS20 (40S Ribosomal protein S20) pseudogene Contains ESTs, STSs. GSSs and a putative CpG island, complete sequence	Homo sapiens	36,684	23-Nov-99
		GB_PR3 HS356B7	20733	AL031714	Human DNA sequence from clone 356B7 on chromosome 16 Contains the UBE21 gene for ubiquitin-conjugating enzyme E2I (homologous to yeast UBC9), and an RPS20 (40S Ribosomal protein S20) pseudogene. Contains ESTs, STSs GSSs and a putative CpG island, complete sequence.	Homo sapiens	39,621	23-Nov-99
		GB_PR1 HSEF1AL1	1815	X16870	Human DNA for elongation factor 1-alpha (clone lambda-1)	Homo sapiens	37,462	12-Jun-90
rxa01218	552	GB_PR3 HS257I9	90695	AL031773	Human DNA sequence from clone 257I9 on chromosome 6q25 1-26 Contains gene similar to Cytochrome B, CA repeat, GSS, complete sequence	Homo sapiens	35,897	23-Nov-99
		GB_PR3 HS287L14	112831	Z95325	Human DNA sequence from clone 287L14 on chromosome Xq21 1-21 33 Contains STSs and GSSs, complete sequence	Homo sapiens	37,778	23-Nov-99

TABLE 4: ALIGNMENT RESULTS

		GB_EST8:AA035251	493	AA035251	zk23d09.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471377 3', mRNA sequence	Homo sapiens	40,191	10-MAY-1997
rxa01229	1401	GB_PR4 HUAC002394	107910	AC002394	Human Chromosome 16 BAC clone CIT987SK-A-211C6, complete sequence	Homo sapiens	33,633	23-Nov-99
		GB_OV:AF138905	1678	AF138905	Gallus gallus NK class homeodomain transcription factor NKX3 2 mRNA, complete cds	Gallus gallus	30,556	4-Sep-99
		GB_PAT:AR031772	30001	AR031772	Sequence 1 from patent US 5866410	Unknown	34,304	29-Sep-99
rxa01231	366	GB_EST25 AI295169	507	AI295169	LP08720 3prime LP Drosophila melanogaster larval-early pupal pOT2 Drosophila melanogaster cDNA clone LP08720 3prime, mRNA sequence	Drosophila melanogaster	38,279	01-DEC-1998
		GB_EST25.AI297653	512	AI297653	LP12002 3prime LP Drosophila melanogaster larval-early pupal pOT2 Drosophila melanogaster cDNA clone LP12002 3prime, mRNA sequence	Drosophila melanogaster	36,893	01-DEC-1998
		GB_EST21:AA951454	677	AA951454	LD31920 5prime LD Drosophila melanogaster embryo pOT2 Drosophila melanogaster cDNA clone LD31920 5prime, mRNA sequence	Drosophila melanogaster	44,167	24-Nov-98
rxa01234	507	GB_GSS12 AQ365352	431	AQ365352	nbxb0063L13f CUGI Rice BAC Library Oryza sativa genomic clone nbxb0063L13f, genomic survey sequence	Oryza sativa	34,577	3-Feb-99
		GB_PR4 AC007544	119034	AC007544	Homo sapiens Human 12p11-37 2-54 4 BAC RPCI11-12D15 (Roswell Park Cancer Institute Human BAC Library) complete sequence	Homo sapiens	34,350	29-OCT-1999
		GB_PR4 AC007544	119034	AC007544	Homo sapiens Human 12p11-37 2-54 4 BAC RPCI11-12D15 (Roswell Park Cancer Institute Human BAC Library) complete sequence	Homo sapiens	37,988	29-OCT-1999
rxa01237	564	GB_GSS1 AG009269	706	AG009269	Homo sapiens genomic DNA, 21q region, clone: 31C6X11, genomic survey sequence	Homo sapiens	36,328	14-Apr-99
		GB_GSS1 AG009269	706	AG009269	Homo sapiens genomic DNA, 21q region, clone 31C6X11, genomic survey sequence	Homo sapiens	37,391	14-Apr-99
rxa01246	630	GB_HTG2 AC007646	180133	AC007646	Drosophila melanogaster chromosome 3 clone BACR03J04 (D687) RPCI-98 03 J 4 map 87F-87F strain y, cn bw sp, *** SEQUENCING IN PROGRESS ***, 10 unordered pieces	Drosophila melanogaster	38,188	2-Aug-99
		GB_HTG2 AC007646	180133	AC007646	Drosophila melanogaster chromosome 3 clone BACR03J04 (D687) RPCI-98 03 J 4 map 87F-87F strain y, cn bw sp, *** SEQUENCING IN PROGRESS ***, 10 unordered pieces.	Drosophila melanogaster	38,188	2-Aug-99
		GB_HTG4 AC009492	212394	AC009492	Homo sapiens clone NH0423F09, *** SEQUENCING IN PROGRESS ***, 2 unordered pieces	Homo sapiens	38,762	29-OCT-1999
rxa01249	471	GB_EST7 W84105	361	W84105	T2969 MVAT4 bloodstream form of serodeme WRATat1 1 Trypanosoma brucei rhodesiense cDNA 5', mRNA sequence.	Trypanosoma brucei rhodesiense	38,261	12-Aug-96
		GB_EST7 W84105	361	W84105	T2969 MVAT4 bloodstream form of serodeme WRATat1 1 Trypanosoma brucei rhodesiense cDNA 5', mRNA sequence	Trypanosoma brucei rhodesiense	33,894	12-Aug-96
rxa01251	432	GB_RO AC005240	41830	AC005240	Mus musculus clone UWGC magap from 14D1-D2 (T-cell Receptor Alpha Locus), complete sequence	Mus musculus	41,463	8-Jul-98
		GB_RO AC004101	39491	AC004101	Mouse Cosmid ma53a016 from 14D1-D2, complete sequence	Mus musculus	41,463	2-Feb-98
		GB_HTG3 AC009837	162287	AC009837	Homo sapiens chromosome 17 clone 550_K_23 map 17, *** SEQUENCING IN PROGRESS ***, 13 unordered pieces	Homo sapiens	36,131	2-Sep-99
rxa01263	1035	GB_PR4 AC005919	156300	AC005919	Homo sapiens chromosome 17, clone hRPK 142_H_19, complete sequence	Homo sapiens	39,822	18-Nov-98
		GB_PR4 AC005919	156300	AC005919	Homo sapiens chromosome 17, clone hRPK 142_H_19, complete sequence	Homo sapiens	38,319	18-Nov-98
		GB_HTG1 CEY71A12_3	110000	AL021390	Caenorhabditis elegans chromosome I clone Y71A12, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Caenorhabditis elegans	36,884	15-Sep-99
rxa01266	1158	GB_HTG4 AC010775	165565	AC010775	Homo sapiens clone 2_G_17, *** SEQUENCING IN PROGRESS ***, 14 unordered pieces	Homo sapiens	38,670	20-OCT-1999
		GB_HTG4.AC010775	165565	AC010775	Homo sapiens clone 2_G_17, *** SEQUENCING IN PROGRESS ***, 14 unordered pieces	Homo sapiens	38,670	20-OCT-1999
		GB_HTG4:AC010775	165565	AC010775	Homo sapiens clone 2_G_17, *** SEQUENCING IN PROGRESS ***, 14 unordered pieces	Homo sapiens	36,131	20-OCT-1999
rxa01267	1437	GB_PR3 AF070717	100793	AF070717	Homo sapiens BAC clone 393I22 from 8q21, complete sequence	Homo sapiens	38,826	2-Jul-98
		GB_BA2 MPU34931	2571	U34931	Mycoplasma pulmonis FtsZ (ftsZ) gene, complete cds, methionyl-tRNA synthetase (metG) gene, partial cds	Mycoplasma pulmonis	37,092	30-MAY-1996
		GB_EST25 AI322057	638	AI322057	SWOv3MCAM09A04SK Onchocerca volvulus molting L3 larva cDNA (SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWOv3MCAM09A04 5', mRNA sequence	Onchocerca volvulus	40,566	22-DEC-1998
rxa01268	963	GB_HTG3 AC010878	288945	AC010878	Homo sapiens clone NH0230E20, *** SEQUENCING IN PROGRESS ***, 65 unordered pieces	Homo sapiens	36,496	25-Sep-99
		GB_HTG3 AC010878	288945	AC010878	Homo sapiens clone NH0230E20, *** SEQUENCING IN PROGRESS ***, 65 unordered pieces	Homo sapiens	36,496	25-Sep-99
		GB_HTG3:AC010878	288945	AC010878	Homo sapiens clone NH0230E20, *** SEQUENCING IN PROGRESS ***, 65 unordered pieces	Homo sapiens	36,354	25-Sep-99

TABLE 4: ALIGNMENT RESULTS

rxa01271	1935	GB_BA2:U67549	14561	U67549	Methanococcus jannaschii section 91 of 150 of the complete genome.	Methanococcus jannaschii	37,841	28-Jan-98
		GB_PR2 HSJ836N17	111694	AL049539	Human DNA sequence from clone RP5-836N17 on chromosome 20q11 1-11 21, complete sequence.	Homo sapiens	34,872	22-Nov-99
		GB_OV AF089743	30676	AF089743	Morone saxatilis homeodomain protein Hox-A10 (Hoxa10), homeodomain protein Hox-A9 (Hoxa9), homeodomain protein Hox-A7 (Hoxa7), homeodomain protein Hox-A5 (Hoxa5), and homeodomain protein Hox-A4 (Hoxa4) genes, complete cds	Morone saxatilis	36,738	2-Aug-99
rxa01273	1557	GB_PR3 AC004070	110192	AC004070	Human Chromosome X, complete sequence	Homo sapiens	37,679	29-Jan-98
		GB_PR2 AC002410	96217	AC002410	Human BAC clone RG264L19 from 7p15-p21, complete sequence	Homo sapiens	38,587	11-Aug-97
		GB_PR2:AC002410	96217	AC002410	Human BAC clone RG264L19 from 7p15-p21, complete sequence	Homo sapiens	37,035	11-Aug-97
rxa01275	1041	GB_EST8.C03322	357	C03322	C03322 Human heart cDNA (YNakamura) Homo sapiens cDNA clone 3NHC1263, mRNA sequence.	Homo sapiens	35,393	30-Jul-96
		GB_EST4 R92079	410	R92079	yp96g02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE.195314 5', mRNA sequence	Homo sapiens	37,010	25-Aug-95
		GB_EST4 H57724	461	H57724	yr21a12 r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE.205918 5', mRNA sequence	Homo sapiens	37,281	05-OCT-1995
rxa01276	567	GB_OM:OCMYLC1	962	X54041	Rabbit mRNA for myosin light chain 1	Oryctolagus cuniculus	40,503	26-Nov-90
		GB_PR3 AC005383	123110	AC005383	Homo sapiens chromosome 10 clone CIT987SK-1144G6 map 10q25 1, complete sequence	Homo sapiens	38,930	31-OCT-1998
		GB_RO RATPTPECA	2155	D78610	Rat mRNA for protein tyrosine phosphatase epsilon C, partial cds	Rattus norvegicus	37,770	5-Feb-99
rxa01281	885	GB_HTG4 AC009366	199607	AC009366	Drosophila melanogaster chromosome 3L/79D4 clone RPCI98-48E10, *** SEQUENCING IN PROGRESS ***, 31 unordered pieces	Drosophila melanogaster	34,025	16-OCT-1999
		GB_HTG4 AC009366	199607	AC009366	Drosophila melanogaster chromosome 3L/79D4 clone RPCI98-48E10, *** SEQUENCING IN PROGRESS ***, 31 unordered pieces	Drosophila melanogaster	34,025	16-OCT-1999
		GB_HTG4 AC009366	199607	AC009366	Drosophila melanogaster chromosome 3L/79D4 clone RPCI98-48E10, *** SEQUENCING IN PROGRESS ***, 31 unordered pieces	Drosophila melanogaster	34,386	16-OCT-1999
rxa01282	903	GB_GSS11 AQ263970	363	AQ263970	CITBI-E1-2503H24 TF CITBI-E1 Homo sapiens genomic clone 2503H24, genomic survey sequence.	Homo sapiens	40,361	27-OCT-1998
		GB_GSS1 FR0025959	603	AL018794	F.rubripes GSS sequence, clone 165E10aE1, genomic survey sequence.	Fugu rubripes	34,824	10-DEC-1997
		GB_GSS9 AQ102435	334	AQ102435	HS_3038_B2_D09_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3038 Col=18 Row=H, genomic survey sequence	Homo sapiens	37,624	27-Aug-98
rxa01294	789	GB_PL2 AC007258	144422	AC007258	Arabidopsis thaliana chromosome I BAC F23H11 genomic sequence, complete sequence	Arabidopsis thaliana	39,453	16-Jun-99
		GB_EST17 T04634	491	T04634	681 Lambda-PRL1 Arabidopsis thaliana cDNA clone SBD1T7P, mRNA sequence.	Arabidopsis thaliana	38,693	6-Nov-97
		GB_PL2:AC007258	144422	AC007258	Arabidopsis thaliana chromosome I BAC F23H11 genomic sequence, complete sequence	Arabidopsis thaliana	36,170	16-Jun-99
rxa01295	1098	GB_HTG3 AC009803	235360	AC009803	Homo sapiens clone RPCI11-1028N23, *** SEQUENCING IN PROGRESS ***, 47 unordered pieces.	Homo sapiens	38,662	24-Sep-99
		GB_HTG3 AC009803	235360	AC009803	Homo sapiens clone RPCI11-1028N23, *** SEQUENCING IN PROGRESS ***, 47 unordered pieces	Homo sapiens	38,662	24-Sep-99
		GB_IN2 AC004333	63178	AC004333	Drosophila melanogaster DNA sequence (P1 DS05969 (D229)), complete sequence	Drosophila melanogaster	39,252	20-Jun-98
rxa01296	1206	GB_PR4 AC004961	68130	AC004961	Homo sapiens clone DJ1098J04, complete sequence	Homo sapiens	39,409	5-Jun-99
		GB_GSS14 AQ525299	447	AQ525299	HS_5227_B2_H03_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=803 Col=6 Row=P, genomic survey sequence.	Homo sapiens	37,330	11-MAY-1999
		GB_BA2:BFU78108	1900	U78108	Bacteroides fragilis NAD(H) glutamate dehydrogenase (gdhB) gene, complete cds	Bacteroides fragilis	40,509	15-Jul-98
rxa01301	648	GB_PR4 AC007051	167810	AC007051	Homo sapiens chromosome 3, clone hRPK 44_A_1, complete sequence	Homo sapiens	38,498	11-Jun-99
		GB_PR4 AC007919	184989	AC007919	Homo sapiens 3q26 2-27 BAC RPCI11-408H1 (Roswell Park Cancer Institute Human BAC Library) complete sequence	Homo sapiens	35,139	09-OCT-1999
		GB_EST11 AA252547	454	AA252547	zp87g09 r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE 627232 5' similar to gb D13748 EUKARYOTIC INITIATION FACTOR 4A-I (HUMAN),, mRNA sequence	Homo sapiens	38,538	12-MAR-1997
rxa01304	609	GB_HTG2 AC006779	119562	AC006779	Caenorhabditis elegans clone Y47D7, *** SEQUENCING IN PROGRESS ***, 32 unordered pieces	Caenorhabditis elegans	32,888	25-Feb-99
		GB_HTG2 AC006779	119562	AC006779	Caenorhabditis elegans clone Y47D7, *** SEQUENCING IN PROGRESS ***, 32 unordered pieces	Caenorhabditis elegans	32,888	25-Feb-99

TABLE 4: ALIGNMENT RESULTS

		GB_VI:BHT1UL	37000	Z78205	Bovine herpesvirus type 1 UL22-35 genes.	Bovine herpesvirus 1	38,047	14-Aug-96
rxa01306	1131	GB_GSS8:AQ047475	420	AQ047475	cLM-1c5-t cLM Giardia intestinalis genomic, genomic survey sequence	Giardia intestinalis	38,902	14-Jul-98
		GB_PL1:CR1433P	1464	X79445	C reinhardtii mRNA for 14-3-3 protein	Chlamydomonas reinhardtii	39,640	06-OCT-1995
		GB_PR3:HSJ878I13	122400	AL049591	Human DNA sequence from clone 878I13 on chromosome Xq23-25 Contains a pseudogene similar to alpha tubulin, ESTs, STSs, GSSs, complete sequence.	Homo sapiens	35,624	23-Nov-99
rxa01310	450	GB_HTG3.AC010530	274508	AC010530	Homo sapiens chromosome 16 clone RPCI-11_167P11, *** SEQUENCING IN PROGRESS ***, 19 unordered pieces	Homo sapiens	38,462	15-Sep-99
		GB_HTG3 AC010530	274508	AC010530	Homo sapiens chromosome 16 clone RPCI-11_167P11, *** SEQUENCING IN PROGRESS ***, 19 unordered pieces.	Homo sapiens	38,462	15-Sep-99
		GB_HTG3 AC010530	274508	AC010530	Homo sapiens chromosome 16 clone RPCI-11_167P11, *** SEQUENCING IN PROGRESS ***, 19 unordered pieces	Homo sapiens	32,063	15-Sep-99
rxa01313								
rxa01315	774	GB_BA2 AF031037	1472	AF031037	Neisseria meningitidis chloramphenicol acetyltransferase gene, complete cds	Neisseria meningitidis	35,638	21-Apr-98
		GB_GSS11:AQ326599	662	AQ326599	nbxb0037P01r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0037P01r, genomic survey sequence	Oryza sativa	34,817	8-Jan-99
		GB_HTG1 PFMAL13PA	80518	AL109815	Plasmodium falciparum chromosome 13 strain 3D7, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Plasmodium falciparum	34,935	19-Aug-99
rxa01316	426	GB_HTG3 AC010133	154773	AC010133	Homo sapiens clone NH0118E09, *** SEQUENCING IN PROGRESS ***, 5 unordered pieces	Homo sapiens	33,414	13-Sep-99
		GB_HTG3:AC010133	154773	AC010133	Homo sapiens clone NH0118E09, *** SEQUENCING IN PROGRESS ***, 5 unordered pieces.	Homo sapiens	33,414	13-Sep-99
		GB_HTG3 AC010133	154773	AC010133	Homo sapiens clone NH0118E09, *** SEQUENCING IN PROGRESS ***, 5 unordered pieces	Homo sapiens	38,186	13-Sep-99
rxa01317	543	GB_BA2 U67560	12215	U67560	Methanococcus jannaschii section 102 of 150 of the complete genome	Methanococcus jannaschii	38,476	28-Jan-98
		GB_BA2 U67560	12215	U67560	Methanococcus jannaschii section 102 of 150 of the complete genome	Methanococcus jannaschii	35,867	28-Jan-98
rxa01318	1425	GB_BA1 MTV038	16094	AL021933	Mycobacterium tuberculosis H37Rv complete genome, segment 24/162	Mycobacterium tuberculosis	51,266	17-Jun-98
		GB_IN1.CELC41A3	37149	U41541	Caenorhabditis elegans cosmid C41A3.	Caenorhabditis elegans	36,887	08-DEC-1995
		GB_HTG3.AC011298	205637	AC011298	Homo sapiens clone NH0118M12, *** SEQUENCING IN PROGRESS ***, 19 unordered pieces	Homo sapiens	35,760	05-OCT-1999
rxa01326	489	GB_BA1.PAL249201	3390	AJ249201	Prevotella albensis ftsQ (partial), ftsA and ftsZ genes and ORF-fts (partial).	Prevotella albensis	37,708	27-Aug-99
		GB_BA1:PAL249201	3390	AJ249201	Prevotella albensis ftsQ (partial), ftsA and ftsZ genes and ORF-fts (partial).	Prevotella albensis	37,474	27-Aug-99
rxa01330								
rxa01331	2520	GB_HTG1 HSAJ02553	142807	AJ002553	Homo sapiens chromosome 11 clone 1118i22 map q13, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Homo sapiens	26,237	14-Nov-97
		GB_HTG1 HSAJ02553	142807	AJ002553	Homo sapiens chromosome 11 clone 1118i22 map q13, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	26,237	14-Nov-97
		GB_PR3 AC005304	164017	AC005304	Homo sapiens chromosome 17, clone hRPK 131_K_5, complete sequence	Homo sapiens	35,318	25-Jul-98
rxa01333	1128	GB_BA1 CGU43536	3464	U43536	Corynebacterium glutamicum heat shock, ATP-binding protein (clpB) gene, complete cds	Corynebacterium glutamicum	38,075	13-MAR-1997
		GB_OM:BTPRLP	924	X15975	Bovine mRNA for prolactin (PRL) related protein	Bos taurus	40,901	22-DEC-1994
		GB_OM BTPRLP	924	X15975	Bovine mRNA for prolactin (PRL) related protein	Bos taurus	39,580	22-DEC-1994
rxa01336	726	GB_BA1 AP000064	247695	AP000064	Aeropyrum pernix genomic DNA, section 7/7	Aeropyrum pernix	37,881	22-Jun-99
		GB_BA1:AP000064	247695	AP000064	Aeropyrum pernix genomic DNA, section 7/7	Aeropyrum pernix	36,161	22-Jun-99
		GB_EST1:T05458	363	T05458	EST03347 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCY86, mRNA sequence.	Homo sapiens	43,798	30-Jun-93

TABLE 4: ALIGNMENT RESULTS

rxa01337	1536	GB_PR2:AP000215	100000	AP000215	Homo sapiens genomic DNA, chromosome 21q22.3-ter, Ter region, clone f27E1-T1136, segment 1/4, complete sequence.	Homo sapiens	36,438	20-Nov-99
		GB_PR2:AP000215	100000	AP000215	Homo sapiens genomic DNA, chromosome 21q22 3-ter, Ter region, clone f27E1-T1136, segment 1/4, complete sequence.	Homo sapiens	35,827	20-Nov-99
		GB_PR2.AP000337	53553	AP000337	Homo sapiens genomic DNA, chromosome 21q22 3-ter, Ter region, clone T1957, complete sequence.	Homo sapiens	36,043	20-Nov-99
rxa01342	626	GB_EST35 AI814229	544	AI814229	wj70e01.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2408184 3', mRNA sequence	Homo sapiens	36,803	24-Aug-99
		GB_EST35 AI814229	544	AI814229	wj70e01.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2408184 3', mRNA sequence	Homo sapiens	36,688	24-Aug-99
rxa01348	615	GB_HTG3 AC011246	210407	AC011246	Homo sapiens clone NH0498O20, *** SEQUENCING IN PROGRESS ***, 29 unordered pieces	Homo sapiens	39,101	04-OCT-1999
		GB_HTG3:AC011246	210407	AC011246	Homo sapiens clone NH0498O20, *** SEQUENCING IN PROGRESS ***, 29 unordered pieces	Homo sapiens	39,101	04-OCT-1999
		GB_PL1.ZMB32120	3093	X54212	Z mays mRNA for b-32 protein, putative regulatory factor of zein expression (clone b-32 120)	Zea mays	35,902	18-Jan-93
rxa01349	900	GB_IN1:CELK10G6	33588	AF016669	Caenorhabditis elegans cosmid K10G6	Caenorhabditis elegans	40,251	8-Aug-97
		GB_IN1 CELK10G6	33588	AF016669	Caenorhabditis elegans cosmid K10G6	Caenorhabditis elegans	36,842	8-Aug-97
rxa01357	426	GB_BA1:MTCY274	39991	Z74024	Mycobacterium tuberculosis H37Rv complete genome, segment 126/162	Mycobacterium tuberculosis	36,058	19-Jun-98
		GB_BA1.MLCB250	40603	Z97369	Mycobacterium leprae cosmid B250.	Mycobacterium leprae	59,294	27-Aug-99
		GB_BA2.SKZ86111	7860	Z86111	Streptomyces lividans rpsP, trmD, rplS, sipW, sipX, sipY, sipZ, mutT genes and 4 open reading frames	Streptomyces lividans	57,882	27-OCT-1999
rxa01359	1305	GB_BA1 D87820	7217	D87820	Vibrio cholerae non-O1 gene for N-acetylglucosamine 6-phosphate deacetylase, NagC, NagE, complete cds.	Vibrio cholerae non-O1	38,152	17-OCT-1997
		GB_PR3.AC004540	131757	AC004540	Homo sapiens PAC clone DJ1066K24 from 7p15, complete sequence	Homo sapiens	35,714	9-Apr-98
		GB_PR2 HSU44119	450	U44119	Human der(9) chromosome breakpoint region alpha 1(V) collagen chain (COL5A1) gene, partial intron 24, and imperfect LINE-1 element of Xp21 2	Homo sapiens	38,085	14-Jan-97
rxa01362	3677	GB_EST30 AI665031	602	AI665031	605005H05.x1 605 - Endosperm cDNA library from Schmidt lab Zea mays cDNA, mRNA sequence	Zea mays	42,308	11-MAY-1999
		GB_EST34 AI795319	661	AI795319	605005H05 y2 605 - Endosperm cDNA library from Schmidt lab Zea mays cDNA, mRNA sequence	Zea mays	38,729	2-Jul-99
		GB_HTG3 AC008387	151804	AC008387	Homo sapiens chromosome 5 clone CIT-HSPC_229P9, *** SEQUENCING IN PROGRESS ***, 74 unordered pieces	Homo sapiens	38,023	3-Aug-99
rxa01366	513	GB_IN1.AF007166	1392	AF007166	Anopheles gambiae serine protease 14D mRNA, complete cds.	Anopheles gambiae	41,379	14-Jul-97
		GB_GSS13 AQ475498	476	AQ475498	CITBI-E1-2589F13 TR CITBI-E1 Homo sapiens genomic clone 2589F13, genomic survey sequence.	Homo sapiens	40,511	23-Apr-99
		GB_IN1:AF007166	1392	AF007166	Anopheles gambiae serine protease 14D mRNA, complete cds	Anopheles gambiae	40,000	14-Jul-97
rxa01367	525	GB_EST28 AI489958	591	AI489958	EST248297 tomato ovary, TAMU Lycopersicon esculentum cDNA clone cLED14O8, mRNA sequence.	Lycopersicon esculentum	38,186	29-Jun-99
		GB_GSS13 AQ475498	476	AQ475498	CITBI-E1-2589F13 TR CITBI-E1 Homo sapiens genomic clone 2589F13, genomic survey sequence.	Homo sapiens	37,405	23-Apr-99
		GB_EST28:AI489958	591	AI489958	EST248297 tomato ovary, TAMU Lycopersicon esculentum cDNA clone cLED14O8, mRNA sequence	Lycopersicon esculentum	35,882	29-Jun-99
rxa01370								
rxa01372	614	GB_HTG5:AC011644	164746	AC011644	Homo sapiens clone 14_K_21, *** SEQUENCING IN PROGRESS ***, 8 unordered pieces	Homo sapiens	33,715	5-Nov-99
		GB_HTG5 AC011644	164746	AC011644	Homo sapiens clone 14_K_21, *** SEQUENCING IN PROGRESS ***, 8 unordered pieces	Homo sapiens	35,821	5-Nov-99
rxa01378	1878	GB_IN1 DMBR42I17	155168	AL121806	Drosophila melanogaster clone BACR42I17	Drosophila melanogaster	36,373	10-OCT-1999
		GB_IN2 AC005714	177740	AC005714	Drosophila melanogaster, chromosome 2R, region 58D4-58E2, BAC clone BACR48M13, complete sequence.	Drosophila melanogaster	36,234	01-MAY-1999

TABLE 4: ALIGNMENT RESULTS

		GB_IN2:AC005639	188288	AC005639	Drosophila melanogaster, chromosome 2R, region 59E3-59F4, BAC clone BACR48M01, complete sequence.	Drosophila melanogaster	36,275	6-Jan-99
rxa01379	1042	GB_HTG4 AC010031	132106	AC010031	Drosophila melanogaster chromosome 3L/70C1 clone RPCI98-2M20, *** SEQUENCING IN PROGRESS ***, 69 unordered pieces.	Drosophila melanogaster	35,368	16-OCT-1999
		GB_HTG4 AC010031	132106	AC010031	Drosophila melanogaster chromosome 3L/70C1 clone RPCI98-2M20, *** SEQUENCING IN PROGRESS ***, 69 unordered pieces	Drosophila melanogaster	35,368	16-OCT-1999
		GB_HTG3 AC009932	68745	AC009932	Homo sapiens clone 114_O_12, LOW-PASS SEQUENCE SAMPLING.	Homo sapiens	36,337	05-OCT-1999
rxa01380	2322	GB_BA1 SC5F2A	40105	AL049587	Streptomyces coelicolor cosmid 5F2A	Streptomyces coelicolor	39,699	24-MAY-1999
		GB_BA1:BPTEX	2701	X95386	B pertussis tex gene.	Bordetella pertussis	59,687	31-Jul-96
		GB_BA1.SC5F2A	40105	AL049587	Streptomyces coelicolor cosmid 5F2A.	Streptomyces coelicolor	41,024	24-MAY-1999
rxa01384	1839	GB_GSS15:AQ613816	598	AQ613816	HS_5118_B1_F06_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=694 Col=11 Row=L, genomic survey sequence	Homo sapiens	39,300	15-Jun-99
		GB_GSS15.AQ613816	598	AQ613816	HS_5118_B1_F06_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=694 Col=11 Row=L, genomic survey sequence	Homo sapiens	36,455	15-Jun-99
rxa01390	780	GB_BA2 CGL012293	2952	AJ012293	Corynebacterium glutamicum ilvD gene.	Corynebacterium glutamicum	40,413	01-OCT-1999
		GB_PR4 AC006213	160754	AC006213	Homo sapiens, clone hRPK 15_A_1, complete sequence	Homo sapiens	35,724	16-Jan-99
		GB_PL2.ATF24G24	99856	AL049488	Arabidopsis thaliana DNA chromosome 4, BAC clone F24G24 (ESSA project)	Arabidopsis thaliana	35,925	27-Aug-99
rxa01391	813	GB_HTG2.AC006171	44733	AC006171	Homo sapiens chromosome 10 clone LA10NC01_15_E_11 map 10q26 3, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces.	Homo sapiens	35,031	09-DEC-1998
		GB_HTG2:AC006171	44733	AC006171	Homo sapiens chromosome 10 clone LA10NC01_15_E_11 map 10q26 3, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces.	Homo sapiens	35,031	09-DEC-1998
		GB_HTG2 AC006171	44733	AC006171	Homo sapiens chromosome 10 clone LA10NC01_15_E_11 map 10q26 3, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces	Homo sapiens	38,035	09-DEC-1998
rxa01396	381	GB_BA2:AE000775	14358	AE000775	Aquifex aeolicus section 107 of 109 of the complete genome	Aquifex aeolicus	43,085	25-MAR-1998
		GB_EST26:AI329024	471	AI329024	a9c02ne f1 Neurospora crassa evening cDNA library Neurospora crassa cDNA clone a9c02ne 5', mRNA sequence.	Neurospora crassa	39,286	28-DEC-1998
		GB_EST26 AI329043	401	AI329043	a9d06ne.f1 Neurospora crassa evening cDNA library Neurospora crassa cDNA clone a9d06ne 5', mRNA sequence	Neurospora crassa	44,484	28-DEC-1998
rxa01397	543	GB_BA2.AE000775	14358	AE000775	Aquifex aeolicus section 107 of 109 of the complete genome	Aquifex aeolicus	41,121	25-MAR-1998
		GB_BA1 BSTMSPRS	3211	X16518	B.subtilis prs,tms,and ctc (partial) genes for PRPP synthetase and two undefined gene products	Bacillus subtilis	41,255	30-Sep-93
		GB_EST4.H21691	382	H21691	yl29b01.r1 Soares breast 3NbHBst Homo sapiens cDNA clone IMAGE 159625 5' similar to SP.XPEC_CERAE P33194 POSSIBLE DNA-REPAIR PROTEIN XP-E ,, mRNA sequence	Homo sapiens	35,407	6-Jul-95
rxa01400	1623	GB_GSS11 AQ264714	353	AQ264714	CITBI-E1-2502C17 TR CITBI-E1 Homo sapiens genomic clone 2502C17, genomic survey sequence.	Homo sapiens	40,227	27-OCT-1998
		GB_BA1 TFENTRA	2803	M58480	Thiobacillus ferrooxidans nitrogen metabolism regulator (ntrA) gene, complete cds	Thiobacillus ferrooxidans	39,960	26-Apr-93
		GB_BA1:NPSDHCDBA	5596	Y07709	N pharaonis sdhC, sdhD, sdhB and sdhA genes	Natronomonas pharaonis	38,003	2-Sep-96
rxa01401	384	GB_HTG4 AC006583	110000	AC006583	Homo sapiens chromosome 3p21 3 clone RPCI11-491D6, *** SEQUENCING IN PROGRESS ***, 90 unordered pieces	Homo sapiens	32,718	21-OCT-1999
		GB_HTG4 AC006583	110000	AC006583	Homo sapiens chromosome 3p21.3 clone RPCI11-491D6, *** SEQUENCING IN PROGRESS ***, 90 unordered pieces	Homo sapiens	32,718	21-OCT-1999
		GB_HTG4 AC011291	173585	AC011291	Homo sapiens chromosome unknown clone NH0067G07, WORKING DRAFT SEQUENCE, in unordered pieces	Homo sapiens	33,596	29-OCT-1999
rxa01402	597	GB_BA1.CAJ10319	5368	AJ010319	Corynebacterium glutamicum amtP, glnB, glnD genes and partial ftsY and srp genes	Corynebacterium glutamicum	39,389	14-MAY-1999
		GB_HTG4 AC010066	187240	AC010066	Drosophila melanogaster chromosome 3L/72A4 clone RPCI98-25O1, *** SEQUENCING IN PROGRESS ***, 70 unordered pieces	Drosophila melanogaster	33,681	16-OCT-1999
		GB_HTG4 AC010066	187240	AC010066	Drosophila melanogaster chromosome 3L/72A4 clone RPCI98-25O1, *** SEQUENCING IN PROGRESS ***, 70 unordered pieces.	Drosophila melanogaster	33,681	16-OCT-1999

TABLE 4: ALIGNMENT RESULTS

rxa01403	771	GB_BA1:SC6E10	23990	AL109661	Streptomyces coelicolor cosmid 6E10.	Streptomyces coelicolor A3(2)	39,136	5-Aug-99
		GB_GSS12 AQ396728	608	AQ396728	mgxb0002E02f CUGI Rice Blast BAC Library Magnaporthe grisea genomic clone mgxb0002E02f, genomic survey sequence	Magnaporthe grisea	36,626	06-MAR-1999
		GB_BA1:SC6E10	23990	AL109661	Streptomyces coelicolor cosmid 6E10	Streptomyces coelicolor A3(2)	41,403	5-Aug-99
rxa01405	579	GB_PL2:AF111709	52684	AF111709	Oryza sativa subsp indica Retrosat 1 retrotransposon and Ty3-Gypsy type Retrosat 2 retrotransposon, complete sequences, and unknown genes	Oryza sativa subsp indica	34,888	26-Apr-99
		GB_GSS3 B88760	696	B88760	RPCI11-24L19 TPC RPCI-11 Homo sapiens genomic clone RPCI-11-24L19, genomic survey sequence.	Homo sapiens	37,204	9-Apr-99
		GB_STS:G52436	696	G52436	SHGC-85004 Human Homo sapiens STS genomic, sequence tagged site	Homo sapiens	37,204	25-Jun-99
rxa01409	845	GB_HTG5:AC008019	190459	AC008019	Mus musculus, *** SEQUENCING IN PROGRESS ***, 16 unordered pieces.	Mus musculus	39,924	16-Nov-99
		GB_PR4:AC006236	127593	AC006236	Homo sapiens chromosome 17, clone hCIT.162_E_12, complete sequence.	Homo sapiens	33,907	29-DEC-1998
		GB_HTG5:AC008019	190459	AC008019	Mus musculus, *** SEQUENCING IN PROGRESS ***, 16 unordered pieces	Mus musculus	40,819	16-Nov-99
rxa01413	723	GB_OV:AF038947	1617	AF038947	Ambystoma tigrinum red cone visual pigment mRNA, complete cds	Ambystoma tigrinum	35,846	16-DEC-1998
		GB_BA1 MSGB577COS	37770	L01263	M leprae genomic dna sequence, cosmid b577	Mycobacterium leprae	38,042	14-Jun-96
		GB_PR3 AC002558	102064	AC002558	Homo sapiens chromosome 17, clone hRPC867C24, complete sequence.	Homo sapiens	36,820	31-OCT-1997
rxa01414	630	GB_PL1:SC5610	37730	Z38060	S cerevisiae chromosome IX sequence derived from lambda clones 5610-5004	Saccharomyces cerevisiae	38,782	20-Aug-97
		GB_PL1 YSCDIN1	2969	M58012	S.cerevisiae ribonucleotide reductase DNA damage-inducible regulatory subunit (DIN1) gene, 5' end	Saccharomyces cerevisiae	35,877	27-Apr-93
		GB_EST18.AA689161	624	AA689161	ET2100 Trypanosoma brucei rhodesiense ZAP II library Trypanosoma brucei rhodesiense cDNA 5', mRNA sequence.	Trypanosoma brucei rhodesiense	37,150	15-DEC-1997
rxa01417	720	GB_PL1 SC8419	30507	Z49701	S.cerevisiae chromosome IV cosmid 8419	Saccharomyces cerevisiae	36,248	11-Aug-97
		GB_PL1 SCPRP28G	2452	X56934	S.cerevisiae PRP28 gene.	Saccharomyces cerevisiae	45,036	9-Feb-95
rxa01421		GB_BA1:BACPEPFA	4654	M29035	B.subtilis bacillopeptidase F (bpr) gene, complete cds	Bacillus subtilis	37,324	06-MAR-1995
rxa01422	1095	GB_EST24.AU033392	344	AU033392	AU033392 Dictyostelium discoideum SL (H Urushihara) Dictyostelium discoideum cDNA clone SLA715, mRNA sequence.	Dictyostelium discoideum	38,953	28-Apr-99
		GB_EST14 AA399243	301	AA399243	zt57d02 s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE 726435 3' similar to SW:NIDO_HUMAN P14543 NIDOGEN PRECURSOR ;, mRNA sequence	Homo sapiens	45,183	12-Aug-97
		GB_PR2 AC002037	53897	AC002037	Human Chromosome 11 Overlapping Cosmids cSRL72g7 and cSRL140b8, complete sequence	Homo sapiens	37,500	6-Aug-97
rxa01425	1008	GB_PR4:AC005908	196501	AC005908	Homo sapiens 12p13 3 BAC RPCI11-476M19 (Roswell Park Cancer Institute Human BAC Library) complete sequence	Homo sapiens	34,410	20-Jan-99
		GB_PR4:AF111169	183916	AF111169	Homo sapiens chromosome 14 BAC containing gene for KIAA0759 and other possible new transcripts, complete sequence.	Homo sapiens	40,635	19-Jul-99
		GB_HTG2 AC008284	146797	AC008284	Drosophila melanogaster chromosome 3 clone BACR03M22 (D1000) RPCI-98 03.M 22 map 96C-96D strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 137 unordered pieces.	Drosophila melanogaster	35,822	2-Aug-99
rxa01429	741	GB_EST25 AI300084	635	AI300084	qn59f02.x1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE 1902555 3', mRNA sequence	Homo sapiens	37,753	1-Feb-99
		GB_EST18 AA706612	949	AA706612	ah26c02.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone 1239938 3', mRNA sequence	Homo sapiens	37,361	12-Jan-99
		GB_EST35.AI817084	598	AI817084	wj76g07.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE 2408796 3', mRNA sequence	Homo sapiens	38,627	24-Aug-99
rxa01434	3075	GB_PL1:CAC49C10	37825	AL033497	C.albicans cosmid Ca49C10	Candida albicans	34,724	10-Nov-98
		GB_GSS3 B10423	1217	B10423	F19F22-T7 IGF Arabidopsis thaliana genomic clone F19F22, genomic survey sequence.	Arabidopsis thaliana	36,003	14-MAY-1997
		GB_PL1 CAC49C10	37825	AL033497	C albicans cosmid Ca49C10	Candida albicans	33,794	10-Nov-98

TABLE 4: ALIGNMENT RESULTS

rxa01439	669	GB_BA2:AF049897	9196	AF049897	Corynebacterium glutamicum N-acetylglutamylphosphate reductase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds	Corynebacterium glutamicum	41,564	1-Jul-98
		GB_BA1 CGARGCJBD	4355	X86157	C.glutamicum argC, argJ, argB, argD, and argF genes	Corynebacterium glutamicum	41,564	25-Jul-96
		GB_BA2:AF049897	9196	AF049897	Corynebacterium glutamicum N-acetylglutamylphosphate reductase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds	Corynebacterium glutamicum	39,486	1-Jul-98
rxa01440	1131	GB_PAT:E16763	2517	E16763	gDNA encoding aspartate transferase (AAT)	Corynebacterium glutamicum	42,188	28-Jul-99
		GB_EST20:AA870569	423	AA870569	vq23c09 r1 Barstead stromal cell line MPLRB8 Mus musculus cDNA clone IMAGE 1095088 5' similar to TR:Q14468 Q14468 KIAA0047 ;, mRNA sequence	Mus musculus	42,066	16-MAR-1998
		GB_EST18 AA726390	436	AA726390	vu40b04.r1 Barstead mouse myotubes MPLRB5 Mus musculus cDNA clone IMAGE.1193839 5', mRNA sequence	Mus musculus	41,228	2-Jan-98
rxa01441	1152	GB_EST32.AV053763	252	AV053763	AV053763 Mus musculus pancreas C57BL/6J adult Mus musculus cDNA clone 1810028E06, mRNA sequence.	Mus musculus	45,238	23-Jun-99
		GB_EST20:AA870569	423	AA870569	vq23c09 r1 Barstead stromal cell line MPLRB8 Mus musculus cDNA clone IMAGE 1095088 5' similar to TR:Q14468 Q14468 KIAA0047 ,, mRNA sequence	Mus musculus	39,643	16-MAR-1998
		GB_EST18 AA726390	436	AA726390	vu40b04 r1 Barstead mouse myotubes MPLRB5 Mus musculus cDNA clone IMAGE.1193839 5', mRNA sequence	Mus musculus	39,953	2-Jan-98
rxa01445	1116	GB_PR4:AC007786	229061	AC007786	Homo sapiens chromosome 19, BAC 41855 (CIT-B-32o4), complete sequence.	Homo sapiens	39,545	11-Jun-99
		GB_PR3.AC003957	126581	AC003957	Homo sapiens chromosome 17, clone hCIT 457_L_16, complete sequence	Homo sapiens	36,579	09-MAY-1998
		GB_OV:AF108420	46626	AF108420	Fugu rubripes prohormone convertase PACE4 (PACE4) gene, partial cds, and 1-aminocyclopropane-carboxilate synthase (ACC), recombination-activating protein 1 (RAG1), and recombination-activating protein 2 (RAG2) genes, complete cds	Fugu rubripes	39,187	17-MAR-1999
rxa01447	972	GB_PL2 AF049112	1436	AF049112	Zea mays retrotransposon Cinful prpol mRNA, partial cds	Zea mays	38,268	1-Feb-99
		GB_EST36 AV190070	360	AV190070	AV190070 Yuji Kohara unpublished cDNA Strain N2 hermaphrodite embryo Caenorhabditis elegans cDNA clone yk566e10 5', mRNA sequence	Caenorhabditis elegans	40,390	22-Jul-99
		GB_EST9 AA103228	477	AA103228	mo22h07 r1 Life Tech mouse embryo 13 5dpc 10666014 Mus musculus cDNA clone IMAGE.554365 5' similar to gb:J00068 ACTIN, ALPHA SKELETAL MUSCLE (HUMAN), gb M12866 Mouse skeletal muscle actin mRNA, complete cds (MOUSE);, mRNA sequence	Mus musculus	40,411	29-OCT-1996
rxa01448	1290	GB_BA1 CGFDA	3371	X17313	Corynebacterium glutamicum fda gene for fructose-bisphosphate aldolase (EC 4 1 2 13).	Corynebacterium glutamicum	100,000	12-Sep-93
		GB_PL2:ENU75428	4443	U75428	Emericella nidulans acid trehalase precursor (treA) gene, complete cds	Emericella nidulans	36,271	15-MAY-1997
		GB_BA1.CGFDA	3371	X17313	Corynebacterium glutamicum fda gene for fructose-bisphosphate aldolase (EC 4 1 2 13)	Corynebacterium glutamicum	37,872	12-Sep-93
rxa01452	402	GB_BA1:MTV017	67200	AL021897	Mycobacterium tuberculosis H37Rv complete genome; segment 48/162	Mycobacterium tuberculosis	57,246	24-Jun-99
		GB_BA1:MLCB1222	34714	AL049491	Mycobacterium leprae cosmid B1222	Mycobacterium leprae	34,872	27-Aug-99
		GB_BA2:S71532	914	S71532	che=cholesterol esterase [Streptomyces lavendulae, H646-SY2, Genomic, 914 nt]	Streptomyces lavendulae	38,701	8-Nov-94
rxa01456	645	GB_GSS3 B16150	663	B16150	347A15 TP CIT978SKA1 Homo sapiens genomic clone A-347A15, genomic survey sequence	Homo sapiens	34,394	4-Jun-98
		GB_HTG3 AC004157	132090	AC004157	Plasmodium falciparum chromosome 12 clone 3D7, *** SEQUENCING IN PROGRESS ***, 9 unordered pieces	Plasmodium falciparum	34,165	23-Sep-99
		GB_HTG3 AC004157	132090	AC004157	Plasmodium falciparum chromosome 12 clone 3D7, *** SEQUENCING IN PROGRESS ***, 9 unordered pieces	Plasmodium falciparum	34,165	23-Sep-99
rxa01457	798	GB_HTG3 AC011009	158335	AC011009	Homo sapiens clone 2_I_22, LOW-PASS SEQUENCE SAMPLING	Homo sapiens	39,490	29-Sep-99
		GB_HTG3 AC011009	158335	AC011009	Homo sapiens clone 2_I_22, LOW-PASS SEQUENCE SAMPLING	Homo sapiens	39,490	29-Sep-99
		GB_HTG3.AC011009	158335	AC011009	Homo sapiens clone 2_I_22, LOW-PASS SEQUENCE SAMPLING	Homo sapiens	39,125	29-Sep-99

TABLE 4: ALIGNMENT RESULTS

rxa01459	933	GB_HTG3:AC008670	113564	AC008670	Homo sapiens chromosome 5 clone CIT978SKB_36O1, *** SEQUENCING IN PROGRESS ***, 43 unordered pieces	Homo sapiens	39,022	3-Aug-99
		GB_HTG3 AC008670	113564	AC008670	Homo sapiens chromosome 5 clone CIT978SKB_36O1, *** SEQUENCING IN PROGRESS ***, 43 unordered pieces	Homo sapiens	39,022	3-Aug-99
		GB_IN2.CELT05A8	33896	AF040652	Caenorhabditis elegans cosmid T05A8	Caenorhabditis elegans	35,699	16-Jun-99
rxa01460	417	GB_HTG3 AC009186	48600	AC009186	Homo sapiens chromosome 5 clone CIT978SKB_148I14, *** SEQUENCING IN PROGRESS ***, 3 ordered pieces	Homo sapiens	41,278	07-OCT-1999
		GB_HTG3 AC009186	48600	AC009186	Homo sapiens chromosome 5 clone CIT978SKB_148I14, *** SEQUENCING IN PROGRESS ***, 3 ordered pieces.	Homo sapiens	41,278	07-OCT-1999
		GB_HTG3:AC009186	48600	AC009186	Homo sapiens chromosome 5 clone CIT978SKB_148I14, *** SEQUENCING IN PROGRESS ***, 3 ordered pieces.	Homo sapiens	35,162	07-OCT-1999
rxa01463	1287	GB_PR3:HS326L13	127247	Z82170	Human DNA sequence from PAC 326L13 containing brain-4 mRNA ESTs and polymorphic CA repeat	Homo sapiens	37,956	23-Nov-99
		GB_HTG1.HS439A6	49379	AL031723	Homo sapiens chromosome 16 clone LA16-439A6, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Homo sapiens	38,035	23-Nov-99
		GB_HTG1.HS439A6	49379	AL031723	Homo sapiens chromosome 16 clone LA16-439A6, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	38,035	23-Nov-99
rxa01469	1155	GB_EST31.AI701691	349	AI701691	we81c04 x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE 2347494 3' similar to gb L19686_rna1 MACROPHAGE MIGRATION INHIBITORY FACTOR (HUMAN),, mRNA sequence	Homo sapiens	39,806	3-Jun-99
		GB_EST15 AA480256	389	AA480256	ne31f04.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE 898975 3' similar to gb:L19686_rna1 MACROPHAGE MIGRATION INHIBITORY FACTOR (HUMAN),, mRNA sequence	Homo sapiens	42,705	14-Aug-97
		GB_IN2 AF153269	1308	AF153269	Tetrahymena thermophila dynein heavy chain (DYH10) gene, partial cds	Tetrahymena thermophila	32,489	10-Jun-99
rxa01470	549	GB_PL2 ATF3L17	94319	AL080283	Arabidopsis thaliana DNA chromosome 4, BAC clone F3L17 (ESSA project)	Arabidopsis thaliana	37,615	24-Jun-99
		GB_PL2 ATF3L17	94319	AL080283	Arabidopsis thaliana DNA chromosome 4, BAC clone F3L17 (ESSA project)	Arabidopsis thaliana	35,946	24-Jun-99
rxa01471	930	GB_EST11.AA233898	460	AA233898	zr49b12 s1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:666719 3', mRNA sequence	Homo sapiens	40,570	6-Aug-97
		GB_EST11.AA234033	428	AA234033	zr49b12 r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE 666719 5' similar to contains Alu repetitive element,, mRNA sequence	Homo sapiens	36,277	6-Aug-97
rxa01472		GB_PL2 AF084971	1874	AF084971	Catharanthus roseus G-box binding protein 1 (GBF1) mRNA, complete cds	Catharanthus roseus	36,821	7-Jul-99
rxa01473	888	GB_PL2:AC002329	76170	AC002329	DNA sequence of Arabidopsis thaliana BAC F5J6 from chromosome IV, complete sequence	Arabidopsis thaliana	35,780	18-Nov-97
		GB_HTG3:AC009485	190706	AC009485	Homo sapiens clone NH0324G03, *** SEQUENCING IN PROGRESS ***, 6 unordered pieces	Homo sapiens	39,649	04-OCT-1999
		GB_HTG3.AC009485	190706	AC009485	Homo sapiens clone NH0324G03, *** SEQUENCING IN PROGRESS ***, 6 unordered pieces.	Homo sapiens	39,649	04-OCT-1999
rxa01474	669	GB_PR2.HSP373C6	85654	AL022393	Homo sapiens DNA sequence from P1 p373c6 on chromosome 6p21 31-21.33 Contains zinc finger proteins, pseudogenes, ESTs and STS	Homo sapiens	33,934	22-Nov-99
		GB_EST4 H30893	485	H30893	yp43e11 r1 Soares retina N2b5HR Homo sapiens cDNA clone IMAGE 190220 5' similar to contains Alu repetitive element;, mRNA sequence	Homo sapiens	37,866	16-Aug-95
		GB_PL2 ATAC005398	80238	AC005398	Arabidopsis thaliana chromosome II BAC T6B13 genomic sequence, complete sequence	Arabidopsis thaliana	38,640	30-OCT-1998
rxa01475	549	GB_PL1:AB024028	70952	AB024028	Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone K1G2, complete sequence	Arabidopsis thaliana	40,520	20-Nov-99
		GB_HTG2 AC007940	159279	AC007940	Homo sapiens clone 44_C_14, *** SEQUENCING IN PROGRESS ***, 12 unordered pieces	Homo sapiens	36,044	1-Jul-99
		GB_HTG2 AC007940	159279	AC007940	Homo sapiens clone 44_C_14, *** SEQUENCING IN PROGRESS ***, 12 unordered pieces.	Homo sapiens	36,044	1-Jul-99
rxa01476	465	GB_PL1 AB009087	1074	AB009087	Chlamydomonas sp mRNA for alternative oxidase, partial cds	Chlamydomonas sp	38,596	05-DEC-1997
		GB_PL1.AB009087	1074	AB009087	Chlamydomonas sp. mRNA for alternative oxidase, partial cds	Chlamydomonas sp	39,519	05-DEC-1997
rxa01479	363	GB_HTG1 HSJ136J15	148579	AL118496	Homo sapiens chromosome X clone RP1-136J15, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	39,886	23-Nov-99

TABLE 4: ALIGNMENT RESULTS

		GB_HTG1:HSJ136J15	148579	AL118496	Homo sapiens chromosome X clone RP1-136J15, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Homo sapiens	39,886	23-Nov-99
		GB_HTG2 AC007579	134344	AC007579	Drosophila melanogaster chromosome 2 clone BACR07M03 (D607) RPCI-98 07 M 3 map 53A-53B strain y, cn bw sp, *** SEQUENCING IN PROGRESS ***, 108 unordered pieces	Drosophila melanogaster	39,266	2-Aug-99
rxa01484	669	GB_PR3.AF064858	193387	AF064858	Homo sapiens chromosome 21q22 3 BAC 28F9, complete sequence	Homo sapiens	38,281	2-Jun-98
		GB_GSS10:AQ207755	496	AQ207755	HS_3026_B1_G04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3026 Col=7 Row=N, genomic survey sequence	Homo sapiens	37,150	18-Sep-98
		GB_PR3.AF064858	193387	AF064858	Homo sapiens chromosome 21q22 3 BAC 28F9, complete sequence	Homo sapiens	38,379	2-Jun-98
rxa01485	2175	GB_IN1.CEY50E8A	61864	AL117200	Caenorhabditis elegans cosmid Y50E8A, complete sequence	Caenorhabditis elegans	39,617	19-Nov-99
		GB_IN1.CEY50E8A	61864	AL117200	Caenorhabditis elegans cosmid Y50E8A, complete sequence	Caenorhabditis elegans	34,349	19-Nov-99
		GB_PL1:AB028606	61510	AB028606	Arabidopsis thaliana genomic DNA, chromosome 5, BAC clone.F16F17, complete sequence	Arabidopsis thaliana	34,858	20-Nov-99
rxa01488	1071	GB_BA1:CGPROMF10	60	X90358	C glutamicum DNA for promoter fragment F10	Corynebacterium glutamicum	65,000	4-Nov-96
		GB_EST10:AA183656	465	AA183656	mt20f08 r1 Soares mouse 3NbMS Mus musculus cDNA clone IMAGE 621639 5' similar to WP.T02C12 2 CE01062 ,, mRNA sequence	Mus musculus	35,333	17-Feb-97
		GB_EST9 AA110912	309	AA110912	mm02c01.r1 Stratagene mouse kidney (#937315) Mus musculus cDNA clone IMAGE 520320 5' similar to WP T02C12.2 CE01062 ,, mRNA sequence.	Mus musculus	37,662	4-Feb-97
rxa01492	927	GB_EST16 AA589576	567	AA589576	vl49b06 s1 Stratagene mouse skin (#937313) Mus musculus cDNA clone IMAGE 975539 3' similar to gb M63488 REPLICATION PROTEIN A 70 KD DNA-BINDING SUBUNIT (HUMAN),, mRNA sequence	Mus musculus	34,104	16-Sep-97
		GB_EST28 AU051490	865	AU051490	AU051490 Sugano mouse brain mncb Mus musculus cDNA clone MNCb-2105 5', mRNA sequence	Mus musculus	29,837	18-MAR-1999
		GB_EST32:AI738234	609	AI738234	606044C01 x2 606 - Ear tissue cDNA library from Schmidt lab Zea mays cDNA, mRNA sequence	Zea mays	38,291	16-Jun-99
rxa01494	1119	GB_PR4:AC007106	172188	AC007106	Homo sapiens chromosome 4 clone C0383J20 map 4p16, complete sequence	Homo sapiens	35,108	2-Jun-99
		GB_BA2:AE001093	14097	AE001093	Archaeoglobus fulgidus section 14 of 172 of the complete genome.	Archaeoglobus fulgidus	38,113	15-DEC-1997
		GB_PR4.AC007106	172188	AC007106	Homo sapiens chromosome 4 clone C0383J20 map 4p16, complete sequence	Homo sapiens	34,657	2-Jun-99
rxa01497	1041	GB_BA2 SCJ1	36925	AL109962	Streptomyces coelicolor cosmid J1	Streptomyces coelicolor A3(2)	50,722	24-Sep-99
		GB_BA1 MTY20B11	36330	Z95121	Mycobacterium tuberculosis H37Rv complete genome, segment 139/162	Mycobacterium tuberculosis	40,238	17-Jun-98
		GB_BA1.PAU12891	4062	U12891	Pseudomonas aeruginosa PAO substrain OT684 pyoverdine gene transcriptional regulator PvdS (pvdS) gene, complete cds	Pseudomonas aeruginosa	39,856	03-OCT-1996
rxa01501	411	GB_PAT I78757	2203	I78757	Sequence 13 from patent US 5693781.	Unknown	61,364	3-Apr-98
		GB_PAT I92046	2203	I92046	Sequence 13 from patent US 5726299	Unknown	61,364	01-DEC-1998
		GB_PR4:AC002427	101098	AC002427	Homo sapiens BAC clone GS011E15 from 5q31, complete sequence	Homo sapiens	42,250	02-DEC-1998
rxa01504	732	GB_HTG3:AC008954	23046	AC008954	Homo sapiens chromosome 5 clone CITB-H1_2340N2, *** SEQUENCING IN PROGRESS ***, 51 unordered pieces	Homo sapiens	37,830	3-Aug-99
		GB_HTG3 AC008954	23046	AC008954	Homo sapiens chromosome 5 clone CITB-H1_2340N2, *** SEQUENCING IN PROGRESS ***, 51 unordered pieces	Homo sapiens	37,830	3-Aug-99
		GB_BA1:QPHQSOP	4068	L28041	Plasmid QpH1 (from Coxiella burnetii) qsopA and qsopB genes, promoter region.	Plasmid QpH1	37,517	14-Jul-95
rxa01505	621	GB_SY:SYNM13GAL	66	M10216	Bacteriophage M13gt102 N-terminal beta-galactosidase gene (lac+ phenotype).	unidentified cloning vector	62,121	27-Apr-93
		GB_SY SYNM13GAL	66	M10216	Bacteriophage M13gt102 N-terminal beta-galactosidase gene (lac+ phenotype)	unidentified cloning vector	62,121	27-Apr-93
		GB_BA2 BJU56817	2892	U56817	Bradyrhizobium japonicum aconitase (acnA) gene, complete cds	Bradyrhizobium japonicum	40,214	13-Nov-96
rxa01506	534	GB_BA1 MTCY98	31225	Z83860	Mycobacterium tuberculosis H37Rv complete genome, segment 103/162.	Mycobacterium tuberculosis	38,274	17-Jun-98
		GB_BA1 MTCY98	31225	Z83860	Mycobacterium tuberculosis H37Rv complete genome, segment 103/162.	Mycobacterium tuberculosis	33,710	17-Jun-98
rxa01507	546	GB_RO D89731	1815	D89731	Rattus norvegicus mRNA for AIM-1, complete cds	Rattus norvegicus	38,125	7-Feb-99

TABLE 4: ALIGNMENT RESULTS

		GB_RO:D89731	1815	D89731	Rattus norvegicus mRNA for AIM-1, complete cds.	Rattus norvegicus	34,600	7-Feb-99
rxa01518								
rxa01519	870	GB_HTG2 AC007929	123885	AC007929	Drosophila melanogaster chromosome 3 clone BACR05C11 (D759) RPCI-98 05 C 11 map 95A-95C strain y, cn bw sp, *** SEQUENCING IN PROGRESS ***, 85 unordered pieces.	Drosophila melanogaster	34,075	2-Aug-99
		GB_HTG2 AC007929	123885	AC007929	Drosophila melanogaster chromosome 3 clone BACR05C11 (D759) RPCI-98 05 C 11 map 95A-95C strain y, cn bw sp, *** SEQUENCING IN PROGRESS***, 85 unordered pieces	Drosophila melanogaster	34,075	2-Aug-99
		GB_PL2 AC011437	95310	AC011437	Arabidopsis thaliana chromosome III BAC F7O18 genomic sequence, complete sequence	Arabidopsis thaliana	37,280	2-Nov-99
rxa01520								
rxa01523	1074	GB_GSS11 AQ270206	389	AQ270206	HS_2037_A1_G10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2037 Col=19 Row=M, genomic survey sequence	Homo sapiens	38,046	3-Nov-98
		GB_GSS14 AQ588624	480	AQ588624	CITBI-E1-2643C9 TF CITBI-E1 Homo sapiens genomic clone 2643C9, genomic survey sequence	Homo sapiens	36,875	7-Jun-99
		GB_HTG1 CEY80D3	245017	AL020988	Caenorhabditis elegans chromosome V clone Y80D3, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Caenorhabditis elegans	35,646	6-Sep-99
rxa01525	1845	GB_PR3 HS560B9	99074	Z98751	Human DNA sequence from PAC 560B9 on chromosome 1q24-1q25 Contains profilin-like pseudogene, 60S ribosomal protein L4 pseudogene RNA binding protein, ESTs, GSS	Homo sapiens	37,981	23-Nov-99
		GB_PR3.HS560B9	99074	Z98751	Human DNA sequence from PAC 560B9 on chromosome 1q24-1q25 Contains profilin-like pseudogene, 60S ribosomal protein L4 pseudogene RNA binding protein, ESTs, GSS	Homo sapiens	37,982	23-Nov-99
rxa01527								
rxa01536	1365	GB_HTG3.AC010745	193862	AC010745	Homo sapiens clone NH0549D18, *** SEQUENCING IN PROGRESS ***, 30 unordered pieces	Homo sapiens	35,277	21-Sep-99
		GB_HTG3:AC010745	193862	AC010745	Homo sapiens clone NH0549D18, *** SEQUENCING IN PROGRESS ***, 30 unordered pieces	Homo sapiens	35,277	21-Sep-99
		GB_HTG3 AC010745	193862	AC010745	Homo sapiens clone NH0549D18, *** SEQUENCING IN PROGRESS ***, 30 unordered pieces.	Homo sapiens	35,958	21-Sep-99
rxa01539	2289	GB_BA1.CGPROMF10	60	X90358	C.glutamicum DNA for promoter fragment F10	Corynebacterium glutamicum	61,667	4-Nov-96
		GB_HTG3:AC011577	151996	AC011577	Homo sapiens clone 12_P_19, LOW-PASS SEQUENCE SAMPLING	Homo sapiens	35,554	07-OCT-1999
		GB_HTG3:AC011577	151996	AC011577	Homo sapiens clone 12_P_19, LOW-PASS SEQUENCE SAMPLING	Homo sapiens	35,554	07-OCT-1999
rxa01540	825	GB_EST10 AA152819	491	AA152819	mq67e04 r1 Soares 2NbMT Mus musculus cDNA clone IMAGE.583806 5', mRNA sequence	Mus musculus	39,040	18-Feb-97
		GB_EST29 AI616027	481	AI616027	mq67e04.y1 Soares 2NbMT Mus musculus cDNA clone IMAGE 583806 5', mRNA sequence	Mus musculus	36,688	21-Apr-99
		GB_GSS6.AQ843942	468	AQ843942	LMAJFV1_lm03d08 x2 Leishmania major FV1 random genomic library Leishmania major genomic clone LMAJFV1_lm03d08 3', genomic survey sequence	Leishmania major	40,899	04-OCT-1999
rxa01543	2889	GB_BA2 ECOUW67_0	110000	U18997	Escherichia coli K-12 chromosomal region from 67.4 to 76 0 minutes	Escherichia coli	36,618	15-Sep-99
		GB_BA2.ECOUW67_0	110000	U18997	Escherichia coli K-12 chromosomal region from 67.4 to 76 0 minutes	Escherichia coli	38,415	15-Sep-99
		GB_BA2 AE000397	14820	AE000397	Escherichia coli K-12 MG1655 section 287 of 400 of the complete genome	Escherichia coli	37,594	12-Nov-98
rxa01544	723	GB_EST37 AI977486	479	AI977486	EST272080 Schistosoma mansoni male, Phil LoVerde/Joe Merrick Schistosoma mansoni cDNA clone SMMAM80 5' end, mRNA sequence	Schistosoma mansoni	44,156	27-Aug-99
		GB_VI.AF056119	564	AF056119	HIV-1 isolate z560 from Zimbabwe, envelope glycoprotein V3-V5 region (env) gene, partial cds	Human immunodeficiency virus type 1	35,874	26-Sep-98
		GB_VI AF056119	564	AF056119	HIV-1 isolate z560 from Zimbabwe, envelope glycoprotein V3-V5 region (env) gene, partial cds	Human immunodeficiency virus type 1	37,229	26-Sep-98
rxa01545	1374	GB_HTG1 CEY53C10_1	110000	Z93340	Caenorhabditis elegans chromosome I clone Y53C10, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Caenorhabditis elegans	36,885	4-Nov-98
		GB_HTG1 CEY53C10_1	110000	Z93340	Caenorhabditis elegans chromosome I clone Y53C10, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Caenorhabditis elegans	36,885	4-Nov-98

TABLE 4: ALIGNMENT RESULTS

		GB_HTG1:CEY47H9_1	110000	Z92853	Caenorhabditis elegans chromosome I clone Y47H9, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Caenorhabditis elegans	30,285	4-Sep-98
rxa01546	819	GB_GSS3.B58207	420	B58207	CIT-HSP-2012C11.TR CIT-HSP Homo sapiens genomic clone 2012C11, genomic survey sequence	Homo sapiens	45,228	20-Jun-98
		GB_IN1 HAU02678	623	U02678	Helicoverpa armigera mitochondrion D-loop, partial 12S rRNA gene, and partial tRNA-Met gene	Mitochondrion Helicoverpa armigera	37,500	27-OCT-1993
		GB_EST19:AA769027	473	AA769027	oa78g01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE 1318416 3' similar to TR Q92617 Q92617 MYELOBLAST KIAA0220 ;, mRNA sequence.	Homo sapiens	39,583	28-Jan-98
rxa01547	786	GB_EST26:AU002373	837	AU002373	AU002373 Bombyx mori p50(Daizo) Bombyx mori cDNA clone mg0832, mRNA sequence	Bombyx mori	37,698	15-Jan-99
		GB_EST30 AV025617	494	AV025617	AV025617 Mus musculus adult C57BL/6J lung Mus musculus cDNA clone 1200014J18, mRNA sequence	Mus musculus	38,316	31-Aug-99
		GB_EST26.AU002373	837	AU002373	AU002373 Bombyx mori p50(Daizo) Bombyx mori cDNA clone mg0832, mRNA sequence	Bombyx mori	36,767	15-Jan-99
rxa01548	1131	GB_IN1 PFARBPCA	8841	M88097	Plasmodium vivax reticulocyte binding protein 1 gene, complete cds	Plasmodium vivax	37,077	26-Apr-93
		GB_PAT I55034	1985	I55034	Sequence 2 from patent US 5646247	Unknown.	38,250	07-OCT-1997
		GB_OV.GGNEUROMP	1112	Y09597	G gallus mRNA for NeuroM protein	Gallus gallus	37,104	15-OCT-1997
rxa01549	1727	GB_PR4 HSLONPG01	2443	AF059296	Homo sapiens LON protease (LON) gene, nuclear gene encoding mitochondrial protein, exon 1.	Homo sapiens	39,401	11-Apr-99
		GB_EST33 AI770254	555	AI770254	SAL2.F12 Black Tiger Shrimp Whole Cephalothorax UniZap library Penaeus monodon cDNA clone SAL2.F12 5' similar to muscle myosin heavy chain, mRNA sequence	Penaeus monodon	40,325	28-Jun-99
		GB_PR1:HSU02389	3179	U02389	Human hLON ATP-dependent protease mRNA, nuclear gene encoding mitochondrial protein, complete cds	Homo sapiens	38,868	27-Jan-95
rxa01552	1101	GB_HTG4.AC011192	144277	AC011192	Homo sapiens clone hRPK 53_A_1, *** SEQUENCING IN PROGRESS ***, 9 unordered pieces.	Homo sapiens	36,296	19-OCT-1999
		GB_HTG4.AC011192	144277	AC011192	Homo sapiens clone hRPK 53_A_1, *** SEQUENCING IN PROGRESS ***, 9 unordered pieces	Homo sapiens	36,296	19-OCT-1999
		GB_HTG3.AC011203	70518	AC011203	Homo sapiens chromosome 3 clone 78_O_24 map 3, LOW-PASS SEQUENCE SAMPLING	Homo sapiens	36,440	03-OCT-1999
rxa01554	2265	GB_EST27 AA957437	340	AA957437	UI-R-E1-fy-g-02-0-UI s1 UI-R-E1 Rattus norvegicus cDNA clone UI-R-E1-fy-g-02-0-UI 3', mRNA sequence	Rattus norvegicus	39,039	4-Jul-99
		GB_PL2:SPBC19G7	37727	AL021839	S pombe chromosome II cosmid c19G7.	Schizosaccharomyces pombe	36,991	17-Nov-99
		GB_PL1 HVPROTZ	703	X05902	Barley mRNA fragment for protein Z	Hordeum vulgare	36,390	13-Jul-95
rxa01557	939	GB_EST24 AI167051	429	AI167051	xylem est 822 Poplar xylem Lambda ZAPII library Populus balsamifera subsp. trichocarpa cDNA 5', mRNA sequence	Populus balsamifera subsp. trichocarpa	40,326	03-DEC-1998
		GB_PL2 AC007259	97146	AC007259	Arabidopsis thaliana chromosome I BAC T28P6 genomic sequence, complete sequence	Arabidopsis thaliana	34,442	17-Aug-99
rxa01560		GB_PL2 AC007259	97146	AC007259	Arabidopsis thaliana chromosome I BAC T28P6 genomic sequence, complete sequence	Arabidopsis thaliana	34,967	17-Aug-99
rxa01574	1158	GB_PR3.AC005242	160262	AC005242	Homo sapiens chromosome 17, clone hRPK.118_F_13, complete sequence	Homo sapiens	35,727	22-Jul-98
		GB_PR3:AC005242	160262	AC005242	Homo sapiens chromosome 17, clone hRPK 118_F_13, complete sequence.	Homo sapiens	33,969	22-Jul-98
		GB_HTG2:AC007604	167373	AC007604	Homo sapiens chromosome 16 clone 344L6, *** SEQUENCING IN PROGRESS***, 85 unordered pieces	Homo sapiens	36,028	20-MAY-1999
rxa01575	1143	GB_PR4:AC004738	147404	AC004738	Homo sapiens Chromosome 15q11-q13 PAC clone pDJ351h23 from the Prader-Willi/Angelman Syndrome region, complete sequence	Homo sapiens	37,312	25-Nov-98
		GB_PR3 AC005250	94336	AC005250	Homo sapiens BAC clone RG318M05 from 7q22-q31.1, complete sequence	Homo sapiens	38,201	3-Jul-98
		GB_GSS11 AQ300376	487	AQ300376	HS_2206_A2_D05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2206 Col=10 Row=G, genomic survey sequence	Homo sapiens	35,345	16-DEC-1998
rxa01577	498	GB_BA1 MTY15C10	33050	Z95436	Mycobacterium tuberculosis H37Rv complete genome, segment 154/162	Mycobacterium tuberculosis	58,385	17-Jun-98
		GB_BA2:AF030975	2511	AF030975	Aeromonas salmonicida chaperonin GroES and chaperonin GroEL genes, complete cds	Aeromonas salmonicida	41,322	2-Apr-98
		GB_EST7 W33355	488	W33355	mb97g01 r1 Soares mouse p3NMF19 5 Mus musculus cDNA clone IMAGE 337392 5' similar to gb:X58196_cds1 M.musculus H19 mRNA (MOUSE),, mRNA sequence	Mus musculus	40,230	11-Sep-96
rxa01579	507	GB_GSS1 GGA300114	662	AJ231964	Gallus gallus anonymous sequence from Cosmid mapping to chicken chromosome 3 (Cosmid 30 - Contig 14), genomic survey sequence	Gallus gallus	38,023	25-Aug-98

TABLE 4: ALIGNMENT RESULTS

		GB_GSS1:GGA300114	662	AJ231964	Gallus gallus anonymous sequence from Cosmid mapping to chicken chromosome 3 (Cosmid 30 - Contig 14), genomic survey sequence	Gallus gallus	38,608	25-Aug-98
rxa01585	750	GB_PR4 AC004815	120538	AC004815	Homo sapiens clone 82F9, complete sequence	Homo sapiens	35,383	8-Sep-99
		GB_PR2 AP000151	100000	AP000151	Homo sapiens genomic DNA, chromosome 21q22.2, DSCR region, clone D47-S479, segment 3/16, complete sequence	Homo sapiens	39,722	20-Nov-99
		GB_PR2 AP000151	100000	AP000151	Homo sapiens genomic DNA, chromosome 21q22 2, DSCR region, clone D47-S479, segment 3/16, complete sequence	Homo sapiens	34,683	20-Nov-99
rxa01586	392	GB_GSS5.AQ791385	522	AQ791385	HS_5268_A2_C05_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=844 Col=10 Row=E, genomic survey sequence	Homo sapiens	43,235	3-Aug-99
		GB_EST15:AA463774	255	AA463774	aa09f10 r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE 812779 5' similar to gb:X07868_rna1 PUTATIVE INSULIN-LIKE GROWTH FACTOR II ASSOCIATED (HUMAN),contains element PTR7 repetitive element ,, mRNA sequence	Homo sapiens	42,045	10-Jun-97
rxa01590		GB_PR1 AP000010	100000	AP000010	Homo sapiens genomic DNA of 21q22 2 Down Syndrome region, segment 3/13	Homo sapiens	38,684	24-Apr-99
rxa01592	1425	GB_HTG2 AC008163	135300	AC008163	Homo sapiens clone NH0005B09, *** SEQUENCING IN PROGRESS ***, 1 unordered pieces	Homo sapiens	34,141	31-Jul-99
		GB_HTG2.AC008163	135300	AC008163	Homo sapiens clone NH0005B09, *** SEQUENCING IN PROGRESS ***, 1 unordered pieces	Homo sapiens	34,141	31-Jul-99
		GB_HTG3 AC009231	181006	AC009231	Homo sapiens clone NH0350I24, *** SEQUENCING IN PROGRESS ***, 2 unordered pieces	Homo sapiens	36,767	6-Aug-99
rxa01595	1083	GB_BA1.MTCI125	37432	Z98268	Mycobacterium tuberculosis H37Rv complete genome, segment 76/162	Mycobacterium tuberculosis	57,955	17-Jun-98
		GB_BA1:MTHYPROT	2544	X98295	M tuberculosis TlyA gene	Mycobacterium tuberculosis	57,955	2-Jun-98
		GB_BA1.U00021	39193	U00021	Mycobacterium leprae cosmid L247	Mycobacterium leprae	35,261	29-Sep-94
rxa01597	1305	GB_HTG3 AC009462	103046	AC009462	Drosophila melanogaster chromosome 3 clone BACR27G04 (D985) RPCI-98 27 G.4 map 90E-90E strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 88 unordered pieces	Drosophila melanogaster	38,898	30-Aug-99
		GB_HTG3 AC009462	103046	AC009462	Drosophila melanogaster chromosome 3 clone BACR27G04 (D985) RPCI-98 27.G 4 map 90E-90E strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 88 unordered pieces.	Drosophila melanogaster	38,898	30-Aug-99
		GB_HTG2:AC006889	267118	AC006889	Caenorhabditis elegans clone Y65B4, *** SEQUENCING IN PROGRESS ***, 6 unordered pieces	Caenorhabditis elegans	36,236	26-Feb-99
rxa01598	1086	GB_EST2 R02663	397	R02663	ye80a04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE 124014 5', mRNA sequence	Homo sapiens	36,272	31-MAR-1995
		GB_EST6 W03663	346	W03663	za65b08.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE 297399 5', mRNA sequence.	Homo sapiens	42,775	19-Apr-96
		GB_IN2:AC007765	163403	AC007765	Drosophila melanogaster, chromosome 2L, region 23C1-23C5, P1 clones DS02190 and DS00906, complete sequence	Drosophila melanogaster	38,351	9-Jun-99
rxa01600	792	GB_STS.G39530	822	G39530	Z22942 Zebrafish AB Danio rerio STS genomic, sequence tagged site	Danio rerio	41,242	31-Jul-98
		GB_STS:G39530	822	G39530	Z22942 Zebrafish AB Danio rerio STS genomic, sequence tagged site	Danio rerio	41,242	31-Jul-98
		GB_PR3:HSDJ991C6	128995	AL078599	Human DNA sequence from clone 991C6 on chromosome 6q14 1-15, complete sequence.	Homo sapiens	35,188	23-Nov-99
rxa01602	1653	GB_EST38.AW033000	685	AW033000	EST276559 tomato callus, TAMU Lycopersicon esculentum cDNA clone cLEC19N6, mRNA sequence	Lycopersicon esculentum	44,706	15-Sep-99
		GB_PL2 SPAC3C7	35052	Z99568	S pombe chromosome I cosmid c3C7	Schizosaccharomyces pombe	38,158	29-Nov-99
		GB_PL2.SPAC3C7	35052	Z99568	S pombe chromosome I cosmid c3C7.	Schizosaccharomyces pombe	37,888	29-Nov-99
rxa01605	1638	GB_HTG3 AC008689	145122	AC008689	Homo sapiens chromosome 5 clone CIT978SKB_61G23, *** SEQUENCING IN PROGRESS ***, 44 unordered pieces	Homo sapiens	35,448	3-Aug-99
		GB_HTG3 AC008689	145122	AC008689	Homo sapiens chromosome 5 clone CIT978SKB_61G23, *** SEQUENCING IN PROGRESS ***, 44 unordered pieces	Homo sapiens	35,448	3-Aug-99

TABLE 4: ALIGNMENT RESULTS

		GB_HTG3:AC009175	233932	AC009175	Homo sapiens chromosome 5 clone RPCI-PAC_241C15, *** SEQUENCING IN PROGRESS ***, 94 unordered pieces	Homo sapiens	37,423	3-Aug-99
rxa01610	852	GB_BA1 ECU82664	139818	U82664	Escherichia coli minutes 9 to 11 genomic sequence	Escherichia coli	34,198	11-Jan-97
		GB_BA1:ECU82664	139818	U82664	Escherichia coli minutes 9 to 11 genomic sequence	Escherichia coli	36,949	11-Jan-97
		GB_BA1:D90845	19366	D90845	E coli genomic DNA, Kohara clone #356(46.1-46 5 min).	Escherichia coli	39,808	21-MAR-1997
rxa01611	480	GB_PR3:AC005581	39601	AC005581	Homo sapiens chromosome 19, cosmid R31237, complete sequence	Homo sapiens	38,901	1-Sep-98
		GB_EST35 AI809560	443	AI809560	wf30h09 x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2357153 3', mRNA sequence	Homo sapiens	35,989	7-Jul-99
		GB_EST25:AI279953	416	AI279953	qh90b02 x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE 1854219 3', mRNA sequence	Homo sapiens	35,276	27-Jan-99
rxa01612								
rxa01618	507	GB_GSS14 AQ506815	616	AQ506815	RPCI-11-316B19 TV RPCI-11 Homo sapiens genomic clone RPCI-11-316B19, genomic survey sequence	Homo sapiens	41,901	29-Apr-99
		GB_HTG2:AC007512	168140	AC007512	Homo sapiens clone hRPK.96_A_1, *** SEQUENCING IN PROGRESS ***, 14 unordered pieces	Homo sapiens	39,549	07-MAY-1999
		GB_HTG2:AC007512	168140	AC007512	Homo sapiens clone hRPK 96_A_1, *** SEQUENCING IN PROGRESS ***, 14 unordered pieces	Homo sapiens	39,549	07-MAY-1999
rxa01619	1098	GB_BA1.ECOUW93	338534	U14003	Escherichia coli K-12 chromosomal region from 92 8 to 00 1 minutes	Escherichia coli	39,459	17-Apr-96
		GB_BA2 AE000497	10334	AE000497	Escherichia coli K-12 MG1655 section 387 of 400 of the complete genome.	Escherichia coli	39,459	12-Nov-98
		GB_BA1:ECOLEUX	2147	M96355	Escherichia coli leucine tRNA gene and ORF1 gene, complete cds	Escherichia coli	41,434	26-Jul-95
rxa01622	726	GB_PR4.AC007664	162470	AC007664	Homo sapiens, complete sequence.	Homo sapiens	37,006	18-Sep-99
		GB_PR4:AC002472	147100	AC002472	Homo sapiens Chromosome 22q11 2 PAC Clone p_n5 In BCRL2-GGT Region, complete sequence.	Homo sapiens	33,058	13-Sep-99
		GB_BA1:SYCSLRG	135638	D64005	Synechocystis sp PCC6803 complete genome, 24/27, 3002966-3138603	Synechocystis sp.	38,755	13-Feb-99
rxa01623	834	GB_HTG4 AC007422	156484	AC007422	Homo sapiens clone hRPK.68_A_1, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces.	Homo sapiens	36,759	23-OCT-1999
		GB_HTG4:AC007422	156484	AC007422	Homo sapiens clone hRPK 68_A_1, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces	Homo sapiens	36,759	23-OCT-1999
		GB_HTG4 AC007422	156484	AC007422	Homo sapiens clone hRPK.68_A_1, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces.	Homo sapiens	33,495	23-OCT-1999
rxa01624	468	GB_BA2:AE001816	10007	AE001816	Thermotoga maritima section 128 of 136 of the complete genome.	Thermotoga maritima	38,852	2-Jun-99
		GB_RO CCPH20	2152	X56332	Cavia cobaya mRNA for PH-20 protein	Cavia porcellus	38,293	20-Feb-91
		GB_PAT.I89388	2152	I89388	Sequence 1 from patent US 5721348	Unknown	38,293	10-Aug-98
rxa01628	1137	GB_BA1:CGPROPGEN	2936	Y12537	C glutamicum proP gene	Corynebacterium glutamicum	37,882	17-Nov-98
		GB_IN1:CET06E6	33238	Z81117	Caenorhabditis elegans cosmid T06E6, complete sequence	Caenorhabditis elegans	38,330	2-Sep-99
		GB_HTG2.AC006916	157093	AC006916	Caenorhabditis elegans clone Y9C9, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces	Caenorhabditis elegans	36,519	24-Feb-99
rxa01630	1200	GB_PR3 AC004945	167372	AC004945	Homo sapiens PAC clone DJ0997N05 from 7q11 23-q21 1, complete sequence	Homo sapiens	34,996	26-Sep-98
		GB_PR4:AC006385	173508	AC006385	Homo sapiens clone NH0559J05, complete sequence	Homo sapiens	32,525	05-MAY-1999
		GB_PR3:AC004945	167372	AC004945	Homo sapiens PAC clone DJ0997N05 from 7q11 23-q21 1, complete sequence	Homo sapiens	37,972	26-Sep-98
rxa01634	675	GB_PR4:AC005901	156763	AC005901	Homo sapiens chromosome 17, clone hRPK 15_K_2, complete sequence	Homo sapiens	35,736	20-Jan-99
		GB_PR4:AC005901	156763	AC005901	Homo sapiens chromosome 17, clone hRPK 15_K_2, complete sequence	Homo sapiens	35,549	20-Jan-99
rxa01635	864	GB_HTG3 AC008590	268470	AC008590	Homo sapiens chromosome 5 clone CIT-HSPC_575D19, *** SEQUENCING IN PROGRESS ***, 235 unordered pieces	Homo sapiens	35,370	3-Aug-99
		GB_HTG3.AC008590	268470	AC008590	Homo sapiens chromosome 5 clone CIT-HSPC_575D19, *** SEQUENCING IN PROGRESS ***, 235 unordered pieces	Homo sapiens	35,370	3-Aug-99
		GB_HTG3 AC008590	268470	AC008590	Homo sapiens chromosome 5 clone CIT-HSPC_575D19, *** SEQUENCING IN PROGRESS ***, 235 unordered pieces	Homo sapiens	38,571	3-Aug-99
rxa01638	1023	GB_HTG3 AC008261	93735	AC008261	Arabidopsis thaliana chromosome III clone TAMU-T4P13, *** SEQUENCING IN PROGRESS ***, 1 ordered pieces	Arabidopsis thaliana	37,200	10-Aug-99

TABLE 4: ALIGNMENT RESULTS

		GB_HTG3:AC008261	93735	AC008261	Arabidopsis thaliana chromosome III clone TAMU-T4P13, *** SEQUENCING IN PROGRESS ***, 1 ordered pieces	Arabidopsis thaliana	37,200	10-Aug-99
		GB_HTG3 AC008261	93735	AC008261	Arabidopsis thaliana chromosome III clone TAMU-T4P13, *** SEQUENCING IN PROGRESS ***, 1 ordered pieces.	Arabidopsis thaliana	32,637	10-Aug-99
rxa01641	1494	GB_PR3 HS681N20	130263	AL031670	Human DNA sequence from clone 681N20 on chromosome 20p12 1-13 Contains FTLL1(ferritin, light polypeptide-like 1), a gene similar to Zinc finger, C3HC4 type (RING finger), weakly similar to SW GOLI_DROME Q06003 GOLIATH PROTEIN, ESTs, STS, GSS, CA repeat (D20S889), CpG Islands, complete sequence	Homo sapiens	34,676	23-Nov-99
		GB_HTG4 AC011177	168660	AC011177	Homo sapiens clone 11_L_8, *** SEQUENCING IN PROGRESS ***, 7 unordered pieces.	Homo sapiens	36,234	29-OCT-1999
		GB_HTG4 AC011177	168660	AC011177	Homo sapiens clone 11_L_8, *** SEQUENCING IN PROGRESS ***, 7 unordered pieces	Homo sapiens	36,234	29-OCT-1999
rxa01642	1365	GB_BA1 MTY15F10	38204	Z94121	Mycobacterium tuberculosis H37Rv complete genome; segment 161/162	Mycobacterium tuberculosis	37,723	17-Jun-98
		GB_BA1:SC3C3	31382	AL031231	Streptomyces coelicolor cosmid 3C3.	Streptomyces coelicolor	39,602	10-Aug-98
		GB_BA1:SCU33176	1238	U33176	Streptomyces coelicolor serine protease gene, complete cds.	Streptomyces coelicolor	41,467	9-Jan-96
rxa01643	549	GB_IN1:CEZC101	26147	Z93395	Caenorhabditis elegans cosmid ZC101, complete sequence	Caenorhabditis elegans	36,280	23-Jul-99
		GB_EST16 C47058	360	C47058	C47058 Yuji Kohara unpublished cDNA Strain N2 hermaphrodite embryo Caenorhabditis elegans cDNA clone yk432e11 5', mRNA sequence	Caenorhabditis elegans	39,944	18-OCT-1999
		GB_HTG1 CEY54E2_1	110000	Z92861	Caenorhabditis elegans chromosome II clone Y54E2, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Caenorhabditis elegans	36,280	29-Jul-98
rxa01645	729	GB_BA1 MTV025	121125	AL022121	Mycobacterium tuberculosis H37Rv complete genome, segment 155/162	Mycobacterium tuberculosis	60,310	24-Jun-99
		GB_BA1 MLCB2407	35615	AL023596	Mycobacterium leprae cosmid B2407	Mycobacterium leprae	37,378	27-Aug-99
		GB_BA1 MSGB577COS	37770	L01263	M leprae genomic dna sequence, cosmid b577	Mycobacterium leprae	57,829	14-Jun-96
rxa01646	942	GB_BA1 MSGB577COS	37770	L01263	M leprae genomic dna sequence, cosmid b577.	Mycobacterium leprae	53,781	14-Jun-96
		GB_BA1.MLCB2407	35615	AL023596	Mycobacterium leprae cosmid B2407	Mycobacterium leprae	39,348	27-Aug-99
		GB_BA1:MTV025	121125	AL022121	Mycobacterium tuberculosis H37Rv complete genome, segment 155/162	Mycobacterium tuberculosis	53,503	24-Jun-99
rxa01647	1293	GB_GSS1.CNS010VB	837	AL099473	Drosophila melanogaster genome survey sequence T7 end of BAC BACN05B20 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence	Drosophila melanogaster	39,412	26-Jul-99
		GB_EST1.T55021	429	T55021	yb42e09.r1 Stratagene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE 73864 5', mRNA sequence	Homo sapiens	39,730	6-Feb-95
		GB_EST38:AL120803	505	AL120803	DKFZp762E202_r1 762 (synonym. hmel2) Homo sapiens cDNA clone DKFZp762E202 5', mRNA sequence	Homo sapiens	40,476	27-Sep-99
rxa01656	1020	GB_BA1:MTCY1A10	25949	Z95387	Mycobacterium tuberculosis H37Rv complete genome, segment 117/162	Mycobacterium tuberculosis	37,771	17-Jun-98
		GB_BA1 MLCL581	36225	Z96801	Mycobacterium leprae cosmid L581.	Mycobacterium leprae	40,041	24-Jun-97
		GB_PL2:ATAC003028	106448	AC003028	Arabidopsis thaliana chromosome II BAC F16M14 genomic sequence, complete sequence	Arabidopsis thaliana	57,692	22-Jul-98
rxa01658	1856	GB_BA1:MTV014	58280	AL021646	Mycobacterium tuberculosis H37Rv complete genome, segment 137/162	Mycobacterium tuberculosis	38,877	18-Jun-98
		GB_BA1 MTV030	29256	AL021428	Mycobacterium tuberculosis H37Rv complete genome; segment 4/162	Mycobacterium tuberculosis	57,048	17-Jun-98
		GB_BA1:MTV014	58280	AL021646	Mycobacterium tuberculosis H37Rv complete genome, segment 137/162	Mycobacterium tuberculosis	40,511	18-Jun-98
rxa01659	669	GB_HTG3 AC008604	136016	AC008604	Homo sapiens chromosome 5 clone CIT978SKB_109F8, *** SEQUENCING IN PROGRESS ***, 79 unordered pieces.	Homo sapiens	35,106	3-Aug-99
		GB_HTG3:AC008604	136016	AC008604	Homo sapiens chromosome 5 clone CIT978SKB_109F8, *** SEQUENCING IN PROGRESS ***, 79 unordered pieces	Homo sapiens	35,106	3-Aug-99
		GB_HTG3 AC011403	124903	AC011403	Homo sapiens chromosome 5 clone CIT978SKB_3P13, *** SEQUENCING IN PROGRESS ***, 7 ordered pieces	Homo sapiens	33,997	06-OCT-1999
rxa01663	981	GB_HTG2:AC006799	278007	AC006799	Caenorhabditis elegans clone Y51H7, *** SEQUENCING IN PROGRESS ***, 7 unordered pieces.	Caenorhabditis elegans	34,787	23-Feb-99

TABLE 4: ALIGNMENT RESULTS

		GB_HTG2:AC006799	278007	AC006799	Caenorhabditis elegans clone Y51H7, *** SEQUENCING IN PROGRESS ***, 7 unordered pieces.	Caenorhabditis elegans	34,787	23-Feb-99
		GB_HTG2 AC006799	278007	AC006799	Caenorhabditis elegans clone Y51H7, *** SEQUENCING IN PROGRESS ***, 7 unordered pieces.	Caenorhabditis elegans	39,148	23-Feb-99
rxa01665	843	GB_BA1.CGU43535	2531	U43535	Corynebacterium glutamicum multidrug resistance protein (cmr) gene, complete cds	Corynebacterium glutamicum	37,353	9-Apr-97
		GB_IN2 AF062971	359	AF062971	Anoplodactylus portus 28S ribosomal RNA gene, partial sequence	Anoplodactylus portus	42,462	20-Apr-99
		GB_EST31:AU062109	544	AU062109	AU062109 Dictyostelium discoideum SL (H Urushihara) Dictyostelium discoideum cDNA clone SLH629, mRNA sequence.	Dictyostelium discoideum	34,810	20-MAY-1999
rxa01669	1038	GB_BA2 CGU89648	1105	U89648	Corynebacterium glutamicum unidentified sequence involved in histidine biosynthesis, partial sequence	Corynebacterium glutamicum	65,152	30-MAR-1999
		GB_IN1 DMC86E4	29352	AL021086	Drosophila melanogaster cosmid clone 86E4	Drosophila melanogaster	39,289	27-Apr-99
		GB_PL1 ENY13759	3141	Y13759	Emericella nidulans abfB gene.	Emericella nidulans	38,552	05-MAR-1999
rxa01671	1272	GB_PH MPU46938	15664	U46938	Mycobacterium phage DS6A, Spe1/Nhe1 G fragment sequence	Mycobacterium phage DS6A	60,751	29-Jun-96
		GB_PAT I31047	15664	I31047	Sequence 3 from patent US 5582969	Unknown	60,751	6-Feb-97
		GB_PAT I36863	15664	I36863	Sequence 3 from patent US 5612182.	Unknown.	60,751	13-MAY-1997
rxa01672	465	GB_GSS14.AQ512046	462	AQ512046	HS_5113_B1_B10_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=689 Col=19 Row=D, genomic survey sequence.	Homo sapiens	40,882	05-MAY-1999
		GB_GSS13 AQ475012	253	AQ475012	CITBI-E1-2592A3 TR CITBI-E1 Homo sapiens genomic clone 2592A3, genomic survey sequence	Homo sapiens	35,417	23-Apr-99
		GB_GSS14 AQ512046	462	AQ512046	HS_5113_B1_B10_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=689 Col=19 Row=D, genomic survey sequence	Homo sapiens	35,106	05-MAY-1999
rxa01673	1158	GB_HTG5 AC010988	176452	AC010988	Homo sapiens clone NH0570F04, WORKING DRAFT SEQUENCE, 1 unordered pieces	Homo sapiens	37,489	11-Nov-99
		GB_HTG5:AC010988	176452	AC010988	Homo sapiens clone NH0570F04, WORKING DRAFT SEQUENCE, 1 unordered pieces	Homo sapiens	35,492	11-Nov-99
rxa01675	534	GB_EST19 AA797620	497	AA797620	vw26b03 r1 Soares mouse mammary gland NbMMG Mus musculus cDNA clone IMAGE:1244909 5', mRNA sequence.	Mus musculus	44,318	10-Feb-98
		GB_IN2 AF076597	846	AF076597	Dictyostelium discoideum ubiquitin-conjugating enzyme protein UbcC (ubcC) mRNA, complete cds	Dictyostelium discoideum	37,149	30-Jul-98
		GB_EST22:C94466	698	C94466	C94466 Dictyostelium discoideum SS (H Urushihara) Dictyostelium discoideum cDNA clone SSL136, mRNA sequence	Dictyostelium discoideum	33,647	15-Jun-98
rxa01676	879	GB_IN1.CELR03H10	35080	U29382	Caenorhabditis elegans cosmid R03H10	Caenorhabditis elegans	40,951	22-Jun-95
		GB_EST37:AI998397	584	AI998397	701545552 A thaliana, Columbia Col-0, rosette-2 Arabidopsis thaliana cDNA clone 701545552, mRNA sequence	Arabidopsis thaliana	37,333	8-Sep-99
		GB_GSS14 AQ551731	577	AQ551731	RPCI-11-383J4 TJ RPCI-11 Homo sapiens genomic clone RPCI-11-383J4, genomic survey sequence.	Homo sapiens	39,321	28-MAY-1999
rxa01677	867	GB_PL2 ATF6I18	122322	AL022198	Arabidopsis thaliana DNA chromosome 4, BAC clone F6I18 (ESSA project).	Arabidopsis thaliana	34,335	27-Aug-99
		GB_PL2:ATF6I18	122322	AL022198	Arabidopsis thaliana DNA chromosome 4, BAC clone F6I18 (ESSA project)	Arabidopsis thaliana	34,895	27-Aug-99
		GB_OV:XLSDK2	2306	Y10350	X laevis mRNA for nuclear protein SDK2.	Xenopus laevis	36,538	2-Apr-98
rxa01681	756	GB_HTG3 AC010798	172575	AC010798	Homo sapiens chromosome 18 clone 470_B_24 map 18, *** SEQUENCING IN PROGRESS ***, 7 unordered pieces	Homo sapiens	37,116	23-Sep-99
		GB_HTG3 AC010798	172575	AC010798	Homo sapiens chromosome 18 clone 470_B_24 map 18, *** SEQUENCING IN PROGRESS ***, 7 unordered pieces.	Homo sapiens	37,116	23-Sep-99
		GB_PL2:AF085231	3158	AF085231	Arabidopsis thaliana phytochelatin synthase 1 (AtPCS1) gene, complete cds	Arabidopsis thaliana	42,149	3-Jun-99
rxa01685	702	GB_HTG1 CEY48A6	296699	Z92854	Caenorhabditis elegans chromosome III clone Y48A6, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Caenorhabditis elegans	37,393	31-Jul-98
		GB_HTG1 CEY48A6	296699	Z92854	Caenorhabditis elegans chromosome III clone Y48A6, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Caenorhabditis elegans	37,393	31-Jul-98
		GB_HTG1:CEY48A6	296699	Z92854	Caenorhabditis elegans chromosome III clone Y48A6, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Caenorhabditis elegans	32,946	31-Jul-98

TABLE 4: ALIGNMENT RESULTS

rxa01686	564	GB_EST35:AV156415	240	AV156415	AV156415 Mus musculus head C57BL/6J 12-day embryo Mus musculus cDNA clone 3000002G04, mRNA sequence	Mus musculus	40,417	7-Jul-99
		GB_GSS15 AQ611518	597	AQ611518	HS_5084_B2_H01_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=660 Col=2 Row=P, genomic survey sequence.	Homo sapiens	41,848	15-Jun-99
		GB_BA1 PDIORAB	5467	Z48918	P diminuta iorA and iorB genes for isoquinoline 1-oxidoreductase	Brevundimonas diminuta	36,709	15-Aug-95
rxa01693	1545	GB_IN1:CEF46B6	36616	Z70780	Caenorhabditis elegans cosmid F46B6, complete sequence	Caenorhabditis elegans	36,856	04-DEC-1998
		GB_EST5:L44364	362	L44364	HUMEST1G5 Human thymus NSTH II Homo sapiens cDNA, mRNA sequence	Homo sapiens	38,136	17-Jan-96
		GB_PR2:AF009282	414	AF009282	Homo sapiens clone FBF3 Cri-du-chat region mRNA	Homo sapiens	46,809	17-Aug-97
rxa01694	1023	GB_BA1:CGA224946	2408	AJ224946	Corynebacterium glutamicum DNA for L-Malate quinone oxidoreductase.	Corynebacterium glutamicum	100,000	11-Aug-98
		GB_EST7 W22650	715	W22650	71B2 Human retina cDNA Tsp509I-cleaved sublibrary Homo sapiens cDNA not directional, mRNA sequence.	Homo sapiens	37,538	06-MAY-1996
		GB_PR4:AC005343	137213	AC005343	Homo sapiens Chromosome 12p13.3 BAC RPCI11-21K20 (Roswell Park Cancer Institute Human BAC Library) complete sequence	Homo sapiens	38,048	2-Apr-99
rxa01696	1302	GB_BA1.MSGB1529CS	36985	L78824	Mycobacterium leprae cosmid B1529 DNA sequence	Mycobacterium leprae	67,442	15-Jun-96
		GB_BA1.SC6A5	43632	AL049485	Streptomyces coelicolor cosmid 6A5	Streptomyces coelicolor	66,821	24-MAR-1999
		GB_BA1 MTV003	13246	AL008883	Mycobacterium tuberculosis H37Rv complete genome, segment 125/162	Mycobacterium tuberculosis	38,802	17-Jun-98
rxa01697	1080	GB_PL2:HNNHAHR	2559	L76588	Helianthus annuus homeodomain protein 1 mRNA, complete cds	Helianthus annuus	38,257	02-OCT-1997
		GB_PL2:HNNHAHR	2559	L76588	Helianthus annuus homeodomain protein 1 mRNA, complete cds	Helianthus annuus	37,196	02-OCT-1997
rxa01701	472	GB_BA2:AF069748	2103	AF069748	Pseudomonas chlororaphis polyurethanase esterase A (pueA) gene, complete cds	Pseudomonas chlororaphis	39,130	4-Apr-99
		GB_BA2 AF069748	2103	AF069748	Pseudomonas chlororaphis polyurethanase esterase A (pueA) gene, complete cds	Pseudomonas chlororaphis	40,271	4-Apr-99
rxa01703	1236	GB_BA1 CGFDA	3371	X17313	Corynebacterium glutamicum fda gene for fructose-bisphosphate aldolase (EC 4 1 2 13)	Corynebacterium glutamicum	100,000	12-Sep-93
		GB_EST18 AA728419	340	AA728419	33598 CD4-6 Arabidopsis thaliana cDNA clone K2C9RP, mRNA sequence	Arabidopsis thaliana	36,176	5-Jan-98
		GB_PL2:ATU90439	93639	U90439	Arabidopsis thaliana chromosome II BAC T06D20 genomic sequence, complete sequence	Arabidopsis thaliana	35,381	21-Jul-97
rxa01709	555	GB_OV.AF033670	2353	AF033670	Gallus gallus T-Box protein 4 (TBX4) mRNA, complete cds.	Gallus gallus	37,917	9-Jun-98
		GB_EST5:H85635	533	H85635	ys88c04 r1 Soares retina N2b5HR Homo sapiens cDNA clone IMAGE:221862 5', mRNA sequence	Homo sapiens	36,735	14-Nov-95
		GB_EST35 AI829867	427	AI829867	wj58c05 x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE 2407016 3', mRNA sequence.	Homo sapiens	40,299	26-Aug-99
rxa01711	1281	GB_GSS10 AQ217798	441	AQ217798	HS_2007_A1_A04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2007 Col=7 Row=A, genomic survey sequence.	Homo sapiens	38,292	19-Sep-98
		GB_PAT:E05055	2053	E05055	DNA encoding D-threonine aldolase(DTA)	Xanthomonas oryzae	36,475	29-Sep-97
		GB_PR3 HSJ570L12	143508	AL049589	Human DNA sequence from clone 570L12 on chromosome Xq13 1-21 1 Contains the PGK1 gene for phosphoglycerate kinase 1, the gene for a novel protein similar to TAF2G (TATA box binding protein (TBP)-associated factor, RNA polymerase II, G, 32kD) (TAFII31)), ESTs, STS, GSSs and a putative CpG island, complete sequence.	Homo sapiens	36,262	23-Nov-99
rxa01714								
rxa01715	819	GB_BA1 MTCY441	35187	Z80225	Mycobacterium tuberculosis H37Rv complete genome, segment 118/162.	Mycobacterium tuberculosis	36,216	18-Jun-98
		GB_BA1 SC1B5	14866	AL023517	Streptomyces coelicolor cosmid 1B5	Streptomyces coelicolor	56,807	11-MAY-1998
		GB_BA1 MSGB1912CS	38503	L01536	M leprae genomic dna sequence, cosmid b1912	Mycobacterium leprae	55,651	14-Jun-96
rxa01729	642	GB_BA2 CORCSLYS	2821	M89931	Corynebacterium glutamicum beta C-S lyase (aecD) and branched-chain amino acid uptake carrier (brnQ) genes, complete cds, and hypothetical protein Yhbw (yhbw) gene, partial cds.	Corynebacterium glutamicum	41,993	4-Jun-98

TABLE 4: ALIGNMENT RESULTS

		GB_HTG4:AC010037	166249	AC010037	Drosophila melanogaster chromosome 3L/66B6 clone RPCI98-6E4, *** SEQUENCING IN PROGRESS ***, 52 unordered pieces	Drosophila melanogaster	34,951	16-OCT-1999
		GB_HTG4:AC010037	166249	AC010037	Drosophila melanogaster chromosome 3L/66B6 clone RPCI98-6E4, *** SEQUENCING IN PROGRESS ***, 52 unordered pieces.	Drosophila melanogaster	34,951	16-OCT-1999
rxa01731	822	GB_GSS3 B83621	616	B83621	RPCI11-16H17.TPB RPCI-11 Homo sapiens genomic clone RPCI-11-16H17, genomic survey sequence	Homo sapiens	40,899	9-Apr-99
		GB_GSS3 B82563	586	B82563	RPCI11-16N17 TP RPCI-11 Homo sapiens genomic clone RPCI-11-16N17, genomic survey sequence.	Homo sapiens	40,235	9-Apr-99
		GB_HTG3 AC009074	45999	AC009074	Homo sapiens chromosome 16 clone RPCI-11_323C21, *** SEQUENCING IN PROGRESS ***, 27 unordered pieces	Homo sapiens	36,783	3-Aug-99
rxa01734	657	GB_GSS14 AQ545618	327	AQ545618	CITBI-E1-2636O13.TR CITBI-E1 Homo sapiens genomic clone 2636O13, genomic survey sequence.	Homo sapiens	38,154	28-MAY-1999
		GB_HTG2:AC006629	27659	AC006629	Caenorhabditis elegans clone F12E12, *** SEQUENCING IN PROGRESS***, 1 unordered pieces	Caenorhabditis elegans	35,658	23-Feb-99
		GB_HTG2 AC006629	27659	AC006629	Caenorhabditis elegans clone F12E12, *** SEQUENCING IN PROGRESS ***, 1 unordered pieces	Caenorhabditis elegans	35,714	23-Feb-99
rxa01738	837	GB_HTG1 CNS01DSB	222193	AL121768	Homo sapiens chromosome 14 clone R-976B16, *** SEQUENCING IN PROGRESS ***, in ordered pieces	Homo sapiens	36,978	05-OCT-1999
		GB_HTG1:CNS01DSB	222193	AL121768	Homo sapiens chromosome 14 clone R-976B16, *** SEQUENCING IN PROGRESS ***, in ordered pieces	Homo sapiens	36,978	05-OCT-1999
		GB_HTG5:AC011170	171788	AC011170	Homo sapiens clone 10_L_13, *** SEQUENCING IN PROGRESS ***, 14 unordered pieces.	Homo sapiens	35,259	5-Nov-99
rxa01741	921	GB_IN1:CEK04G11	34190	Z78544	Caenorhabditis elegans cosmid K04G11, complete sequence	Caenorhabditis elegans	35,055	6-Sep-99
		GB_HTG2 AC005995	170023	AC005995	Homo sapiens clone DJ0042M02, *** SEQUENCING IN PROGRESS ***, 13 unordered pieces	Homo sapiens	33,624	23-Apr-99
		GB_HTG2 AC005995	170023	AC005995	Homo sapiens clone DJ0042M02, *** SEQUENCING IN PROGRESS ***, 13 unordered pieces	Homo sapiens	33,624	23-Apr-99
rxa01742	627	GB_EST30 AI658116	497	AI658116	fc22e07 y1 Zebrafish WashU MPIMG EST Danio rerio cDNA 5' similar to TR Q15883 Q15883 X104 ,, mRNA sequence	Danio rerio	35,604	06-MAY-1999
		GB_HTG1 CEY60A9	275370	AL022281	Caenorhabditis elegans chromosome X clone Y60A9, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Caenorhabditis elegans	35,610	2-Sep-99
		GB_HTG1 CEY60A9	275370	AL022281	Caenorhabditis elegans chromosome X clone Y60A9, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Caenorhabditis elegans	35,610	2-Sep-99
rxa01748	903	GB_GSS13 AQ447364	439	AQ447364	mgxb0006N01r CUGI Rice Blast BAC Library Magnaporthe grisea genomic clone mgxb0006N01r, genomic survey sequence	Magnaporthe grisea	34,889	8-Apr-99
		GB_PR2 HSJ247G22	120487	AL096866	Human DNA sequence from clone RP1-247G22 on chromosome 6p12 2-21 2, complete sequence	Homo sapiens	39,310	22-Nov-99
		GB_GSS5.AQ811603	375	AQ811603	HS_5460_B1_C09_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=1036 Col=17 Row=F, genomic survey sequence	Homo sapiens	38,133	25-Aug-99
rxa01749	1740	GB_HTG5 AC009544	211057	AC009544	Homo sapiens chromosome 11 clone RP11-85D24 map 11, WORKING DRAFT SEQUENCE, 14 unordered pieces	Homo sapiens	37,433	19-Nov-99
		GB_HTG5:AC009544	211057	AC009544	Homo sapiens chromosome 11 clone RP11-85D24 map 11, WORKING DRAFT SEQUENCE, 14 unordered pieces	Homo sapiens	37,069	19-Nov-99
rxa01750								
rxa01752	1584	GB_PR1 HUMPROFILX	17630	M96943	Human profilaggrin gene exons 1-3, 5' end	Homo sapiens	36,352	27-Apr-93
		GB_PL2:AF049174	535	AF049174	Tolypocladium inflatum NRRL 28024 28S ribosomal RNA gene, partial sequence	Tolypocladium inflatum	40,187	03-MAR-1999
		GB_BA1.MLCL458	43839	AL049478	Mycobacterium leprae cosmid L458	Mycobacterium leprae	40,322	27-Aug-99
rxa01753	1662	GB_PR1 HUMPROFILX	17630	M96943	Human profilaggrin gene exons 1-3, 5' end	Homo sapiens	36,794	27-Apr-93
		GB_PL1:YSCFBPA	2202	J03207	S cerevisiae fructose-1,6-bisphosphatase (FBP) gene, complete cds	Saccharomyces cerevisiae	37,762	27-Apr-93

TABLE 4: ALIGNMENT RESULTS

		GB_PL2:YSCL8039	31806	U19103	Saccharomyces cerevisiae chromosome XII cosmid 8039.	Saccharomyces cerevisiae	37,685	22-Aug-97
rxa01754								
rxa01760	405	GB_IN1:CELF43C9	34037	U40427	Caenorhabditis elegans cosmid F43C9	Caenorhabditis elegans	40,945	16-Nov-95
		GB_IN1.CELF43C9	34037	U40427	Caenorhabditis elegans cosmid F43C9.	Caenorhabditis elegans	35,484	16-Nov-95
		GB_RO.MUSOP5F	3405	D14816	Mouse osteopontin gene, 5' flanking region	Mus musculus	35,264	4-Feb-99
rxa01761	4587	GB_PR4:AC004600	133863	AC004600	Homo sapiens Chromosome 15q11-q13 PAC clone pDJ373b1 containing Angelman Syndrome gene (UBE3A), complete sequence	Homo sapiens	37,037	11-MAR-1999
		GB_PR3 AC004259	118684	AC004259	Human Chromosome 15q11-q13 PAC clone pDJ14i12 containing Angelman Syndrome gene (UBE3A), complete sequence	Homo sapiens	37,037	3-Jun-98
		GB_PR4 AC004600	133863	AC004600	Homo sapiens Chromosome 15q11-q13 PAC clone pDJ373b1 containing Angelman Syndrome gene (UBE3A), complete sequence	Homo sapiens	35,995	11-MAR-1999
rxa01765	1065	GB_EST31 AI694883	370	AI694883	we52h02 x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE 2344755 3', mRNA sequence	Homo sapiens	39,566	3-Jun-99
		GB_EST6 W08057	341	W08057	mb37e05 r1 Soares mouse p3NMF19.5 Mus musculus cDNA clone IMAGE 331616 5' similar to gb Z23090 HEAT SHOCK 27 KD PROTEIN (HUMAN), gb L11609 Mus musculus heat shock protein 25 (MOUSE),, mRNA sequence.	Mus musculus	37,353	5-Sep-96
		GB_IN1:CELC39D10	40897	U39678	Caenorhabditis elegans cosmid C39D10	Caenorhabditis elegans	39,590	2-Nov-95
rxa01767	588	GB_IN1:CEF16H9	21721	Z50005	Caenorhabditis elegans cosmid F16H9, complete sequence	Caenorhabditis elegans	36,667	2-Sep-99
		GB_IN1 CECC4	32063	Z81490	Caenorhabditis elegans cosmid CC4, complete sequence	Caenorhabditis elegans	35,094	2-Sep-99
		GB_HTG1:CEY26D4	156152	AL022595	Caenorhabditis elegans chromosome I clone Y26D4, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Caenorhabditis elegans	33,276	7-Sep-99
rxa01768								
rxa01769	564	GB_HTG4:AC010034	130818	AC010034	Drosophila melanogaster clone RPCI98-4O3, *** SEQUENCING IN PROGRESS ***, 63 unordered pieces	Drosophila melanogaster	35,740	16-OCT-1999
		GB_HTG4 AC010034	130818	AC010034	Drosophila melanogaster clone RPCI98-4O3, *** SEQUENCING IN PROGRESS ***, 63 unordered pieces.	Drosophila melanogaster	35,740	16-OCT-1999
		GB_EST1 D36647	360	D36647	CELK035EZF Yuji Kohara unpublished cDNA Caenorhabditis elegans cDNA clone yk35e12 5', mRNA sequence	Caenorhabditis elegans	37,870	8-Aug-94
rxa01770	3888	GB_IN1.SUSENDO16C	4692	L34680	Strongylocentrotus purpuratus calcium-binding protein (endo16) mRNA, complete cds	Strongylocentrotus purpuratus	39,337	21-Jul-94
		GB_EST31:AF121176	535	AF121176	AF121176 Homo sapiens liver (Chang L-Y) Homo sapiens cDNA clone PFTTA2-2, mRNA sequence	Homo sapiens	39,626	24-MAY-1999
		GB_PR1 AB011149	5134	AB011149	Homo sapiens mRNA for KIAA0577 protein, complete cds	Homo sapiens	38,279	10-Apr-98
rxa01771	825	GB_BA1 CGPROPGEN	2936	Y12537	C glutamicum proP gene.	Corynebacterium glutamicum	100,000	17-Nov-98
		GB_EST33 AI778471	545	AI778471	EST259350 tomato susceptible, Cornell Lycopersicon esculentum cDNA clone cLES5M16, mRNA sequence	Lycopersicon esculentum	41,187	29-Jun-99
		GB_IN1.CET11F9	37714	Z74042	Caenorhabditis elegans cosmid T11F9, complete sequence	Caenorhabditis elegans	38,077	23-Nov-98
rxa01773	600	GB_HTG2 U82212	46387	U82212	Homo sapiens chromosome 10 clone LA10NC01_23_C_3 map 10q26 1-10q26 2, *** SEQUENCING IN PROGRESS ***, 1 ordered pieces.	Homo sapiens	42,142	09-DEC-1998
		GB_HTG2 U82212	46387	U82212	Homo sapiens chromosome 10 clone LA10NC01_23_C_3 map 10q26 1-10q26 2, *** SEQUENCING IN PROGRESS ***, 1 ordered pieces	Homo sapiens	42,142	09-DEC-1998
		GB_HTG2:U82212	46387	U82212	Homo sapiens chromosome 10 clone LA10NC01_23_C_3 map 10q26 1-10q26 2, *** SEQUENCING IN PROGRESS ***, 1 ordered pieces.	Homo sapiens	37,748	09-DEC-1998
rxa01774	849	GB_HTG1 HSA557H15	228174	AL078590	Homo sapiens chromosome 6 clone RP11-557H15, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Homo sapiens	38,054	23-Nov-99

TABLE 4: ALIGNMENT RESULTS

		GB_HTG1:HSA557H15	228174	AL078590	Homo sapiens chromosome 6 clone RP11-557H15, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Homo sapiens	38,054	23-Nov-99
		GB_PL2.YSCH9998	35600	U00030	Saccharomyces cerevisiae chromosome VIII cosmid 9998	Saccharomyces cerevisiae	39,110	2-Sep-97
rxa01775	687	GB_PR3 HS37J18	131427	Z98747	Human DNA sequence from clone 37J18 on chromosome 1p36 2-36 3 Contains a putative novel gene, ESTs and GSSs, complete sequence	Homo sapiens	35,036	23-Nov-99
		GB_HTG2 AC007475	185087	AC007475	Drosophila melanogaster chromosome 2 clone BACR04E21 (D592) RPCI-98 04 E 21 map 49A-49B strain y, cn bw sp, *** SEQUENCING IN PROGRESS ***, 36 unordered pieces	Drosophila melanogaster	37,333	2-Aug-99
		GB_HTG2 AC007475	185087	AC007475	Drosophila melanogaster chromosome 2 clone BACR04E21 (D592) RPCI-98 04.E 21 map 49A-49B strain y, cn bw sp, *** SEQUENCING IN PROGRESS***, 36 unordered pieces	Drosophila melanogaster	37,333	2-Aug-99
rxa01776	1575	GB_GSS10 AQ174954	416	AQ174954	HS_3211_B2_C03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3211 Col=6 Row=F, genomic survey sequence.	Homo sapiens	43,171	17-OCT-1998
		GB_PR1 HSFGF6	1032	X57075	H sapiens FGF6 gene.	Homo sapiens	41,196	15-Feb-95
		GB_PR2:HSAC000055	93578	AC000055	Human PAC clone DJ073F11 from Xq23, complete sequence	Homo sapiens	35,080	14-Nov-96
rxa01777	582	GB_BA2.AF076997	15398	AF076997	Comamonas testosteroni PtL5 cryptic plasmid pPT1, complete sequence	Comamonas testosteroni	37,805	30-Nov-99
		GB_BA2:AF076997	15398	AF076997	Comamonas testosteroni PtL5 cryptic plasmid pPT1, complete sequence	Comamonas testosteroni	35,529	30-Nov-99
rxa01778	1260	GB_PR3:AC002981	153568	AC002981	Homo sapiens Xp22 BAC GS279A12 (Genome Systems) complete sequence	Homo sapiens	37,305	22-Jan-98
		GB_EST29 AI587176	384	AI587176	tr54c10 x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2222130 3', mRNA sequence	Homo sapiens	37,240	14-MAY-1999
		GB_PR1:HSCP450	1346	X65962	H sapiens mRNA for cytochrome P-450	Homo sapiens	38,908	29-MAY-1992
rxa01779	1542	GB_EST19 AA202518	661	AA202518	LD02757 5prime LD Drosophila melanogaster embryo BlueScript Drosophila melanogaster cDNA clone LD02757 5prime, mRNA sequence.	Drosophila melanogaster	40,212	27-Nov-98
		GB_EST34 AI805834	453	AI805834	te52b03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE 2090285 3' similar to contains Alu repetitive element,, mRNA sequence	Homo sapiens	38,000	7-Jul-99
		GB_EST30.AI648920	754	AI648920	uk32h03 x1 Sugano mouse kidney mkia Mus musculus cDNA clone IMAGE 1970741 3' similar to WP:Y76A2B 5 CE19277 ;, mRNA sequence	Mus musculus	36,967	30-Apr-99
rxa01780	498	GB_GSS8 AQ038759	670	AQ038759	CIT-HSP-2325O13.TV CIT-HSP Homo sapiens genomic clone 2325O13, genomic survey sequence.	Homo sapiens	32,645	11-Jul-98
		GB_GSS8 AQ038759	670	AQ038759	CIT-HSP-2325O13.TV CIT-HSP Homo sapiens genomic clone 2325O13, genomic survey sequence.	Homo sapiens	39,474	11-Jul-98
rxa01781	384	GB_IN1.CELF52G3	42696	AF026212	Caenorhabditis elegans cosmid F52G3	Caenorhabditis elegans	39,314	25-Sep-97
		GB_GSS14 AQ579313	877	AQ579313	nbxb0084O07r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0084O07r, genomic survey sequence.	Oryza sativa	36,053	2-Jun-99
		GB_VI HAV19AE3	3441	X95259	Human adenovirus type 19a early region 3 genes.	Human adenovirus type 19a	38,624	9-Jul-97
rxa01782	519	GB_IN1.DMSED5	930	X78219	D melanogaster (Barton) SED5 mRNA	Drosophila melanogaster	38,372	21-Apr-95
		GB_IN2.L49408	83527	L49408	Drosophila melanogaster DNA sequence (P1 DS02740 (D27)), complete sequence	Drosophila melanogaster	35,992	17-Jul-98
		GB_STS:G46002	398	G46002	Z556_1 Zebrafish AB Danio rerio STS genomic clone Z556 5', sequence tagged site	Danio rerio	33,920	23-MAR-1999
rxa01783	360	GB_VI CITV18420	19259	Y18420	Citrus tristeza virus complete genome, isolate T385	Citrus tristeza virus	41,457	6-Apr-99
		GB_IN1 DMSED5	930	X78219	D melanogaster (Barton) SED5 mRNA	Drosophila melanogaster	45,802	21-Apr-95
		GB_VI.CTY18368	2759	Y18368	Citrus tristeza virus defective RNA, strain T411	Citrus tristeza virus	41,457	6-Apr-99
rxa01785	699	GB_BA2 AF121000	19751	AF121000	Corynebacterium glutamicum strain 22243 R-plasmid pAG1, complete sequence.	Corynebacterium glutamicum	40,529	14-Apr-99
		GB_PR2 HS1014D13	71263	AL022311	Human DNA sequence from clone 1014D13 on chromosome 22q13 1-13 2 Contains ESTs, STSs, and a CpG island, complete sequence	Homo sapiens	35,362	23-Nov-99
		GB_BA2 AF121000	19751	AF121000	Corynebacterium glutamicum strain 22243 R-plasmid pAG1, complete sequence	Corynebacterium glutamicum	38,012	14-Apr-99
rxa01787	816	GB_RO:RATSIALYLA	1128	L13445	Rat sialyltransferase gene family related mRNA, complete cds	Rattus norvegicus	35,012	26-Jul-93
		GB_PR3 HSN75H12	46144	Z84496	Human DNA sequence from cosmid N75H12 on chromosome 22q12-qter	Homo sapiens	37,738	23-Nov-99

TABLE 4: ALIGNMENT RESULTS

		GB_GSS13:AQ496514	532	AQ496514	HS_5118_B2_F05_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=694 Col=10 Row=L, genomic survey sequence	Homo sapiens	39,238	28-Apr-99
rxa01788								
rxa01789	765	GB_BA1:MTV029	3279	AL021427	Mycobacterium tuberculosis H37Rv complete genome, segment 1/162	Mycobacterium tuberculosis	39,229	17-Jun-98
		GB_BA1 MTORIREP	8400	X92504	M tuberculosis origin of replication and genes rnpA, rpmH, dnaA, dnaN, recF	Mycobacterium tuberculosis	36,328	26-Aug-97
		GB_GSS4 AQ729452	763	AQ729452	HS_5474_A1_G07_T7AHS_5474_A1 RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=1050 Col=13 Row=M, genomic survey sequence	Homo sapiens	39,451	15-Jul-99
rxa01790	183	GB_EST37 AI935426	436	AI935426	wo84d02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE.2462019 3' similar to TR.O00193 O00193 SMALL ACIDIC PROTEIN. ;, mRNA sequence	Homo sapiens	39,877	2-Sep-99
		GB_GSS11 AQ265301	621	AQ265301	CITBI-E1-2509K16.TF CITBI-E1 Homo sapiens genomic clone 2509K16, genomic survey sequence.	Homo sapiens	45,856	27-OCT-1998
		GB_HTG2.AC007596	199300	AC007596	Homo sapiens chromosome 16 clone 116B6, *** SEQUENCING IN PROGRESS ***, 42 unordered pieces	Homo sapiens	37,572	20-MAY-1999
rxa01791	486	GB_PL2:ATAC004521	104797	AC004521	Arabidopsis thaliana chromosome II BAC F4I1 genomic sequence, complete sequence	Arabidopsis thaliana	43,167	12-MAY-1998
		GB_GSS13 AQ436125	508	AQ436125	HS_5049_B2_G12_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=625 Col=24 Row=N, genomic survey sequence	Homo sapiens	32,762	31-MAR-1999
		GB_GSS12 AQ342410	674	AQ342410	RPCI11-121E5.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-121E5, genomic survey sequence	Homo sapiens	37,269	06-MAY-1999
rxa01792	396	GB_STS:KLAJ9905	178	AJ229905	Kluyveromyces lactis DNA fragment for sequence tagged site, clone okam5e06r	Kluyveromyces lactis	42,697	20-Nov-98
		GB_STS.KLAJ9905	178	AJ229905	Kluyveromyces lactis DNA fragment for sequence tagged site, clone okam5e06r	Kluyveromyces lactis	42,697	20-Nov-98
		GB_GSS15 AQ612295	472	AQ612295	HS_5121_A2_D09_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=697 Col=18 Row=G, genomic survey sequence	Homo sapiens	40,885	15-Jun-99
rxa01793	357	GB_GSS3 B82515	613	B82515	RPCI11-16J10.TV RPCI-11 Homo sapiens genomic clone RPCI-11-16J10, genomic survey sequence	Homo sapiens	40,164	9-Apr-99
		GB_PR2.CNS0000B	196287	AL049829	Human chromosome 14 DNA sequence *** IN PROGRESS *** BAC R-124D2 of RPCI-11 library from chromosome 14 of Homo sapiens (Human), complete sequence	Homo sapiens	33,621	27-OCT-1999
		GB_OV AF001393	4329	AF001393	Oryzias latipes Medaka OG-12 (MOG-12) mRNA, complete cds	Oryzias latipes	35,511	30-Sep-99
rxa01794	357	GB_GSS15.AQ644157	665	AQ644157	RPCI93-DpnII-29O12.TV RPCI93-DpnII Trypanosoma brucei genomic clone RPCI93-DpnII-29O12, genomic survey sequence	Trypanosoma brucei	39,894	8-Jul-99
		GB_GSS15:AQ657704	665	AQ657704	Sheared DNA-24C24.TR Sheared DNA Trypanosoma brucei genomic clone Sheared DNA-24C24, genomic survey sequence	Trypanosoma brucei	37,110	23-Jun-99
		GB_OV.GGU25125	6418	U25125	Gallus gallus preprogastrin gene, complete cds	Gallus gallus	40,584	06-MAY-1995
rxa01796	897	GB_PR3 HS404G5	119737	AL035695	Human DNA sequence from clone 404G5 on chromosome 6q24 1-25 2. Contains part of a human estrogen receptor gene, STSs and GSSs, complete sequence	Homo sapiens	34,793	23-Nov-99
		GB_PR1:HSPTP1CHG	8545	X82818	H sapiens PTP1C/HCP gene	Homo sapiens	35,531	26-Jun-97
		GB_PR3.HS404G5	119737	AL035695	Human DNA sequence from clone 404G5 on chromosome 6q24 1-25 2 Contains part of a human estrogen receptor gene, STSs and GSSs, complete sequence	Homo sapiens	37,058	23-Nov-99
rxa01799	1317	GB_HTG3 AC010869	38000	AC010869	Leishmania major chromosome 35 clone L7195 strain Friedlin, *** SEQUENCING IN PROGRESS ***, 4 unordered pieces	Leishmania major	40,522	02-OCT-1999
		GB_HTG3 AC010869	38000	AC010869	Leishmania major chromosome 35 clone L7195 strain Friedlin, *** SEQUENCING IN PROGRESS ***, 4 unordered pieces	Leishmania major	40,522	02-OCT-1999
		GB_OM:SSU12574	2190	U12574	Sus scrofa myogenic regulatory factor MyoD (myoD) gene, complete cds	Sus scrofa	37,068	10-Feb-96
rxa01800	843	GB_PH C2PVCG	22172	L48605	Bacteriophage c2 complete genome	Lactococcus bacteriophage c2	36,747	14-MAR-1996
		GB_EST38 AW066009	641	AW066009	687004F08 y1 687 - Early embryo from Delaware Zea mays cDNA, mRNA sequence	Zea mays	40,000	12-OCT-1999
		GB_PH.C2PVCG	22172	L48605	Bacteriophage c2 complete genome	Lactococcus bacteriophage c2	36,867	14-MAR-1996

TABLE 4: ALIGNMENT RESULTS

rxa01803	1083	GB_BA2:SCJ1	36925	AL109962	Streptomyces coelicolor cosmid J1.	Streptomyces coelicolor A3(2)	54,267	24-Sep-99
		GB_BA1.PAU12891	4062	U12891	Pseudomonas aeruginosa PAO substrain OT684 pyoverdine gene transcriptional regulator PvdS (pvdS) gene, complete cds	Pseudomonas aeruginosa	37,841	03-OCT-1996
		GB_HTG6:AC010203	230460	AC010203	Homo sapiens clone RP11-175P13, *** SEQUENCING IN PROGRESS ***, 48 unordered pieces	Homo sapiens	35,185	03-DEC-1999
rxa01804	444	GB_EST24 AI189912	784	AI189912	qd33e07 x1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:1725540 3' similar to gb:Z23064_cds1 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN G (HUMAN),, mRNA sequence	Homo sapiens	40,000	28-OCT-1998
		GB_EST24 AI189912	784	AI189912	qd33e07 x1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE 1725540 3' similar to gb Z23064_cds1 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN G (HUMAN);, mRNA sequence	Homo sapiens	35,294	28-OCT-1998
rxa01805	453	GB_PR2 HSU73628	32289	U73628	Human chromosome 11 101h11 cosmid, complete sequence	Homo sapiens	36,099	19-Jun-97
		GB_PR2:HSU73628	32289	U73628	Human chromosome 11 101h11 cosmid, complete sequence.	Homo sapiens	35,227	19-Jun-97
rxa01806	603	GB_IN1:CELK02E7	36535	AF025465	Caenorhabditis elegans cosmid K02E7	Caenorhabditis elegans	37,479	23-Sep-97
		GB_HTG3 AC011217	157261	AC011217	Homo sapiens clone 7_J_14, LOW-PASS SEQUENCE SAMPLING.	Homo sapiens	33,333	03-OCT-1999
		GB_HTG3:AC011217	157261	AC011217	Homo sapiens clone 7_J_14, LOW-PASS SEQUENCE SAMPLING.	Homo sapiens	33,333	03-OCT-1999
rxa01809	1299	GB_HTG3:AC010759	155875	AC010759	Homo sapiens clone 1_K_15, *** SEQUENCING IN PROGRESS ***, 15 unordered pieces	Homo sapiens	37,920	22-Sep-99
		GB_HTG3 AC010759	155875	AC010759	Homo sapiens clone 1_K_15, *** SEQUENCING IN PROGRESS ***, 15 unordered pieces.	Homo sapiens	37,920	22-Sep-99
		GB_HTG2 AC006235	190842	AC006235	Homo sapiens clone hRPK 520_J_4, *** SEQUENCING IN PROGRESS ***, 5 unordered pieces	Homo sapiens	36,019	17-Jul-99
rxa01813	789	GB_PR4.AC004047	134649	AC004047	Homo sapiens chromosome 4 clone B150J4 map 4q25, complete sequence.	Homo sapiens	36,205	01-DEC-1998
		GB_HTG2 HS1012F16	74539	AL080274	Homo sapiens chromosome 20 clone RP5-1012F16, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	35,032	03-DEC-1999
		GB_HTG2.HS1012F16	74539	AL080274	Homo sapiens chromosome 20 clone RP5-1012F16, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Homo sapiens	35,032	03-DEC-1999
rxa01815	915	GB_PR3:AC005740	186780	AC005740	Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence	Homo sapiens	37,315	01-OCT-1998
		GB_HTG3 AC008328	114617	AC008328	Drosophila melanogaster chromosome 2 clone BACR09A04 (D860) RPCI-98 09 A 4 map 28B-28C strain y, cn bw sp, *** SEQUENCING IN PROGRESS ***, 74 unordered pieces	Drosophila melanogaster	30,516	6-Aug-99
		GB_HTG3 AC008328	114617	AC008328	Drosophila melanogaster chromosome 2 clone BACR09A04 (D860) RPCI-98 09 A 4 map 28B-28C strain y, cn bw sp, *** SEQUENCING IN PROGRESS ***, 74 unordered pieces	Drosophila melanogaster	30,516	6-Aug-99
rxa01816	855	GB_PR3.AC003101	208396	AC003101	Homo sapiens chromosome 17, clone HRPC41C23, complete sequence	Homo sapiens	34,272	5-Jun-98
		GB_EST23:AI144656	492	AI144656	UI-R-BT0-pl-f-04-0-UI.s1 UI-R-BT0 Rattus norvegicus cDNA clone UI-R-BT0-pl-f-04-0-UI 3', mRNA sequence	Rattus norvegicus	37,526	5-Jul-99
		GB_GSS11:AQ341706	506	AQ341706	RPCI11-120J20 TJ RPCI-11 Homo sapiens genomic clone RPCI-11-120J20, genomic survey sequence.	Homo sapiens	40,789	06-MAY-1999
rxa01817	756	GB_BA2.AF030176	7000	AF030176	Rhodococcus opacus putative transposase gene, partial cds, and putative FAD synthetase, putative short-chain dehydrogenase/reductase, maleylacetate reductase (macA), and putative transcription factor genes, complete cds	Rhodococcus opacus	42,577	5-Aug-98
		GB_EST19:AA263350	423	AA263350	LD06495 5prime LD Drosophila melanogaster embryo BlueScript Drosophila melanogaster cDNA clone LD06495 5prime, mRNA sequence	Drosophila melanogaster	38,955	27-Nov-98
		GB_EST19.AA202194	368	AA202194	LD02304.5prime LD Drosophila melanogaster embryo BlueScript Drosophila melanogaster cDNA clone LD02304 5prime, mRNA sequence	Drosophila melanogaster	39,891	27-Nov-98
rxa01820	1497	GB_BA2:AF030176	7000	AF030176	Rhodococcus opacus putative transposase gene, partial cds, and putative FAD synthetase, putative short-chain dehydrogenase/reductase, maleylacetate reductase (macA), and putative transcription factor genes, complete cds	Rhodococcus opacus	41,799	5-Aug-98
		GB_EST32 AI728582	666	AI728582	BNLGHi11124 Six-day Cotton fiber Gossypium hirsutum cDNA 5' similar to (U64918) ATGP1 [Arabidopsis thaliana], mRNA sequence.	Gossypium hirsutum	37,915	11-Jun-99

TABLE 4: ALIGNMENT RESULTS

		GB_BA2:AF030176	7000	AF030176	Rhodococcus opacus putative transposase gene, partial cds; and putative FAD synthetase, putative short-chain dehydrogenase/reductase, maleylacetate reductase (macA), and putative transcription factor genes, complete cds.	Rhodococcus opacus	37,127	5-Aug-98
rxa01825	393	GB_HTG1 HSJCF13	293368	AJ239320	Homo sapiens chromosome X clone cosmid 244B12 map Xq13, *** SEQUENCING IN PROGRESS ***, in ordered pieces	Homo sapiens	34,748	28-Sep-99
		GB_HTG1.HSJCF13	293368	AJ239320	Homo sapiens chromosome X clone cosmid 244B12 map Xq13, *** SEQUENCING IN PROGRESS ***, in ordered pieces.	Homo sapiens	34,748	28-Sep-99
		GB_HTG1 AP000568	136627	AP000568	Homo sapiens chromosome 21 clone B753B2 map 21q21 2, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Homo sapiens	34,884	07-OCT-1999
rxa01831	585	GB_IN2:AF047757	408	AF047757	Trichogramma australicum internal transcribed spacer 2, complete sequence.	Trichogramma australicum	38,390	10-Jul-98
		GB_EST18 AA687516	513	AA687516	ns58h11 r1 NCI_CGAP_Pr22 Homo sapiens cDNA clone IMAGE 1187877 5' similar to gb X15341 CYTOCHROME C OXIDASE POLYPEPTIDE VIA-LIVER (HUMAN),, mRNA sequence	Homo sapiens	35,057	11-DEC-1997
		GB_EST18:AA687516	513	AA687516	ns58h11.r1 NCI_CGAP_Pr22 Homo sapiens cDNA clone IMAGE:1187877 5' similar to gb X15341 CYTOCHROME C OXIDASE POLYPEPTIDE VIA-LIVER (HUMAN),, mRNA sequence.	Homo sapiens	37,624	11-DEC-1997
rxa01834	825	GB_PL2.T8F5	87192	AC004512	Arabidopsis thaliana chromosome 1 BAC T8F5 sequence, complete sequence	Arabidopsis thaliana	38,101	22-Jul-98
		GB_PR4:AC007677	166949	AC007677	Homo sapiens clone NH0086N01, complete sequence	Homo sapiens	35,888	28-Sep-99
		GB_PR4.AC007677	166949	AC007677	Homo sapiens clone NH0086N01, complete sequence	Homo sapiens	36,906	28-Sep-99
rxa01842	1041	GB_HTG3:AC009183	145694	AC009183	Drosophila melanogaster chromosome 3 clone BACR39F04 (D839) RPCI-98 39 F.4 map 85F-85F strain y, cn bw sp, *** SEQUENCING IN PROGRESS***, 139 unordered pieces	Drosophila melanogaster	40,430	16-Sep-99
		GB_HTG3 AC009183	145694	AC009183	Drosophila melanogaster chromosome 3 clone BACR39F04 (D839) RPCI-98 39 F.4 map 85F-85F strain y, cn bw sp, *** SEQUENCING IN PROGRESS ***, 139 unordered pieces	Drosophila melanogaster	40,430	16-Sep-99
		GB_HTG5.AC008338	136685	AC008338	Drosophila melanogaster chromosome X clone BACR30J04 (D908) RPCI-98 30 J 4 map 19C-19E strain y, cn bw sp, *** SEQUENCING IN PROGRESS***, 93 unordered pieces	Drosophila melanogaster	40,527	15-Nov-99
rxa01844	303	GB_HTG2.AC007597	163880	AC007597	Homo sapiens chromosome 16 clone RPCI-11_137H10, *** SEQUENCING IN PROGRESS ***, 3 ordered pieces.	Homo sapiens	34,564	20-Jul-99
		GB_HTG2.AC007597	163880	AC007597	Homo sapiens chromosome 16 clone RPCI-11_137H10, *** SEQUENCING IN PROGRESS ***, 3 ordered pieces.	Homo sapiens	34,564	20-Jul-99
		GB_HTG3.AC009998	163590	AC009998	Homo sapiens chromosome 15 clone BAC 573G7 map 15q24, LOW-PASS SEQUENCE SAMPLING	Homo sapiens	40,816	10-Sep-99
rxa01845	531	GB_OV AF012348	4921	AF012348	Gallus gallus smooth muscle gamma actin (gamma actin) gene, complete cds	Gallus gallus	37,333	17-MAR-1998
		GB_BA1.D85417	7984	D85417	Propionibacterium freudenreichii hemY, hemH, hemB, hemX, hemR and hemL genes, complete cds	Propionibacterium freudenreichii	45,243	6-Feb-99
		GB_BA1:D85417	7984	D85417	Propionibacterium freudenreichii hemY, hemH, hemB, hemX, hemR and hemL genes, complete cds	Propionibacterium freudenreichii	40,232	6-Feb-99
rxa01846	382	GB_HTG1 HSJ323A24	278948	AL121750	Homo sapiens chromosome 4 clone RP3-323A24, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Homo sapiens	34,840	23-Nov-99
		GB_HTG1 HSJ323A24	278948	AL121750	Homo sapiens chromosome 4 clone RP3-323A24, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Homo sapiens	34,840	23-Nov-99
		GB_PR2:HS181C9	92472	Z98743	Human DNA sequence from clone 181C9 on chromosome 22q13 2-13 33.Contains a PHAPI2 Leucine Rich Acidic Nuclear Protein pseudogene, part of a putative novel gene, ESTs, STSs and GSSs, complete sequence	Homo sapiens	42,480	23-Nov-99
rxa01847	858	GB_PR3 AC004893	103738	AC004893	Homo sapiens PAC clone DJ0808A01 from 7q21 1-q31 1, complete sequence	Homo sapiens	38,321	03-OCT-1998
		GB_HTG4 AC010182_3	110000	AC010182	Homo sapiens chromosome 12q seeders clone RPCI11-185N2, *** SEQUENCING IN PROGRESS ***, 172 unordered pieces	Homo sapiens	36,998	15-Sep-99
		GB_HTG4 AC010182_3	110000	AC010182	Homo sapiens chromosome 12q seeders clone RPCI11-185N2, *** SEQUENCING IN PROGRESS ***, 172 unordered pieces.	Homo sapiens	36,998	15-Sep-99
rxa01856	669	GB_GSS15:AQ612487	433	AQ612487	HS_5122_A1_B07_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=698 Col=13 Row=C, genomic survey sequence	Homo sapiens	39,723	15-Jun-99

TABLE 4: ALIGNMENT RESULTS

		GB_PR4:AC005876	89817	AC005876	citb_188_i_5, complete sequence.	Homo sapiens	39,567	5-Nov-99
		GB_PR4 AC005876	89817	AC005876	citb_188_i_5, complete sequence	Homo sapiens	36,677	5-Nov-99
rxa01857	774	GB_PR3:HS742C19	122748	AL031846	Human DNA sequence from clone RP4-742C19 on chromosome 22, complete sequence.	Homo sapiens	33,506	29-Nov-99
		GB_PR2:HSJ1100I6	161525	AL110503	Human DNA sequence from clone RP5-1100I6 on chromosome 20 Contains a novel mRNA, GSSs and a CpG Island, complete sequence	Homo sapiens	37,450	22-Nov-99
		GB_HTG6 AC009893	186769	AC009893	Homo sapiens chromosome 8 clone RP11-4P3, *** SEQUENCING IN PROGRESS ***, 5 unordered pieces	Homo sapiens	37,368	23-Nov-99
rxa01858								
rxa01870	798	GB_RO AC004155	128026	AC004155	Mus musculus DNA from BAC 10818 containing the Ercc-4 gene, complete sequence.	Mus musculus	37,387	19-Feb-98
		GB_RO:AC004155	128026	AC004155	Mus musculus DNA from BAC 10818 containing the Ercc-4 gene, complete sequence	Mus musculus	37,707	19-Feb-98
		GB_BA2 AF144563	5971	AF144563	Thermobifida fusca beta-1,4-exocellulase E6 precursor (celF) gene, complete cds, and unknown genes.	Thermobifida fusca	38,619	21-Jun-99
rxa01871	1086	GB_BA2 AF079304	3350	AF079304	Eikenella corrodens type IV pilin (pilA1), type IV pilin (pilA2), putative fimbrial protein (pilB), and putative hemagglutinin protein (hagA) genes, complete cds	Eikenella corrodens	40,465	15-Jul-99
		GB_BA1:ECECPHAG	3589	Z12609	E corrodens ecpA and ecpB genes encoding type 4 N-methylphenylalanine pilin and hag1 gene for hemagglutinin protein.	Eikenella corrodens	40,517	5-Aug-92
		GB_BA2 AE001707	19518	AE001707	Thermotoga maritima section 19 of 136 of the complete genome	Thermotoga maritima	38,124	2-Jun-99
rxa01874	448	GB_EST6 N51407	505	N51407	yz17a08.s1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE 283286 3', mRNA sequence	Homo sapiens	35,735	14-Feb-96
		GB_EST29 AI619782	374	AI619782	ty53b03 x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE 2282765 3', mRNA sequence.	Homo sapiens	38,966	21-Apr-99
		GB_EST36.AI885047	466	AI885047	wl89a01 x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2432040 3', mRNA sequence	Homo sapiens	37,419	1-Sep-99
rxa01875	969	GB_EST13:AA356276	291	AA356276	EST64843 Jurkat T-cells VI Homo sapiens cDNA 5' end, mRNA sequence.	Homo sapiens	41,667	21-Apr-97
		GB_EST22 AI050653	443	AI050653	ub38f03 r1 Soares 2NbMT Mus musculus cDNA clone IMAGE 1380029 5', mRNA sequence.	Mus musculus	38,851	9-Jul-98
		GB_GSS1.CNS0022Z	1101	AL061786	Drosophila melanogaster genome survey sequence T7 end of BAC # BACR05B21 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence	Drosophila melanogaster	39,039	3-Jun-99
rxa01877	1194	GB_HTG4:AC009849	114993	AC009849	Drosophila melanogaster chromosome 2 clone BACR07H08 (D864) RPCI-98 07 H.8 map 31B-31C strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 55 unordered pieces	Drosophila melanogaster	37,274	25-OCT-1999
		GB_HTG4 AC009849	114993	AC009849	Drosophila melanogaster chromosome 2 clone BACR07H08 (D864) RPCI-98 07 H 8 map 31B-31C strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 55 unordered pieces	Drosophila melanogaster	37,274	25-OCT-1999
		GB_IN2 AC005454	84367	AC005454	Drosophila melanogaster, chromosome 2R, region 31C1-31D6, P1 clone DS08879, complete sequence	Drosophila melanogaster	38,679	15-DEC-1998
rxa01879	1056	GB_PR2 CNS0000Q	192932	AL049874	Human chromosome 14 DNA sequence *** IN PROGRESS *** BAC R-1042B17 of RPCI-11 library from chromosome 14 of Homo sapiens (Human), complete sequence	Homo sapiens	37,094	7-Jul-99
		GB_HTG2:AC006732	159453	AC006732	Caenorhabditis elegans clone Y32G9, *** SEQUENCING IN PROGRESS ***, 9 unordered pieces	Caenorhabditis elegans	34,862	23-Feb-99
		GB_HTG2.AC006732	159453	AC006732	Caenorhabditis elegans clone Y32G9, *** SEQUENCING IN PROGRESS ***, 9 unordered pieces	Caenorhabditis elegans	34,862	23-Feb-99
rxa01896	759	GB_BA1:SC2G5	38404	AL035478	Streptomyces coelicolor cosmid 2G5	Streptomyces coelicolor	38,420	11-Jun-99
		GB_PL1 AP000570	157903	AP000570	Oryza sativa genomic DNA, chromosome 1, clone P0711E10.	Oryza sativa	40,272	03-DEC-1999
		GB_BA1 SC2G5	38404	AL035478	Streptomyces coelicolor cosmid 2G5.	Streptomyces coelicolor	40,270	11-Jun-99
rxa01899	909	GB_BA1 MTV002	56414	AL008967	Mycobacterium tuberculosis H37Rv complete genome, segment 122/162	Mycobacterium tuberculosis	38,702	17-Jun-98
		GB_BA1 MTV002	56414	AL008967	Mycobacterium tuberculosis H37Rv complete genome, segment 122/162	Mycobacterium tuberculosis	38,229	17-Jun-98
rxa01902	1182	GB_HTG6.AC009893	186769	AC009893	Homo sapiens chromosome 8 clone RP11-4P3, *** SEQUENCING IN PROGRESS ***, 5 unordered pieces	Homo sapiens	34,868	23-Nov-99
		GB_OV:D84063	2363	D84063	Oryzias latipes Bf/C2 mRNA, complete cds	Oryzias latipes	38,074	6-Feb-99

TABLE 4: ALIGNMENT RESULTS

		GB_HTG6:AC009893	186769	AC009893	Homo sapiens chromosome 8 clone RP11-4P3, *** SEQUENCING IN PROGRESS ***, 5 unordered pieces.	Homo sapiens	35,616	23-Nov-99
rxa01903	302	GB_BA1.MSGILVB	4210	L49392	Mycobacterium avium acetolactate synthase (ilvBN) and acetohydroxy acid isomeroreductase (ilvC) gene, complete cds.	Mycobacterium avium	38,667	11-DEC-1996
		GB_PR3:AC004833	68890	AC004833	Homo sapiens PAC clone DJ0547C10 from 7p21-p22, complete sequence	Homo sapiens	34,615	5-Nov-98
		GB_PR3 AC004833	68890	AC004833	Homo sapiens PAC clone DJ0547C10 from 7p21-p22, complete sequence.	Homo sapiens	42,712	5-Nov-98
rxa01904	546	GB_HTG2 AC006740	200965	AC006740	Caenorhabditis elegans clone Y38B5, *** SEQUENCING IN PROGRESS ***, 12 unordered pieces.	Caenorhabditis elegans	34,074	25-Feb-99
		GB_HTG2 AC006695	33622	AC006695	Caenorhabditis elegans clone W06H8, *** SEQUENCING IN PROGRESS ***, 1 unordered pieces	Caenorhabditis elegans	35,556	23-Feb-99
		GB_HTG2 AC006695	33622	AC006695	Caenorhabditis elegans clone W06H8, *** SEQUENCING IN PROGRESS ***, 1 unordered pieces.	Caenorhabditis elegans	35,556	23-Feb-99
rxa01905	654	GB_IN1:CEW04G3	32158	Z68014	Caenorhabditis elegans cosmid W04G3, complete sequence.	Caenorhabditis elegans	38,730	2-Sep-99
		GB_PL2:AF067082	6947	AF067082	Apium graveolens mannitol dehydrogenase (Mtd) gene, complete cds	Apium graveolens	38,242	30-Sep-98
		GB_IN1:CEW04G3	32158	Z68014	Caenorhabditis elegans cosmid W04G3, complete sequence	Caenorhabditis elegans	36,834	2-Sep-99
rxa01906	588	GB_PL1.AB012242	78973	AB012242	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone. K24G6, complete sequence	Arabidopsis thaliana	39,071	20-Nov-99
		GB_EST6:N49608	454	N49608	yy58g01.s1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE 277776 3', mRNA sequence.	Homo sapiens	43,603	14-Feb-96
		GB_EST6 N49609	452	N49609	yy58g02 s1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE 277778 3', mRNA sequence.	Homo sapiens	43,307	14-Feb-96
rxa01907	735	GB_HTG3.AC009437	159691	AC009437	Homo sapiens chromosome 11 clone 56_G_09 map 11, *** SEQUENCING IN PROGRESS ***, 10 unordered pieces	Homo sapiens	36,226	22-Aug-99
		GB_HTG3:AC009437	159691	AC009437	Homo sapiens chromosome 11 clone 56_G_09 map 11, *** SEQUENCING IN PROGRESS ***, 10 unordered pieces	Homo sapiens	36,226	22-Aug-99
		GB_HTG3 AC009437	159691	AC009437	Homo sapiens chromosome 11 clone 56_G_09 map 11, *** SEQUENCING IN PROGRESS ***, 10 unordered pieces	Homo sapiens	38,483	22-Aug-99
rxa01908	969	GB_PR3 HS90G24	154414	AL008723	Human DNA sequence from clone 90G24 on chromosome 22 Contains the RFPL2 gene for RET finger protein-like 2, an Immunoglobulin Lambda Light Chain C region (IGLC) pseudogene, the gene for SAAT1 (low affinity sodium glucose cotransporter (sodium solute symporter family)) and a Cleavage and Polyadenylation Specific Factor CPSF 160 kD subunit pseudogene Contains ESTs, GSSs and three putative CpG islands, complete sequence.	Homo sapiens	37,331	23-Nov-99
		GB_EST25.AI316482	972	AI316482	uj60g12 y1 Sugano mouse liver mlia Mus musculus cDNA clone IMAGE 1924390 5' similar to gb M12529 APOLIPOPROTEIN E PRECURSOR (HUMAN), gb D00466 Mouse apolipoprotein E gene (MOUSE),, mRNA sequence.	Mus musculus	36,800	17-DEC-1998
		GB_EST27.AI398904	556	AI398904	NCW10G7T7 Westergaards Neurospora crassa cDNA clone W10G7 3', mRNA sequence.	Neurospora crassa	38,095	8-Feb-99
rxa01909	970	GB_HTG1 HSJ658I14	133423	AL109845	Homo sapiens chromosome 1 clone RP4-658I14, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	40,520	23-Nov-99
		GB_HTG1.HSJ658I14	133423	AL109845	Homo sapiens chromosome 1 clone RP4-658I14, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	40,520	23-Nov-99
		GB_HTG1:HSJ658I14	133423	AL109845	Homo sapiens chromosome 1 clone RP4-658I14, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	36,364	23-Nov-99
rxa01910	969	GB_PR2 CNS00008	218956	AL049831	Human chromosome 14 DNA sequence *** IN PROGRESS *** BAC R-330O19 of RPCI-11 library from chromosome 14 of Homo sapiens (Human), complete sequence	Homo sapiens	35,393	29-Jun-99
		GB_PR2:CNS00008	218956	AL049831	Human chromosome 14 DNA sequence *** IN PROGRESS *** BAC R-330O19 of RPCI-11 library from chromosome 14 of Homo sapiens (Human), complete sequence	Homo sapiens	38,405	29-Jun-99
		GB_HTG5 AC009217	118561	AC009217	Drosophila melanogaster chromosome X clone BACR41N19 (D907) RPCI-98 41 N 19 map 19A-19C strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 78 unordered pieces	Drosophila melanogaster	36,765	16-Nov-99
rxa01911	1062	GB_HTG2:AC002317	94882	AC002317	Homo sapiens chromosome 17 clone HCIT7H10 map 17, *** SEQUENCING IN PROGRESS ***, 8 unordered pieces.	Homo sapiens	36,654	20-Feb-98
		GB_HTG2 AC002317	94882	AC002317	Homo sapiens chromosome 17 clone HCIT7H10 map 17, *** SEQUENCING IN PROGRESS ***, 8 unordered pieces	Homo sapiens	36,654	20-Feb-98

TABLE 4: ALIGNMENT RESULTS

		GB_HTG2:AC002317	94882	AC002317	Homo sapiens chromosome 17 clone HCIT7H10 map 17, *** SEQUENCING IN PROGRESS ***, 8 unordered pieces	Homo sapiens	37,012	20-Feb-98
rxa01923	873	GB_HTG2:AC006844	299782	AC006844	Caenorhabditis elegans clone Y108G3Y, *** SEQUENCING IN PROGRESS***, 4 unordered pieces.	Caenorhabditis elegans	37,176	24-Feb-99
		GB_HTG2 AC006844	299782	AC006844	Caenorhabditis elegans clone Y108G3Y, *** SEQUENCING IN PROGRESS ***, 4 unordered pieces.	Caenorhabditis elegans	37,176	24-Feb-99
		GB_BA1.ECOUW76	225419	U00039	E. coli chromosomal region from 76 0 to 81.5 minutes	Escherichia coli	38,902	7-Nov-96
rxa01930	1074	GB_BA1 CGPAN	2164	X96580	C glutamicum panB, panC & xylB genes	Corynebacterium glutamicum	100,000	11-MAY-1999
		GB_HTG2.AC007598	248427	AC007598	Homo sapiens chromosome 16 clone 165M1, *** SEQUENCING IN PROGRESS ***, 105 unordered pieces.	Homo sapiens	38,469	20-MAY-1999
		GB_HTG2.AC007598	248427	AC007598	Homo sapiens chromosome 16 clone 165M1, *** SEQUENCING IN PROGRESS ***, 105 unordered pieces	Homo sapiens	38,469	20-MAY-1999
rxa01931	777	GB_IN1:CEH12I19	37427	Z98851	Caenorhabditis elegans cosmid H12I19, complete sequence	Caenorhabditis elegans	32,763	18-DEC-1998
		GB_HTG1.CEY37A1	316170	Z93243	Caenorhabditis elegans chromosome IV clone Y37A1, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Caenorhabditis elegans	32,763	03-DEC-1998
		GB_HTG1 CEY37A1	316170	Z93243	Caenorhabditis elegans chromosome IV clone Y37A1, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Caenorhabditis elegans	32,763	03-DEC-1998
rxa01941	558	GB_EST25:AI313927	520	AI313927	uj38h06.x1 Sugano mouse kidney mkia Mus musculus cDNA clone IMAGE 1922267 3' similar to TR:O09047 O09047 COMPLEMENT COMPONENT 3A RECEPTOR 1 ,, mRNA sequence.	Mus musculus	41,148	17-DEC-1998
		GB_RO:AF053757	8308	AF053757	Mus musculus complement C3a anaphylatoxin receptor (C3ar) gene, complete cds	Mus musculus	38,649	30-Jul-98
		GB_RO:MMU77461	2657	U77461	Mus musculus anaphylatoxin C3a receptor gene, complete cds	Mus musculus	38,649	28-MAY-1997
rxa01942	723	GB_BA1 BRLPTSG	3163	L18875	Brevibacterium lactofermentum phosphoenolpyruvate sugar phosphotransferase (ptsG) gene, complete cds	Brevibacterium lactofermentum	67,407	01-OCT-1993
		GB_BA1.CORPTSMA	2656	L18874	Corynebacterium glutamicum phosphoenolpyruvate sugar phosphotransferase (ptsM) mRNA, complete cds	Corynebacterium glutamicum	100,000	24-Nov-94
		GB_BA1 CORPTSMA	2656	L18874	Corynebacterium glutamicum phosphoenolpyruvate sugar phosphotransferase (ptsM) mRNA, complete cds	Corynebacterium glutamicum	37,008	24-Nov-94
rxa01944	1095	GB_HTG2:AC004840	162485	AC004840	Homo sapiens clone DJ0607J02, *** SEQUENCING IN PROGRESS ***, 12 unordered pieces	Homo sapiens	36,287	12-Jun-98
		GB_HTG2 AC004840	162485	AC004840	Homo sapiens clone DJ0607J02, *** SEQUENCING IN PROGRESS ***, 12 unordered pieces	Homo sapiens	36,287	12-Jun-98
		GB_VI MCU60315	190289	U60315	Molluscum contagiosum virus subtype 1, complete genome	Molluscum contagiosum virus subtype 1	37,650	17-Aug-96
rxa01945	2115	GB_GSS15.AQ632158	445	AQ632158	RPCI-11-473F7.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-473F7, genomic survey sequence	Homo sapiens	38,095	17-Jun-99
		GB_GSS15.AQ632158	445	AQ632158	RPCI-11-473F7.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-473F7, genomic survey sequence.	Homo sapiens	40,275	17-Jun-99
rxa01957	585	GB_EST16.C35275	300	C35275	C35275 Yuji Kohara unpublished cDNA Strain N2 hermaphrodite embryo Caenorhabditis elegans cDNA clone yk427e6 3', mRNA sequence.	Caenorhabditis elegans	37,698	18-OCT-1999
		GB_IN2 CELC29H12	42635	U23169	Caenorhabditis elegans cosmid C29H12	Caenorhabditis elegans	34,477	13-Jul-95
		GB_GSS1.CNS00GP0	1101	AL072364	Drosophila melanogaster genome survey sequence T7 end of BAC BACR33I08 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence	Drosophila melanogaster	34,321	3-Jun-99
rxa01958	630	GB_PR1:HSIL1RECA	12565	X64532	H sapiens gene for interleukin-1 receptor antagonist	Homo sapiens	42,079	25-Jun-97
		GB_PR3 HSU65590	33414	U65590	Homo sapiens IL-1 receptor antagonist IL-1Ra (IL-1RN) gene, alternatively spliced forms, complete cds.	Homo sapiens	42,079	21-DEC-1997
		GB_GSS11 AQ293677	476	AQ293677	HS_2254_A2_C03_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2254 Col=6 Row=E, genomic survey sequence	Homo sapiens	36,772	15-DEC-1998
rxa01959								
rxa01960								

TABLE 4: ALIGNMENT RESULTS

rxa01961	603	GB_BA2 U67460	12589	U67460	Methanococcus jannaschii section 2 of 150 of the complete genome	Methanococcus jannaschii	36,013	28-Jan-98
		GB_EST25:AI260761	626	AI260761	LP04729 3prime LP Drosophila melanogaster larval-early pupal pOT2 Drosophila melanogaster cDNA clone LP04729 3prime, mRNA sequence	Drosophila melanogaster	39,130	17-Nov-98
		GB_EST25:AI294890	554	AI294890	LP08371 3prime LP Drosophila melanogaster larval-early pupal pOT2 Drosophila melanogaster cDNA clone LP08371 3prime, mRNA sequence	Drosophila melanogaster	38,940	01-DEC-1998
rxa01962	693	GB_BA2 U67460	12589	U67460	Methanococcus jannaschii section 2 of 150 of the complete genome	Methanococcus jannaschii	34,795	28-Jan-98
		GB_BA2.U67460	12589	U67460	Methanococcus jannaschii section 2 of 150 of the complete genome	Methanococcus jannaschii	37,666	28-Jan-98
rxa01963	784	GB_PR4 AC006397	91460	AC006397	Homo sapiens BAC clone GS170I02 from 7p21-p15 1, complete sequence	Homo sapiens	35,401	17-Feb-99
		GB_PR3 AC005565	39441	AC005565	Homo sapiens chromosome 16, cosmid clone 444B9 (LANL), complete sequence.	Homo sapiens	37,891	30-Aug-98
		GB_PR2 D86999	40778	D86999	Homo sapiens immunoglobulin lambda gene locus DNA, clone 22A12	Homo sapiens	38,212	5-Nov-99
rxa01964	1426	GB_GSS13:AQ465174	437	AQ465174	HS_5109_A2_C07_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=685 Col=14 Row=E, genomic survey sequence	Homo sapiens	40,084	23-Apr-99
		GB_GSS13 AQ457528	599	AQ457528	HS_5087_A1_H06_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=663 Col=11 Row=O, genomic survey sequence	Homo sapiens	36,728	23-Apr-99
		GB_GSS13 AQ454028	527	AQ454028	HS_5171_B1_D12_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=747 Col=23 Row=H, genomic survey sequence	Homo sapiens	37,137	21-Apr-99
rxa01965	684	GB_IN2 AC004283	80095	AC004283	Drosophila melanogaster DNA sequence (P1 DS05557 (D152)), complete sequence	Drosophila melanogaster	36,982	29-Aug-98
		GB_EST28:AI541584	585	AI541584	SD02734 5prime SD Drosophila melanogaster Schneider L2 cell culture pOT2 Drosophila melanogaster cDNA clone SD02734 5prime, mRNA sequence	Drosophila melanogaster	38,375	22-MAR-1999
		GB_EST22:AI013385	434	AI013385	EST208060 Normalized rat spleen, Bento Soares Rattus sp cDNA clone RSPBK32 3' end, mRNA sequence	Rattus sp	42,126	31-Jan-99
rxa01966	780	GB_GSS1 CNS00AMI	810	AL055260	Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR21F10 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence	Drosophila melanogaster	37,592	4-Jun-99
		GB_HTG3 AC009567	164147	AC009567	Homo sapiens chromosome 4 clone 21_G_20 map 4, *** SEQUENCING IN PROGRESS ***, 14 unordered pieces	Homo sapiens	35,844	29-Sep-99
		GB_HTG3.AC009567	164147	AC009567	Homo sapiens chromosome 4 clone 21_G_20 map 4, *** SEQUENCING IN PROGRESS ***, 14 unordered pieces	Homo sapiens	35,844	29-Sep-99
rxa01968	1281	GB_PR4 AC005146	157653	AC005146	Homo sapiens 12q24 2 PAC RPCI1-157K6 (Roswell Park Cancer Institute Human PAC library) complete sequence	Homo sapiens	40,620	11-Nov-98
		GB_PR4:AC006549	174844	AC006549	Homo sapiens, complete sequence	Homo sapiens	34,202	26-Nov-99
		GB_PR2.HSAC002070	165197	AC002070	Human BAC clone 7E17 from 12q, complete sequence.	Homo sapiens	36,482	12-MAY-1997
rxa01969	489	GB_SY:SCU53587	4546	U53587	Artificial Corynebacterium glutamicum IS1207-derived transposon transposase genes, complete cds, and 3'5"-aminoglycoside phosphotransferase (aphA-3) gene, complete cds.	synthetic construct	98,160	06-MAY-1996
		GB_PAT I43826	1452	I43826	Sequence 1 from patent US 5633154	Unknown	98,963	07-OCT-1997
		GB_BA1 CGIS1207	1453	X96962	C glutamicum insertion sequence IS1207 and transposase gene.	Corynebacterium glutamicum	98,755	01-MAY-1997
rxa01973								
rxa01974	1908	GB_PL1 SC9320A	24000	Z68329	S cerevisiae chromosome IV cosmid 9320A	Saccharomyces cerevisiae	36,528	11-Aug-97
		GB_PL1 SC9320X	22253	Z70202	S cerevisiae chromosome IV cosmid 9320X.	Saccharomyces cerevisiae	36,528	11-Aug-97
		GB_PR4 AC006210	186986	AC006210	Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence	Homo sapiens	38,351	31-DEC-1998

TABLE 4: ALIGNMENT RESULTS

rxa01976	1644	GB_BA2:CGU13922	4412	U13922	Corynebacterium glutamicum putative type II 5-cytosoine methyltransferase (cglIIM) and putative type II restriction endonuclease (cglIIR) and putative type I or type III restriction endonuclease (clgIIR) genes, complete cds.	Corynebacterium glutamicum	47,727	3-Feb-98
		GB_BA2:CGU13922	4412	U13922	Corynebacterium glutamicum putative type II 5-cytosoine methyltransferase (cglIIM) and putative type II restriction endonuclease (cglIIR) and putative type I or type III restriction endonuclease (clgIIR) genes, complete cds	Corynebacterium glutamicum	37,515	3-Feb-98
rxa01977	699	GB_PR3:HS426F10	91640	AL023586	Human DNA sequence from clone 426F10 on chromosome 1p36 21-36.33 Contains EST, CA repeat, STS, complete sequence	Homo sapiens	38,295	23-Nov-99
		GB_GSS6 AQ823696	587	AQ823696	HS_3228_A1_D10_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3228 Col=19 Row=G, genomic survey sequence.	Homo sapiens	37,637	26-Aug-99
		GB_VI.HS3DNA1	892	M29629	Varicella-zoster virus (VZV) DNA, 5' end	Human herpesvirus 3	33,857	2-Aug-93
rxa01982	1281	GB_EST8 AA009257	472	AA009257	mh02g07 r1 Soares mouse embryo NbME13 5 14 5 Mus musculus cDNA clone IMAGE.441372 5', mRNA sequence.	Mus musculus	36,017	26-Jul-96
		GB_EST8 AA009257	472	AA009257	mh02g07 r1 Soares mouse embryo NbME13 5 14 5 Mus musculus cDNA clone IMAGE 441372 5', mRNA sequence	Mus musculus	38,710	26-Jul-96
rxa01987	336	GB_PR4:AC009330	174768	AC009330	Homo sapiens clone RP11-83M17 from 7q31, complete sequence.	Homo sapiens	33,036	09-DEC-1999
		GB_HTG6 AC007300	171472	AC007300	Drosophila melanogaster chromosome 2 clone BACR09I15 (D570) RPCI-98 09 I 15 map 32A-32A strain y, cn bw sp, *** SEQUENCING IN PROGRESS ***, 43 unordered pieces	Drosophila melanogaster	38,782	07-DEC-1999
		GB_HTG3 AC009542	160367	AC009542	Homo sapiens chromosome 7, *** SEQUENCING IN PROGRESS ***, 17 unordered pieces	Homo sapiens	35,065	27-Aug-99
rxa01988	549	GB_IN1 AC002446	50978	AC002446	Drosophila melanogaster (P1 DS06754 (D83)) DNA sequence, complete sequence	Drosophila melanogaster	38,920	19-Aug-97
		GB_PR3.HSU19H10	43303	AL021182	Human DNA sequence from cosmid U19H10 on chromosome X Contains ESTs and CA repeat	Homo sapiens	39,006	23-Nov-99
		GB_PR3 HSU19H10	43303	AL021182	Human DNA sequence from cosmid U19H10 on chromosome X Contains ESTs and CA repeat	Homo sapiens	38,447	23-Nov-99
rxa01990	1022	GB_GSS9 AQ100628	382	AQ100628	HS_3054_B2_A05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3054 Col=10 Row=B, genomic survey sequence.	Homo sapiens	38,320	27-Aug-98
		GB_EST14 AA406679	338	AA406679	MBAFCZ2F12T3A Brugia malayi adult female cDNA (SAW96MLW-BmAF) Brugia malayi cDNA clone AFCZ2F12 5', mRNA sequence	Brugia malayi	38,039	01-MAY-1997
		GB_EST21 AA991134	600	AA991134	BSBmMFSZ06C1SK Brugia malayi microfilaria cDNA (SAW94LS-BmMf) Brugia malayi cDNA clone BSBmMFSZ06C1 5', mRNA sequence.	Brugia malayi	40,090	5-Jun-98
rxa01991	996	GB_HTG3 AC007559	156374	AC007559	Homo sapiens clone NH0364J06, *** SEQUENCING IN PROGRESS ***, 29 unordered pieces	Homo sapiens	35,931	13-Aug-99
		GB_HTG3 AC007559	156374	AC007559	Homo sapiens clone NH0364J06, *** SEQUENCING IN PROGRESS ***, 29 unordered pieces	Homo sapiens	35,931	13-Aug-99
		GB_HTG3.AC007559	156374	AC007559	Homo sapiens clone NH0364J06, *** SEQUENCING IN PROGRESS ***, 29 unordered pieces	Homo sapiens	36,120	13-Aug-99
rxa01992								
rxa01996	660	GB_BA1 XCXPSGEN	5324	X59079	X campestris xps E, F, G, H, I, and J genes for protein secretion and pathogenicity functions	Xanthomonas campestris	38,447	12-Sep-93
		GB_GSS15 AQ659461	394	AQ659461	Sheared DNA-5C7.TR Sheared DNA Trypanosoma brucei genomic clone Sheared DNA-5C7, genomic survey sequence.	Trypanosoma brucei	49,180	23-Jun-99
		GB_GSS4:AQ741049	713	AQ741049	HS_2272_A2_B02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2272 Col=4 Row=C, genomic survey sequence	Homo sapiens	39,614	16-Jul-99
rxa01999	594	GB_HTG2 AC007321	159558	AC007321	Homo sapiens clone NH0507C01, *** SEQUENCING IN PROGRESS ***, 4 unordered pieces	Homo sapiens	34,524	16-Apr-99
		GB_HTG2 AC007321	159558	AC007321	Homo sapiens clone NH0507C01, *** SEQUENCING IN PROGRESS ***, 4 unordered pieces	Homo sapiens	34,524	16-Apr-99
		GB_HTG2 AC007321	159558	AC007321	Homo sapiens clone NH0507C01, *** SEQUENCING IN PROGRESS ***, 4 unordered pieces	Homo sapiens	35,094	16-Apr-99
rxa02001	1281	GB_BA1 D90917	154619	D90917	Synechocystis sp PCC6803 complete genome, 27/27, 3418852-3573470	Synechocystis sp	50,474	7-Feb-99
		GB_BA1 MTV016	53662	AL021841	Mycobacterium tuberculosis H37Rv complete genome, segment 143/162.	Mycobacterium tuberculosis	39,223	23-Jun-99
		GB_BA1 BSUB0006	210440	Z99109	Bacillus subtilis complete genome (section 6 of 21) from 999501 to 1209940	Bacillus subtilis	36,445	26-Nov-97
rxa02004	230	GB_HTG3 AC011491	162134	AC011491	Homo sapiens chromosome 19 clone CIT978SKB_180A7, *** SEQUENCING IN PROGRESS ***, 161 unordered pieces	Homo sapiens	37,383	07-OCT-1999

TABLE 4: ALIGNMENT RESULTS

		GB_HTG3:AC011491	162134	AC011491	Homo sapiens chromosome 19 clone CIT978SKB_180A7, *** SEQUENCING IN PROGRESS ***, 161 unordered pieces	Homo sapiens	37,383	07-OCT-1999
		GB_HTG3:AC011357	160676	AC011357	Homo sapiens chromosome 5 clone CIT-HSPC_362D12, *** SEQUENCING IN PROGRESS ***, 42 unordered pieces.	Homo sapiens	54,585	06-OCT-1999
rxa02006	595	GB_HTG2 AC006901	294136	AC006901	Caenorhabditis elegans clone Y74A11X, *** SEQUENCING IN PROGRESS ***, 81 unordered pieces.	Caenorhabditis elegans	37,500	26-Feb-99
		GB_HTG2 AC006901	294136	AC006901	Caenorhabditis elegans clone Y74A11X, *** SEQUENCING IN PROGRESS ***, 81 unordered pieces.	Caenorhabditis elegans	37,500	26-Feb-99
		GB_HTG1 CEY70C5	224525	Z98878	Caenorhabditis elegans chromosome V clone Y70C5, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Caenorhabditis elegans	36,021	28-Aug-97
rxa02007	756	GB_BA2 CGL012293	2952	AJ012293	Corynebacterium glutamicum ilvD gene	Corynebacterium glutamicum	100,000	01-OCT-1999
		GB_PR4:AC006285	150172	AC006285	Homo sapiens, complete sequence.	Homo sapiens	38,740	15-Nov-99
		GB_PR4.AC006285	150172	AC006285	Homo sapiens, complete sequence.	Homo sapiens	38,701	15-Nov-99
rxa02009	223	GB_PR4.AC004926	153556	AC004926	Homo sapiens PAC clone DJ0910H09 from 7q21 1-q21.2, complete sequence	Homo sapiens	38,462	17-Feb-99
		GB_PR2 AP000053	100000	AP000053	Homo sapiens genomic DNA, chromosome 21q22.1, segment 24/28, complete sequence.	Homo sapiens	37,674	20-Nov-99
		GB_PR2:AP000121	100000	AP000121	Homo sapiens genomic DNA of 21q22 1, GART and AML related, SLC5A3-f4A4 region, segment 4/8, complete sequence.	Homo sapiens	37,674	25-Sep-99
rxa02013	649	GB_BA1 MTCI237	27030	Z94752	Mycobacterium tuberculosis H37Rv complete genome, segment 46/162	Mycobacterium tuberculosis	39,308	17-Jun-98
		GB_HTG4 AC010885	201581	AC010885	Homo sapiens chromosome unknown clone NH0368K23, WORKING DRAFT SEQUENCE, in unordered pieces	Homo sapiens	37,206	29-OCT-1999
		GB_HTG4 AC010885	201581	AC010885	Homo sapiens chromosome unknown clone NH0368K23, WORKING DRAFT SEQUENCE, in unordered pieces	Homo sapiens	37,206	29-OCT-1999
rxa02014	630	GB_HTG3 AC010769	119431	AC010769	Homo sapiens chromosome 15 clone 28_B_17 map 15, LOW-PASS SEQUENCE SAMPLING	Homo sapiens	33,816	22-Sep-99
		GB_HTG3.AC010769	119431	AC010769	Homo sapiens chromosome 15 clone 28_B_17 map 15, LOW-PASS SEQUENCE SAMPLING	Homo sapiens	33,816	22-Sep-99
		GB_EST34:AI783738	320	AI783738	tu45b07 x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2253973 3', mRNA sequence	Homo sapiens	37,855	1-Jul-99
rxa02019	524	GB_EST15 AA473289	318	AA473289	vd44g09 r1 Barstead MPLRB1 Mus musculus cDNA clone IMAGE 803488 5', mRNA sequence	Mus musculus	38,153	18-Jun-97
		GB_HTG1 CEY102A5_3	110000	Z99711	Caenorhabditis elegans chromosome V clone Y102A5, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Caenorhabditis elegans	38,867	9-Jun-98
		GB_HTG1 CEY102A5_3	110000	Z99711	Caenorhabditis elegans chromosome V clone Y102A5, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Caenorhabditis elegans	38,867	9-Jun-98
rxa02021	1071	GB_BA1 CGDNAAROP	2612	X85965	C glutamicum ORF3 and aroP gene	Corynebacterium glutamicum	99,905	30-Nov-97
		GB_BA1.CGDAPE	1966	X81379	C glutamicum dapE gene and orf2	Corynebacterium glutamicum	36,406	8-Aug-95
		GB_BA1 SCI7	34893	AL096743	Streptomyces coelicolor cosmid I7	Streptomyces coelicolor	36,782	1-Jul-99
rxa02023	891	GB_BA1 CGDAPE	1966	X81379	C.glutamicum dapE gene and orf2	Corynebacterium glutamicum	99,864	8-Aug-95
		GB_PR3 AC004067	161326	AC004067	Homo sapiens chromosome 4 clone B366O24 map 4q25, complete sequence	Homo sapiens	39,651	8-Nov-98
		GB_HTG3.AC009725	145005	AC009725	Mus musculus chromosome 6 clone 388_N_17 map 6, *** SEQUENCING IN PROGRESS ***, 2 ordered pieces	Mus musculus	38,215	01-OCT-1999
rxa02032	693	GB_PR4 AC006961	171419	AC006961	Homo sapiens chromosome 18, clone RP11-31P16, complete sequence	Homo sapiens	37,703	19-Nov-99
		GB_PR4 AC006961	171419	AC006961	Homo sapiens chromosome 18, clone RP11-31P16, complete sequence	Homo sapiens	40,839	19-Nov-99
rxa02036	504	GB_PR2 HSDJ799G3	127639	AL078624	Human DNA sequence from clone RP4-799G3 on chromosome 1q42 11-42 3, complete sequence	Homo sapiens	35,657	22-Nov-99
		GB_BA1 AOPCZA361	37941	AJ223998	Amycolatopsis orientalis cosmid PCZA361	Amycolatopsis orientalis	46,341	29-MAR-1999
		GB_PL1 ATDNADAL1	8747	Y14851	Arabidopsis thaliana dal1 gene	Arabidopsis thaliana	35,223	23-Sep-97
rxa02039	863	GB_PR3:AC005609	157970	AC005609	Homo sapiens chromosome 5, BAC clone 203o13 (LBNL H155), complete sequence	Homo sapiens	37,176	4-Sep-98

TABLE 4: ALIGNMENT RESULTS

		GB_HTG3:AC008468	245016	AC008468	Homo sapiens chromosome 5 clone CIT-HSPC_365B8, *** SEQUENCING IN PROGRESS ***, 14 unordered pieces	Homo sapiens	36,842	3-Aug-99
		GB_HTG3 AC008468	245016	AC008468	Homo sapiens chromosome 5 clone CIT-HSPC_365B8, *** SEQUENCING IN PROGRESS ***, 14 unordered pieces.	Homo sapiens	36,842	3-Aug-99
rxa02040	551	GB_HTG3 AC009303	198549	AC009303	Homo sapiens clone NH0098C01, *** SEQUENCING IN PROGRESS ***, 2 unordered pieces	Homo sapiens	35,424	13-Aug-99
		GB_HTG3:AC009303	198549	AC009303	Homo sapiens clone NH0098C01, *** SEQUENCING IN PROGRESS ***, 2 unordered pieces	Homo sapiens	35,424	13-Aug-99
		GB_HTG3 AC009303	198549	AC009303	Homo sapiens clone NH0098C01, *** SEQUENCING IN PROGRESS ***, 2 unordered pieces	Homo sapiens	32,597	13-Aug-99
rxa02045	384	GB_EST3.R23812	459	R23812	yh34g05.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE 131672 5', mRNA sequence.	Homo sapiens	47,273	20-Apr-95
		GB_EST19 AA778733	611	AA778733	af88d02.s1 Soares_testis_NHT Homo sapiens cDNA clone 1049091 3', mRNA sequence.	Homo sapiens	38,806	5-Feb-98
		GB_PR2.HSU59185	2529	U59185	Human putative monocarboxylate transporter (MCT) mRNA, complete cds	Homo sapiens	43,164	03-OCT-1997
rxa02046	540	GB_HTG3 AC005507	196595	AC005507	Plasmodium falciparum chromosome 12 clone 3D7, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces.	Plasmodium falciparum	37,218	23-Sep-99
		GB_HTG3 AC005507	196595	AC005507	Plasmodium falciparum chromosome 12 clone 3D7, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces.	Plasmodium falciparum	37,218	23-Sep-99
		GB_EST1 T09984	330	T09984	0540m7 gmbPfHB3 1, G Roman Reddy Plasmodium falciparum genomic clone 0540m, mRNA sequence.	Plasmodium falciparum	32,121	29-Nov-93
rxa02049	732	GB_PL1:ATHCOLR	1098	M37778	A.thaliana middle repetative sequence.	Arabidopsis thaliana	33,755	27-Apr-93
		GB_PL2 ATAC006954	87035	AC006954	Arabidopsis thaliana chromosome II BAC F25P17 genomic sequence, complete sequence.	Arabidopsis thaliana	33,755	7-Apr-99
		GB_EST33 AI779067	495	AI779067	EST259946 tomato susceptible, Cornell Lycopersicon esculentum cDNA clone cLES7C7, mRNA sequence.	Lycopersicon esculentum	35,223	29-Jun-99
rxa02050	918	GB_HTG2 AC008307	91654	AC008307	Drosophila melanogaster chromosome 3 clone BACR03D22 (D709) RPCI-98 03 D.22 map 86F-87A strain y, cn bw sp, *** SEQUENCING IN PROGRESS ***, 94 unordered pieces	Drosophila melanogaster	36,182	2-Aug-99
		GB_HTG2 AC008307	91654	AC008307	Drosophila melanogaster chromosome 3 clone BACR03D22 (D709) RPCI-98 03 D 22 map 86F-87A strain y, cn bw sp, *** SEQUENCING IN PROGRESS***, 94 unordered pieces	Drosophila melanogaster	36,182	2-Aug-99
		GB_EST31 AU060923	663	AU060923	AU060923 Dictyostelium discoideum SL (H Urushihara) Dictyostelium discoideum cDNA clone SLC248, mRNA sequence.	Dictyostelium discoideum	39,388	20-MAY-1999
rxa02051	621	GB_EST16 C43896	369	C43896	C43896 Yuji Kohara unpublished cDNA Strain N2 hermaphrodite embryo Caenorhabditis elegans cDNA clone yk336c10 5', mRNA sequence	Caenorhabditis elegans	41,160	18-OCT-1999
		GB_EST16 C40413	360	C40413	C40413 Yuji Kohara unpublished cDNA Strain N2 hermaphrodite embryo Caenorhabditis elegans cDNA clone yk230e7 5', mRNA sequence	Caenorhabditis elegans	42,090	18-OCT-1999
		GB_EST36 AV191515	360	AV191515	AV191515 Yuji Kohara unpublished cDNA Strain N2 hermaphrodite embryo Caenorhabditis elegans cDNA clone yk594g6 5', mRNA sequence.	Caenorhabditis elegans	40,833	22-Jul-99
rxa02053	702	GB_IN1:AF035264	6397	AF035264	Drosophila melanogaster POU domain protein (pdm-1) gene, promoter region and exon 1	Drosophila melanogaster	36,888	04-DEC-1997
		GB_BA1 MTV036	24055	AL021931	Mycobacterium tuberculosis H37Rv complete genome; segment 19/162	Mycobacterium tuberculosis	37,647	17-Jun-98
		GB_EST30 AI658116	497	AI658116	fc22e07.y1 Zebrafish WashU MPIMG EST Danio rerio cDNA 5' similar to TR Q15883 Q15883 X104 ;, mRNA sequence	Danio rerio	41,129	06-MAY-1999
rxa02057	654	GB_PAT.E14601	4394	E14601	Brevibacterium lactofermentum gene for alpha-ketoglutaric acid dehydrogenase	Corynebacterium glutamicum	96,667	28-Jul-99
		GB_BA1.D84102	4394	D84102	Corynebacterium glutamicum DNA for 2-oxoglutarate dehydrogenase, complete cds	Corynebacterium glutamicum	96,667	6-Feb-99
		GB_PAT.E14601	4394	E14601	Brevibacterium lactofermentum gene for alpha-ketoglutaric acid dehydrogenase.	Corynebacterium glutamicum	38,199	28-Jul-99
rxa02058	675	GB_GSS9 AQ129748	432	AQ129748	HS_2254_B1_H03_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2254 Col=5 Row=P, genomic survey sequence	Homo sapiens	40,000	23-Sep-98
		GB_PL2:T15B16	90596	AF104919	Arabidopsis thaliana BAC T15B16	Arabidopsis thaliana	35,338	11-Nov-98
		GB_PL2 AC007138	120185	AC007138	Arabidopsis thaliana BAC T7B11 from chromosome IV near 10 cM, complete sequence	Arabidopsis thaliana	39,426	1-Apr-99
rxa02059	618	GB_HTG3 AC008672	131573	AC008672	Homo sapiens chromosome 5 clone CIT978SKB_3B12, *** SEQUENCING IN PROGRESS ***, 71 unordered pieces.	Homo sapiens	40,871	3-Aug-99

TABLE 4: ALIGNMENT RESULTS

		GB_HTG3:AC008672	131573	AC008672	Homo sapiens chromosome 5 clone CIT978SKB_3B12, *** SEQUENCING IN PROGRESS ***, 71 unordered pieces	Homo sapiens	40,871	3-Aug-99
		GB_IN1 DDU06228	2695	U06228	Dictyostelium discoideum CRAC (dagA) gene, complete cds	Dictyostelium discoideum	36,513	1-Feb-95
rxa02066	615	GB_PR2:CNS01DRA	198444	AL110505	Human chromosome 14 DNA sequence *** IN PROGRESS *** BAC R-816J8 of RPCI-11 library from chromosome 14 of Homo sapiens (Human), complete sequence	Homo sapiens	36,903	11-Nov-99
		GB_PR2 HS230G1	125515	Z84466	Homo sapiens DNA sequence from PAC 230G1 on chromosome Xp11 3 Contains EST, STS and GSS, complete sequence.	Homo sapiens	41,751	23-Nov-99
		GB_PR2.CNS01DRA	198444	AL110505	Human chromosome 14 DNA sequence *** IN PROGRESS *** BAC R-816J8 of RPCI-11 library from chromosome 14 of Homo sapiens (Human), complete sequence.	Homo sapiens	36,589	11-Nov-99
rxa02067	579	GB_HTG3.AC009543	159209	AC009543	Homo sapiens chromosome 11 clone 63_H_13 map 11, *** SEQUENCING IN PROGRESS ***, 12 unordered pieces	Homo sapiens	35,366	07-OCT-1999
		GB_HTG3.AC009543	159209	AC009543	Homo sapiens chromosome 11 clone 63_H_13 map 11, *** SEQUENCING IN PROGRESS ***, 12 unordered pieces	Homo sapiens	35,366	07-OCT-1999
		GB_PR2.HS230G1	125515	Z84466	Homo sapiens DNA sequence from PAC 230G1 on chromosome Xp11 3 Contains EST, STS and GSS, complete sequence.	Homo sapiens	36,348	23-Nov-99
rxa02069	702	GB_BA1 MTCI61	13540	Z98260	Mycobacterium tuberculosis H37Rv complete genome, segment 53/162	Mycobacterium tuberculosis	36,642	17-Jun-98
		GB_BA1.MTCI61	13540	Z98260	Mycobacterium tuberculosis H37Rv complete genome, segment 53/162	Mycobacterium tuberculosis	39,474	17-Jun-98
rxa02070	1245	GB_BA2 AE001112	14704	AE001112	Archaeoglobus fulgidus section 167 of 172 of the complete genome.	Archaeoglobus fulgidus	39,352	15-DEC-1997
		GB_PR3.HSDJ47M23	129320	AL096816	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone dJ47M23, complete sequence	Homo sapiens	40,413	23-Nov-99
		GB_HTG3 AC009139	152666	AC009139	Homo sapiens chromosome 16 clone RPCI-11_538I12, *** SEQUENCING IN PROGRESS ***, 27 unordered pieces	Homo sapiens	35,275	3-Aug-99
rxa02076	657	GB_EST34:AI789138	594	AI789138	uk51e02 y1 Sugano mouse kidney mkia Mus musculus cDNA clone IMAGE:1972538 5' similar to WP:R10H10.7 CE06298 TYROSINE-PROTEIN KINASE LIKE ;, mRNA sequence	Mus musculus	43,041	2-Jul-99
		GB_GSS1.FR0013995	552	AL005239	F.rubripes GSS sequence, clone 137O18aC6, genomic survey sequence.	Fugu rubripes	37,079	18-Sep-97
		GB_GSS3:B27548	642	B27548	F19J9TFB IGF Arabidopsis thaliana genomic clone F19J9, genomic survey sequence.	Arabidopsis thaliana	37,056	13-OCT-1997
rxa02080	930	GB_GSS15:AQ652136	411	AQ652136	Sheared DNA-7M23 TR Sheared DNA Trypanosoma brucei genomic clone Sheared DNA-7M23, genomic survey sequence.	Trypanosoma brucei	39,259	22-Jun-99
		GB_GSS15.AQ652498	450	AQ652498	Sheared DNA-22K16 TR Sheared DNA Trypanosoma brucei genomic clone Sheared DNA-22K16, genomic survey sequence	Trypanosoma brucei	39,597	22-Jun-99
		GB_HTG3 AC009683	171597	AC009683	Homo sapiens chromosome 8 clone 76_N_5 map 8, *** SEQUENCING IN PROGRESS ***, 10 unordered pieces	Homo sapiens	37,053	29-Sep-99
rxa02081	1752	GB_OV.BSU43200	2070	U43200	Boreogadus saida antifreeze glycopeptide AFGP polyprotein precursor gene, complete cds	Boreogadus saida	37,016	12-MAY-1997
		GB_BA2:AE001615	12401	AE001615	Chlamydia pneumoniae section 31 of 103 of the complete genome	Chlamydophila pneumoniae	36,385	08-MAR-1999
		GB_OV:BSU43200	2070	U43200	Boreogadus saida antifreeze glycopeptide AFGP polyprotein precursor gene, complete cds	Boreogadus saida	37,672	12-MAY-1997
rxa02084	468	GB_PR4.AC007382	80547	AC007382	Homo sapiens clone NH0288C18, complete sequence	Homo sapiens	41,138	8-Sep-99
		GB_GSS4 AQ731530	508	AQ731530	HS_5543_A2_A05_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=1119 Col=10 Row=A, genomic survey sequence	Homo sapiens	36,245	15-Jul-99
		GB_PR4.AC007382	80547	AC007382	Homo sapiens clone NH0288C18, complete sequence	Homo sapiens	35,398	8-Sep-99
rxa02089	594	GB_PR2.AP000031	149298	AP000031	Homo sapiens genomic DNA, chromosome 21q22.1, segment 2/28, complete sequence.	Homo sapiens	38,699	20-Nov-99
		GB_PR2:AP000135	111894	AP000135	Homo sapiens genomic DNA of 21q22 1, GART and AML, f43D11-119B8 region, segment 10/10, complete sequence.	Homo sapiens	38,699	25-Sep-99
		GB_PR2 AP000213	100000	AP000213	Homo sapiens genomic DNA, chromosome 21q22 1, D21S226-AML region, clone f43D11-119B8, segment 11/12, complete sequence	Homo sapiens	38,699	20-Nov-99
rxa02090	924	GB_PL2 ATAC006841	123183	AC006841	Arabidopsis thaliana chromosome II BAC F3K23 genomic sequence, complete sequence	Arabidopsis thaliana	39,826	6-Apr-99
		GB_PL1 SCXV55KB	54719	Z70678	S cerevisiae chromosome XV DNA, 54 7 kb region	Saccharomyces cerevisiae	37,817	16-MAY-1997

TABLE 4: ALIGNMENT RESULTS

		GB_PR1:D87675	301692	D87675	Homo sapiens DNA for amyloid precursor protein, complete cds.	Homo sapiens	39,140	22-Sep-97
rxa02091	774	GB_BA2 AF031929	2675	AF031929	Lactobacillus helveticus cochaperonin GroES and chaperonin GroEL genes, complete cds; and DNA mismatch repair enzyme (hexA) gene, partial cds	Lactobacillus helveticus	35,509	8-Aug-98
		GB_BA1 CGU43536	3464	U43536	Corynebacterium glutamicum heat shock, ATP-binding protein (clpB) gene, complete cds	Corynebacterium glutamicum	39,124	13-MAR-1997
		GB_BA1 RCFBC	3874	X03476	Rhodopseudomonas sphaeroides fbc operon (fbcF, fbcB, fbcC genes).	Rhodobacter sphaeroides	36,478	10-Feb-99
rxa02094	840	GB_RO MMHC188A7	120990	AF109719	Mus musculus casein kinase 2 beta subunit (gMCK2) gene, partial cds; BAT4, NG20 (NG20), BAT3, BAT2, AIF-1, B144, lymphotoxin beta, TNF, and TNF beta genes, complete cds, IKBL gene, partial cds, and unknown gene	Mus musculus	38,118	25-OCT-1999
		GB_EST10 AA168948	549	AA168948	ms39c08.r1 Life Tech mouse embryo 13 5dpc 10666014 Mus musculus cDNA clone IMAGE.613934 5' similar to gb U15980 Mus musculus (MOUSE),, mRNA sequence	Mus musculus	40,789	19-DEC-1996
		GB_EST24 AI101223	348	AI101223	EST210512 Normalized rat brain, Bento Soares Rattus sp cDNA clone RBRBK04 3' end, mRNA sequence	Rattus sp	40,634	31-Jan-99
rxa02097	3495	GB_BA2 RMU31512	1974	U31512	Rhizobium meliloti RmDEGP (degP) gene, complete cds	Sinorhizobium meliloti	39,159	05-MAR-1996
		GB_EST15:AA502050	346	AA502050	ng57c04 s1 NCI_CGAP_Lip2 Homo sapiens cDNA clone IMAGE 938886 similar to contains Alu repetitive element;, mRNA sequence	Homo sapiens	40,751	18-Aug-97
		GB_EST16:AA589883	400	AA589883	vl80h08.r1 Stratagene mouse diaphragm (#937303) Mus musculus cDNA clone IMAGE 987039 5' similar to gb:M75716 Mus musculus alpha-1 protease inhibitor 2 (MOUSE);, mRNA sequence	Mus musculus	35,427	16-Sep-97
rxa02102	1281	GB_IN2:AF135118	10830	AF135118	Drosophila melanogaster laminin alpha1,2 (wing blister) mRNA, complete cds	Drosophila melanogaster	36,926	23-MAY-1999
		GB_IN1:AC002516	48158	AC002516	Drosophila melanogaster (P1 DS01068 (D37)) DNA sequence, complete sequence	Drosophila melanogaster	37,838	28-Aug-97
		GB_GSS3:B09866	1194	B09866	T16G20-Sp6 TAMU Arabidopsis thaliana genomic clone T16G20, genomic survey sequence	Arabidopsis thaliana	35,332	14-MAY-1997
rxa02103	519	GB_GSS3 B09866	1194	B09866	T16G20-Sp6 TAMU Arabidopsis thaliana genomic clone T16G20, genomic survey sequence	Arabidopsis thaliana	36,310	14-MAY-1997
		GB_EST34:AV165661	290	AV165661	AV165661 Mus musculus head C57BL/6J 13-day embryo Mus musculus cDNA clone 3110038F04, mRNA sequence.	Mus musculus	37,716	6-Jul-99
		GB_RO:AC002121	84056	AC002121	Genomic sequence from Mouse 11, complete sequence	Mus musculus	39,096	10-Jul-97
rxa02104	1245	GB_BA2:ECOUW67_0	110000	U18997	Escherichia coli K-12 chromosomal region from 67.4 to 76 0 minutes	Escherichia coli	39,024	22-Dec-94
		GB_BA2 AE000394	12221	AE000394	Escherichia coli K-12 MG1655 section 284 of 400 of the complete genome.	Escherichia coli	39,024	12-Nov-98
		GB_BA1 ECORNPBW	4434	D90212	E coli rnpB gene and ORFs	Escherichia coli	45,255	7-Feb-99
rxa02107								
rxa02108	732	GB_BA1 D90912	128598	D90912	Synechocystis sp PCC6803 complete genome, 14/27, 1719644-1848241	Synechocystis sp	38,095	7-Feb-99
		GB_GSS13 AQ498890	431	AQ498890	HS_5154_A1_E06_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=730 Col=11 Row=I, genomic survey sequence.	Homo sapiens	37,150	28-Apr-99
		GB_BA1 D90912	128598	D90912	Synechocystis sp PCC6803 complete genome, 14/27, 1719644-1848241.	Synechocystis sp.	38,781	7-Feb-99
rxa02109	1044	GB_IN2 AC001658	91019	AC001658	Drosophila melanogaster DNA sequence (P1 DS00913 (D24)), complete sequence.	Drosophila melanogaster	35,687	17-Jul-98
		GB_EST19:AA802304	581	AA802304	GM04170.5prime GM Drosophila melanogaster ovary BlueScript Drosophila melanogaster cDNA clone GM04170 5prime, mRNA sequence.	Drosophila melanogaster	40,451	25-Nov-98
		GB_EST35 AI822653	733	AI822653	L0-1173T3 Ice plant Lambda Uni-Zap XR expression library, 0 hours NaCl treatment Mesembryanthemum crystallinum cDNA clone L0-1173 5' similar to Profilin 1 (AF092547) [Ricinus communis, mRNA sequence	Mesembryanthemum crystallinum	36,957	12-Jul-99
rxa02114	509	GB_BA1 SMU94899	2379	U94899	Sinorhizobium meliloti dissimilatory nitrous oxide reduction proteins NosY, NosL and NosX genes, complete cds	Sinorhizobium meliloti	42,744	6-Sep-97
		GB_BA1 SMU94899	2379	U94899	Sinorhizobium meliloti dissimilatory nitrous oxide reduction proteins NosY, NosL and NosX genes, complete cds.	Sinorhizobium meliloti	39,486	6-Sep-97
rxa02117	597	GB_BA2:AF094575	18754	AF094575	Streptococcus pneumoniae serotype 19A DexB (dexB) gene, partial sequence, capsular polysaccharide biosynthesis operon, complete sequence, and oligopeptide permease AliA (aliA) gene, partial cds	Streptococcus pneumoniae	40,480	9-Sep-99

TABLE 4: ALIGNMENT RESULTS

		GB_BA2:AF105113	5832	AF105113	Streptococcus pneumoniae type 19A putative oligosaccharide repeat unit transporter (cps19AJ) gene, partial cds; UDP-N-acetyl glucosamine-2-epimerase (cps19AK), glucose-1-phosphate thymidylyl transferase (cps19AL), dTDP-4-keto-6-deoxyglucose-3,5-epimerase (cps19AM), dTDP-glucose-4,6 dehydratase (cps19AN), and dTDP-L-rhamnose synthase (cps19AO) genes, complete cds, and AliA (aliA) gene, partial cds	Streptococcus pneumoniae	40,652	9-Sep-99
		GB_EST9 AA073381	429	AA073381	mm93a12 r1 Stratagene mouse heart (#937316) Mus musculus cDNA clone IMAGE 535966 5' similar to gb X03765 Mouse mRNA for cytoplasmatic beta-actin (MOUSE),, mRNA sequence	Mus musculus	46,341	15-Feb-97
rxa02121	828	GB_PR4.AC004874	95983	AC004874	Homo sapiens PAC clone DJ0744D13 from 7q11, complete sequence	Homo sapiens	40,791	21-Nov-98
		GB_EST14 AA418305	440	AA418305	zv96g05 s1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE 767672 3', mRNA sequence	Homo sapiens	40,093	16-OCT-1997
		GB_BA2.U32763	12021	U32763	Haemophilus influenzae Rd section 78 of 163 of the complete genome	Haemophilus influenzae Rd	37,715	29-MAY-1998
rxa02123	1494	GB_BA1.MTCY10D7	39800	Z79700	Mycobacterium tuberculosis H37Rv complete genome, segment 44/162	Mycobacterium tuberculosis	62,083	17-Jun-98
		GB_BA1:MTCY10D7	39800	Z79700	Mycobacterium tuberculosis H37Rv complete genome, segment 44/162	Mycobacterium tuberculosis	38,462	17-Jun-98
		GB_GSS15 AQ639831	649	AQ639831	927P1-20A2 TV 927P1 Trypanosoma brucei genomic clone 927P1-20A2, genomic survey sequence.	Trypanosoma brucei	36,124	8-Jul-99
rxa02124	2079	GB_PR2:HS242N11	167514	AL023655	Human DNA sequence from clone 242N11 on chromosome 6p22 3-23. Contains ESTs, STSs, GSSs, genomic marker D6S285, and ca and gaaa repeat polymorphisms, complete sequence	Homo sapiens	33,866	23-Nov-99
		GB_PR2 HS242N11	167514	AL023655	Human DNA sequence from clone 242N11 on chromosome 6p22 3-23 Contains ESTs, STSs, GSSs, genomic marker D6S285, and ca and gaaa repeat polymorphisms, complete sequence	Homo sapiens	36,342	23-Nov-99
rxa02125	924	GB_HTG1.CEY116A8_4	110000	Z98858	Caenorhabditis elegans chromosome IV clone Y116A8, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Caenorhabditis elegans	36,615	23-Jan-98
		GB_IN1:CEY116A8B	29344	AL021469	Caenorhabditis elegans cosmid Y116A8B, complete sequence	Caenorhabditis elegans	36,615	23-Nov-98
		GB_HTG1:CEY116A8_4	110000	Z98858	Caenorhabditis elegans chromosome IV clone Y116A8, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Caenorhabditis elegans	36,615	23-Jan-98
rxa02129	357	GB_HTG5 AC007809	141122	AC007809	Drosophila melanogaster chromosome 3 clone BACR45M03 (D718) RPCI-98 45.M.3 map 88C-88C strain y, cn bw sp, *** SEQUENCING IN PROGRESS ***, 98 unordered pieces	Drosophila melanogaster	37,255	16-Nov-99
		GB_IN2 CELT02C5	36267	U55374	Caenorhabditis elegans cosmid T02C5.	Caenorhabditis elegans	41,834	08-OCT-1999
		GB_IN1:CEZC101	26147	Z93395	Caenorhabditis elegans cosmid ZC101, complete sequence	Caenorhabditis elegans	38,873	23-Jul-99
rxa02132								
rxa02137	921	GB_EST16 C48630	360	C48630	C48630 Yuji Kohara unpublished cDNA Strain N2 hermaphrodite embryo Caenorhabditis elegans cDNA clone yk459c11 5', mRNA sequence.	Caenorhabditis elegans	39,326	18-OCT-1999
		GB_GSS12 AQ381854	597	AQ381854	RPCI11-137P5.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-137P5, genomic survey sequence.	Homo sapiens	37,879	21-MAY-1999
		GB_HTG3 AC010253	74835	AC010253	Homo sapiens chromosome 5 clone CIT-HSPC_432B14, *** SEQUENCING IN PROGRESS ***, 34 unordered pieces	Homo sapiens	35,082	15-Sep-99
rxa02138	465	GB_BA1:SC6G10	36734	AL049497	Streptomyces coelicolor cosmid 6G10.	Streptomyces coelicolor	40,047	24-MAR-1999
		GB_BA1 MSGB1554CS	36548	L78814	Mycobacterium leprae cosmid B1554 DNA sequence	Mycobacterium leprae	60,991	15-Jun-96
		GB_BA1 MSGB1551CS	36548	L78813	Mycobacterium leprae cosmid B1551 DNA sequence	Mycobacterium leprae	60,991	15-Jun-96
rxa02141	531	GB_HTG2 AC003118	98940	AC003118	Homo sapiens chromosome 1, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces	Homo sapiens	34,008	24-Nov-97
		GB_HTG2 AC003118	98940	AC003118	Homo sapiens chromosome 1, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces	Homo sapiens	34,008	24-Nov-97
		GB_PR3 HS395P12	147724	AL022310	Human DNA sequence from clone 395P12 on chromosome 1q24-25 Contains the TXGP1 gene for tax-transcriptionally activated glycoprotein 1 (34kD) (OX40 ligand, OX40L) and a GOT2 (Aspartate Aminotransferase, mitochondrial precursor, EC 2.6 1.1, Transaminase A, Glutamate Oxaloacetate Transaminase-2) pseudogene Contains ESTs, STSs and GSSs, complete sequence	Homo sapiens	34,008	23-Nov-99

TABLE 4: ALIGNMENT RESULTS

rxa02146	750	GB_BA1:SC6G10	36734	AL049497	Streptomyces coelicolor cosmid 6G10.	Streptomyces coelicolor	36,167	24-MAR-1999
		GB_HTG6:AC008224	199774	AC008224	Drosophila melanogaster chromosome 3 clone BACR29J02 (D817) RPCI-98 29 J 2 map 83D-83D strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 37 unordered pieces	Drosophila melanogaster	36,437	24-Nov-99
		GB_GSS12 AQ407179	476	AQ407179	HS_5088_A2_G01_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=664 Col=2 Row=M, genomic survey sequence.	Homo sapiens	37,143	17-MAR-1999
rxa02151	1311	GB_PR3 AC000074	44450	AC000074	Homo sapiens Chromosome 22q11 2 Cosmid Clone 20b In DGCR Region, complete sequence	Homo sapiens	37,798	31-OCT-1998
		GB_PR2.HSAC002122	79931	AC002122	Human unknown clone GS293J04 from 5p15 2, complete sequence	Homo sapiens	36,064	27-MAY-1997
		GB_PR2.HSAC002122	79931	AC002122	Human unknown clone GS293J04 from 5p15.2, complete sequence	Homo sapiens	35,051	27-MAY-1997
rxa02152	525	GB_PAT AR009990	2793	AR009990	Sequence 1 from patent US 5756677	Unknown.	44,311	04-DEC-1998
		GB_IN1 AF027735	3060	AF027735	Nephila clavipes minor ampullate silk protein MiSp1 mRNA, partial cds	Nephila clavipes	44,311	23-Apr-98
		GB_PAT I95876	2793	I95876	Sequence 1 from patent US 5733771	Unknown.	44,311	01-DEC-1998
rxa02163	876	GB_PR3 HSJ1175I6	96276	AL049538	Human DNA sequence from clone 1175I6 on chromosome 20 Contains the gene for Ras inhibitor JC265 (Ras association (RalGDS/AF-6) domain containing protein), ESTs, STSs, GSSs and two putative CpG islands, complete sequence	Homo sapiens	36,385	23-Nov-99
		GB_GSS4:AQ690740	975	AQ690740	nbxb0082N18f CUGI Rice BAC Library Oryza sativa genomic clone nbxb0082N18f, genomic survey sequence.	Oryza sativa	39,474	1-Jul-99
		GB_PH.SVVWBORF	6051	X72092	Streptomyces venezuelae bacteriophage VWB orfs	Bacteriophage VWB	41,416	24-Aug-95
rxa02164	1698	GB_BA2 AF000579	8931	AF000579	Bordetella bronchiseptica LysR transcriptional activator homolog (bbuR), urease accessory protein D (ureD), urease structural subunit A (ureA), urease accessory protein J (ureJ), urease structural subunits B (ureB) and C (ureC), urease accessory proteins EF (ureEF) and G (ureG) genes, complete cds	Bordetella bronchiseptica	38,005	23-Feb-98
		GB_PR3.HS431P23	147971	AL009178	Human DNA sequence from clone 431P23 on chromosome 6q27 Contains the first coding exon of the MLLT4 gene for myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog), translocated to, 4 (AF-6, Afadin, MLLT-4, ALL-1 fusion partner), and a Serine Palmitoyltransferase 2 (EC 2.3.1.50, Long Chain Base Biosynthesis protein 2, LCB-2, SPT-2) pseudogene Contains ESTs, STss, GSSs, and a putative CpG island, complete sequence	Homo sapiens	35,604	23-Nov-99
		GB_PR2 AB016897	331211	AB016897	Homo sapiens genomic DNA, chromosome 6q27, complete sequence	Homo sapiens	38,314	20-Nov-99
rxa02165	735	GB_IN2.AF079177	2159	AF079177	Theileria parva strain KNP2 p67 surface antigen (p67) gene, complete cds	Theileria parva	39,207	09-MAR-1999
		GB_IN2 AF079176	2285	AF079176	Theileria parva strain Hluhluwe3 p67 surface antigen (p67) gene, complete cds.	Theileria parva	39,049	09-MAR-1999
		GB_EST27:AI397572	482	AI397572	NCSC5G2T3 Subtracted Conidial Neurospora crassa cDNA clone SC5G2 5', mRNA sequence	Neurospora crassa	38,936	8-Feb-99
rxa02166	300	GB_BA1:MLCB1351	38936	Z95117	Mycobacterium leprae cosmid B1351	Mycobacterium leprae	37,627	24-Jun-97
		GB_BA1:MLCB1351	38936	Z95117	Mycobacterium leprae cosmid B1351	Mycobacterium leprae	40,741	24-Jun-97
rxa02168	2937	GB_BA1.MAFASGEN	10520	X87822	B ammoniagenes FAS gene	Corynebacterium ammoniagenes	61,515	03-OCT-1996
		GB_BA1 MLCL458	43839	AL049478	Mycobacterium leprae cosmid L458.	Mycobacterium leprae	50,292	27-Aug-99
		GB_PR3:HSL19H1	40145	Z68164	Human DNA sequence from cosmid L19H1, Huntington's Disease Region, chromosome 4p16 3, containing multiple EST matches	Homo sapiens	37,621	23-Nov-99
rxa02169	969	GB_RO MMA3CA212	4784	X94406	Mus musculus partial b3 gene for alpha3 subunit of L-type Ca2+ channel, exons 2-13	Mus musculus	37,620	24-Nov-99
		GB_RO RATCACH3B	2525	M88751	Rat calcium channel beta subunit-III mRNA, complete cds	Rattus norvegicus	36,345	27-MAY-1994
		GB_RO MMU20372	2469	U20372	Mus musculus voltage-dependent calcium channel beta-3 subunit (CCHB3) mRNA, complete cds	Mus musculus	36,865	02-MAR-1996
rxa02170	897	GB_HTG6:AC005497	212097	AC005497	Homo sapiens chromosome 17 clone RP11-952N18 map 17, *** SEQUENCING IN PROGRESS ***, 2 ordered pieces	Homo sapiens	36,101	20-Nov-99
		GB_HTG6 AC005497	212097	AC005497	Homo sapiens chromosome 17 clone RP11-952N18 map 17, *** SEQUENCING IN PROGRESS ***, 2 ordered pieces.	Homo sapiens	37,570	20-Nov-99
		GB_PR2 AP000104	100000	AP000104	Homo sapiens genomic DNA of 21q22 1, GART and AML related, Q78C10-149C3 region, segment 7/20, complete sequence	Homo sapiens	34,871	25-Sep-99
rxa02172	462	GB_EST24 AI170522	367	AI170522	EST216450 Normalized rat lung, Bento Soares Rattus sp cDNA clone RLUCO75 3' end, mRNA sequence	Rattus sp.	38,904	20-Jan-99

TABLE 4: ALIGNMENT RESULTS

		GB_GSS13:AQ430048	538	AQ430048	HS_5061_B2_G09_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=637 Col=18 Row=N, genomic survey sequence	Homo sapiens	37,143	31-MAR-1999
		GB_GSS4 AQ701704	589	AQ701704	HS_2130_A1_E03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2130 Col=5 Row=I, genomic survey sequence	Homo sapiens	35,280	7-Jul-99
rxa02177	1056	GB_HTG4 AC009403	198495	AC009403	Homo sapiens clone DJ1015O24, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces.	Homo sapiens	37,154	28-OCT-1999
		GB_HTG4:AC009403	198495	AC009403	Homo sapiens clone DJ1015O24, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces	Homo sapiens	37,154	28-OCT-1999
		GB_PR2.AP000094	100000	AP000094	Homo sapiens genomic DNA of 21q22 1, GART and AML related, B335D16-P10G11 region, segment 4/7, complete sequence	Homo sapiens	38,536	25-Sep-99
rxa02178								
rxa02180	1581	GB_BA1:SC6C5	18160	AL034492	Streptomyces coelicolor cosmid 6C5	Streptomyces coelicolor	53,635	14-DEC-1998
		GB_HTG4.AC011121	172050	AC011121	Homo sapiens chromosome 11 clone 364_C_06 map 11, *** SEQUENCING IN PROGRESS ***, 9 ordered pieces	Homo sapiens	37,170	14-OCT-1999
		GB_HTG4:AC011121	172050	AC011121	Homo sapiens chromosome 11 clone 364_C_06 map 11, *** SEQUENCING IN PROGRESS ***, 9 ordered pieces	Homo sapiens	37,170	14-OCT-1999
rxa02181	801	GB_PL1 STU76701	3049	U76701	Solanum tuberosum NADH nitrate reductase (StNR2) mRNA, complete cds	Solanum tuberosum	38,846	18-Nov-96
		GB_EST36 AI896605	633	AI896605	EST266048 tomato callus, TAMU Lycopersicon esculentum cDNA clone cLEC16C12, mRNA sequence.	Lycopersicon esculentum	39,671	27-Jul-99
		GB_EST38:AW035744	620	AW035744	EST281898 tomato callus, TAMU Lycopersicon esculentum cDNA clone cLEC36M13, mRNA sequence.	Lycopersicon esculentum	40,555	15-Sep-99
rxa02183								
rxa02185	702	GB_BA1.MTV043	68848	AL022004	Mycobacterium tuberculosis H37Rv complete genome, segment 40/162	Mycobacterium tuberculosis	38,793	24-Jun-99
		GB_BA1:MSGB1935CS	40085	L04666	M leprae genomic sequence, cosmid b1935	Mycobacterium leprae	38,067	14-Jun-96
		GB_BA1:MLCB57	38029	Z99494	Mycobacterium leprae cosmid B57	Mycobacterium leprae	38,067	10-Feb-99
rxa02186	321	GB_BA2:CNSPAX03	307120	AJ248285	Pyrococcus abyssi complete genome; segment 3/6	Pyrococcus abyssi	35,873	9-Sep-99
		GB_HTG3 AC010677	116108	AC010677	Homo sapiens clone MS2304L04, *** SEQUENCING IN PROGRESS ***, 4 unordered pieces.	Homo sapiens	39,145	04-OCT-1999
		GB_HTG3 AC010677	116108	AC010677	Homo sapiens clone MS2304L04, *** SEQUENCING IN PROGRESS ***, 4 unordered pieces	Homo sapiens	39,145	04-OCT-1999
rxa02187	2322	GB_EST33.AI779784	362	AI779784	EST260663 tomato susceptible, Cornell Lycopersicon esculentum cDNA clone cLES9K1, mRNA sequence	Lycopersicon esculentum	41,011	29-Jun-99
		GB_EST33 AI779784	362	AI779784	EST260663 tomato susceptible, Cornell Lycopersicon esculentum cDNA clone cLES9K1, mRNA sequence	Lycopersicon esculentum	41,011	29-Jun-99
rxa02199	693	GB_PR3:AC005274	205150	AC005274	Homo sapiens chromosome 17, clone hRPK 1090_M_7, complete sequence	Homo sapiens	36,337	29-Jul-98
		GB_HTG2:AC007732	110348	AC007732	Homo sapiens chromosome 17 clone hRPC 1030_A_12 map 17, *** SEQUENCING IN PROGRESS ***, 7 unordered pieces.	Homo sapiens	35,924	5-Jun-99
		GB_IN1:DMU11052	4871	U11052	Drosophila melanogaster peroxidasin precursor mRNA, complete cds	Drosophila melanogaster	39,873	26-Jan-95
rxa02203	501	GB_EST17:AA642571	323	AA642571	nq73c08 s1 NCI_CGAP_Pr22 Homo sapiens cDNA clone IMAGE 1157966 3' similar to TR G9372 G9372 UBIQUITIN ,, mRNA sequence	Homo sapiens	49,485	27-OCT-1997
		GB_EST27.AI425489	312	AI425489	my32e11.y1 Barstead mouse pooled organs MPLRB4 Mus musculus cDNA clone IMAGE 697580 5', mRNA sequence.	Mus musculus	40,514	09-MAR-1999
		GB_EST23 AI154481	308	AI154481	ua03h07.r1 Soares 2NbMT Mus musculus cDNA clone IMAGE:1345693 5', mRNA sequence	Mus musculus	42,748	30-Sep-98
rxa02206	1059	GB_PR2.AP000269	70932	AP000269	Homo sapiens genomic DNA, chromosome 21q22.1, D21S226-AML region, clone T293, complete sequence	Homo sapiens	39,306	20-Nov-99
		GB_PL1 D32140	1360	D32140	Cyanidioschyzon merolae DNA for actin, complete cds	Cyanidioschyzon merolae	37,331	7-Feb-99
		GB_PR2 AP000269	70932	AP000269	Homo sapiens genomic DNA, chromosome 21q22 1, D21S226-AML region, clone T293, complete sequence	Homo sapiens	35,481	20-Nov-99

TABLE 4: ALIGNMENT RESULTS

rxa02207	898	GB_EST21:AA982901	442	AA982901	vx59f07.r1 Stratagene mouse macrophage (#937306) Mus musculus cDNA clone IMAGE:1279525 5' similar to gb:X59543_rna1RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE M1 CHAIN (HUMAN), gb.K02927 Mouse ribonucleotide reductase subunit M1 mRNA, complete (MOUSE);, mRNA sequence	Mus musculus	42,141	27-MAY-1998
		GB_EST8:W85369	558	W85369	mf48h04.r1 Soares mouse embryo NbME13 5 14.5 Mus musculus cDNA clone IMAGE.408343 5' similar to gb K02927 Mouse ribonucleotide reductase subunit M1 mRNA, complete (MOUSE),, mRNA sequence.	Mus musculus	39,964	12-Sep-96
rxa02211		GB_PAT E14824	2379	E14824	cDNA encoding M1 subunit of human ribonucleotide reductase	Homo sapiens	36,812	28-Jul-99
rxa02212	621	GB_HTG3:AC009518	241128	AC009518	Homo sapiens chromosome 7, *** SEQUENCING IN PROGRESS ***, 68 unordered pieces	Homo sapiens	36,542	1-Sep-99
		GB_HTG3:AC009518	241128	AC009518	Homo sapiens chromosome 7, *** SEQUENCING IN PROGRESS ***, 68 unordered pieces	Homo sapiens	36,542	1-Sep-99
		GB_HTG3.AC009518	241128	AC009518	Homo sapiens chromosome 7, *** SEQUENCING IN PROGRESS ***, 68 unordered pieces.	Homo sapiens	41,362	1-Sep-99
rxa02216	329	GB_HTG2 AC007641	102402	AC007641	Mus musculus chromosome 10 clone 644_M_8 map 10, *** SEQUENCING IN PROGRESS ***, 7 unordered pieces.	Mus musculus	31,307	22-MAY-1999
		GB_HTG2.AC007641	102402	AC007641	Mus musculus chromosome 10 clone 644_M_8 map 10, *** SEQUENCING IN PROGRESS ***, 7 unordered pieces	Mus musculus	31,307	22-MAY-1999
		GB_HTG2 AC007641	102402	AC007641	Mus musculus chromosome 10 clone 644_M_8 map 10, *** SEQUENCING IN PROGRESS ***, 7 unordered pieces	Mus musculus	32,198	22-MAY-1999
rxa02217	786	GB_RO RNU91516	1540	U91516	Rattus norvegicus oxytocin receptor (OTR) gene, promoter region	Rattus norvegicus	36,256	25-Nov-97
		GB_RO.RNU91516	1540	U91516	Rattus norvegicus oxytocin receptor (OTR) gene, promoter region.	Rattus norvegicus	37,176	25-Nov-97
rxa02218	390	GB_HTG3 AC008656	43033	AC008656	Homo sapiens chromosome 5 clone CIT978SKB_194J6, *** SEQUENCING IN PROGRESS ***, 64 unordered pieces	Homo sapiens	39,894	3-Aug-99
		GB_HTG3:AC008656	43033	AC008656	Homo sapiens chromosome 5 clone CIT978SKB_194J6, *** SEQUENCING IN PROGRESS ***, 64 unordered pieces.	Homo sapiens	39,894	3-Aug-99
		GB_HTG3:AC008656	43033	AC008656	Homo sapiens chromosome 5 clone CIT978SKB_194J6, *** SEQUENCING IN PROGRESS ***, 64 unordered pieces	Homo sapiens	37,598	3-Aug-99
rxa02219	1509	GB_PR3.HS475N16	113109	AL035587	Human DNA sequence from clone 475N16 on chromosome 6p12 3-21.2, complete sequence.	Homo sapiens	36,266	23-Nov-99
		GB_PR3 HS475N16	113109	AL035587	Human DNA sequence from clone 475N16 on chromosome 6p12.3-21 2, complete sequence	Homo sapiens	35,255	23-Nov-99
		GB_EST10.AA142336	411	AA142336	ms07f02 r1 Stratagene mouse skin (#937313) Mus musculus cDNA clone IMAGE.606267 5' similar to SW.RCA1_YEAST P40341 MITOCHONDRIAL RESPIRATORY CHAIN COMPLEXES ASSEMBLY PROTEIN RCA1 ;, mRNA sequence	Mus musculus	38,398	12-Feb-97
rxa02221	1485	GB_PR3:AC002422	160091	AC002422	Human Chromosome X, complete sequence	Homo sapiens	38,435	30-Jan-98
		GB_HTG2.AC006755	199917	AC006755	Caenorhabditis elegans clone Y40C5, *** SEQUENCING IN PROGRESS ***, 1 unordered pieces	Caenorhabditis elegans	39,229	23-Feb-99
		GB_HTG2 AC006755	199917	AC006755	Caenorhabditis elegans clone Y40C5, *** SEQUENCING IN PROGRESS ***, 1 unordered pieces	Caenorhabditis elegans	39,229	23-Feb-99
rxa02223	601	GB_HTG6 AC008224	199774	AC008224	Drosophila melanogaster chromosome 3 clone BACR29J02 (D817) RPCI-98 29 J 2 map 83D-83D strain y, cn bw sp, *** SEQUENCING IN PROGRESS ***, 37 unordered pieces	Drosophila melanogaster	35,333	24-Nov-99
		GB_HTG3 AC011511	158296	AC011511	Homo sapiens chromosome 19 clone CITB-H1_2369P2, *** SEQUENCING IN PROGRESS ***, 57 unordered pieces	Homo sapiens	35,593	07-OCT-1999
		GB_HTG3.AC011511	158296	AC011511	Homo sapiens chromosome 19 clone CITB-H1_2369P2, *** SEQUENCING IN PROGRESS ***, 57 unordered pieces	Homo sapiens	35,593	07-OCT-1999
rxa02226	1156	GB_HTG2:AC006890	298195	AC006890	Caenorhabditis elegans clone Y67D8x, *** SEQUENCING IN PROGRESS ***, 23 unordered pieces.	Caenorhabditis elegans	36,810	24-Feb-99
		GB_HTG2:AC006890	298195	AC006890	Caenorhabditis elegans clone Y67D8x, *** SEQUENCING IN PROGRESS ***, 23 unordered pieces.	Caenorhabditis elegans	35,433	24-Feb-99
		GB_HTG2:AC006890	298195	AC006890	Caenorhabditis elegans clone Y67D8x, *** SEQUENCING IN PROGRESS ***, 23 unordered pieces	Caenorhabditis elegans	36,810	24-Feb-99

TABLE 4: ALIGNMENT RESULTS

rxa02227	741	GB_EST5:H98835	440	H98835	yx14f12.s1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:261743 3', mRNA sequence.	Homo sapiens	38,182	15-DEC-1995
		GB_EST5.N25530	586	N25530	yx76c03 s1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE 267652 3', mRNA sequence.	Homo sapiens	37,543	29-DEC-1995
		GB_BA1 CGU43535	2531	U43535	Corynebacterium glutamicum multidrug resistance protein (cmr) gene, complete cds	Corynebacterium glutamicum	38,812	9-Apr-97
rxa02230	660	GB_EST16:AA570388	527	AA570388	nk62c08 s1 NCI_CGAP_Sch1 Homo sapiens cDNA clone IMAGE 1018094 3' similar to contains element MSR1 repetitive element ,, mRNA sequence	Homo sapiens	41,096	9-Sep-97
		GB_PR2 HSU43030	1539	U43030	Human cardiotrophin-1 (CTF1) mRNA, complete cds	Homo sapiens	36,335	9-Jan-96
		GB_IN1 CELK08B5	35728	U41022	Caenorhabditis elegans cosmid K08B5	Caenorhabditis elegans	35,387	30-Nov-95
rxa02231	879	GB_PL2:ATAC006429	94818	AC006429	Arabidopsis thaliana chromosome II BAC F15K19 genomic sequence, complete sequence	Arabidopsis thaliana	33,687	23-Apr-99
		GB_PR3 AC004554	195142	AC004554	Homo sapiens Xp22 BAC GSHB-590J6 (Genome Systems Human BAC library) complete sequence	Homo sapiens	38,921	30-MAY-1998
		GB_HTG2 AC007853	116280	AC007853	Drosophila melanogaster chromosome 3 clone BACR03L02 (D766) RPCI-98 03 L 2 map 96B-96C strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 80 unordered pieces	Drosophila melanogaster	36,237	2-Aug-99
rxa02238	408	GB_BA1 MTCY21B4	39150	Z80108	Mycobacterium tuberculosis H37Rv complete genome, segment 62/162	Mycobacterium tuberculosis	52,206	23-Jun-98
		GB_BA1 MTCY21B4	39150	Z80108	Mycobacterium tuberculosis H37Rv complete genome, segment 62/162	Mycobacterium tuberculosis	36,935	23-Jun-98
		GB_VI AF105451	801	AF105451	HIV-1 isolate A-DII-07 from Italy, envelope glycoprotein, C2-V5 region (env) gene, partial cds	Human immunodeficiency virus type 1	40,864	25-Apr-99
rxa02244	1656	GB_PR1 AB016195	10558	AB016195	Homo sapiens ELK1 pseudogene (ELK2) and immunoglobulin heavy chain gamma pseudogene (IGHGP)	Homo sapiens	38,929	9-Apr-99
		GB_PR3 HSN21F1	39212	Z94162	Human DNA sequence from cosmid N21F1 on chromosome 22 Contains exon trap and STS, complete sequence	Homo sapiens	38,763	23-Nov-99
		GB_IN1 DMAC001648	51989	AC001648	Drosophila melanogaster (P1 DS03431 (D102)) DNA sequence, complete sequence	Drosophila melanogaster	36,884	22-Apr-97
rxa02254	800	GB_GSS12 AQ360240	541	AQ360240	HS_5035_A2_E07_T7 RPCI11 Human Male BAC Library Homo sapiens genomic clone Plate=611 Col=14 Row=I, genomic survey sequence	Homo sapiens	36,386	06-MAR-1999
		GB_GSS11 AQ258453	620	AQ258453	nbxb0020L15f CUGI Rice BAC Library Oryza sativa genomic clone nbxb0020L15f, genomic survey sequence	Oryza sativa	36,271	23-OCT-1998
		GB_GSS14 AQ577777	568	AQ577777	nbxb0091L17f CUGI Rice BAC Library Oryza sativa genomic clone nbxb0091L17f, genomic survey sequence.	Oryza sativa	39,456	2-Jun-99
rxa02255	1059	GB_PR4 AC006332	153477	AC006332	Homo sapiens clone NH0376O14, complete sequence	Homo sapiens	35,019	11-Nov-99
		GB_PAT E02669	1197	E02669	DNA encoding Bacillus sp L-lactic acid dehydrogenase	Bacillus sp	39,719	29-Sep-97
		GB_PL1:YSCBOI2	3201	D38310	Yeast BOI2 gene for Boi2p	Saccharomyces cerevisiae	35,769	8-Feb-99
rxa02266	636	GB_BA1 REGIONB	4961	Z13995	N meningitidis lipA and lipB genes for LipA and LipB proteins	Neisseria meningitidis	35,691	29-DEC-1993
		GB_HTG1 AP000568	136627	AP000568	Homo sapiens chromosome 21 clone B753B2 map 21q21 2, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	37,500	07-OCT-1999
		GB_HTG1 AP000568	136627	AP000568	Homo sapiens chromosome 21 clone B753B2 map 21q21 2, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Homo sapiens	37,500	07-OCT-1999
rxa02267	996	GB_PR4 AC007283	127361	AC007283	Homo sapiens clone NH0536I18, complete sequence	Homo sapiens	37,155	28-Sep-99
		GB_IN1 CEC54C6	35500	Z77131	Caenorhabditis elegans cosmid C54C6, complete sequence	Caenorhabditis elegans	38,280	23-Nov-98
		GB_HTG3 AC008905	129915	AC008905	Homo sapiens chromosome 5 clone CITB-H1_2259I14, *** SEQUENCING IN PROGRESS ***, 40 unordered pieces.	Homo sapiens	35,895	3-Aug-99
rxa02271	681	GB_HTG3 AC007441	219832	AC007441	Drosophila melanogaster chromosome 3 clone BACR10E03 (D690) RPCI-98 10 E 3 map 88A-88B strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 188 unordered pieces	Drosophila melanogaster	33,284	08-OCT-1999
		GB_HTG3 AC007441	219832	AC007441	Drosophila melanogaster chromosome 3 clone BACR10E03 (D690) RPCI-98 10 E 3 map 88A-88B strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 188 unordered pieces	Drosophila melanogaster	33,284	08-OCT-1999
		GB_HTG2 AC008029	123186	AC008029	Drosophila melanogaster chromosome 3 clone BACR01C11 (D819) RPCI-98 01 C.11 map 84D-84D strain y, cn bw sp, *** SEQUENCING IN PROGRESS ***, 92 unordered pieces	Drosophila melanogaster	34,315	2-Aug-99

TABLE 4: ALIGNMENT RESULTS

rxa02279	1581	GB_IN1:AC003121	69822	AC003121	Drosophila melanogaster (P1 DS00329 (D89)) DNA sequence, complete sequence.	Drosophila melanogaster	38,046	26-Nov-97
		GB_IN1:AC003121	69822	AC003121	Drosophila melanogaster (P1 DS00329 (D89)) DNA sequence, complete sequence	Drosophila melanogaster	39,220	26-Nov-97
		GB_BA1:MTCY39	38500	Z74025	Mycobacterium tuberculosis H37Rv complete genome; segment 89/162	Mycobacterium tuberculosis	39,685	17-Jun-98
rxa02280								
rxa02286	672	GB_BA1 MTV025	121125	AL022121	Mycobacterium tuberculosis H37Rv complete genome, segment 155/162	Mycobacterium tuberculosis	36,953	24-Jun-99
		GB_PL2 AC002130	114738	AC002130	The sequence of BAC F1N21 from Arabidopsis thaliana chromosome 1, complete sequence	Arabidopsis thaliana	39,216	8-Jan-98
		GB_PL2 AC007259	97146	AC007259	Arabidopsis thaliana chromosome I BAC T28P6 genomic sequence, complete sequence	Arabidopsis thaliana	36,090	17-Aug-99
rxa02287	675	GB_HTG3 AC009281	221178	AC009281	Homo sapiens chromosome 15 clone 8_C_22 map 15, *** SEQUENCING IN PROGRESS ***, 49 unordered pieces	Homo sapiens	35,565	12-Aug-99
		GB_HTG3 AC009281	221178	AC009281	Homo sapiens chromosome 15 clone 8_C_22 map 15, *** SEQUENCING IN PROGRESS ***, 49 unordered pieces	Homo sapiens	35,565	12-Aug-99
		GB_RO MUSMURINC	4597	M65736	Mouse murinoglobulin mRNA, complete cds	Mus musculus	38,485	27-Apr-93
rxa02294	498	GB_EST19 AA813194	398	AA813194	ai80g12 s1 Soares_testis_NHT Homo sapiens cDNA clone 1377190 3', mRNA sequence	Homo sapiens	36,797	31-DEC-1998
		GB_EST19:AA813194	398	AA813194	ai80g12 s1 Soares_testis_NHT Homo sapiens cDNA clone 1377190 3', mRNA sequence	Homo sapiens	33,417	31-DEC-1998
rxa02295	903	GB_PAT:I89451	18318	I89451	Sequence 6 from patent US 5721354	Unknown	38,839	10-Aug-98
		GB_VI HCU33331	18535	U33331	Human cytomegalovirus Toledo strain UL/b' region	human herpesvirus 5	38,839	27-Jan-96
		GB_PR3 HS550H1	108803	AL035420	Human DNA sequence from clone 550H1 on chromosome 20q11 1-11 22 Contains a pseudogene similar to HIGH MOBILITY GROUP PROTEIN 2A, a novel mRNA, ESTs, STSs, GSSs and CpG Islands, complete sequence	Homo sapiens	38,796	23-Nov-99
rxa02296	612	GB_BA2:AF065312	1694	AF065312	Yersinia pestis hypothetical protein (yceG) gene, partial cds, thymidylate kinase (tmk) gene, complete cds; and putative DNA polymerase III delta' subunit (holB) gene, partial cds	Yersinia pestis	41,351	16-Nov-99
		GB_PR3 HS550H1	108803	AL035420	Human DNA sequence from clone 550H1 on chromosome 20q11 1-11 22 Contains a pseudogene similar to HIGH MOBILITY GROUP PROTEIN 2A, a novel mRNA, ESTs, STSs, GSSs and CpG Islands, complete sequence	Homo sapiens	37,919	23-Nov-99
		GB_PR3 HS550H1	108803	AL035420	Human DNA sequence from clone 550H1 on chromosome 20q11 1-11 22 Contains a pseudogene similar to HIGH MOBILITY GROUP PROTEIN 2A, a novel mRNA, ESTs, STSs, GSSs and CpG Islands, complete sequence.	Homo sapiens	37,607	23-Nov-99
rxa02297	1260	GB_BA2 AF065312	1694	AF065312	Yersinia pestis hypothetical protein (yceG) gene, partial cds, thymidylate kinase (tmk) gene, complete cds, and putative DNA polymerase III delta' subunit (holB) gene, partial cds	Yersinia pestis	39,683	16-Nov-99
		GB_RO:AF007836	5655	AF007836	Rattus norvegicus rab3 effector (RIM) mRNA, alternatively spliced, complete cds	Rattus norvegicus	37,844	15-Aug-97
		GB_IN2:EGU27015	2394	U27015	Echinococcus granulosus 18S ribosomal RNA gene, complete sequence	Echinococcus granulosus	38,710	16-Jul-96
rxa02298	1782	GB_BA2:AF116184	540	AF116184	Corynebacterium glutamicum L-aspartate-alpha-decarboxylase precursor (panD) gene, complete cds	Corynebacterium glutamicum	44,231	02-MAY-1999
		GB_BA2 AF116184	540	AF116184	Corynebacterium glutamicum L-aspartate-alpha-decarboxylase precursor (panD) gene, complete cds	Corynebacterium glutamicum	42,007	02-MAY-1999
rxa02300	456	GB_BA2 AF116184	540	AF116184	Corynebacterium glutamicum L-aspartate-alpha-decarboxylase precursor (panD) gene, complete cds	Corynebacterium glutamicum	46,250	02-MAY-1999
		GB_BA1 MTV004	69350	AL009198	Mycobacterium tuberculosis H37Rv complete genome, segment 144/162	Mycobacterium tuberculosis	39,602	18-Jun-98
		GB_EST22 AI048692	172	AI048692	ub30g04 r1 Soares 2NbMT Mus musculus cDNA clone IMAGE 1379286 5', mRNA sequence	Mus musculus	43,284	8-Jul-98
rxa02301	840	GB_HTG3:AC008573	205755	AC008573	Homo sapiens chromosome 5 clone CIT-HSPC_551I11, *** SEQUENCING IN PROGRESS ***, 95 unordered pieces	Homo sapiens	35,115	3-Aug-99
		GB_HTG3 AC008573	205755	AC008573	Homo sapiens chromosome 5 clone CIT-HSPC_551I11, *** SEQUENCING IN PROGRESS ***, 95 unordered pieces	Homo sapiens	35,115	3-Aug-99

TABLE 4: ALIGNMENT RESULTS

		GB_HTG3:AC008573	205755	AC008573	Homo sapiens chromosome 5 clone CIT-HSPC_551I11, *** SEQUENCING IN PROGRESS ***, 95 unordered pieces	Homo sapiens	36,527	3-Aug-99
rxa02302	1002	GB_HTG6 AC008076	200000	AC008076	Homo sapiens chromosome 4, *** SEQUENCING IN PROGRESS ***, 18 unordered pieces	Homo sapiens	34,884	02-DEC-1999
		GB_HTG3 AC008930	258026	AC008930	Homo sapiens chromosome 5 clone CITB-H1_2292M9, *** SEQUENCING IN PROGRESS ***, 166 unordered pieces	Homo sapiens	36,945	3-Aug-99
		GB_HTG3 AC008930	258026	AC008930	Homo sapiens chromosome 5 clone CITB-H1_2292M9, *** SEQUENCING IN PROGRESS ***, 166 unordered pieces	Homo sapiens	36,945	3-Aug-99
rxa02303								
rxa02304	1014	GB_PAT A69720	53789	A69720	Sequence 3 from Patent WO9807868	unidentified	36,915	07-MAY-1999
		GB_BA1:AMM223012	53784	AJ223012	Amycolatopsis mediterranei genes encoding rifamycin polyketide synthases, ORFs 1 to 5	Amycolatopsis mediterranei	36,915	9-Feb-98
		GB_BA2 AF040570	76199	AF040570	Amycolatopsis mediterranei rifamycin biosynthetic gene cluster	Amycolatopsis mediterranei	36,915	5-Feb-98
rxa02307								
rxa02308	552	GB_HTG3:AC009340	110415	AC009340	Drosophila melanogaster chromosome 2 clone BACR04E19 (D1026) RPCI-98 04 E.19 map 34A-34E strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 103 unordered pieces	Drosophila melanogaster	36,066	27-Aug-99
		GB_HTG3 AC009340	110415	AC009340	Drosophila melanogaster chromosome 2 clone BACR04E19 (D1026) RPCI-98 04.E 19 map 34A-34E strain y, cn bw sp, *** SEQUENCING IN PROGRESS ***, 103 unordered pieces	Drosophila melanogaster	36,066	27-Aug-99
		GB_IN2 AC005656	48443	AC005656	Drosophila melanogaster, chromosome 2R, region 34B6-34C2, P1 clone DS08787, complete sequence	Drosophila melanogaster	46,154	6-Feb-99
rxa02314	564	GB_HTG5 AC011247	206436	AC011247	Homo sapiens clone NH0541E12, WORKING DRAFT SEQUENCE, 1 unordered pieces.	Homo sapiens	36,201	13-Nov-99
		GB_HTG5 AC011247	206436	AC011247	Homo sapiens clone NH0541E12, WORKING DRAFT SEQUENCE, 1 unordered pieces	Homo sapiens	35,036	13-Nov-99
		GB_HTG3:AC011152	142616	AC011152	Homo sapiens clone 7_H_4, LOW-PASS SEQUENCE SAMPLING.	Homo sapiens	35,548	01-OCT-1999
rxa02324	1209	GB_BA2:AF110185	20302	AF110185	Burkholderia pseudomallei strain 1026b DbhB (dbhB), general secretory pathway protein D (gspD), general secretory pathway protein E (gspE), general secretory pathway protein F (gspF), GspC (gspC), general secretory pathway protein G (gspG), general secretory pathway protein H (gspH), general secretory pathway protein I (gspI), general secretory pathway protein J (gspJ), general secretory pathway protein K (gspK), general secretory pathway protein L (gspL), general secretory pathway protein M (gspM), and general secretory pathway protein N (gspN) genes, complete cds, and unknown genes	Burkholderia pseudomallei	39,670	2-Aug-99
		GB_BA1 PSEAMNH	5215	D90216	P. chlororaphis genes for amidase (EC 3 5 1 4) and for nitrile hydratase (EC 4 2 1 84).	Pseudomonas chlororaphis	51,254	7-Feb-99
		GB_PAT:E12519	4775	E12519	Nucleotide sequence of Rhodococcus rhodochrous genomic DNA region containing amidase and nitrilehydratase genes.	Rhodococcus rhodochrous	51,646	24-Jun-98
rxa02325	990	GB_BA1 CGPYC	3728	Y09548	Corynebacterium glutamicum pyc gene	Corynebacterium glutamicum	100,000	08-MAY-1998
		GB_PR4 AC006079	178109	AC006079	Homo sapiens chromosome 17, clone hRPK.855_D_21, complete sequence	Homo sapiens	37,807	12-DEC-1998
		GB_GSS8:AQ036832	441	AQ036832	CIT-HSP-2334L1.TF CIT-HSP Homo sapiens genomic clone 2334L1, genomic survey sequence	Homo sapiens	42,359	11-Jul-98
rxa02331	489	GB_PL1 YSKGA11	4159	M68870	Kluyveromyces lactis transcriptional activator (GAL11) gene, complete cds	Kluyveromyces lactis	40,252	14-MAY-1993
		GB_PR2 HSAY18950	584	Y18950	Homo sapiens partial gene for caspase-9, intronic sequence (584 bp)	Homo sapiens	40,529	08-OCT-1999
		GB_PL1 YSKGA11	4159	M68870	Kluyveromyces lactis transcriptional activator (GAL11) gene, complete cds	Kluyveromyces lactis	38,679	14-MAY-1993
rxa02336	303	GB_BA1 CGU35023	3195	U35023	Corynebacterium glutamicum thiosulfate sulfurtransferase (thtR) gene, partial cds, acyl CoA carboxylase (accBC) gene, complete cds	Corynebacterium glutamicum	35,548	16-Jan-97
		GB_PL2 AF114171	183990	AF114171	Sorghum bicolor BAC clone 25 M18, complete sequence	Sorghum bicolor	41,414	25-Apr-99
		GB_PR4 AC006324	157310	AC006324	Homo sapiens clone DJ1164F05, complete sequence	Homo sapiens	41,786	11-Nov-99
rxa02337	1446	GB_BA1 CGU35023	3195	U35023	Corynebacterium glutamicum thiosulfate sulfurtransferase (thtR) gene, partial cds, acyl CoA carboxylase (accBC) gene, complete cds	Corynebacterium glutamicum	100,000	16-Jan-97

TABLE 4: ALIGNMENT RESULTS

		GB_BA1:MTCY22G8	22550	Z95585	Mycobacterium tuberculosis H37Rv complete genome; segment 49/162.	Mycobacterium tuberculosis	38,072	17-Jun-98
		GB_PR2.HSAY18950	584	Y18950	Homo sapiens partial gene for caspase-9, intronic sequence (584 bp)	Homo sapiens	42,949	08-OCT-1999
rxa02339	515	GB_PR2 HS149A16	173354	AL021937	Human DNA sequence from clone 149A16 on chromosome 22q12-13 Contains an IGLC (Immunoglobulin Lambda Chain C) pseudogene, the RFPL3 and RFPL3S genes for Ret finger protein-like 3 and Ret finger protein-like 3 antisense respectively, a gene for a novel Immunoblobulin Lambda Chain V family protein, a novel gene for a protein similar to mouse RGDS (RALGDS, RALGEF, Guanine Nucleotide Dissociation Stimulator A) and rabbit oncogene RSC, a novel gene for the human ortholog of worm F16A11 2 and bacterial and archea-bacterial predicted proteins, a novel gene for a protein similar to BPI (Bacterial Permeability-Increasing Protein) and rabbit LBP (Liposaccharide-Binding Protein), and a the 5' part of a novel gene Contains ESTs, STSs, GSSs, genomic marker D22S1175, a ca repeat polymorphism and putative CpG islands, complete sequence.	Homo sapiens	37,376	23-Nov-99
		GB_HTG3 AC009726	177618	AC009726	Homo sapiens chromosome 18 clone 263_O_14 map 18, *** SEQUENCING IN PROGRESS ***, 12 unordered pieces.	Homo sapiens	37,037	29-Aug-99
		GB_HTG3.AC009726	177618	AC009726	Homo sapiens chromosome 18 clone 263_O_14 map 18, *** SEQUENCING IN PROGRESS ***, 12 unordered pieces	Homo sapiens	37,037	29-Aug-99
rxa02340	1188	GB_VI.AF063866	236120	AF063866	Melanoplus sanguinipes entomopoxvirus, complete genome	Melanoplus sanguinipes entomopoxvirus	34,480	22-DEC-1998
		GB_HTG4 AC011089	171283	AC011089	Homo sapiens chromosome 2 clone 303_K_20 map 2, *** SEQUENCING IN PROGRESS ***, 25 ordered pieces	Homo sapiens	37,757	14-OCT-1999
		GB_HTG4 AC011089	171283	AC011089	Homo sapiens chromosome 2 clone 303_K_20 map 2, *** SEQUENCING IN PROGRESS ***, 25 ordered pieces	Homo sapiens	37,757	14-OCT-1999
rxa02341	609	GB_GSS14 AQ580594	303	AQ580594	RPCI-11-452K5 TJ RPCI-11 Homo sapiens genomic clone RPCI-11-452K5, genomic survey sequence	Homo sapiens	38,305	7-Jun-99
		GB_GSS12 AQ393454	561	AQ393454	CITBI-E1-2556E3 TR CITBI-E1 Homo sapiens genomic clone 2556E3, genomic survey sequence	Homo sapiens	37,882	06-MAR-1999
		GB_GSS14:AQ507468	627	AQ507468	RPCI-11-298O19 TJ RPCI-11 Homo sapiens genomic clone RPCI-11-298O19, genomic survey sequence	Homo sapiens	38,480	29-Apr-99
rxa02347	444	GB_PR3 AC005549	147416	AC005549	Homo sapiens chromosome 17, clone hRPK 215_E_13, complete sequence	Homo sapiens	39,909	22-Sep-98
		GB_PR3.AC005549	147416	AC005549	Homo sapiens chromosome 17, clone hRPK 215_E_13, complete sequence	Homo sapiens	33,784	22-Sep-98
		GB_GSS8 B92789	742	B92789	CIT-HSP-2164J8 TR CIT-HSP Homo sapiens genomic clone 2164J8, genomic survey sequence	Homo sapiens	39,409	25-Jun-98
rxa02349								
rxa02352	578	GB_EST19 AA738949	396	AA738949	vv68d12.r1 Stratagene mouse skin (#937313) Mus musculus cDNA clone IMAGE 1227575 5', mRNA sequence	Mus musculus	36,023	14-Jan-98
		GB_GSS14 AQ526017	500	AQ526017	HS_5329_A2_F02_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=905 Col=4 Row=K, genomic survey sequence	Homo sapiens	38,537	11-MAY-1999
		GB_PR3 U82695	167460	U82695	Homo sapiens cosmid LM1937 from Xq28	Homo sapiens	38,421	3-Jan-98
rxa02356	1119	GB_BA1:MTCY16B7	43430	Z81331	Mycobacterium tuberculosis H37Rv complete genome, segment 123/162.	Mycobacterium tuberculosis	39,087	17-Jun-98
		GB_BA1:SRMSIK	2384	Y08921	S reticuli gene encoding Msik protein and orf1	Streptomyces reticuli	58,356	21-MAR-1997
		GB_BA1 MSGY414A	40121	AD000007	Mycobacterium tuberculosis sequence from clone y414a	Mycobacterium tuberculosis	58,423	03-DEC-1996
rxa02358	414	GB_BA1 BSUB0021	215534	Z99124	Bacillus subtilis complete genome (section 21 of 21) from 3999281 to 4214814	Bacillus subtilis	36,829	26-Nov-97
		GB_PR3 HSDA22P16	103367	AL049641	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone DA22P16, complete sequence	Homo sapiens	36,430	23-Nov-99
		GB_BA1 BSUB0021	215534	Z99124	Bacillus subtilis complete genome (section 21 of 21) from 3999281 to 4214814	Bacillus subtilis	37,440	26-Nov-97
rxa02360	2556	GB_EST21:AA970555	420	AA970555	oo94h05 s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE 1573881 3' similar to gb X61970 PROTEASOME ZETA CHAIN (HUMAN);, mRNA sequence.	Homo sapiens	36,905	20-MAY-1998

TABLE 4: ALIGNMENT RESULTS

		GB_GSS4:AQ739589	909	AQ739589	HS_5381_B2_G06_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=957 Col=12 Row=N, genomic survey sequence.	Homo sapiens	44,912	16-Jul-99
		GB_IN1 CEY53H1C	37004	AL117201	Caenorhabditis elegans cosmid Y53H1C, complete sequence	Caenorhabditis elegans	38,436	19-Nov-99
rxa02361	774	GB_IN2.CELK04F10	35413	AF039719	Caenorhabditis elegans cosmid K04F10	Caenorhabditis elegans	36,891	26-MAY-1999
		GB_PL1:AB011477	78181	AB011477	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone MHK7, complete sequence	Arabidopsis thaliana	37,095	20-Nov-99
		GB_PL1:AB011477	78181	AB011477	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone MHK7, complete sequence	Arabidopsis thaliana	36,794	20-Nov-99
rxa02362	3822	GB_EST10.AA178985	357	AA178985	zp12g08 s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE 609278 3', mRNA sequence	Homo sapiens	39,875	31-DEC-1996
		GB_GSS4 AQ710468	555	AQ710468	HS_5336_A2_B09_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=912 Col=18 Row=C, genomic survey sequence	Homo sapiens	39,820	13-Jul-99
		GB_EST37 AI986900	380	AI986900	rs19a09 y1 Sommer Pristionchus Pristionchus pacificus cDNA clone IMAGE 5' similar to WP.C06A1 1 CE02114 TRANSITIONAL ENDOPLASMIC RETICULUM ATPASE HOMOLOG 1 ,, mRNA sequence	Pristionchus pacificus	42,105	1-Sep-99
rxa02367	732	GB_BA2 SCF76	18292	AL121600	Streptomyces coelicolor cosmid F76	Streptomyces coelicolor A3(2)	40,195	29-Sep-99
		GB_SY SCU53587	4546	U53587	Artificial Corynebacterium glutamicum IS1207-derived transposon transposase genes, complete cds, and 3'5"-aminoglycoside phosphotransferase (aphA-3) gene, complete cds	synthetic construct	36,755	06-MAY-1996
		GB_PAT E16763	2517	E16763	gDNA encoding aspartate transferase (AAT)	Corynebacterium glutamicum	38,687	28-Jul-99
rxa02368								
rxa02374	744	GB_PL2 AC010924	80442	AC010924	Arabidopsis thaliana chromosome 1 BAC T24D18 sequence, complete sequence.	Arabidopsis thaliana	39,261	6-Nov-99
		GB_VI HE1CG	152261	X14112	Herpes simplex virus (HSV) type 1 complete genome	human herpesvirus 1	39,856	17-Apr-97
		GB_VI:HS1ULR	108360	D10879	Herpes simplex virus type 1 long unique region UL	human herpesvirus 1	39,856	3-Feb-99
rxa02381	1146	GB_BA1 CGPROAGEN	1783	X82929	C glutamicum proA gene.	Corynebacterium glutamicum	98,974	23-Jan-97
		GB_BA1 CGPROAGEN	1783	X82929	C glutamicum proA gene	Corynebacterium glutamicum	37,156	23-Jan-97
		GB_GSS10 AQ215523	445	AQ215523	HS_2259_B2_F03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2259 Col=6 Row=L, genomic survey sequence	Homo sapiens	40,674	19-Sep-98
rxa02383	736	GB_EST35 AI810729	450	AI810729	tt86h09.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE 2248481 3', mRNA sequence.	Homo sapiens	41,568	7-Jul-99
		GB_EST22 AI048725	347	AI048725	ub31d01 r1 Soares 2NbMT Mus musculus cDNA clone IMAGE 1379329 5', mRNA sequence	Mus musculus	39,412	8-Jul-98
		GB_EST15 AA466288	431	AA466288	vh34c01 r1 Barstead mouse pooled organs MPLRB4 Mus musculus cDNA clone IMAGE:888864 5', mRNA sequence	Mus musculus	39,336	11-Jun-97
rxa02387	885	GB_PR3 AC004687	175120	AC004687	Homo sapiens chromosome 17, clone hRPC.1171_I_10, complete sequence	Homo sapiens	34,518	26-Jun-98
		GB_PR3 AC004687	175120	AC004687	Homo sapiens chromosome 17, clone hRPC 1171_I_10, complete sequence	Homo sapiens	38,551	26-Jun-98
		GB_GSS15:AQ604975	536	AQ604975	HS_2135_B2_G04_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2135 Col=8 Row=N, genomic survey sequence	Homo sapiens	39,321	10-Jun-99
rxa02390	792	GB_BA2 SC51A	42527	AL121596	Streptomyces coelicolor cosmid 51A	Streptomyces coelicolor A3(2)	38,804	28-Sep-99
		GB_BA2 AF073776	5138	AF073776	Pseudomonas aeruginosa MexZ (mexZ), complete cds, and mexGH operon, complete sequence	Pseudomonas aeruginosa	37,245	19-OCT-1998
		GB_BA1 AB015853	5461	AB015853	Pseudomonas aeruginosa gene for MexX and MexY, complete cds	Pseudomonas aeruginosa	40,641	13-Nov-98
rxa02393	405	GB_BA1 RCU57682	86896	U57682	Rhodobacter capsulatus cosmids 143-147, complete sequence	Rhodobacter capsulatus	44,246	7-Feb-97
		GB_PL2 T2K10	88037	AC005966	Arabidopsis thaliana chromosome 1 BAC T2K10 sequence, complete sequence	Arabidopsis thaliana	42,455	10-Feb-99
		GB_PL2 T24H24	88848	AF075598	Arabidopsis thaliana BAC T24H24	Arabidopsis thaliana	34,826	3-Aug-98
rxa02395	2013	GB_BA1 SC5F2A	40105	AL049587	Streptomyces coelicolor cosmid 5F2A	Streptomyces coelicolor	51,688	24-MAY-1999
		GB_BA1 CGBETPGEN	2339	X93514	C glutamicum betP gene	Corynebacterium glutamicum	48,877	8-Sep-97

TABLE 4: ALIGNMENT RESULTS

		GB_PL2:AF015436	682	AF015436	Liquidambar formosana internal transcribed spacer 1, 5.8S ribosomal RNA gene; and internal transcribed spacer 2, complete sequence	Liquidambar formosana	36,217	1-Feb-99
rxa02396	402	GB_BA2 AE000070	9973	AE000070	Rhizobium sp. NGR234 plasmid pNGR234a, section 7 of 46 of the complete plasmid sequence	Rhizobium sp NGR234	35,572	12-DEC-1997
		GB_BA2:AE000070	9973	AE000070	Rhizobium sp. NGR234 plasmid pNGR234a, section 7 of 46 of the complete plasmid sequence	Rhizobium sp NGR234	37,436	12-DEC-1997
		GB_BA1 CVAJ677	1087	AJ000677	Chromatium vinosum recA gene	Allochromatium vinosum	37,500	8-Aug-97
rxa02398	1725	GB_PR1:HUMJUNA	3622	J04111	Human c-jun proto oncogene (JUN), complete cds, clone hCJ-1	Homo sapiens	37,806	6-Jan-95
		GB_EST35.AL041724	462	AL041724	DKFZp434O0317_r1 434 (synonym htes3) Homo sapiens cDNA clone DKFZp434O0317 5', mRNA sequence	Homo sapiens	40,260	29-Sep-99
		GB_PAT I96176	3622	I96176	Sequence 13 from patent US 5734039.	Unknown	37,806	01-DEC-1998
rxa02403	888	GB_BA1.CGACEB	3024	X78491	C glutamicum (ATCC 13032) aceB gene	Corynebacterium glutamicum	47,410	13-Jan-95
		GB_BA1 CORACEB	2725	L27123	Corynebacterium glutamicum malate synthase (aceB) gene, complete cds	Corynebacterium glutamicum	43,981	8-Jun-95
		GB_IN1 CEK06A4	34006	Z70755	Caenorhabditis elegans cosmid K06A4, complete sequence	Caenorhabditis elegans	37,875	23-Nov-98
rxa02406	672	GB_EST22.AI062160	629	AI062160	GH01261 5prime GH Drosophila melanogaster head pOT2 Drosophila melanogaster cDNA clone GH01261 5prime, mRNA sequence	Drosophila melanogaster	37,687	24-Nov-98
		GB_PR1 HSRPIILS	6732	X63564	H.sapiens mRNA for RNA polymerase II largest subunit	Homo sapiens	36,486	13-Feb-92
		GB_PR1.HSRPIILS	6732	X63564	H sapiens mRNA for RNA polymerase II largest subunit	Homo sapiens	38,813	13-Feb-92
rxa02407	495	GB_BA1 MTCY130	32514	Z73902	Mycobacterium tuberculosis H37Rv complete genome, segment 59/162	Mycobacterium tuberculosis	54,321	17-Jun-98
		GB_BA1.MSGY151	37036	AD000018	Mycobacterium tuberculosis sequence from clone y151	Mycobacterium tuberculosis	40,000	10-DEC-1996
		GB_EST19 AA391133	474	AA391133	LD10081 5prime LD Drosophila melanogaster embryo BlueScript Drosophila melanogaster cDNA clone LD10081 5prime, mRNA sequence	Drosophila melanogaster	38,015	27-Nov-98
rxa02408	1035	GB_PAT:I92047	551	I92047	Sequence 14 from patent US 5726299.	Unknown	46,000	01-DEC-1998
		GB_PAT I78759	549	I78759	Sequence 15 from patent US 5693781.	Unknown	45,438	3-Apr-98
		GB_PAT I92048	549	I92048	Sequence 15 from patent US 5726299.	Unknown.	45,438	01-DEC-1998
rxa02409	660	GB_EST19:AA438982	672	AA438982	LD13390 5prime LD Drosophila melanogaster embryo BlueScript Drosophila melanogaster cDNA clone LD13390 5prime, mRNA sequence	Drosophila melanogaster	36,130	27-Nov-98
		GB_EST28 AI513795	635	AI513795	GH26887 5prime GH Drosophila melanogaster head pOT2 Drosophila melanogaster cDNA clone GH26887 5prime, mRNA sequence	Drosophila melanogaster	38,840	16-MAR-1999
		GB_HTG3 AC009601	40300	AC009601	Leishmania major chromosome 35 clone L165 strain Friedlin, *** SEQUENCING IN PROGRESS ***, 2 ordered pieces	Leishmania major	35,759	30-Sep-99
rxa02412	603	GB_BA1 AB020624	1605	AB020624	Corynebacterium glutamicum murI gene for D-glutamate racemase, complete cds	Corynebacterium glutamicum	40,237	24-Jul-99
		GB_EST19.AA756805	646	AA756805	vv72b10.r1 Stratagene mouse skin (#937313) Mus musculus cDNA clone IMAGE 1227931 5' similar to gb D21261 SM22-ALPHA HOMOLOG (HUMAN),, mRNA sequence	Mus musculus	34,483	21-Jan-98
		GB_RO AF149291	1388	AF149291	Mus musculus transgelin mRNA, complete cds	Mus musculus	37,540	8-Jun-99
rxa02417	2247	GB_GSS14 AQ554774	813	AQ554774	RPCI-11-436G15 TV RPCI-11 Homo sapiens genomic clone RPCI-11-436G15, genomic survey sequence	Homo sapiens	34,649	28-MAY-1999
		GB_GSS4 AQ713076	500	AQ713076	HS_5384_A2_C05_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=960 Col=10 Row=E, genomic survey sequence	Homo sapiens	35,200	13-Jul-99
		GB_STS:G47161	448	G47161	Z15758_1 Zebrafish AB Danio rerio STS genomic clone Z15758 5', sequence tagged site	Danio rerio	39,910	23-MAR-1999
rxa02421	933	GB_HTG2 AC005708	76712	AC005708	Drosophila melanogaster chromosome 2 clone DS08537 (D425) map 50C1-50C2 strain y2, cn bw sp, *** SEQUENCING IN PROGRESS ***, 20 unordered pieces	Drosophila melanogaster	36,207	15-Jan-99
		GB_HTG3 AC005812	76721	AC005812	Drosophila melanogaster chromosome 2 clone DS07345 (D445) map 50C1-50C2 strain y, cn bw sp, *** SEQUENCING IN PROGRESS ***, 8 unordered pieces	Drosophila melanogaster	36,205	20-Sep-99
		GB_HTG2:AC005673	77023	AC005673	Drosophila melanogaster chromosome 2 clone DS00096 (D427) map 50C1-50C4 strain y, cn bw sp, *** SEQUENCING IN PROGRESS ***, 12 unordered pieces	Drosophila melanogaster	39,321	30-Jul-99
rxa02425	653	GB_BA1 PFPHCOAHL	2700	Y13067	Pseudomonas fluorescens genes encoding p-hydroxycinnamoyl CoA hydratase/lyase and vanillin NAD+ oxidoreductase	Pseudomonas fluorescens	40,854	05-MAY-1998

TABLE 4: ALIGNMENT RESULTS

		GB_EST27:AI438343	610	AI438343	SWOvAFCAP31F09SK Onchocerca volvulus adult female cDNA (SAW98MLW-OvAF) Onchocerca volvulus cDNA clone SWOvAFCAP31F09 5', mRNA sequence	Onchocerca volvulus	41,244	09-MAR-1999
		GB_BA1 XANHRPA1A	1824	M99173	Xanthomonas campstris HrpA1 gene, complete cds.	Xanthomonas campestris	37,520	14-Sep-93
rxa02427	510	GB_OV:CCA245635	2455	AJ245635	Cyprinus carpio IL-1 gene for interleukin-1-beta	Cyprinus carpio	35,614	5-Aug-99
		GB_OV.AB010701	1213	AB010701	Cyprinus carpio mRNA for interleukin-1 beta, complete cds	Cyprinus carpio	36,821	29-Jan-98
		GB_OV CCA245635	2455	AJ245635	Cyprinus carpio IL-1 gene for interleukin-1-beta	Cyprinus carpio	35,060	5-Aug-99
rxa02428	1257	GB_IN1 CEY40B1B	29313	AL032636	Caenorhabditis elegans cosmid Y40B1B, complete sequence	Caenorhabditis elegans	37,068	12-Nov-99
		GB_GSS12 AQ374513	640	AQ374513	RPCI11-145N15 TJ RPCI-11 Homo sapiens genomic clone RPCI-11-145N15, genomic survey sequence	Homo sapiens	35,636	20-MAY-1999
		GB_IN1 CEY40B1B	29313	AL032636	Caenorhabditis elegans cosmid Y40B1B, complete sequence	Caenorhabditis elegans	32,800	12-Nov-99
rxa02430	309	GB_BA1 MTCY1A11	30850	Z78020	Mycobacterium tuberculosis H37Rv complete genome, segment 83/162	Mycobacterium tuberculosis	64,610	17-Jun-98
		GB_PR4:AC004998	135572	AC004998	Homo sapiens clone DJ164D05, complete sequence	Homo sapiens	41,118	17-Jun-99
		GB_PR2 AC002091	161799	AC002091	Genomic sequence from Human 17, complete sequence	Homo sapiens	36,393	9-Sep-97
rxa02433	723	GB_HTG5 AC009754	212978	AC009754	Homo sapiens chromosome 15 clone RP11-519C12, WORKING DRAFT SEQUENCE, 16 ordered pieces	Homo sapiens	33,008	17-Nov-99
		GB_HTG5 AC009754	212978	AC009754	Homo sapiens chromosome 15 clone RP11-519C12, WORKING DRAFT SEQUENCE, 16 ordered pieces	Homo sapiens	39,716	17-Nov-99
		GB_PR4 HUAC003108	164564	AC003108	Human Chromosome 16 BAC clone CIT987SK-327O24, complete sequence	Homo sapiens	35,180	23-Nov-99
rxa02437	933	GB_IN2 AC005650	60019	AC005650	Drosophila melanogaster, chromosome 2R, region 59B4-59B7, P1 clone DS02885, complete sequence	Drosophila melanogaster	40,397	30-Jan-99
		GB_IN2 AC005650	60019	AC005650	Drosophila melanogaster, chromosome 2R, region 59B4-59B7, P1 clone DS02885, complete sequence	Drosophila melanogaster	37,719	30-Jan-99
		GB_RO AF081193	2250	AF081193	Mus musculus calcium and DAG-regulated guanine nucleotide exchange factor I mRNA, complete cds	Mus musculus	37,835	28-Nov-98
rxa02443	1077	GB_HTG4.AC009370	59409	AC009370	Drosophila melanogaster chromosome 3L/75C1 clone RPCI98-35F4, *** SEQUENCING IN PROGRESS ***, 40 unordered pieces	Drosophila melanogaster	35,460	16-OCT-1999
		GB_HTG4 AC009370	59409	AC009370	Drosophila melanogaster chromosome 3L/75C1 clone RPCI98-35F4, *** SEQUENCING IN PROGRESS ***, 40 unordered pieces	Drosophila melanogaster	35,460	16-OCT-1999
		GB_EST9 AA081445	311	AA081445	zn18a01.r1 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone IMAGE 547752 5', mRNA sequence	Homo sapiens	36,334	21-OCT-1996
rxa02444	1401	GB_BA2 SCF76	18292	AL121600	Streptomyces coelicolor cosmid F76	Streptomyces coelicolor A3(2)	39,226	29-Sep-99
		GB_PR2 HS1022J11	137658	AL049765	Human DNA sequence from clone 1022J11 on chromosome 20q13 13-13 2, complete sequence	Homo sapiens	35,444	23-Nov-99
		GB_HTG1 AC002345	132645	AC002345	Homo sapiens chromosome 17 clone 20D5, *** SEQUENCING IN PROGRESS ***, 10 unordered pieces	Homo sapiens	35,106	25-Aug-97
rxa02452	303	GB_GSS14 AQ579499	825	AQ579499	nbxb0084D17f CUGI Rice BAC Library Oryza sativa genomic clone nbxb0084D17f, genomic survey sequence	Oryza sativa	39,535	2-Jun-99
		GB_GSS14 AQ579499	825	AQ579499	nbxb0084D17f CUGI Rice BAC Library Oryza sativa genomic clone nbxb0084D17f, genomic survey sequence	Oryza sativa	36,213	2-Jun-99
rxa02454	1365	GB_HTG3 AC007810	140175	AC007810	Drosophila melanogaster chromosome 3 clone BACR14A01 (D720) RPCI-98 14 A 1 map 90C-90C strain y, cn bw sp, *** SEQUENCING IN PROGRESS ***, 89 unordered pieces	Drosophila melanogaster	33,931	17-Sep-99
		GB_HTG3 AC007810	140175	AC007810	Drosophila melanogaster chromosome 3 clone BACR14A01 (D720) RPCI-98 14 A 1 map 90C-90C strain y, cn bw sp, *** SEQUENCING IN PROGRESS***, 89 unordered pieces	Drosophila melanogaster	33,931	17-Sep-99
		GB_PR3 AC005339	32360	AC005339	Homo sapiens chromosome 19, cosmid R33729, complete sequence	Homo sapiens	38,131	30-Jul-98
rxa02457	1233	GB_HTG3 AC009346	105005	AC009346	Drosophila melanogaster chromosome 3 clone BACR03P13 (D672) RPCI-98 03 P 13 map 83A-83B strain y, cn bw sp, *** SEQUENCING IN PROGRESS ***, 83 unordered pieces	Drosophila melanogaster	36,829	27-Aug-99
		GB_EST20 AA820427	436	AA820427	LD24042 5prime LD Drosophila melanogaster embryo pOT2 Drosophila melanogaster cDNA clone LD24042 5prime, mRNA sequence	Drosophila melanogaster	38,018	25-Feb-99

TABLE 4: ALIGNMENT RESULTS

		GB_HTG3:AC009346	105005	AC009346	Drosophila melanogaster chromosome 3 clone BACR03P13 (D672) RPCI-98 03.P.13 map 83A-83B strain y, cn bw sp, *** SEQUENCING IN PROGRESS ***, 83 unordered pieces	Drosophila melanogaster	36,829	27-Aug-99
rxa02459	858	GB_BA2 AF114233	1852	AF114233	Corynebacterium glutamicum 5-enolpyruvylshikimate 3-phosphate synthase (aroA) gene, complete cds	Corynebacterium glutamicum	99,248	7-Feb-99
		GB_HTG1 CEY45F10_2	110000	Z93245	Caenorhabditis elegans chromosome IV clone Y45F10, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Caenorhabditis elegans	35,621	17-Sep-97
		GB_HTG1 CEY45F10_2	110000	Z93245	Caenorhabditis elegans chromosome IV clone Y45F10, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Caenorhabditis elegans	35,621	17-Sep-97
rxa02460								
rxa02461	531	GB_EST10 AA153371	590	AA153371	ms02a12 r1 Stratagene mouse embryonic carcinoma (#937317) Mus musculus cDNA clone IMAGE:605758 5' similar to gb M24194 GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN (HUMAN), gb X75313 M.musculus (MOUSE),, mRNA sequence.	Mus musculus	39,203	11-Feb-97
		GB_EST10 AA153371	590	AA153371	ms02a12 r1 Stratagene mouse embryonic carcinoma (#937317) Mus musculus cDNA clone IMAGE:605758 5' similar to gb M24194 GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN (HUMAN), gb X75313 M musculus (MOUSE),, mRNA sequence	Mus musculus	41,920	11-Feb-97
rxa02464	1323	GB_HTG4:AC008754	86446	AC008754	Homo sapiens chromosome 19 clone CITB-E1_3023J11, *** SEQUENCING IN PROGRESS ***, 73 unordered pieces	Homo sapiens	36,064	31-OCT-1999
		GB_HTG4 AC008754	86446	AC008754	Homo sapiens chromosome 19 clone CITB-E1_3023J11, *** SEQUENCING IN PROGRESS ***, 73 unordered pieces	Homo sapiens	36,064	31-OCT-1999
		GB_HTG4 AC008754	86446	AC008754	Homo sapiens chromosome 19 clone CITB-E1_3023J11, *** SEQUENCING IN PROGRESS ***, 73 unordered pieces	Homo sapiens	37,589	31-OCT-1999
rxa02465	522	GB_PR3.AC004960	143834	AC004960	Homo sapiens PAC clone DJ1098B01 from 7q11 23-q21, complete sequence	Homo sapiens	35,010	5-Nov-98
		GB_GSS9.AQ122158	428	AQ122158	HS_3083_A1_E10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3083 Col=19 Row=I, genomic survey sequence.	Homo sapiens	39,720	22-Sep-98
		GB_BA2:AF053227	840	AF053227	Photobacterium leiognathi probable flavin reductase (luxG) gene, complete cds	Photobacterium leiognathi	37,572	12-Jun-98
rxa02466	187	GB_EST21:AA942401	825	AA942401	LD26583.5prime LD Drosophila melanogaster embryo pOT2 Drosophila melanogaster cDNA clone LD26583 5prime, mRNA sequence	Drosophila melanogaster	37,705	25-Nov-98
		GB_GSS12 AQ400564	485	AQ400564	HS_5064_A1_G09_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=640 Col=17 Row=M, genomic survey sequence	Homo sapiens	38,043	13-MAR-1999
		GB_GSS12 AQ400564	485	AQ400564	HS_5064_A1_G09_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=640 Col=17 Row=M, genomic survey sequence	Homo sapiens	37,647	13-MAR-1999
rxa02467	348	GB_HTG2 AC005718	149592	AC005718	Drosophila melanogaster chromosome 2 clone DS02336 (D440) map 60C8-60D2 strain y, cn bw sp, *** SEQUENCING IN PROGRESS ***, 68 unordered pieces.	Drosophila melanogaster	40,525	30-Jul-99
		GB_HTG2 AC005718	149592	AC005718	Drosophila melanogaster chromosome 2 clone DS02336 (D440) map 60C8-60D2 strain y, cn bw sp, *** SEQUENCING IN PROGRESS ***, 68 unordered pieces	Drosophila melanogaster	40,525	30-Jul-99
		GB_PR3.AC004217	103319	AC004217	Homo sapiens 12q24 1 PAC RPCI3-521E19 (Roswell Park Cancer Institute Human PAC library) complete sequence	Homo sapiens	37,389	2-Jun-98
rxa02472	414	GB_GSS12 AQ413964	550	AQ413964	RPCI-11-207C17 TV RPCI-11 Homo sapiens genomic clone RPCI-11-207C17, genomic survey sequence	Homo sapiens	37,870	23-MAR-1999
		GB_IN2 CELR09H3	10687	U58740	Caenorhabditis elegans cosmid R09H3	Caenorhabditis elegans	37,408	26-MAY-1999
		GB_GSS13 AQ488397	734	AQ488397	RPCI-11-243H14 TV RPCI-11 Homo sapiens genomic clone RPCI-11-243H14, genomic survey sequence.	Homo sapiens	37,569	24-Apr-99
rxa02473	864	GB_HTG1 CEY7A5	235922	AL021576	Caenorhabditis elegans chromosome X clone Y7A5, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Caenorhabditis elegans	38,561	19-Aug-99
		GB_HTG1 CEY7A5	235922	AL021576	Caenorhabditis elegans chromosome X clone Y7A5, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Caenorhabditis elegans	38,561	19-Aug-99
		GB_IN1 CEY7A5A	68270	AL034489	Caenorhabditis elegans cosmid Y7A5A, complete sequence	Caenorhabditis elegans	38,081	18-DEC-1998

TABLE 4: ALIGNMENT RESULTS

rxa02475	1278	GB_BA1:AB009078	2686	AB009078	Brevibacterium saccharolyticum gene for L-2.3-butanediol dehydrogenase, complete cds.	Brevibacterium saccharolyticum	99,217	13-Feb-99
		GB_PH AF074945	15644	AF074945	Mycoplasma arthritidis bacteriophage MAV1, complete genome	Mycoplasma arthritidis bacteriophage MAV1	36,876	27-Jul-99
		GB_BA1 MTV008	63033	AL021246	Mycobacterium tuberculosis H37Rv complete genome, segment 108/162	Mycobacterium tuberculosis	37,520	17-Jun-98
rxa02478	1338	GB_HTG1 AC002419	128340	AC002419	Homo sapiens chromosome X clone bWXD40, *** SEQUENCING IN PROGRESS ***, 2 unordered pieces	Homo sapiens	34,700	12-Aug-97
		GB_PR3:AC004073	79612	AC004073	Human Chromosome X, complete sequence	Homo sapiens	34,700	29-Jan-98
		GB_HTG1 AC002419	128340	AC002419	Homo sapiens chromosome X clone bWXD40, *** SEQUENCING IN PROGRESS ***, 2 unordered pieces	Homo sapiens	34,700	12-Aug-97
rxa02482	933	GB_OV:AF077329	1645	AF077329	Coturnix coturnix pro-alpha2(I) collagen mRNA, partial cds.	Coturnix coturnix	40,202	3-Feb-99
		GB_PL2.SFU59150	2854	U59150	Sartorya fumigata nucleolar protein AfCbf5p (AfCBF5p) mRNA, complete cds.	Aspergillus fumigatus	36,789	1-Jan-98
		GB_BA2 AE000106	12554	AE000106	Rhizobium sp NGR234 plasmid pNGR234a, section 43 of 46 of the complete plasmid sequence	Rhizobium sp. NGR234	36,630	12-DEC-1997
rxa02483	936	GB_HTG1:AC002345	132645	AC002345	Homo sapiens chromosome 17 clone 20D5, *** SEQUENCING IN PROGRESS***, 10 unordered pieces	Homo sapiens	37,942	25-Aug-97
		GB_HTG1.AC002345	132645	AC002345	Homo sapiens chromosome 17 clone 20D5, *** SEQUENCING IN PROGRESS ***, 10 unordered pieces	Homo sapiens	37,942	25-Aug-97
		GB_PR4 AF118569	24070	AF118569	Homo sapiens angiotensin I converting enzyme precursor (DCP1) gene, alternative splice products, complete cds	Homo sapiens	37,352	28-OCT-1999
rxa02484	624	GB_BA1 RLSPRLVCP	3696	Y09534	R.leguminosarum Symbiosis Plasmid DNA, rlvCP gene	Rhizobium leguminosarum	38,003	26-Feb-97
		GB_BA2 RLU23040	3931	U23040	Rhizobium leguminosarum bv viciae putative glycerol-3-phosphate transport protein (ugpC) gene, partial cds, and chemoreceptor protein (mcpA), putative 2-hydroxychromene-2-carboxylate isomerase, and putative alcohol dehydrogenase genes, complete cds	Rhizobium leguminosarum bv viciae	38,003	26-Aug-96
		GB_BA1 NGORBKGME	1580	L07845	Neisseria gonorrhoeae ribokinase (rbk) gene, 3' end; ADP-L-glycero-D-mannoheptose epimerase (gme) gene, complete cds	Neisseria gonorrhoeae	46,939	11-OCT-1995
rxa02486	759	GB_IN1:CELM02D8	40876	U41034	Caenorhabditis elegans cosmid M02D8	Caenorhabditis elegans	38,358	30-Nov-95
		GB_IN2.CELC36C5	41596	AF016444	Caenorhabditis elegans cosmid C36C5	Caenorhabditis elegans	38,482	08-OCT-1999
		GB_HTG3.AC011467	188118	AC011467	Homo sapiens chromosome 19 clone CIT-HSPC_457E21, *** SEQUENCING IN PROGRESS ***, 59 unordered pieces	Homo sapiens	37,954	07-OCT-1999
rxa02488	392	GB_HTG2 AC006765	274498	AC006765	Caenorhabditis elegans clone Y43H11, *** SEQUENCING IN PROGRESS ***, 7 unordered pieces	Caenorhabditis elegans	38,961	23-Feb-99
		GB_HTG2 AC006765	274498	AC006765	Caenorhabditis elegans clone Y43H11, *** SEQUENCING IN PROGRESS ***, 7 unordered pieces	Caenorhabditis elegans	38,961	23-Feb-99
		GB_HTG4:AC010035	173152	AC010035	Drosophila melanogaster chromosome 3L/74B2 clone RPCO98-6H1, *** SEQUENCING IN PROGRESS ***, 60 unordered pieces.	Drosophila melanogaster	38,010	16-OCT-1999
rxa02489	724	GB_GSS8.AQ050210	796	AQ050210	nbxb0003cD08r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0003H15r, genomic survey sequence	Oryza sativa	40,201	24-MAR-1999
		GB_PL1 D87819	2036	D87819	Oryza sativa mRNA for sucrose transporter, complete cds	Oryza sativa	39,356	26-DEC-1997
		GB_STS G53565	627	G53565	SHGC-83995 Human Homo sapiens STS genomic, sequence tagged site	Homo sapiens	40,237	25-Jun-99
rxa02495	2691	GB_BA1 MTCY19H9	20679	Z83857	Mycobacterium tuberculosis H37Rv complete genome, segment 129/162	Mycobacterium tuberculosis	40,853	18-Jun-98
		GB_BA1 MTCY19H9	20679	Z83857	Mycobacterium tuberculosis H37Rv complete genome, segment 129/162	Mycobacterium tuberculosis	40,358	18-Jun-98
		GB_HTG1 HSDJ901O8	114599	AL078461	Homo sapiens chromosome 20 clone RP5-901O8 map q11 1-11 23, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Homo sapiens	34,059	25-Nov-99
rxa02496	930	GB_EST36 AV201062	373	AV201062	AV201062 Yuji Kohara unpublished cDNA Caenorhabditis elegans cDNA clone yk250f11 5', mRNA sequence	Caenorhabditis elegans	41,287	26-Jul-99
		GB_IN1 CELC10F3	40172	AF022968	Caenorhabditis elegans cosmid C10F3.	Caenorhabditis elegans	35,217	10-Sep-97

TABLE 4: ALIGNMENT RESULTS

		GB_EST29:AI612578	357	AI612578	TENG0372 T. Cruzi epimastigote normalised cDNA Library Trypanosoma cruzi cDNA clone n715.r 5', mRNA sequence	Trypanosoma cruzi	39,474	7-Jul-99
rxa02498	927	GB_BA2.CGU31225	1817	U31225	Corynebacterium glutamicum L-proline NADP+ 5-oxidoreductase (proC) gene, complete cds	Corynebacterium glutamicum	92,580	2-Aug-96
		GB_PR2 AP000197	100000	AP000197	Homo sapiens genomic DNA, chromosome 21q22 1, D21S226-AML region, clone B355D16-T1073, segment 3/8, complete sequence	Homo sapiens	36,344	20-Nov-99
		GB_PR2 AP000093	100000	AP000093	Homo sapiens genomic DNA of 21q22 1, GART and AML related, B335D16-P10G11 region, segment 3/7, complete sequence	Homo sapiens	36,344	25-Sep-99
rxa02500	222	GB_BA1 MTCY20G9	37218	Z77162	Mycobacterium tuberculosis H37Rv complete genome, segment 25/162	Mycobacterium tuberculosis	58,257	17-Jun-98
		GB_BA1 U00018	42991	U00018	Mycobacterium leprae cosmid B2168	Mycobacterium leprae	44,776	01-MAR-1994
		GB_BA1:SCE68	38084	AL079345	Streptomyces coelicolor cosmid E68	Streptomyces coelicolor A3(2)	37,624	16-Jul-99
rxa02505	294	GB_RO MM2B4J	289	X00621	Mouse hybridoma 2B4 gene fragment (J-region) for T-cell receptor	Mus musculus	36,364	10-Nov-95
		GB_RO MUSTCBJB1	2276	K02802	Mouse T-cell receptor germline beta-chain J-beta-2 gene cluster, including J-beta-[2 1,2.2,2.3,2 4,2 5,2 psi,2 6] genes	Mus musculus	32,862	27-Apr-93
		GB_RO MMAE000665	199101	AE000665	Mus musculus TCR beta locus from bases 501860 to 700960 (section 3 of 3) of the complete sequence	Mus musculus	36,879	4-Sep-97
rxa02506								
rxa02510	759	GB_OM PIGMTNADP	1585	M86719	Pig mitochondrial NADP-isocitrate dehydrogenase mRNA, 3' end	Sus scrofa	36,963	12-Jun-93
		GB_EST17 AA629042	359	AA629042	zu77d08 s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE 744015 3', mRNA sequence	Homo sapiens	37,184	16-OCT-1997
		GB_EST20 AA837524	528	AA837524	oe31d07 s1 NCI_CGAP_Pr25 Homo sapiens cDNA clone IMAGE 1410157 similar to gb X69391 60S RIBOSOMAL PROTEIN L6 (HUMAN),, mRNA sequence	Homo sapiens	40,039	26-Feb-98
rxa02514	857	GB_PR2 CNS01DS9	175148	AL121694	Human chromosome 14 DNA sequence *** IN PROGRESS *** BAC R-701B16 of RPCI-11 library from chromosome 14 of Homo sapiens (Human), complete sequence.	Homo sapiens	35,185	8-Nov-99
		GB_PR4 AC006222	165643	AC006222	Homo sapiens, clone hRPK 12_A_1, complete sequence	Homo sapiens	33,411	15-Jan-99
		GB_PR4 AC006222	165643	AC006222	Homo sapiens, clone hRPK 12_A_1, complete sequence	Homo sapiens	35,629	15-Jan-99
rxa02518	534	GB_BA1 MTV007	32806	AL021184	Mycobacterium tuberculosis H37Rv complete genome, segment 64/162	Mycobacterium tuberculosis	57,965	17-Jun-98
		GB_EST16 AA576027	231	AA576027	nm57e05 s1 NCI_CGAP_Br3 Homo sapiens cDNA clone IMAGE 1072352 3' similar to TR G1001455 G1001455 HYPOTHETICAL 141 7 KD PROTEIN ,, mRNA sequence	Homo sapiens	47,674	9-Sep-97
		GB_BA2 AE000226	10466	AE000226	Escherichia coli K-12 MG1655 section 116 of 400 of the complete genome.	Escherichia coli	38,447	12-Nov-98
rxa02519	1752	GB_IN2:DMNRG2	8574	AF050085	Drosophila melanogaster neuroglian (nrg) gene, exons 3-6, 7a, 7b and alternatively spliced products, complete cds	Drosophila melanogaster	38,498	5-Aug-98
		GB_IN2:AC004322	32480	AC004322	Drosophila melanogaster DNA sequence (P1 DS01962 (D216)), complete sequence	Drosophila melanogaster	36,126	29-Aug-98
		GB_HTG2.AC008188	129128	AC008188	Drosophila melanogaster chromosome 2 clone BACR08I18 (D660) RPCI-98 08.I 18 map 56A2-56B1 strain y, cn bw sp, *** SEQUENCING IN PROGRESS ***, 72 unordered pieces	Drosophila melanogaster	35,660	2-Aug-99
rxa02520	807	GB_GSS3 B68449	228	B68449	CIT-HSP-2025P8 TF CIT-HSP Homo sapiens genomic clone 2025P8, genomic survey sequence.	Homo sapiens	42,544	21-Jun-98
		GB_HTG3 AC010642	45982	AC010642	Homo sapiens chromosome 19 clone LLNL-R_245B6, *** SEQUENCING IN PROGRESS ***, 26 unordered pieces	Homo sapiens	34,543	16-Sep-99
		GB_HTG3 AC010642	45982	AC010642	Homo sapiens chromosome 19 clone LLNL-R_245B6, *** SEQUENCING IN PROGRESS ***, 26 unordered pieces	Homo sapiens	34,543	16-Sep-99
rxa02521	1566	GB_BA1 SCC22	22115	AL096839	Streptomyces coelicolor cosmid C22	Streptomyces coelicolor	40,885	12-Jul-99
		GB_BA1 BSUB0017	217420	Z99120	Bacillus subtilis complete genome (section 17 of 21) from 3197001 to 3414420	Bacillus subtilis	38,441	26-Nov-97
		GB_BA1 MLCL536	36224	Z99125	Mycobacterium leprae cosmid L536	Mycobacterium leprae	37,233	04-DEC-1998
rxa02524	813	GB_IN1 CELF42H10	28687	L08403	C elegans cosmid F42H10	Caenorhabditis elegans	32,878	22-OCT-1993
		GB_IN1 CEU02289	4824	U02289	Caenorhabditis elegans Bristol N2 GTPase-activating protein (CEGAP) mRNA, partial cds	Caenorhabditis elegans	34,457	11-Jun-94

TABLE 4: ALIGNMENT RESULTS

		GB_IN1:CELF42H10	28687	L08403	C. elegans cosmid F42H10.	Caenorhabditis elegans	34,243	22-OCT-1993
rxa02525	501	GB_EST36:AU076280	416	AU076280	AU076280 Rice green shoot Oryza sativa cDNA clone S10896_11A, mRNA sequence	Oryza sativa	42,671	27-Jul-99
		GB_EST1 D34202	355	D34202	CELK042E5R Yuji Kohara unpublished cDNA Caenorhabditis elegans cDNA clone yk42e5 3', mRNA sequence	Caenorhabditis elegans	42,553	8-Aug-94
		GB_EST1 D34202	355	D34202	CELK042E5R Yuji Kohara unpublished cDNA Caenorhabditis elegans cDNA clone yk42e5 3', mRNA sequence	Caenorhabditis elegans	37,892	8-Aug-94
rxa02534	927	GB_EST15:AA490533	426	AA490533	aa51h04.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE 824503 5', mRNA sequence	Homo sapiens	41,176	15-Aug-97
		GB_PL2 ATFCA3	200252	Z97338	Arabidopsis thaliana DNA chromosome 4, ESSA I FCA contig fragment No 3	Arabidopsis thaliana	35,568	27-Aug-99
		GB_PL2 ATFCA3	200252	Z97338	Arabidopsis thaliana DNA chromosome 4, ESSA I FCA contig fragment No 3	Arabidopsis thaliana	37,376	27-Aug-99
rxa02537	585	GB_HTG4:AC009732	165576	AC009732	Drosophila melanogaster chromosome 2 clone BACR05E17 (D1059) RPCI-98 05 E 17 map 57F-57F strain y; cn bw sp, *** SEQUENCING IN PROGRESS *** 83 unordered pieces	Drosophila melanogaster	30,727	26-OCT-1999
		GB_HTG4 AC009732	165576	AC009732	Drosophila melanogaster chromosome 2 clone BACR05E17 (D1059) RPCI-98 05 E 17 map 57F-57F strain y, cn bw sp, *** SEQUENCING IN PROGRESS ***, 83 unordered pieces.	Drosophila melanogaster	30,727	26-OCT-1999
		GB_HTG4 AC009732	165576	AC009732	Drosophila melanogaster chromosome 2 clone BACR05E17 (D1059) RPCI-98 05 E 17 map 57F-57F strain y, cn bw sp, *** SEQUENCING IN PROGRESS ***, 83 unordered pieces.	Drosophila melanogaster	36,460	26-OCT-1999
rxa02538	795	GB_GSS15 AQ606090	658	AQ606090	HS_5392_A1_E12_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=968 Col=23 Row=I, genomic survey sequence	Homo sapiens	39,369	10-Jun-99
		GB_BA1:AXACE	5323	X94981	A xylinum aceB, aceC, aceD, and aceE genes.	Acetobacter xylinus	37,009	12-Feb-97
		GB_BA1:AXACE	5323	X94981	A xylinum aceB, aceC, aceD, and aceE genes	Acetobacter xylinus	37,879	12-Feb-97
rxa02540	561	GB_BA1:MTY13E10	35019	Z95324	Mycobacterium tuberculosis H37Rv complete genome, segment 18/162	Mycobacterium tuberculosis	51,002	17-Jun-98
		GB_BA1.MTDNAGRP	4644	X58406	M tuberculosis dnaK, grpE, and dnaJ genes	Mycobacterium tuberculosis	51,002	21-OCT-1992
		GB_BA1 AB007847	2400	AB007847	Rhodococcus rhodochrous gene for 3-ketosteroid-delta1-dehydrogenase, complete cds	Rhodococcus rhodochrous	53,723	13-Feb-99
rxa02544	1521	GB_PAT E14041	2776	E14041	gDNA encoding laminaripentaose forming enzyme (LPHase)	Streptomyces sp	47,351	28-Jul-99
		GB_HTG3 AC010592	45971	AC010592	Homo sapiens chromosome 5 clone CIT-HSPC_459H20, *** SEQUENCING IN PROGRESS ***, 38 unordered pieces.	Homo sapiens	37,689	16-Sep-99
		GB_HTG3 AC010592	45971	AC010592	Homo sapiens chromosome 5 clone CIT-HSPC_459H20, *** SEQUENCING IN PROGRESS ***, 38 unordered pieces	Homo sapiens	37,689	16-Sep-99
rxa02545	681	GB_HTG3 AC009016	128095	AC009016	Homo sapiens chromosome 5 clone P1_889E7, *** SEQUENCING IN PROGRESS ***, 67 unordered pieces	Homo sapiens	34,763	3-Aug-99
		GB_HTG3 AC009016	128095	AC009016	Homo sapiens chromosome 5 clone P1_889E7, *** SEQUENCING IN PROGRESS ***, 67 unordered pieces	Homo sapiens	34,763	3-Aug-99
		GB_HTG3 AC009010	72817	AC009010	Homo sapiens chromosome 5 clone P1_1352A1, *** SEQUENCING IN PROGRESS ***, 19 unordered pieces	Homo sapiens	34,763	3-Aug-99
rxa02546	1227	GB_HTG3 AC006519	134365	AC006519	Homo sapiens clone RPCI5-951N9, *** SEQUENCING IN PROGRESS ***, 41 unordered pieces	Homo sapiens	32,868	16-Sep-99
		GB_BA1.D90738	17528	D90738	Escherichia coli genomic DNA (23 0 - 23 4 min).	Escherichia coli	38,674	7-Feb-99
		GB_HTG3.AC006519	134365	AC006519	Homo sapiens clone RPCI5-951N9, *** SEQUENCING IN PROGRESS ***, 41 unordered pieces	Homo sapiens	32,868	16-Sep-99
rxa02549	2826	GB_BA1:CGBPHI16	962	Y12472	C glutamicum DNA, attachment site bacteriophage Phi-16	Corynebacterium glutamicum	41,702	05-MAR-1999
		GB_BA2 AE001095	10592	AE001095	Archaeoglobus fulgidus section 12 of 172 of the complete genome	Archaeoglobus fulgidus	36,817	15-DEC-1997
		GB_EST20 AA887411	587	AA887411	oj37d06 s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE.1500491 3' similar to gb X69908_rna1 ATP SYNTHASE LIPID-BINDING PROTEIN P2 PRECURSOR (HUMAN),, mRNA sequence	Homo sapiens	41,738	9-Jun-98
rxa02552	918	GB_GSS9 AQ129371	377	AQ129371	HS_3045_A2_B07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3045 Col=14 Row=C, genomic survey sequence	Homo sapiens	42,857	23-Sep-98
		GB_GSS14:AQ566979	600	AQ566979	HS_2105_A2_D12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2105 Col=24 Row=G, genomic survey sequence	Homo sapiens	35,443	29-MAY-1999

TABLE 4: ALIGNMENT RESULTS

		GB_IN1:MEPAP	4636	X54422	M.edulis gene for polyphenolic adhesive protein.	Mytilus edulis	35,619	27-MAY-1992
rxa02554	747	GB_PR4:AC004882	171878	AC004882	Homo sapiens PAC clone DJ076B20 from 22, complete sequence	Homo sapiens	37,346	22-OCT-1999
		GB_PR4:AC004882	171878	AC004882	Homo sapiens PAC clone DJ076B20 from 22, complete sequence.	Homo sapiens	38,440	22-OCT-1999
		GB_BA2.U32830	16388	U32830	Haemophilus influenzae Rd section 145 of 163 of the complete genome	Haemophilus influenzae Rd	33,514	29-MAY-1998
rxa02555	726	GB_GSS1.FR0020618	466	AL013501	F rubripes GSS sequence, clone 042H13bD8, genomic survey sequence	Fugu rubripes	40,215	10-DEC-1997
		GB_GSS1:FR0020576	555	AL013459	F rubripes GSS sequence, clone 042H13aE5, genomic survey sequence	Fugu rubripes	35,379	10-DEC-1997
		GB_GSS1:FR0020585	431	AL013468	F rubripes GSS sequence, clone 042H13aH5, genomic survey sequence	Fugu rubripes	39,718	10-DEC-1997
rxa02564	1125	GB_PR3 AC004976	127425	AC004976	Homo sapiens PAC clone DJ1143H19 from 7p14-p15, complete sequence	Homo sapiens	37,364	5-Nov-98
		GB_PR2 HUAC002038	161973	AC002038	Homo sapiens chromosome 2 clone 101B6 map 2p11, complete sequence	Homo sapiens	36,404	30-Jun-97
		GB_HTG3 AC010791	111643	AC010791	Homo sapiens chromosome 17 clone 6_M_14 map 17, *** SEQUENCING IN PROGRESS ***, 8 unordered pieces	Homo sapiens	34,293	22-Sep-99
rxa02568	1753	GB_BA1.FT16SRNAA	1521	Z21931	F tularensis 16S rRNA	Francisella tularensis	39,065	5-Jun-97
		GB_BA1 FT16SRNAB	1520	Z21932	F tularensis 16S rRNA	Francisella tularensis	37,807	16-DEC-1997
		GB_BA1.FP16SRNAA	1518	Z21933	F philomiragia 16S rRNA	Francisella philomiragia	36,380	5-Jun-97
rxa02569	873	GB_GSS13 AQ469518	553	AQ469518	CITBI-E1-2596J20 TR CITBI-E1 Homo sapiens genomic clone 2596J20, genomic survey sequence	Homo sapiens	39,201	23-Apr-99
		GB_GSS12 AQ403903	495	AQ403903	HS_5058_B1_F07_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=634 Col=13 Row=L, genomic survey sequence	Homo sapiens	36,049	13-MAR-1999
		GB_PR2:AF004715	2889	AF004715	Homo sapiens jerky gene product homolog mRNA, complete cds	Homo sapiens	35,689	6-Aug-97
rxa02570	765	GB_BA1 CGU43535	2531	U43535	Corynebacterium glutamicum multidrug resistance protein (cmr) gene, complete cds	Corynebacterium glutamicum	38,165	9-Apr-97
		GB_EST33 AI776398	499	AI776398	EST257498 tomato resistant, Cornell Lycopersicon esculentum cDNA clone cLER18I10, mRNA sequence	Lycopersicon esculentum	42,084	29-Jun-99
		GB_EST23 AI119807	431	AI119807	uc21a06 r1 Soares mouse mammary gland NbMMG Mus musculus cDNA clone IMAGE 1398610 5', mRNA sequence	Mus musculus	40,281	2-Sep-98
rxa02573								
rxa02575	1258	GB_BA1:SCGD3	33779	AL096822	Streptomyces coelicolor cosmid GD3	Streptomyces coelicolor	39,742	8-Jul-99
		GB_RO AC002108	41125	AC002108	Genomic sequence from Mouse 4, complete sequence	Mus musculus	36,100	29-MAY-1997
		GB_PR1 HUMIDS	36845	L35485	Homo sapiens iduronate sulphate sulphatase (IDS) gene, complete cds	Homo sapiens	34,183	16-Aug-94
rxa02576	1545	GB_GSS15 AQ618143	582	AQ618143	HS_5168_B1_H08_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=744 Col=15 Row=P, genomic survey sequence	Homo sapiens	34,874	15-Jun-99
		GB_OV XLFB1A1	2172	X64759	X laevis mRNA for transcription factor (clone XLFB1a1)	Xenopus laevis	38,589	26-Jan-93
		GB_PR4:AC005039	151316	AC005039	Homo sapiens clone NH0512E16, complete sequence	Homo sapiens	33,575	14-Jan-99
rxa02577	1008	GB_PL2.AF034976	7130	AF034976	Pilayella littoralis ribosomal protein S14 (rps14) gene, partial cds, ATPase subunit 8 (atp8) gene, complete cds, tRNA-Ser gene, complete sequence, ribosomal protein S10 (rps10) and ribosomal protein L31 (rpl31) genes, complete cds, tRNA-Ser gene, complete sequence, T7-like RNA polymerase (rpox) gene, complete cds; and unknown genes, mitochondrial genes for mitochondrial products.	Mitochondrion Pilayella littoralis	34,690	22-Jun-98
		GB_EST30:AI655188	456	AI655188	wb67g02 x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE 2310770 3', mRNA sequence	Homo sapiens	39,198	04-MAY-1999
		GB_PL2 AF034976	7130	AF034976	Pilayella littoralis ribosomal protein S14 (rps14) gene, partial cds, ATPase subunit 8 (atp8) gene, complete cds, tRNA-Ser gene, complete sequence, ribosomal protein S10 (rps10) and ribosomal protein L31 (rpl31) genes, complete cds, tRNA-Ser gene, complete sequence, T7-like RNA polymerase (rpox) gene, complete cds, and unknown genes, mitochondrial genes for mitochondrial products.	Mitochondrion Pilayella littoralis	39,959	22-Jun-98
rxa02584	474	GB_PR2 AP000191	100000	AP000191	Homo sapiens genomic DNA, chromosome 21q22 1, D21S226-AML region, clone Q78C10-f32E9, segment 18/21, complete sequence	Homo sapiens	37,199	20-Nov-99
		GB_EST13 AA349881	293	AA349881	EST56832 Infant brain Homo sapiens cDNA 5' end similar to EST containing Alu repeat, mRNA sequence	Homo sapiens	42,466	21-Apr-97

TABLE 4: ALIGNMENT RESULTS

		GB_EST23:AI078215	404	AI078215	oz12h12.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1675175 3' similar to contains Alu repetitive element,contains element THR repetitive element ,, mRNA sequence	Homo sapiens	48,780	29-Sep-98
rxa02585	1104	GB_PR2:AP000115	100000	AP000115	Homo sapiens genomic DNA of 21q22 1, GART and AML related, Q78C10-149C3 region, segment 18/20, complete sequence	Homo sapiens	35,502	25-Sep-99
		GB_PR2 AP000191	100000	AP000191	Homo sapiens genomic DNA, chromosome 21q22 1, D21S226-AML region, clone Q78C10-f32E9, segment 18/21, complete sequence	Homo sapiens	35,502	20-Nov-99
		GB_PR2 AP000047	50188	AP000047	Homo sapiens genomic DNA, chromosome 21q22 1, segment 18/28, complete sequence	Homo sapiens	35,502	20-Nov-99
rxa02588	807	GB_BA1 MTCY8D5	39730	Z92669	Mycobacterium tuberculosis H37Rv complete genome, segment 12/162	Mycobacterium tuberculosis	38,354	18-Jun-98
		GB_BA1 MTCY349	43523	Z83018	Mycobacterium tuberculosis H37Rv complete genome, segment 131/162	Mycobacterium tuberculosis	39,949	17-Jun-98
		GB_HTG2 AC007879	158841	AC007879	Homo sapiens clone NH0309L06, *** SEQUENCING IN PROGRESS ***, 2 unordered pieces	Homo sapiens	36,835	31-Jul-99
rxa02591	1953	GB_BA1:MTCY8D5	39730	Z92669	Mycobacterium tuberculosis H37Rv complete genome, segment 12/162	Mycobacterium tuberculosis	65,398	18-Jun-98
		GB_BA1 MLCL622	42498	Z95398	Mycobacterium leprae cosmid L622	Mycobacterium leprae	63,875	24-Jun-97
		GB_BA1 CHBATP2OP	5477	L08777	Chlorobium limicola atp2 operon	Chlorobium limicola	37,979	26-Apr-93
rxa02593	720	GB_GSS1 CNS0056G	994	AL057090	Drosophila melanogaster genome survey sequence T7 end of BAC # BACR11M23 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence	Drosophila melanogaster	27,206	3-Jun-99
		GB_GSS1 CNS0056G	994	AL057090	Drosophila melanogaster genome survey sequence T7 end of BAC # BACR11M23 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence	Drosophila melanogaster	30,270	3-Jun-99
rxa02598	714	GB_IN1 PFMAL3P5	86829	AL034556	Plasmodium falciparum MAL3P5, complete sequence	Plasmodium falciparum	40,057	04-OCT-1999
		GB_PL1:AB024026	23026	AB024026	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone K15O15, complete sequence	Arabidopsis thaliana	38,865	20-Nov-99
		GB_BA2 AE000930	15553	AE000930	Methanobacterium thermoautotrophicum from bases 1592014 to 1607566 (section 136 of 148) of the complete genome.	Methanobacterium thermoautotrophicum	36,804	15-Nov-97
rxa02600	1521	GB_IN2 AC004301	68620	AC004301	Drosophila melanogaster DNA sequence (P1 DS07134 (D192)), complete sequence	Drosophila melanogaster	36,063	29-MAY-1998
		GB_PL2:AC007504	125021	AC007504	Arabidopsis thaliana chromosome I BAC F13F21 genomic sequence, complete sequence	Arabidopsis thaliana	37,074	9-Jul-99
		GB_PH.AF125520	61670	AF125520	Bacteriophage 933W, complete genome.	Bacteriophage 933W	35,396	16-Apr-99
rxa02601	2112	GB_BA1 MTV026	23740	AL022076	Mycobacterium tuberculosis H37Rv complete genome, segment 157/162	Mycobacterium tuberculosis	38,676	24-Jun-99
		GB_BA2 SSU73128	2331	U73128	Sphingomonas sp A8AN3 catechol 2,3-dioxygenase gene, complete cds and 2-hydroxymuconic semialdehyde hydrolase and 2-hydroxymuconic semialdehyde dehydrogenase genes, partial cds	Sphingomonas sp A8AN3	40,020	1-Feb-99
		GB_BA2 SSU73128	2331	U73128	Sphingomonas sp A8AN3 catechol 2,3-dioxygenase gene, complete cds and 2-hydroxymuconic semialdehyde hydrolase and 2-hydroxymuconic semialdehyde dehydrogenase genes, partial cds	Sphingomonas sp A8AN3	40,101	1-Feb-99
rxa02602	627	GB_PR3 AF006751	3106	AF006751	Homo sapiens ES/130 mRNA, complete cds	Homo sapiens	37,582	10-Jul-98
		GB_PR3:AF006751	3106	AF006751	Homo sapiens ES/130 mRNA, complete cds	Homo sapiens	38,462	10-Jul-98
		GB_GSS9 AQ090116	404	AQ090116	HS_3000_B1_E09_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3000 Col=17 Row=J, genomic survey sequence	Homo sapiens	39,481	26-Aug-98
rxa02604	2199	GB_PL1 CREHIH3G	4358	L41841	Chlamydomonas reinhardtii histone H3, histone H4, histone H2B, and histone H2A genes, complete cds	Chlamydomonas reinhardtii	37,500	16-MAY-1996
		GB_GSS13 AQ455681	621	AQ455681	HS_5068_B1_E01_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=644 Col=1 Row=J, genomic survey sequence.	Homo sapiens	36,246	21-Apr-99
		GB_GSS6 AQ829471	392	AQ829471	HS_5442_A2_F11_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=1018 Col=22 Row=K, genomic survey sequence	Homo sapiens	42,347	27-Aug-99
rxa02606	1494	GB_PAT A26027	2547	A26027	C melassecola gene for extracellular antigen PS1	Corynebacterium melassecola	42,857	2-Apr-95
		GB_BA1 CGCOP1G	2547	X66078	C glutamicum cop1 gene for PS1	Corynebacterium glutamicum	42,857	30-Jun-93

TABLE 4: ALIGNMENT RESULTS

		GB_PR2:AP000134	100000	AP000134	Homo sapiens genomic DNA of 21q22.1, GART and AML, f43D11-119B8 region, segment 9/10, complete sequence	Homo sapiens	36,145	25-Sep-99
rxa02609	372	GB_HTG3:AC009212	125452	AC009212	Drosophila melanogaster chromosome 3 clone BACR01A18 (D669) RPCI-98 01 A 18 map 82E-82F strain y, cn bw sp, *** SEQUENCING IN PROGRESS***, 119 unordered pieces.	Drosophila melanogaster	35,753	23-Aug-99
		GB_HTG3:AC009212	125452	AC009212	Drosophila melanogaster chromosome 3 clone BACR01A18 (D669) RPCI-98 01 A 18 map 82E-82F strain y, cn bw sp, *** SEQUENCING IN PROGRESS***, 119 unordered pieces	Drosophila melanogaster	35,753	23-Aug-99
		GB_HTG2 AC007589	134659	AC007589	Drosophila melanogaster chromosome 3 clone BACR20D10 (D667) RPCI-98 20 D 10 map 82D-82E strain y, cn bw sp, *** SEQUENCING IN PROGRESS ***, 73 unordered pieces	Drosophila melanogaster	35,484	2-Aug-99
rxa02610	1050	GB_BA2 AF073776	5138	AF073776	Pseudomonas aeruginosa MexZ (mexZ), complete cds, and mexGH operon, complete sequence	Pseudomonas aeruginosa	38,323	19-OCT-1998
		GB_BA1 AB015853	5461	AB015853	Pseudomonas aeruginosa gene for MexX and MexY, complete cds	Pseudomonas aeruginosa	38,447	13-Nov-98
		GB_VI:HIM237805	2400	AJ237805	Human immunodeficiency virus type 1 partial envelope gene (gp160), isolate MP255	Human immunodeficiency virus type 1	37,928	15-Jun-99
rxa02617	630	GB_PR2:HSL81781	4041	L81781	Homo sapiens (subclone 7_e4 from P1 H25) DNA sequence, complete sequence	Homo sapiens	38,835	9-Apr-97
		GB_HTG3:AC011430	106902	AC011430	Homo sapiens chromosome 5 clone P1_660D11, *** SEQUENCING IN PROGRESS ***, 28 unordered pieces	Homo sapiens	38,662	06-OCT-1999
		GB_HTG3.AC011430	106902	AC011430	Homo sapiens chromosome 5 clone P1_660D11, *** SEQUENCING IN PROGRESS ***, 28 unordered pieces.	Homo sapiens	38,662	06-OCT-1999
rxa02619	1023	GB_BA1 CGL133719	1839	AJ133719	Corynebacterium glutamicum yjcc gene, amtR gene and citE gene, partial	Corynebacterium glutamicum	100,000	12-Aug-99
		GB_BA1 CGL133719	1839	AJ133719	Corynebacterium glutamicum yjcc gene, amtR gene and citE gene, partial	Corynebacterium glutamicum	100,000	12-Aug-99
		GB_EST18 AA734344	378	AA734344	vv24f02 r1 Stratagene mouse heart (#937316) Mus musculus cDNA clone IMAGE 1223355 5', mRNA sequence	Mus musculus	37,968	7-Jan-98
rxa02620	789	GB_BA1 CGL133719	1839	AJ133719	Corynebacterium glutamicum yjcc gene, amtR gene and citE gene, partial	Corynebacterium glutamicum	100,000	12-Aug-99
		GB_BA1 CGL133719	1839	AJ133719	Corynebacterium glutamicum yjcc gene, amtR gene and citE gene, partial	Corynebacterium glutamicum	100,000	12-Aug-99
		GB_EST16 C27457	252	C27457	C27457 Rice callus cDNA Oryza sativa cDNA clone C51917_1A, mRNA sequence	Oryza sativa	39,044	6-Aug-97
rxa02624	1419	GB_HTG2 AC005995	170023	AC005995	Homo sapiens clone DJ0042M02, *** SEQUENCING IN PROGRESS ***, 13 unordered pieces.	Homo sapiens	38,533	23-Apr-99
		GB_HTG2 AC005995	170023	AC005995	Homo sapiens clone DJ0042M02, *** SEQUENCING IN PROGRESS ***, 13 unordered pieces	Homo sapiens	38,533	23-Apr-99
		GB_PR4:AC004895	152927	AC004895	Homo sapiens clone DJ0810E06, complete sequence	Homo sapiens	38,533	29-MAY-1999
rxa02639	957	GB_BA1 MSGY409	41321	AD000017	Mycobacterium tuberculosis sequence from clone y409.	Mycobacterium tuberculosis	50,370	10-DEC-1996
		GB_BA1 MTCY409	30352	Z97188	Mycobacterium tuberculosis H37Rv complete genome, segment 158/162	Mycobacterium tuberculosis	38,039	17-Jun-98
		GB_HTG2 AC006765	274498	AC006765	Caenorhabditis elegans clone Y43H11, *** SEQUENCING IN PROGRESS***, 7 unordered pieces	Caenorhabditis elegans	35,225	23-Feb-99
rxa02647	585	GB_PAT A45577	1925	A45577	Sequence 1 from Patent WO9519442	Corynebacterium glutamicum	37,545	07-MAR-1997
		GB_PAT A45579	1925	A45579	Sequence 3 from Patent WO9519442	Corynebacterium glutamicum	37,545	07-MAR-1997
		GB_PAT:A45581	1925	A45581	Sequence 5 from Patent WO9519442	Corynebacterium glutamicum	37,545	07-MAR-1997
rxa02649	1125	GB_BA1 D90904	150894	D90904	Synechocystis sp PCC6803 complete genome, 6/27, 630555-781448	Synechocystis sp	37,772	7-Feb-99
		GB_PR3 HS941F9	127587	Z95331	Human DNA sequence from BAC 941F9 on chromosome 22q11 2-qter Contains ESTs, STSs and 3' part of FIBULIN-1 D PRECURSOR like gene, part of a Brain Protein E46 like gene and a CpG island, complete sequence	Homo sapiens	38,748	23-Nov-99
		GB_BA1:D90904	150894	D90904	Synechocystis sp PCC6803 complete genome, 6/27, 630555-781448	Synechocystis sp	36,364	7-Feb-99
rxa02652	702	GB_BA2 AF048749	24454	AF048749	Bacteroides fragilis capsular polysaccharide biosynthesis operon, complete sequence	Bacteroides fragilis	37,464	25-Jun-99
		GB_HTG4 AC009244	318775	AC009244	Homo sapiens chromosome 7, *** SEQUENCING IN PROGRESS ***, 36 unordered pieces	Homo sapiens	35,447	26-OCT-1999

TABLE 4: ALIGNMENT RESULTS

		GB_HTG4:AC009244	318775	AC009244	Homo sapiens chromosome 7, *** SEQUENCING IN PROGRESS ***, 36 unordered pieces.	Homo sapiens	35,447	26-OCT-1999
rxa02655	1107	GB_EST10 AA185699	290	AA185699	mt62d11.r1 Soares 2NbMT Mus musculus cDNA clone IMAGE 634485 5' similar to TR G300372 G300372 CELL GROWTH REGULATING NUCLEOLAR PROTEIN ,, mRNA sequence	Mus musculus	39,510	19-Feb-97
		GB_GSS13 AQ429764	439	AQ429764	HS_5079_A2_C12_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=655 Col=24 Row=E, genomic survey sequence	Homo sapiens	37,701	31-MAR-1999
		GB_GSS8 AQ012380	646	AQ012380	CIT-HSP-2300L9 TF CIT-HSP Homo sapiens genomic clone 2300L9, genomic survey sequence	Homo sapiens	38,874	6-Jun-98
rxa02662	387	GB_HTG2 AC007802	118569	AC007802	Drosophila melanogaster chromosome 2 clone BACR07I11 (D648) RPCI-98 07 I.11 map 58A1-58A2 strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 70 unordered pieces	Drosophila melanogaster	37,696	2-Aug-99
		GB_HTG2 AC007802	118569	AC007802	Drosophila melanogaster chromosome 2 clone BACR07I11 (D648) RPCI-98 07 I 11 map 58A1-58A2 strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 70 unordered pieces	Drosophila melanogaster	37,696	2-Aug-99
		GB_HTG2 AC007802	118569	AC007802	Drosophila melanogaster chromosome 2 clone BACR07I11 (D648) RPCI-98 07 I 11 map 58A1-58A2 strain y, cn bw sp, *** SEQUENCING IN PROGRESS ***, 70 unordered pieces	Drosophila melanogaster	35,616	2-Aug-99
rxa02665	603	GB_HTG1 AC002419	128340	AC002419	Homo sapiens chromosome X clone bWXD40, *** SEQUENCING IN PROGRESS***, 2 unordered pieces	Homo sapiens	32,941	12-Aug-97
		GB_HTG1 AC002419	128340	AC002419	Homo sapiens chromosome X clone bWXD40, *** SEQUENCING IN PROGRESS ***, 2 unordered pieces	Homo sapiens	32,941	12-Aug-97
		GB_GSS15.AQ655091	630	AQ655091	Sheared DNA-21B5 TF Sheared DNA Trypanosoma brucei genomic clone Sheared DNA-21B5, genomic survey sequence	Trypanosoma brucei	41,794	22-Jun-99
rxa02670	705	GB_HTG2 AC006450	177555	AC006450	Homo sapiens chromosome 9 clone hRPK 85_O_21 map 9, *** SEQUENCING IN PROGRESS ***, 2 ordered pieces	Homo sapiens	41,374	15-Jul-99
		GB_HTG2 AC006450	177555	AC006450	Homo sapiens chromosome 9 clone hRPK 85_O_21 map 9, *** SEQUENCING IN PROGRESS ***, 2 ordered pieces	Homo sapiens	41,374	15-Jul-99
		GB_BA1 SPU86147	2268	U86147	Synechococcus PCC7942 UDP-N-acetylmuramate-alanine ligase (murC) gene, partial cds, UDP-N-acetylenolpyruvylglucosamine reductase (murB), and mercuric resistance operon regulatory protein (merR) genes, complete cds	Synechococcus PCC7942	40,177	15-Feb-97
rxa02672	1221	GB_BA1 MTV024	8189	AL022075	Mycobacterium tuberculosis H37Rv complete genome, segment 151/162	Mycobacterium tuberculosis	53,197	17-Jun-98
		GB_BA1 MSGY23	40806	AD000016	Mycobacterium tuberculosis sequence from clone y23	Mycobacterium tuberculosis	37,500	10-DEC-1996
		GB_EST38 AW029724	634	AW029724	EST272979 tomato callus, TAMU Lycopersicon esculentum cDNA clone cLEC28I17 similar to beta-ketoacyl-ACP synthase, putative, mRNA sequence	Lycopersicon esculentum	40,000	15-Sep-99
rxa02673	756	GB_GSS12 AQ356661	518	AQ356661	CITBI-E1-2531G11 TF CITBI-E1 Homo sapiens genomic clone 2531G11, genomic survey sequence.	Homo sapiens	33,022	24-Jan-99
		GB_IN1 CELC50A2	36582	AF036689	Caenorhabditis elegans cosmid C50A2	Caenorhabditis elegans	35,443	05-DEC-1997
		GB_HTG2 AC006702	299864	AC006702	Caenorhabditis elegans clone Y104H12b, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces	Caenorhabditis elegans	35,443	23-Feb-99
rxa02678	1041	GB_HTG1 AP000452	83103	AP000452	Homo sapiens chromosome 11 clone PAC2 map 11q11, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Homo sapiens	35,098	13-Sep-99
		GB_HTG1 AP000452	83103	AP000452	Homo sapiens chromosome 11 clone PAC2 map 11q11 *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	35,098	13-Sep-99
		GB_PR3 HS498I24	58190	AL031057	Human DNA sequence from clone 498I24 on chromosome 6p22 1-22.3 Contains STS, GSS and a CpG island, complete sequence	Homo sapiens	35,328	23-Nov-99
rxa02680	1407	GB_BA1 MLCB268	38859	AL022602	Mycobacterium leprae cosmid B268	Mycobacterium leprae	37,797	27-Aug-99
		GB_BA1 MSGB1554CS	36548	L78814	Mycobacterium leprae cosmid B1554 DNA sequence	Mycobacterium leprae	36,900	15-Jun-96
		GB_BA1.MSGB1551CS	36548	L78813	Mycobacterium leprae cosmid B1551 DNA sequence	Mycobacterium leprae	36,900	15-Jun-96
rxa02683								
rxa02685	780	GB_HTG3 AC008640	198483	AC008640	Homo sapiens chromosome 5 clone CIT978SKB_17P2, *** SEQUENCING IN PROGRESS ***, 70 unordered pieces	Homo sapiens	37,299	3-Aug-99

TABLE 4: ALIGNMENT RESULTS

		GB_HTG3:AC008640	198483	AC008640	Homo sapiens chromosome 5 clone CIT978SKB_17P2, *** SEQUENCING IN PROGRESS ***, 70 unordered pieces	Homo sapiens	37,299	3-Aug-99
		GB_BA2 AE000945	11317	AE000945	Archaeoglobus fulgidus section 162 of 172 of the complete genome	Archaeoglobus fulgidus	38,760	15-DEC-1997
rxa02688	792	GB_BA1 CORPHEA	1088	M13774	C glutamicum pheA gene encoding prephenate dehydratase, complete cds	Corynebacterium glutamicum	100,000	26-Apr-93
		GB_HTG2 AC007554	167095	AC007554	Homo sapiens clone hRPK 74_A_1, *** SEQUENCING IN PROGRESS ***, 10 unordered pieces	Homo sapiens	35,226	14-MAY-1999
		GB_HTG2 AC007554	167095	AC007554	Homo sapiens clone hRPK 74_A_1, *** SEQUENCING IN PROGRESS ***, 10 unordered pieces	Homo sapiens	35,226	14-MAY-1999
rxa02689	465	GB_GSS9 AQ110873	414	AQ110873	CIT-HSP-2378K10 TR CIT-HSP Homo sapiens genomic clone 2378K10, genomic survey sequence	Homo sapiens	34,768	29-Aug-98
		GB_OV DUKFASA	9138	M21635	Duck (A platyrhynchos) S-acyl fatty acid synthase thioesterase gene, complete cds	Anas platyrhynchos	39,177	28-Apr-93
		GB_OV DUKFASA	9138	M21635	Duck (A platyrhynchos) S-acyl fatty acid synthase thioesterase gene, complete cds	Anas platyrhynchos	35,022	28-Apr-93
rxa02690	1221	GB_HTG4.AC010096	223607	AC010096	Homo sapiens chromosome unknown clone NH0364A16, WORKING DRAFT SEQUENCE, in unordered pieces	Homo sapiens	39,301	29-OCT-1999
		GB_HTG4 AC010096	223607	AC010096	Homo sapiens chromosome unknown clone NH0364A16, WORKING DRAFT SEQUENCE, in unordered pieces.	Homo sapiens	39,301	29-OCT-1999
		GB_BA2 AF132788	1411	AF132788	Fischerella muscicola small subunit ribosomal RNA gene, partial sequence	Fischerella muscicola	36,156	1-Sep-99
rxa02693	1899	GB_GSS5 AQ784372	542	AQ784372	HS_3181_A2_H12_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3181 Col=24 Row=O, genomic survey sequence	Homo sapiens	41,546	3-Aug-99
		GB_HTG4 AC010573	80511	AC010573	Drosophila melanogaster chromosome 3L/70C12 clone RPCI98-2M13, *** SEQUENCING IN PROGRESS *** 45 unordered pieces	Drosophila melanogaster	36,839	16-OCT-1999
		GB_EST18 AA696238	640	AA696238	GM05354 5prime GM Drosophila melanogaster ovary BlueScript Drosophila melanogaster cDNA clone GM05354 5prime, mRNA sequence	Drosophila melanogaster	39,523	28-Nov-98
rxa02696	579	GB_BA1 AB003132	4116	AB003132	Corynebacterium glutamicum gene for MurC, FtsQ, FtsZ, complete cds	Corynebacterium glutamicum	100,000	4-Aug-97
		GB_PR4.AC006024	90583	AC006024	Homo sapiens PAC clone DJ1166G19 from 7p12-p11 2, complete sequence	Homo sapiens	36,049	20-Feb-99
		GB_HTG1 HSJ657D12	315458	AL109943	Homo sapiens chromosome X clone RP4-657D12 map q22 1-24, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Homo sapiens	36,475	24-Nov-99
rxa02697	1650	GB_EST20 AA874010	365	AA874010	vw87b05.r1 Stratagene mouse skin (#937313) Mus musculus cDNA clone IMAGE 1261905 5', mRNA sequence	Mus musculus	39,452	19-MAR-1998
		GB_EST30 AI658486	599	AI658486	tu17a09.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE 2251288 3', mRNA sequence	Homo sapiens	37,324	10-MAY-1999
		GB_EST20 AA874010	365	AA874010	vw87b05 r1 Stratagene mouse skin (#937313) Mus musculus cDNA clone IMAGE 1261905 5', mRNA sequence	Mus musculus	39,452	19-MAR-1998
rxa02700	1359	GB_BA1 SCF85	21420	AL110470	Streptomyces coelicolor cosmid F85	Streptomyces coelicolor A3(2)	39,497	1-Sep-99
		GB_HTG5 AC011629	69344	AC011629	Homo sapiens chromosome 15 clone 334_M_8 map 15, LOW-PASS SEQUENCE SAMPLING	Homo sapiens	37,462	13-Nov-99
		GB_HTG3 AC010106	157581	AC010106	Homo sapiens clone NH0575J05, *** SEQUENCING IN PROGRESS ***, 1 unordered pieces	Homo sapiens	36,220	11-Sep-99
rxa02701	1431	GB_BA1 MTCI65	34331	Z95584	Mycobacterium tuberculosis H37Rv complete genome, segment 50/162	Mycobacterium tuberculosis	41,867	17-Jun-98
		GB_BA1 MSGY348	40056	AD000020	Mycobacterium tuberculosis sequence from clone y348	Mycobacterium tuberculosis	43,338	10-DEC-1996
		GB_PR2 AP000117	151516	AP000117	Homo sapiens genomic DNA of 21q22 1, GART and AML related, Q78C10-149C3 region, segment 20/20, complete sequence	Homo sapiens	36,037	25-Sep-99
rxa02712	918	GB_BA2 AF124600	4115	AF124600	Corynebacterium glutamicum chorismate synthase (aroC), shikimate kinase (aroK), and 3-dehydroquinate synthase (aroB) genes, complete cds, and putative cytoplasmic peptidase (pepQ) gene, partial cds	Corynebacterium glutamicum	37,294	04-MAY-1999
		GB_BA2 AF053071	1083	AF053071	Corynebacterium glutamicum dehydroquinate synthetase (aroB) gene, complete cds	Corynebacterium glutamicum	39,675	12-Sep-98
		GB_BA1 BSTHRZ	19861	Z80360	B subtilis thrZ downstream chromosomal region	Bacillus subtilis	34,002	24-Jun-98
rxa02714	552	GB_PL2 ATF9F13	109936	AL080253	Arabidopsis thaliana DNA chromosome 4, BAC clone F9F13 (ESSA project)	Arabidopsis thaliana	39,252	16-Aug-99

TABLE 4: ALIGNMENT RESULTS

		GB_PL2:ATT29H11	87011	AL049659	Arabidopsis thaliana DNA chromosome 3, BAC clone T29H11.	Arabidopsis thaliana	34,249	9-Jun-99
		GB_EST4 H37460	489	H37460	15589 Lambda-PRL2 Arabidopsis thaliana cDNA clone 181N17T7, mRNA sequence	Arabidopsis thaliana	45,869	30-DEC-1997
rxa02715	513	GB_GSS13:AQ454067	534	AQ454067	HS_5176_B1_A09_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=752 Col=17 Row=B, genomic survey sequence	Homo sapiens	40,854	21-Apr-99
		GB_PR3 AC005495	185254	AC005495	Homo sapiens chromosome 17, clone hRPK 293_K_20, complete sequence	Homo sapiens	33,200	30-OCT-1998
		GB_PR3 AC005495	185254	AC005495	Homo sapiens chromosome 17, clone hRPK 293_K_20, complete sequence	Homo sapiens	36,273	30-OCT-1998
rxa02720	825	GB_BA1 AB003132	4116	AB003132	Corynebacterium glutamicum gene for MurC, FtsQ, FtsZ, complete cds	Corynebacterium glutamicum	98,788	4-Aug-97
		GB_BA1 BLFTSZ	5546	Y08964	B.lactofermentum murC, ftsQ or divD & ftsZ genes	Corynebacterium glutamicum	100,000	08-OCT-1998
		GB_HTG4 AC009764	213581	AC009764	Homo sapiens chromosome 11 clone 381_O_22 map 11, *** SEQUENCING IN PROGRESS ***, 40 unordered pieces	Homo sapiens	35,504	21-OCT-1999
rxa02721	861	GB_BA1 BLFTSZ	5546	Y08964	B lactofermentum murC, ftsQ or divD & ftsZ genes.	Corynebacterium glutamicum	98,606	08-OCT-1998
		GB_BA1 AB003132	4116	AB003132	Corynebacterium glutamicum gene for MurC, FtsQ, FtsZ, complete cds	Corynebacterium glutamicum	97,561	4-Aug-97
		GB_BA1 SCI51	40745	AL109848	Streptomyces coelicolor cosmid I51	Streptomyces coelicolor A3(2)	39,110	16-Aug-99
rxa02725	735	GB_BA1.CGU43535	2531	U43535	Corynebacterium glutamicum multidrug resistance protein (cmr) gene, complete cds	Corynebacterium glutamicum	42,043	9-Apr-97
		GB_EST1 D40448	361	D40448	RICS2437A Rice shoot Oryza sativa cDNA, mRNA sequence	Oryza sativa	41,944	11-Nov-94
		GB_BA2 AF038430	8330	AF038430	Thiobacillus neapolitanus carboxysome operon, complete sequence	Thiobacillus neapolitanus	39,202	21-Aug-98
rxa02727	1035	GB_BA1 MTCY270	37586	Z95388	Mycobacterium tuberculosis H37Rv complete genome, segment 96/162	Mycobacterium tuberculosis	37,427	10-Feb-99
		GB_BA1 MTAG84	1458	X77129	M tuberculosis Ag84 (CIE) gene.	Mycobacterium tuberculosis	49,339	21-Jul-95
		GB_BA1 AP000064	247695	AP000064	Aeropyrum pernix genomic DNA, section 7/7	Aeropyrum pernix	38,790	22-Jun-99
rxa02735	828	GB_BA1 TVCPT	1923	X56901	T.vulgaris cpT gene for carboxypeptidase T	Thermoactinomyces vulgaris	37,688	30-OCT-1991
		GB_GSS4:AQ682162	355	AQ682162	HS_5503_B2_C11_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=1079 Col=22 Row=F, genomic survey sequence	Homo sapiens	35,294	28-Jun-99
		GB_EST21:AA915356	456	AA915356	vz29a08 r1 Soares 2NbMT Mus musculus cDNA clone IMAGE 1327862 5', mRNA sequence	Mus musculus	42,609	14-Apr-98
rxa02736	1080	GB_PAT E13655	2260	E13655	gDNA encoding glucose-6-phosphate dehydrogenase	Corynebacterium glutamicum	99,620	24-Jun-98
		GB_GSS13 AQ447106	711	AQ447106	mgxb0004P18f CUGI Rice Blast BAC Library Magnaporthe grisea genomic clone mgxb0004P18f, genomic survey sequence	Magnaporthe grisea	38,158	8-Apr-99
		GB_EST36 AI900850	670	AI900850	sb95c03 y1 Gm-c1012 Glycine max cDNA clone GENOME SYSTEMS CLONE ID Gm-c1012-413 5' similar to SW IF4Z_TOBAC Q40468 EUKARYOTIC INITIATION FACTOR 4A-15 ;, mRNA sequence	Glycine max	37,479	06-DEC-1999
rxa02744	927	GB_PR1 AB026898	270000	AB026898	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds).	Homo sapiens	39,364	15-MAY-1999
		GB_PR1:AB026898	270000	AB026898	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)	Homo sapiens	36,275	15-MAY-1999
		GB_PR2 AP000498	100000	AP000498	Homo sapiens genomic DNA, chromosome 3p21 3, clone 603 to 320, anti-oncogene region, section 1/3	Homo sapiens	39,364	28-Sep-99
rxa02751	597	GB_HTG4 AC010127	189552	AC010127	Homo sapiens chromosome unknown clone NH0002I08, WORKING DRAFT SEQUENCE, in unordered pieces	Homo sapiens	36,149	29-OCT-1999
		GB_HTG4 AC010127	189552	AC010127	Homo sapiens chromosome unknown clone NH0002I08, WORKING DRAFT SEQUENCE, in unordered pieces	Homo sapiens	36,149	29-OCT-1999
		GB_HTG4 AC010127	189552	AC010127	Homo sapiens chromosome unknown clone NH0002I08, WORKING DRAFT SEQUENCE, in unordered pieces.	Homo sapiens	35,924	29-OCT-1999

TABLE 4: ALIGNMENT RESULTS

rxa02756	1014	GB_RO:CRUGIPR	2785	D38103	Hamster mRNA for GIP (gastric inhibitory polypeptide) receptor, complete cds.	Cricetulus sp.	38,501	8-Feb-99
		GB_HTG1 CNS01DRV	224372	AL118558	Homo sapiens chromosome 14 clone R-1017G21, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Homo sapiens	38,667	15-OCT-1999
		GB_HTG1:CNS01DRV	224372	AL118558	Homo sapiens chromosome 14 clone R-1017G21, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Homo sapiens	38,667	15-OCT-1999
rxa02757	669	GB_RO RNU35245	2051	U35245	Rat vacuolar protein sorting homolog r-vps33b mRNA, complete cds	Rattus norvegicus	39,058	15-Jan-97
		GB_RO RNU35245	2051	U35245	Rat vacuolar protein sorting homolog r-vps33b mRNA, complete cds	Rattus norvegicus	37,481	15-Jan-97
rxa02765	882	GB_EST4:H46883	459	H46883	yo19f06 r1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE 178403 5', mRNA sequence.	Homo sapiens	40,132	31-Jul-95
		GB_PL1 NTA6235	3931	AJ006235	Nicotiana tabacum DNA fragment for K-alpha right T-DNA border	Nicotiana tabacum	34,247	6-Feb-99
		GB_HTG3 AC011519	57287	AC011519	Homo sapiens chromosome 19 clone LLNL-F_192H5, *** SEQUENCING IN PROGRESS ***, 36 unordered pieces	Homo sapiens	38,497	07-OCT-1999
rxa02766	516	GB_GSS13:AQ489419	554	AQ489419	RPCI-11-246A3 TV RPCI-11 Homo sapiens genomic clone RPCI-11-246A3, genomic survey sequence	Homo sapiens	37,821	24-Apr-99
		GB_PR3 HS90L6	190837	Z97353	Human DNA sequence from clone 90L6 on chromosome 22q11 21-11.23. Contains an RPL15 (60S Ribosomal Protein L15) pseudogene, ESTs, STSs and GSSs, complete sequence	Homo sapiens	38,160	23-Nov-99
		GB_BA1 MTCY373	35516	Z73419	Mycobacterium tuberculosis H37Rv complete genome, segment 57/162	Mycobacterium tuberculosis	36,701	17-Jun-98
rxa02770	1689	GB_BA2 AF038651	4077	AF038651	Corynebacterium glutamicum dipeptide-binding protein (dciAE) gene, partial cds, adenine phosphoribosyltransferase (apt) and GTP pyrophosphokinase (rel) genes, complete cds, and unknown gene.	Corynebacterium glutamicum	100,000	14-Sep-98
		GB_OV AF061275	6756	AF061275	Ictalurus punctatus estrogen receptor type alpha mRNA, complete cds	Ictalurus punctatus	37,117	31-OCT-1998
		GB_RO MMSCSELN4	3840	X61756	M musculus rearranged T-cell receptor beta variable region (Vb17a)	Mus musculus	37,933	03-DEC-1991
rxa02774	494	GB_HTG2:AF129408	138685	AF129408	Homo sapiens chromosome 21 clone PAC 31K18 map 21q22 3, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Homo sapiens	38,241	04-MAR-1999
		GB_HTG2 AF129408	138685	AF129408	Homo sapiens chromosome 21 clone PAC 31K18 map 21q22 3, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Homo sapiens	38,241	04-MAR-1999
		GB_PR3 AF064859	122571	AF064859	Homo sapiens chromosome 21q22 3 PAC 141B3, complete sequence, containing ribosomal protein homologue pseudogene L23a.	Homo sapiens	37,910	2-Jun-98
rxa02775	348	GB_PR3 HSU19F10	31474	Z81145	Human DNA sequence from cosmid U19F10, between markers DXS366 and DXS87 on chromosome X contains ESTs.	Homo sapiens	36,443	23-Nov-99
		GB_EST11:AA211850	293	AA211850	zr90e04.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE 682974 3' similar to TR G1224065 G1224065 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE ,, mRNA sequence	Homo sapiens	30,479	13-Aug-97
		GB_EST13:AA372532	400	AA372532	EST84441 Colon adenocarcinoma IV Homo sapiens cDNA 5' end, mRNA sequence	Homo sapiens	40,104	21-Apr-97
rxa02776	465	GB_GSS9.AQ096114	383	AQ096114	HS_3030_A2_D11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3030 Col=22 Row=G, genomic survey sequence	Homo sapiens	44,643	27-Aug-98
		GB_RO AF139518	8827	AF139518	Rattus norvegicus A-kinase anchor protein mRNA, complete cds	Rattus norvegicus	39,722	16-Jun-99
		GB_EST32 AI728295	564	AI728295	BNLGHi10386 Six-day Cotton fiber Gossypium hirsutum cDNA 5' similar to (AF076274) contains similarity to rat p47 protein (GB AB002086) [Arabidopsis thaliana], mRNA sequence	Gossypium hirsutum	37,049	11-Jun-99
rxa02777	1230	GB_HTG3:AC009407	207973	AC009407	Homo sapiens clone NH0223I10, *** SEQUENCING IN PROGRESS ***, 16 unordered pieces	Homo sapiens	39,784	21-Aug-99
		GB_HTG3.AC009407	207973	AC009407	Homo sapiens clone NH0223I10, *** SEQUENCING IN PROGRESS ***, 16 unordered pieces	Homo sapiens	39,784	21-Aug-99
		GB_BA2 AE001137	44380	AE001137	Borrelia burgdorferi (section 23 of 70) of the complete genome	Borrelia burgdorferi	39,105	15-DEC-1997
rxa02778	348	GB_EST37 AI940900	668	AI940900	sb79d08 y1 Gm-c1010 Glycine max cDNA clone GENOME SYSTEMS CLONE ID Gm-c1010-1192 5' similar to SW ITRA_SOYBN P01070 TRYPSIN INHIBITORS A AND C PRECURSOR ,, mRNA sequence	Glycine max	35,036	3-Aug-99
		GB_HTG4 AC008940	131864	AC008940	Homo sapiens chromosome 5 clone CITB-H1_2319M24, *** SEQUENCING IN PROGRESS ***, 3 ordered pieces	Homo sapiens	33,043	31-OCT-1999
		GB_HTG4 AC008940	131864	AC008940	Homo sapiens chromosome 5 clone CITB-H1_2319M24, *** SEQUENCING IN PROGRESS ***, 3 ordered pieces	Homo sapiens	33,043	31-OCT-1999

TABLE 4: ALIGNMENT RESULTS

rxa02779	402	GB_PR1:AB020876	100000	AB020876	Homo sapiens genomic DNA of 9q32 anti-oncogene of flat epitherium cancer , segment 8/10.	Homo sapiens	35,000	21-MAY-1999
		GB_EST26 AI339126	415	AI339126	qt06d03 x1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1946789 3' similar to gb L25444 60S RIBOSOMAL PROTEIN L35A (HUMAN),, mRNA sequence	Homo sapiens	35,876	29-DEC-1998
		GB_PR1 AB020876	100000	AB020876	Homo sapiens genomic DNA of 9q32 anti-oncogene of flat epitherium cancer , segment 8/10	Homo sapiens	35,678	21-MAY-1999
rxa02780	450	GB_GSS14 AQ524732	591	AQ524732	HS_5236_A1_D09_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=812 Col=17 Row=G, genomic survey sequence	Homo sapiens	39,726	11-MAY-1999
		GB_PR4 AC006051	38903	AC006051	Homo sapiens 12p13 3 PAC RPCI5-1103G8 (Roswell Park Cancer Institute Human PAC Library) complete sequence.	Homo sapiens	35,068	26-Nov-98
		GB_PR4 AC006051	38903	AC006051	Homo sapiens 12p13 3 PAC RPCI5-1103G8 (Roswell Park Cancer Institute Human PAC Library) complete sequence	Homo sapiens	37,273	26-Nov-98
rxa02781	1314	GB_VI BHV1CGEN	135301	AJ004801	Bovine herpesvirus 1 complete genome	Bovine herpesvirus type 1 1	41,053	11-Jan-99
		GB_BA1:SHGCPIR	107379	X86780	S hygroscopicus gene cluster for polyketide immunosuppressant rapamycin	Streptomyces hygroscopicus	40,551	16-Aug-96
		GB_BA1 SHGCPIR	107379	X86780	S hygroscopicus gene cluster for polyketide immunosuppressant rapamycin	Streptomyces hygroscopicus	39,598	16-Aug-96
rxa02782	1422	GB_IN1 DSV28T23	5218	X60176	D.silvestris clone U28T2 non-LTR retrotransposon DNA (5218 bp)	Drosophila silvestris	38,695	25-MAR-1992
		GB_IN1 DSV28T24	7779	X60177	D silvestris clone U28T2 non-LTR retrotransposon DNA (7779 bp)	Drosophila silvestris	38,844	30-Nov-93
		GB_BA2 MPU34795	24888	U34795	Mycoplasma pneumoniae cosmid pcosMPGT9 25kb EcoRI fragment	Mycoplasma pneumoniae	37,832	06-MAR-1996
rxa02783	672	GB_EST2 R13483	481	R13483	yf77g03 r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE 28494 5', mRNA sequence	Homo sapiens	36,243	12-Apr-95
		GB_HTG3 AC011333	159160	AC011333	Homo sapiens chromosome 5 clone CIT-HSPC_229L21, *** SEQUENCING IN PROGRESS ***, 23 unordered pieces	Homo sapiens	38,246	06-OCT-1999
		GB_HTG3 AC011333	159160	AC011333	Homo sapiens chromosome 5 clone CIT-HSPC_229L21, *** SEQUENCING IN PROGRESS ***, 23 unordered pieces.	Homo sapiens	38,246	06-OCT-1999
rxa02784	309	GB_PR3 HS474A14	107352	AL023285	Human DNA sequence from clone 474A14 on chromosome 1q24 1-25 2 Contains EST, CA repeat, 5'UTR (tenascin-R), GSS, complete sequence	Homo sapiens	37,868	23-Nov-99
		GB_GSS12 AQ374565	441	AQ374565	RPCI11-159P12.TV RPCI-11 Homo sapiens genomic clone RPCI-11-159P12, genomic survey sequence	Homo sapiens	36,522	20-MAY-1999
		GB_GSS5 AQ780184	686	AQ780184	HS_3138_B1_F11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3138 Col=21 Row=L, genomic survey sequence	Homo sapiens	44,186	2-Aug-99
rxa02786	830	GB_PL1 SCYBL033C	1794	Z35794	S cerevisiae chromosome II reading frame ORF YBL033c	Saccharomyces cerevisiae	39,264	11-MAR-1998
		GB_PL1.ECRIB1GN	1747	Z21617	S.cerevisiae RIB1 gene encoding GTP cyclohydrolase II	Saccharomyces cerevisiae	37,118	28-Jan-95
		GB_PAT A38763	1747	A38763	Sequence 1 from Patent WO9411515	Saccharomyces cerevisiae	37,118	05-MAR-1997
rxa02789	669	GB_EST34 AV146372	295	AV146372	AV146372 Mus musculus C57BL/6J 10-11 day embryo Mus musculus cDNA clone 2810453K19, mRNA sequence.	Mus musculus	65,432	3-Jul-99
		GB_GSS5 AQ785226	524	AQ785226	HS_2025_B2_A07_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2025 Col=14 Row=B, genomic survey sequence	Homo sapiens	40,342	3-Aug-99
		GB_BA1 SCE94	38532	AL049628	Streptomyces coelicolor cosmid E94.	Streptomyces coelicolor	35,346	12-Apr-99
rxa02793	825	GB_HTG2:AC006514	247029	AC006514	Homo sapiens clone RPCI11-656E20, *** SEQUENCING IN PROGRESS ***, 90 unordered pieces	Homo sapiens	33,742	1-Apr-99
		GB_HTG2:AC006514	247029	AC006514	Homo sapiens clone RPCI11-656E20, *** SEQUENCING IN PROGRESS ***, 90 unordered pieces	Homo sapiens	33,742	1-Apr-99
		GB_EST22:AI033150	384	AI033150	ow94b01 s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE 1654441 3' similar to TR O02711 O02711 PRO-POL-DUTPASE POLYPROTEIN ,, mRNA sequence.	Homo sapiens	38,951	28-Aug-98
rxa02796	672	GB_OV.AF172144	1101	AF172144	Xenopus laevis potassium channel beta 2 subunit mRNA, partial cds.	Xenopus laevis	40,000	25-Sep-99
		GB_HTG1.AP000572	84439	AP000572	Homo sapiens chromosome 11 clone P28D2 map 11q13, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Homo sapiens	35,725	09-OCT-1999

TABLE 4: ALIGNMENT RESULTS

		GB_HTG1:AP000572	84439	AP000572	Homo sapiens chromosome 11 clone P28D2 map 11q13, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Homo sapiens	35,725	09-OCT-1999
rxa02798	1548	GB_EST10 AA155097	322	AA155097	mr24h12 r1 Soares mouse 3NbMS Mus musculus cDNA clone IMAGE.598439 5', mRNA sequence	Mus musculus	41,195	16-Feb-97
		GB_GSS9.AQ150317	489	AQ150317	HS_3178_B1_F12_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3178 Col=23 Row=L, genomic survey sequence	Homo sapiens	39,549	08-OCT-1998
		GB_BA2 AE001731	10186	AE001731	Thermotoga maritima section 43 of 136 of the complete genome	Thermotoga maritima	35,747	2-Jun-99
rxa02799	396	GB_IN2 AF139876	1562	AF139876	Giardia intestinalis histone H4 gene, complete cds	Giardia intestinalis	34,848	02-OCT-1999
		GB_HTG5 AC011614	176606	AC011614	Drosophila melanogaster chromosome X clone BACR48L05 (D1142) RPCI-98 48 L 5 map 16F-17A strain y, cn bw sp, *** SEQUENCING IN PROGRESS ***, 114 unordered pieces	Drosophila melanogaster	38,817	19-Nov-99
		GB_GSS10 AQ254726	565	AQ254726	EP(3)3517 Drosophila melanogaster EP line Drosophila melanogaster genomic Sequence recovered from Both 5' and 3' ends of P element, genomic survey sequence	Drosophila melanogaster	38,798	28-Jun-99
rxa02812								
rxa02815	552	GB_BA2 PAU32853	1961	U32853	Pseudomonas aeruginosa mucC and mucD genes, complete cds	Pseudomonas aeruginosa	39,925	06-MAR-1996
		GB_BA2 PAU49151	4587	U49151	Pseudomonas aeruginosa alternate sigma factor (algU), mucA, mucB, mucC and mucD genes, complete cds	Pseudomonas aeruginosa	39,925	13-MAR-1996
		GB_BA2.PAU49151	4587	U49151	Pseudomonas aeruginosa alternate sigma factor (algU), mucA, mucB, mucC and mucD genes, complete cds	Pseudomonas aeruginosa	35,922	13-MAR-1996
rxa02817	499	GB_BA1 CORAIA	4705	L09232	Corynebacterium glutamicum acetohydroxy acid synthase (ilvB) and (ilvN) genes, and acetohydroxy acid isomeroreductase (ilvC) gene, complete cds	Corynebacterium glutamicum	38,554	23-Feb-95
		GB_EST22 AI004214	475	AI004214	ot94h01 x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE 1624465 3', mRNA sequence	Homo sapiens	51,092	27-Aug-98
		GB_EST27:AI457904	455	AI457904	tj48b08 x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE 2144727 3', mRNA sequence	Homo sapiens	37,381	13-Apr-99
rxa02818	606	GB_PL1.MZEADH1CM	6167	M32984	Z mays alcohol dehydrogenase (ADH-1 C-m allele) gene, complete cds	Zea mays	33,111	27-Apr-93
		GB_PL1:ZMADH1ALL	6158	X17556	Z mays DNA for Adh1-Cm allele	Zea mays	33,111	23-Jan-92
		GB_PL1:MZEADH1CM	6167	M32984	Z.mays alcohol dehydrogenase (ADH-1 C-m allele) gene, complete cds	Zea mays	38,065	27-Apr-93
rxa02823	370	GB_PL2:AF077130	4392	AF077130	Oryza sativa receptor-like protein kinase gene, complete cds	Oryza sativa	33,243	25-Jul-98
		GB_HTG1 CNS00M8S	214599	AL079302	Homo sapiens chromosome 14 clone R-1089B7, *** SEQUENCING IN PROGRESS ***, in ordered pieces.	Homo sapiens	38,420	15-OCT-1999
		GB_HTG1 CNS00M8S	214599	AL079302	Homo sapiens chromosome 14 clone R-1089B7, *** SEQUENCING IN PROGRESS ***, in ordered pieces	Homo sapiens	38,420	15-OCT-1999
rxa02825	1962	GB_PL1 ZMU17350	1289	U17350	Zea mays thiamine biosynthetic enzyme (thi1-1) mRNA, complete cds	Zea mays	40,710	12-Apr-96
		GB_GSS13.AQ440082	432	AQ440082	HS_5080_B1_B12_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=656 Col=23 Row=D, genomic survey sequence	Homo sapiens	41,121	31-MAR-1999
		GB_EST10 AA141278	579	AA141278	CK01542 3prime CK Drosophila melanogaster embryo BlueScript Drosophila melanogaster cDNA clone CK01542 3prime, mRNA sequence	Drosophila melanogaster	42,424	29-Nov-98
rxa02827	523	GB_BA2:AF054624	6984	AF054624	Lactobacillus sakei transcription-repair coupling factor (mfd) gene, partial cds, L-lactate dehydrogenase (ldhL) gene, complete cds, and unknown genes	Lactobacillus sakei	37,241	12-Jan-99
		GB_BA2 AF023181	6616	AF023181	Listeria monocytogenes transcription-repair coupling factor (mfdL), low temperature requirement B protein (ltrB), and DivIC homolog (divL) genes, complete cds	Listeria monocytogenes	61,228	1-Jan-99
		GB_HTG3 AC009213	114735	AC009213	Drosophila melanogaster chromosome 3 clone BACR09F18 (D812) RPCI-98 09 F 18 map 98D-98D strain y, cn bw sp, *** SEQUENCING IN PROGRESS ***, 109 unordered pieces	Drosophila melanogaster	32,427	23-Aug-99
rxa02838	528	GB_BA2 AE000069	12230	AE000069	Rhizobium sp NGR234 plasmid pNGR234a, section 6 of 46 of the complete plasmid sequence	Rhizobium sp NGR234	57,803	12-DEC-1997
		GB_OM.SSU19994	2004	U19994	Sus scrofa p55 TNF receptor mRNA, complete cds	Sus scrofa	34,848	30-Jan-96
		GB_BA2 AE000069	12230	AE000069	Rhizobium sp NGR234 plasmid pNGR234a, section 6 of 46 of the complete plasmid sequence	Rhizobium sp NGR234	36,505	12-DEC-1997
rxa02840	273	GB_BA2 ECU73857	128824	U73857	Escherichia coli chromosome minutes 6-8	Escherichia coli	100,000	14-Jul-99
		GB_BA2 AE000145	11448	AE000145	Escherichia coli K-12 MG1655 section 35 of 400 of the complete genome	Escherichia coli	100,000	12-Nov-98
		GB_BA1 ECORFABC	3044	X76979	E coli orf302, 0rf303 and orf101 sequence	Escherichia coli	40,672	28-Aug-96

TABLE 4: ALIGNMENT RESULTS

rxa02841	558	GB_GSS4:AQ724171	407	AQ724171	HS_5380_B1_H09_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=956 Col=17 Row=P, genomic survey sequence	Homo sapiens	35,135	14-Jul-99
		GB_PL1 PSFERR	1023	X64417	P.sativum mRNA for ferritin.	Pisum sativum	41,985	30-Jun-93
		GB_PL1:PSFERRI	1023	X73369	P sativum mRNA for ferritin	Pisum sativum	41,985	21-Jul-95
rxa02842	365	GB_EST32.AI723928	435	AI723928	RHIZ1_35_B10 y1_A001 Rhizome1 Sorghum halepense cDNA, mRNA sequence	Sorghum halepense	32,616	11-Jun-99
		GB_PR2 HS212A2	212753	Z95114	Human DNA sequence from clone 212A2 on chromosome 22q12 Contains gene for TNF-inducible protein CG12-1, 3' end of a gene similar to apolipoprotein L, ESTs, STSs, CA repeat, GSSs and CpG islands, complete sequence	Homo sapiens	38,279	23-Nov-99
		GB_OV:AF116856	4634	AF116856	Gallus gallus neurocan core protein precursor, mRNA, complete cds.	Gallus gallus	41,176	20-MAY-1999
rxa02845	615	GB_PR3 AC005934	43699	AC005934	Homo sapiens chromosome 19, cosmid R30813, complete sequence	Homo sapiens	35,225	5-Nov-98
		GB_PR3 AC005340	36705	AC005340	Homo sapiens chromosome 19, cosmid F19544, complete sequence	Homo sapiens	35,225	30-Jul-98
		GB_PR3:AC005934	43699	AC005934	Homo sapiens chromosome 19, cosmid R30813, complete sequence	Homo sapiens	39,153	5-Nov-98
rxa02846	873	GB_GSS5.AQ749564	838	AQ749564	HS_5575_A1_B11_SP6 RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=1151 Col=21 Row=C, genomic survey sequence	Homo sapiens	36,286	19-Jul-99
		GB_GSS5 AQ749564	838	AQ749564	HS_5575_A1_B11_SP6 RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=1151 Col=21 Row=C, genomic survey sequence	Homo sapiens	38,591	19-Jul-99
rxa02847	1135	GB_BA1:MSGB13GS	42923	L78823	Mycobacterium leprae cosmid B13 DNA sequence	Mycobacterium leprae	47,559	15-Jun-96
		GB_HTG4:AC009557	128590	AC009557	Homo sapiens chromosome 15 clone 76_D_16 map 15, LOW-PASS SEQUENCE SAMPLING.	Homo sapiens	36,289	25-OCT-1999
		GB_HTG4:AC009557	128590	AC009557	Homo sapiens chromosome 15 clone 76_D_16 map 15, LOW-PASS SEQUENCE SAMPLING	Homo sapiens	36,289	25-OCT-1999
rxa02848	499	GB_BA1:AB018531	4961	AB018531	Corynebacterium glutamicum dtsR1 and dtsR2 genes, complete cds	Corynebacterium glutamicum	98,397	19-OCT-1998
		GB_PAT:E17019	4961	E17019	Brevibacterium lactofermentum dtsR and dtsR2 genes	Corynebacterium glutamicum	98,397	28-Jul-99
		GB_OM.CFU08596	1780	U08596	Canis familiaris delayed rectifier K+ channel mRNA, partial cds	Canis familiaris	43,265	21-DEC-1994
rxa02849	305	GB_VI AF121950	9395	AF121950	Hepatitis G virus strain Iowan, complete genome	Hepatitis G virus	33,110	24-MAY-1999
		GB_PAT AR049304	9327	AR049304	Sequence 234 from patent US 5824507	Unknown	31,803	29-Sep-99
		GB_PAT:AR026878	9327	AR026878	Sequence 234 from patent US 5856134	Unknown	31,803	29-Sep-99

TABLE 2: GENES IDENTIFIED FROM GENBANK

GenBank™ Accession No.	Gene Name	Gene Function	Reference
A09073	ppg	Phosphoenol pyruvate carboxylase	Bachmann, B. et al. "DNA fragment coding for phosphoenolpyruvat corboxylase, recombinant DNA carrying said fragment, strains carrying the recombinant DNA and method for producing L-aminino acids using said strains," Patent: EP 0358940-A 3 03/21/90
A45579, A45581, A45583, A45585 A45587 ·		Threonine dehydratase	Moeckel, B. et al. "Production of L-isoleucine by means of recombinant micro-organisms with deregulated threonine dehydratase," Patent: WO 9519442-A 5 07/20/95
AB003132	murC; ftsQ; ftsZ		Kobayashi, M. et al. "Cloning, sequencing, and characterization of the ftsZ gene from coryneform bacteria," *Biochem. Biophys. Res. Commun.*, 236(2):383-388 (1997)
AB015023	murC; ftsQ		Wachi, M. et al. "A murC gene from Coryneform bacteria," *Appl. Microbiol. Biotechnol.*, 51(2):223-228 (1999)
AB018530	dtsR		Kimura, E. et al. "Molecular cloning of a novel gene, dtsR, which rescues the detergent sensitivity of a mutant derived from *Brevibacterium lactofermentum*," *Biosci. Biotechnol. Biochem.*, 60(10):1565-1570 (1996)
AB018531	dtsR1; dtsR2		
AB020624	murI	D-glutamate racemase	
AB023377	tkt	transketolase	
AB024708	gltB; gltD	Glutamine 2-oxoglutarate aminotransferase large and small subunits	
AB025424	acn	aconitase	
AB027714	rep	Replication protein	
AB027715	rep; aad	Replication protein; aminoglycoside adenyltransferase	
AF005242	argC	N-acetylglutamate-5-semialdehyde dehydrogenase	
AF005635	glnA	Glutamine synthetase	
AF030405	hisF	cyclase	
AF030520	argG	Argininosuccinate synthetase	
AF031518	argF	Ornithine carbamolytransferase	
AF036932	aroD	3-dehydroquinate dehydratase	

GenBank™ Accession No.	Gene Name	Gene Function	Reference
AF038548	pyc	Pyruvate carboxylase	
AF038651	dciAE; apt; rel	Dipeptide-binding protein; adenine phosphoribosyltransferase; GTP pyrophosphokinase	Wehmeier, L. et al. "The role of the Corynebacterium glutamicum rel gene in (p)ppGpp metabolism," *Microbiology,* 144:1853-1862 (1998)
AF041436	argR	Arginine repressor	
AF045998	impA	Inositol monophosphate phosphatase	
AF048764	argH	Argininosuccinate lyase	
AF049897	argC; argJ; argB; argD; argF; argR; argG; argH	N-acetylglutamylphosphate reductase; ornithine acetyltransferase; N-acetylglutamate kinase; acetylornithine transminase; ornithine carbamoyltransferase; arginine repressor; argininosuccinate synthase; argininosuccinate lyase	
AF050109	inhA	Enoyl-acyl carrier protein reductase	
AF050166	hisG	ATP phosphoribosyltransferase	
AF051846	hisA	Phosphoribosylformimino-5-amino-1-phosphoribosyl-4-imidazolecarboxamide isomerase	
AF052652	metA	Homoserine O-acetyltránsferase	Park, S. et al. "Isolation and analysis of metA, a methionine biosynthetic gene encoding homoserine acetyltransferase in Corynebacterium glutamicum," *Mol. Cells.,* 8(3):286-294 (1998)
AF053071	aroB	Dehydroquinate synthetase	
AF060558	hisH	Glutamine amidotransferase	
AF086704	hisE	Phosphoribosyl-ATP-pyrophosphohydrolase	
AF114233	aroA	5-enolpyruvylshikimate 3-phosphate synthase	
AF116184	panD	L-aspartate-alpha-decarboxylase precursor	Dusch, N. et al. "Expression of the Corynebacterium glutamicum panD gene encoding L-aspartate-alpha-decarboxylase leads to pantothenate overproduction in Escherichia coli," *Appl. Environ. Microbiol.,* 65(4)1530-1539 (1999)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
AF124518	aroD; aroE	3-dehydroquinase; shikimate dehydrogenase	
AF124600	aroC; aroK; aroB; pepQ	Chorismate synthase; shikimate kinase; 3-dehydroquinate synthase; putative cytoplasmic peptidase	
AF145897	inhA		
AF145898	inhA		
AJ001436	ectP	Transport of ectoine, glycine betaine, proline	Peter, H. et al. "Corynebacterium glutamicum is equipped with four secondary carriers for compatible solutes: Identification, sequencing, and characterization of the proline/ectoine uptake system, ProP, and the ectoine/proline/glycine betaine carrier, EctP," *J. Bacteriol.,* 180(22):6005-6012 (1998)
AJ004934	dapD	Tetrahydrodipicolinate succinylase (incomplete[i])	Wehrmann, A. et al. "Different modes of diaminopimelate synthesis and their role in cell wall integrity: A study with Corynebacterium glutamicum," *J. Bacteriol.,* 180(12):3159-3165 (1998)
AJ007732	ppc; secG; amt; ocd; soxA	Phosphoenolpyruvate-carboxylase; ?; high affinity ammonium uptake protein; putative ornithine-cyclodecarboxylase; sarcosine oxidase	
AJ010319	ftsY, glnB, glnD; srp; amtP	Involved in cell division; PII protein; uridylyltransferase (uridylyl-removing enzmye); signal recognition particle; low affinity ammonium uptake protein	Jakoby, M. et al. "Nitrogen regulation in Corynebacterium glutamicum; Isolation of genes involved in biochemical characterization of corresponding proteins," *FEMS Microbiol.,* 173(2):303-310 (1999)
AJ132968	cat	Chloramphenicol aceteyl transferase	
AJ224946	mqo	L-malate: quinone oxidoreductase	Molenaar, D. et al. "Biochemical and genetic characterization of the membrane-associated malate dehydrogenase (acceptor) from Corynebacterium glutamicum," *Eur. J. Biochem.,* 254(2):395-403 (1998)
AJ238250	ndh	NADH dehydrogenase	
AJ238703	porA	Porin	Lichtinger, T. et al. "Biochemical and biophysical characterization of the cell wall porin of Corynebacterium glutamicum: The channel is formed by a low molecular mass polypeptide," *Biochemistry,* 37(43):15024-15032 (1998)
D17429		Transposable element IS31831	Vertes, A.A. et al. "Isolation and characterization of IS31831, a transposable element from Corynebacterium glutamicum," *Mol. Microbiol.,* 11(4):739-746 (1994)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
D84102	odhA	2-oxoglutarate dehydrogenase	Usuda, Y. et al. "Molecular cloning of the Corynebacterium glutamicum (Brevibacterium lactofermentum AJ12036) odhA gene encoding a novel type of 2-oxoglutarate dehydrogenase," *Microbiology,* 142:3347-3354 (1996)
E01358	hdh; hk	Homoserine dehydrogenase; homoserine kinase	Katsumata, R. et al. "Production of L-thereonine and L-isoleucine," Patent: JP 1987232392-A 1 10/12/87
E01359		Upstream of the start codon of homoserine kinase gene	Katsumata, R. et al. "Production of L-thereonine and L-isoleucine," Patent: JP 1987232392-A 2 10/12/87
E01375		Tryptophan operon	
E01376	trpL; trpE	Leader peptide; anthranilate synthase	Matsui, K. et al. "Tryptophan operon, peptide and protein coded thereby, utilization of tryptophan operon gene expression and production of tryptophan," Patent: JP 1987244382-A 1 10/24/87
E01377		Promoter and operator regions of tryptophan operon	Matsui, K. et al. "Tryptophan operon, peptide and protein coded thereby, utilization of tryptophan operon gene expression and production of tryptophan," Patent: JP 1987244382-A 1 10/24/87
E03937		Biotin-synthase	Hatakeyama, K. et al. "DNA fragment containing gene capable of coding biotin synthetase and its utilization," Patent: JP 1992278088-A 1 10/02/92
E04040		Diamino pelargonic acid aminotransferase	Kohama, K. et al. "Gene coding diaminopelargonic acid aminotransferase and desthiobiotin synthetase and its utilization," Patent: JP 1992330284-A 1 11/18/92
E04041		Desthiobiotinsynthetase	Kohama, K. et al. "Gene coding diaminopelargonic acid aminotransferase and desthiobiotin synthetase and its utilization," Patent: JP 1992330284-A 1 11/18/92
E04307		Flavum aspartase	Kurusu, Y. et al. "Gene DNA coding aspartase and utilization thereof," Patent: JP 1993030977-A 1 02/09/93
E04376		Isocitric acid lyase	Katsumata, R. et al. "Gene manifestation controlling DNA," Patent: JP 1993056782-A 3 03/09/93
E04377		Isocitric acid lyase N-terminal fragment	Katsumata, R. et al. "Gene manifestation controlling DNA," Patent: JP 1993056782-A 3 03/09/93
E04484		Prephenate dehydratase	Sotouchi, N. et al. "Production of L-phenylalanine by fermentation," Patent: JP 1993076352-A 2 03/30/93
E05108		Aspartokinase	Fugono, N. et al. "Gene DNA coding Aspartokinase and its use," Patent: JP 1993184366-A 1 07/27/93
E05112		Dihydro-dipichorinate synthetase	Hatakeyama, K. et al. "Gene DNA coding dihydrodipicolinic acid synthetase and its use," Patent: JP 1993184371-A 1 07/27/93

GenBank™ Accession No.	Gene Name	Gene Function	Reference
E05776		Diaminopimelic acid dehydrogenase	Kobayashi, M. et al. "Gene DNA coding Diaminopimelic acid dehydrogenase and its use," Patent: JP 1993284970-A 1 11/02/93
E05779		Threonine synthase	Kohama, K. et al. "Gene DNA coding threonine synthase and its use," Patent: JP 1993284972-A 1 11/02/93
E06110		Prephenate dehydratase	Kikuchi, T. et al. "Production of L-phenylalanine by fermentation method," Patent: JP 1993344881-A 1 12/27/93
E06111		Mutated Prephenate dehydratase	Kikuchi, T. et al. "Production of L-phenylalanine by fermentation method," Patent: JP 1993344881-A 1 12/27/93
E06146		Acetohydroxy acid synthetase	Inui, M. et al. "Gene capable of coding Acetohydroxy acid synthetase and its use," Patent: JP 1993344893-A 1 12/27/93
E06825		Aspartokinase	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E06826		Mutated aspartokinase alpha subunit	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E06827		Mutated aspartokinase alpha subunit	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E07701	secY		Honno, N. et al. "Gene DNA participating in integration of membraneous protein to membrane," Patent: JP 1994169780-A 1 06/21/94
E08177		Aspartokinase	Sato, Y. et al. "Genetic DNA capable of coding Aspartokinase released from feedback inhibition and its utilization," Patent: JP 1994261766-A 1 09/20/94
E08178, E08179, E08180, E08181, E08182		Feedback inhibition-released Aspartokinase	Sato, Y. et al. "Genetic DNA capable of coding Aspartokinase released from feedback inhibition and its utilization," Patent: JP 1994261766-A 1 09/20/94
E08232		Acetohydroxy-acid isomeroreductase	Inui, M. et al. "Gene DNA coding acetohydroxy acid isomeroreductase," Patent: JP 1994277067-A 1 10/04/94
E08234	secE		Asai, Y. et al. "Gene DNA coding for translocation machinery of protein," Patent: JP 1994277073-A 1 10/04/94
E08643		FT aminotransferase and desthiobiotin synthetase promoter region	Hatakeyama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031476-A 1 02/03/95
E08646		Biotin synthetase	Hatakeyama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031476-A 1 02/03/95

GenBank™ Accession No.	Gene Name	Gene Function	Reference
E08649		Aspartase	Kohama, K. et al "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031478-A 1 02/03/95
E08900		Dihydrodipicolinate reductase	Madori, M. et al. "DNA fragment containing gene coding Dihydrodipicolinate acid reductase and utilization thereof," Patent: JP 1995075578-A 1 03/20/95
E08901		Diaminopimelic acid decarboxylase	Madori, M. et al. "DNA fragment containing gene coding Diaminopimelic acid decarboxylase and utilization thereof," Patent: JP 1995075579-A 1 03/20/95
E12594		Serine hydroxymethyltransferase	Hatakeyama, K. et al. "Production of L-trypophan," Patent: JP 1997028391-A 1 02/04/97
E12760, E12759, E12758		transposase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12764		Arginyl-tRNA synthetase; diaminopimelic acid decarboxylase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12767		Dihydrodipicolinic acid synthetase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12770		aspartokinase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12773		Dihydrodipicolinic acid reductase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E13655		Glucose-6-phosphate dehydrogenase	Hatakeyama, K. et al. "Glucose-6-phosphate dehydrogenase and DNA capable of coding the same," Patent: JP 1997224661-A 1 09/02/97
L01508	IlvA	Threonine dehydratase	Moeckel, B. et al. "Functional and structural analysis of the threonine dehydratase of Corynebacterium glutamicum," *J. Bacteriol.*, 174:8065-8072 (1992)
L07603	EC 4.2.1.15	3-deoxy-D-arabinoheptulosonate-7-phosphate synthase	Chen, C. et al. "The cloning and nucleotide sequence of Corynebacterium glutamicum 3-deoxy-D-arabinoheptulosonate-7-phosphate synthase gene," *FEMS Microbiol. Lett.*, 107:223-230 (1993)
L09232	IlvB; ilvN; ilvC	Acetohydroxy acid synthase large subunit; Acetohydroxy acid synthase small subunit; Acetohydroxy acid isomeroreductase	Keilhauer, C. et al. "Isoleucine synthesis in Corynebacterium glutamicum: molecular analysis of the ilvB-ilvN-ilvC operon," *J. Bacteriol.*, 175(17):5595-5603 (1993)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
L18874	PtsM	Phosphoenolpyruvate sugar phosphotransferase	Fouet, A et al. "Bacillus subtilis sucrose-specific enzyme II of the phosphotransferase system: expression in Escherichia coli and homology to enzymes II from enteric bacteria," *PNAS USA,* 84(24):8773-8777 (1987); Lee, J.K. et al. "Nucleotide sequence of the gene encoding the Corynebacterium glutamicum mannose enzyme II and analyses of the deduced protein sequence," *FEMS Microbiol. Lett.,* 119(1-2):137-145 (1994)
L27123	aceB	Malate synthase	Lee, H-S. et al. "Molecular characterization of aceB, a gene encoding malate synthase in Corynebacterium glutamicum," *J. Microbiol. Biotechnol.,* 4(4):256-263 (1994)
L27126		Pyruvate kinase	Jetten, M. S. et al. "Structural and functional analysis of pyruvate kinase from Corynebacterium glutamicum," *Appl. Environ. Microbiol.,* 60(7):2501-2507 (1994)
L28760	aceA	Isocitrate lyase	
L35906	dtxr	Diphtheria toxin repressor	Oguiza, J.A. et al. "Molecular cloning, DNA sequence analysis, and characterization of the Corynebacterium diphtheriae dtxR from Brevibacterium lactofermentum," *J. Bacteriol.,* 177(2):465-467 (1995)
M13774		Prephenate dehydratase	Follettie, M.T. et al. "Molecular cloning and nucleotide sequence of the Corynebacterium glutamicum pheA gene," *J. Bacteriol.,* 167:695-702 (1986)
M16175	5S rRNA		Park, Y-H. et al. "Phylogenetic analysis of the coryneform bacteria by 56 rRNA sequences," *J. Bacteriol.,* 169:1801-1806 (1987)
M16663	trpE	Anthranilate synthase, 5' end	Sano, K. et al. "Structure and function of the trp operon control regions of Brevibacterium lactofermentum, a glutamic-acid-producing bacterium," *Gene,* 52:191-200 (1987)
M16664	trpA	Tryptophan synthase, 3'end	Sano, K. et al. "Structure and function of the trp operon control regions of Brevibacterium lactofermentum, a glutamic-acid-producing bacterium," *Gene,* 52:191-200 (1987)
M25819		Phosphoenolpyruvate carboxylase	O'Regan, M. et al. "Cloning and nucleotide sequence of the Phosphoenolpyruvate carboxylase-coding gene of Corynebacterium glutamicum ATCC13032," *Gene,* 77(2):237-251 (1989)
M85106		23S rRNA gene insertion sequence	Roller, C. et al. "Gram-positive bacteria with a high DNA G+C content are characterized by a common insertion within their 23S rRNA genes," *J. Gen. Microbiol.,* 138:1167-1175 (1992)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
M85107, M85108		23S rRNA gene insertion sequence	Roller, C. et al. "Gram-positive bacteria with a high DNA G+C content are characterized by a common insertion within their 23S rRNA genes," *J. Gen. Microbiol.*, 138:1167-1175 (1992)
M89931	aecD; brnQ; yhbw	Beta C-S lyase; branched-chain amino acid uptake carrier; hypothetical protein yhbw	Rossol, I. et al. "The Corynebacterium glutamicum aecD gene encodes a C-S lyase with alpha, beta-elimination activity that degrades aminoethylcysteine," *J. Bacteriol.*, 174(9):2968-2977 (1992); Tauch, A. et al. "Isoleucine uptake in Corynebacterium glutamicum ATCC 13032 is directed by the brnQ gene product," *Arch. Microbiol.*, 169(4):303-312 (1998)
S59299	trp	Leader gene (promoter)	Herry, D.M. et al. "Cloning of the trp gene cluster from a tryptophan-hyperproducing strain of Corynebacterium glutamicum: identification of a mutation in the trp leader sequence," *Appl. Environ. Microbiol.*, 59(3):791-799 (1993)
U11545	trpD	Anthranilate phosphoribosyltransferase	O'Gara, J.P. and Dunican, L.K. (1994) Complete nucleotide sequence of the Corynebacterium glutamicum ATCC 21850 tpD gene." Thesis, Microbiology Department, University College Galway, Ireland.
U13922	cglIM; cglIR; clgIIR	Putative type II 5-cytosoine methyltransferase; putative type II restriction endonuclease; putative type I or type III restriction endonuclease	Schafer, A. et al. "Cloning and characterization of a DNA region encoding a stress-sensitive restriction system from Corynebacterium glutamicum ATCC 13032 and analysis of its role in intergeneric conjugation with Escherichia coli," *J. Bacteriol.*, 176(23):7309-7319 (1994); Schafer, A. et al. "The Corynebacterium glutamicum cglIM gene encoding a 5-cytosine in an McrBC-deficient Escherichia coli strain," *Gene*, 203(2):95-101 (1997)
U14965	recA		
U31224	ppx		Ankri, S. et al. "Mutations in the Corynebacterium glutamicumproline biosynthetic pathway: A natural bypass of the proA step," *J. Bacteriol.*, 178(15):4412-4419 (1996)
U31225	proC	L-proline: NADP+ 5-oxidoreductase	Ankri, S. et al. "Mutations in the Corynebacterium glutamicumproline biosynthetic pathway: A natural bypass of the proA step," *J. Bacteriol.*, 178(15):4412-4419 (1996)
U31230	obg; proB; unkdh	?;gamma glutamyl kinase;similar to D-isomer specific 2-hydroxyacid dehydrogenases	Ankri, S. et al. "Mutations in the Corynebacterium glutamicumproline biosynthetic pathway: A natural bypass of the proA step," *J. Bacteriol.*, 178(15):4412-4419 (1996)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
U31281	bioB	Biotin synthase	Serebriiskii, I.G., "Two new members of the bio B superfamily: Cloning, sequencing and expression of bio B genes of Methylobacillus flagellatum and Corynebacterium glutamicum," *Gene,* 175:15-22 (1996)
U35023	thtR; accBC	Thiosulfate sulfurtransferase; acyl CoA carboxylase	Jager, W. et al. "A Corynebacterium glutamicum gene encoding a two-domain protein similar to biotin carboxylases and biotin-carboxyl-carrier proteins," *Arch. Microbiol.,* 166(2);76-82 (1996)
U43535	cmr	Multidrug resistance protein	Jager, W. et al. "A Corynebacterium glutamicum gene conferring multidrug resistance in the heterologous host Escherichia coli," *J. Bacteriol.,* 179(7):2449-2451 (1997)
U43536	clpB	Heat shock ATP-binding protein	
U53587	aphA-3	3'5''-aminoglycoside phosphotransferase	
U89648		Corynebacterium glutamicum unidentified sequence involved in histidine biosynthesis, partial sequence	
X04960	trpA; trpB; trpC; trpD; trpE; trpG; trpL	Tryptophan operon	Matsui, K. et al. "Complete nucleotide and deduced amino acid sequences of the Brevibacterium lactofermentum tryptophan operon," *Nucleic Acids Res.,* 14(24):10113-10114 (1986)
X07563	lys A	DAP decarboxylase (meso-diaminopimelate decarboxylase, EC 4.1.1.20)	Yeh, P. et al. "Nucleic sequence of the lysA gene of Corynebacterium glutamicum and possible mechanisms for modulation of its expression," *Mol. Gen. Genet.,* 212(1):112-119 (1988)
X14234	EC 4.1.1.31	Phosphoenolpyruvate carboxylase	Eikmanns, B.J. et al. "The Phosphoenolpyruvate carboxylase gene of Corynebacterium glutamicum: Molecular cloning, nucleotide sequence, and expression," *Mol. Gen. Genet.,* 218(2):330-339 (1989); Lepiniec, L. et al. "Sorghum Phosphoenolpyruvate carboxylase gene family: structure, function and molecular evolution," *Plant. Mol. Biol.,* 21 (3):487-502 (1993)
X17313	fda	Fructose-bisphosphate aldolase	Von der Osten, C.H. et al. "Molecular cloning, nucleotide sequence and fine-structural analysis of the Corynebacterium glutamicum fda gene: structural comparison of C. glutamicum fructose-1, 6-biphosphate aldolase to class I and class II aldolases," *Mol. Microbiol.,*
X53993	dapA	L-2, 3-dihydrodipicolinate synthetase (EC 4.2.1.52)	Bonnassie, S. et al. "Nucleic sequence of the dapA gene from Corynebacterium glutamicum," *Nucleic Acids Res.,* 18(21):6421 (1990)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X54223		AttB-related site	Cianciotto, N. et al. "DNA sequence homology between att B-related sites of Corynebacterium diphtheriae, Corynebacterium ulcerans, Corynebacterium glutamicum , and the attP site of lambdacorynephage," *FEMS. Microbiol, Lett.,* 66:299-302 (1990)
X54740	argS; lysA	Arginyl-tRNA synthetase; Diaminopimelate decarboxylase	Marcel, T. et al. "Nucleotide sequence and organization of the upstream region of the Corynebacterium glutamicum lysA gene," *Mol. Microbiol.,* 4(11):1819-1830 (1990)
X55994	trpL; trpE	Putative leader peptide; anthranilate synthase component 1	Heery, D.M. et al. "Nucleotide sequence of the Corynebacterium glutamicum trpE gene," *Nucleic Acids Res.,* 18(23):7138 (1990)
X56037	thrC	Threonine synthase	Han, K.S. et al. "The molecular structure of the Corynebacterium glutamicum threonine synthase gene," *Mol. Microbiol.,* 4(10):1693-1702 (1990)
X56075	attB-related site	Attachment site	Cianciotto, N. et al. "DNA sequence homology between att B-related sites of Corynebacterium diphtheriae, Corynebacterium ulcerans, Corynebacterium glutamicum , and the attP site of lambdacorynephage," *FEMS. Microbiol, Lett.,* 66:299-302 (1990)
X57226	lysC-alpha; lysC-beta; asd	Aspartokinase-alpha subunit; Aspartokinase-beta subunit; aspartate beta semialdehyde dehydrogenase	Kalinowski, J. et al. "Genetic and biochemical analysis of the Aspartokinase from Corynebacterium glutamicum," *Mol. Microbiol.,* 5(5):1197-1204 (1991); Kalinowski, J. et al. "Aspartokinase genes lysC alpha and lysC beta overlap and are adjacent to the aspertate beta-semialdehyde dehydrogenase gene asd in Corynebacterium glutamicum," *Mol. Gen. Genet.,* 224(3):317-324 (1990)
X59403	gap;pgk; tpi	Glyceraldehyde-3-phosphate; phosphoglycerate kinase; triosephosphate isomerase	Eikmanns, B.J. "Identification, sequence analysis, and expression of a Corynebacterium glutamicum gene cluster encoding the three glycolytic enzymes glyceraldehyde-3-phosphate dehydrogenase, 3-phosphoglycerate kinase, and triosephosphate isomeras," *J. Bacteriol.,* 174(19):6076-6086 (1992)
X59404	gdh	Glutamate dehydrogenase	Bormann, E.R. et al. "Molecular analysis of the Corynebacterium glutamicum gdh gene encoding glutamate dehydrogenase," *Mol. Microbiol.,* 6(3):317-326 (1992)
X60312	lysI	L-lysine permease	Seep-Feldhaus, A.H. et al. "Molecular analysis of the Corynebacterium glutamicum lysI gene involved in lysine uptake," *Mol. Microbiol.,* 5(12):2995-3005 (1991)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X66078	cop1	Ps1 protein	Joliff, G. et al. "Cloning and nucleotide sequence of the csp1 gene encoding PS1, one of the two major secreted proteins of Corynebacterium glutamicum: The deduced N-terminal region of PS1 is similar to the Mycobacterium antigen 85 complex," *Mol. Microbiol.,* 6(16):2349-2362 (1992)
X66112	glt	Citrate synthase	Eikmanns, B.J. et al. "Cloning sequence, expression and transcriptional analysis of the Corynebacterium glutamicum gltA gene encoding citrate synthase," *Microbiol.,* 140:1817-1828 (1994)
X67737	dapB	Dihydrodipicolinate reductase	
X69103	csp2	Surface layer protein PS2	Peyret, J.L. et al. "Characterization of the cspB gene encoding PS2, an ordered surface-layer protein in Corynebacterium glutamicum," *Mol. Microbiol.,* 9(1):97-109 (1993)
X69104		IS3 related insertion element	Bonamy, C. et al. "Identification of IS1206, a Corynebacterium glutamicum IS3-related insertion sequence and phylogenetic analysis," *Mol. Microbiol.,* 14(3):571-581 (1994)
X70959	leuA	Isopropylmalate synthase	Patek, M. et al. "Leucine synthesis in Corynebacterium glutamicum: enzyme activities, structure of leuA, and effect of leuA inactivation on lysine synthesis," *Appl. Environ. Microbiol.,* 60(1):133-140 (1994)
X71489	icd	Isocitrate dehydrogenase (NADP+)	Eikmanns, B.J. et al. "Cloning sequence analysis, expression, and inactivation of the Corynebacterium glutamicum icd gene encoding isocitrate dehydrogenase and biochemical characterization of the enzyme," *J. Bacteriol.,* 177(3):774-782 (1995)
X72855	GDHA	Glutamate dehydrogenase (NADP+)	
X75083, X70584	mtrA	5-methyltryptophan resistance	Heery, D.M. et al. "A sequence from a tryptophan-hyperproducing strain of Corynebacterium glutamicum encoding resistance to 5-methyltryptophan," *Biochem. Biophys. Res. Commun.,* 201(3):1255-1262 (1994)
X75085	recA		Fitzpatrick, R. et al. "Construction and characterization of recA mutant strains of Corynebacterium glutamicum and Brevibacterium lactofermentum," *Appl. Microbiol. Biotechnol.,* 42(4):575-580 (1994)
X75504	aceA; thiX	Partial Isocitrate lyase; ?	Reinscheid, D.J. et al. "Characterization of the isocitrate lyase gene from Corynebacterium glutamicum and biochemical analysis of the enzyme," *J. Bacteriol.,* 176(12):3474-3483 (1994)
X76875		ATPase beta-subunit	Ludwig, W. et al. "Phylogenetic relationships of bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit genes," *Antonie Van Leeuwenhoek,* 64:285-305 (1993)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X77034	tuf	Elongation factor Tu	Ludwig, W. et al. "Phylogenetic relationships of bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit genes," *Antonie Van Leeuwenhoek,* 64:285-305 (1993)
X77384	recA		Billman-Jacobe, H. "Nucleotide sequence of a recA gene from Corynebacterium glutamicum," *DNA Seq.,* 4(6):403-404 (1994)
X78491	aceB	Malate synthase	Reinscheid, D.J. et al. "Malate synthase from Corynebacterium glutamicum pta-ack operon encoding phosphotransacetylase: sequence analysis," *Microbiology,* 140:3099-3108 (1994)
X80629	16S rDNA	16S ribosomal RNA	Rainey, F.A. et al. "Phylogenetic analysis of the genera Rhodococcus and Norcardia and evidence for the evolutionary origin of the genus Norcardia from within the radiation of Rhodococcus species," *Microbiol.,* 141:523-528 (1995)
X81191	gluA; gluB; gluC; gluD	Glutamate uptake system	Kronemeyer, W. et al. "Structure of the gluABCD cluster encoding the glutamate uptake system of Corynebacterium glutamicum," *J. Bacteriol.*, 177(5):1152-1158 (1995)
X81379	dapE	Succinyldiaminopimelate desuccinylase	Wehrmann, A. et al. "Analysis of different DNA fragments of Corynebacterium glutamicum complementing dapE of Escherichia coli," *Microbiology*, 40:3349-56 (1994)
X82061	16S rDNA	16S ribosomal RNA	Ruimy, R. et al. "Phylogeny of the genus Corynebacterium deduced from analyses of small-subunit ribosomal DNA sequences," *Int. J. Syst. Bacteriol.,* 45(4):740-746 (1995)
X82928	asd; lysC	Aspartate-semialdehyde dehydrogenase; ?	Serebrijski, I. et al. "Multicopy suppression by asd gene and osmotic stress-dependent complementation by heterologous proA in proA mutants," *J. Bacteriol.,* 177(24):7255-7260 (1995)
X82929	proA	Gamma-glutamyl phosphate reductase	Serebrijski, I. et al. "Multicopy suppression by asd gene and osmotic stress-dependent complementation by heterologous proA in proA mutants," *J. Bacteriol.,* 177(24):7255-7260 (1995)
X84257	16S rDNA	16S ribosomal RNA	Pascual, C. et al. "Phylogenetic analysis of the genus Corynebacterium based on 16S rRNA gene sequences," *Int. J. Syst. Bacteriol.,* 45(4):724-728 (1995)
X85965	aroP; dapE	Aromatic amino acid permease; ?	Wehrmann, A. et al. "Functional analysis of sequences adjacent to dapE of Corynebacterium glutamicumproline reveals the presence of aroP, which encodes the aromatic amino acid transporter," *J. Bacteriol.,* 177(20):5991-5993 (1995)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X86157	argB; argC; argD; argF; argJ	Acetylglutamate kinase; N-acetyl-gamma-glutamyl-phosphate reductase; acetylornithine aminotransferase; ornithine carbamoyltransferase; glutamate N-acetyltransferase	Sakanyan, V. et al. "Genes and enzymes of the acetyl cycle of arginine biosynthesis in Corynebacterium glutamicum: enzyme evolution in the early steps of the arginine pathway," *Microbiology,* 142:99-108 (1996)
X89084	pta; ackA	Phosphate acetyltransferase; acetate kinase	Reinscheid, D.J. et al. "Cloning, sequence analysis, expression and inactivation of the Corynebacterium glutamicum pta-ack operon encoding phosphotransacetylase and acetate kinase," *Microbiology,* 145:503-513 (1999)
X89850	attB	Attachment site	Le Marrec, C. et al. "Genetic characterization of site-specific integration functions of phi AAU2 infecting "Arthrobacter aureus C70," *J. Bacteriol.,* 178(7):1996-2004 (1996)
X90356		Promoter fragment F1	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology,* 142:1297-1309 (1996)
X90357		Promoter fragment F2	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology,* 142:1297-1309 (1996)
X90358		Promoter fragment F10	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology,* 142:1297-1309 (1996)
X90359		Promoter fragment F13	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology,* 142:1297-1309 (1996)
X90360		Promoter fragment F22	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology,* 142:1297-1309 (1996)
X90361		Promoter fragment F34	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology,* 142:1297-1309 (1996)
X90362		Promoter fragment F37	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology,* 142:1297-1309 (1996)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X90363		Promoter fragment F45	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology,* 142:1297-1309 (1996)
X90364		Promoter fragment F64	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology,* 142:1297-1309 (1996)
X90365		Promoter fragment F75	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology,* 142:1297-1309 (1996)
X90366		Promoter fragment PF101	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology,* 142:1297-1309 (1996)
X90367		Promoter fragment PF104	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology,* 142:1297-1309 (1996)
X90368		Promoter fragment PF109	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology,* 142:1297-1309 (1996)
X93513	amt	Ammonium transport system	Siewe, R.M. et al. "Functional and genetic characterization of the (methyl) ammonium uptake carrier of Corynebacterium glutamicum," *J. Biol. Chem.,* 271(10):5398-5403 (1996)
X93514	betP	Glycine betaine transport system	Peter, H. et al. "Isolation, characterization, and expression of the Corynebacterium glutamicum betP gene, encoding the transport system for the compatible solute glycine betaine," *J. Bacteriol.,* 178(17):5229-5234 (1996)
X95649	orf4		Patek, M. et al. "Identification and transcriptional analysis of the dapB-ORF2-dapA-ORF4 operon of Corynebacterium glutamicum, encoding two enzymes involved in L-lysine synthesis," *Biotechnol. Lett.,* 19:1113-1117 (1997)
X96471	lysE; lysG	Lysine exporter protein; Lysine export regulator protein	Vrljic, M. et al. "A new type of transporter with a new type of cellular function: L-lysine export from Corynebacterium glutamicum," *Mol. Microbiol.,* 22(5):815-826 (1996)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X96580	panB; panC; xylB	3-methyl-2-oxobutanoate hydroxymethyltransferase; pantoate-beta-alanine ligase; xylulokinase	Sahm, H. et al. "D-pantothenate synthesis in Corynebacterium glutamicum and use of panBC and genes encoding L-valine synthesis for D-pantothenate overproduction," *Appl. Environ. Microbiol.*, 65(5):1973-1979 (1999)
X96962		Insertion sequence IS1207 and transposase	
X99289		Elongation factor P	Ramos, A. et al. "Cloning, sequencing and expression of the gene encoding elongation factor P in the amino-acid producer Brevibacterium lactofermentum (Corynebacterium glutamicum ATCC 13869)," *Gene,* 198:217-222 (1997)
Y00140	thrB	Homoserine kinase	Mateos, L.M. et al. "Nucleotide sequence of the homoserine kinase (thrB) gene of the Brevibacterium lactofermentum," *Nucleic Acids Res.*, 15(9):3922 (1987)
Y00151	ddh	Meso-diaminopimelate D-dehydrogenase (EC 1.4.1.16)	Ishino, S. et al. "Nucleotide sequence of the meso-diaminopimelate D-dehydrogenase gene from Corynebacterium glutamicum," *Nucleic Acids Res.*, 15(9):3917 (1987)
Y00476	thrA	Homoserine dehydrogenase	Mateos, L.M. et al. "Nucleotide sequence of the homoserine dehydrogenase (thrA) gene of the Brevibacterium lactofermentum," *Nucleic Acids Res.*, 15(24):10598 (1987)
Y00546	hom; thrB	Homoserine dehydrogenase; homoserine kinase	Peoples, O.P. et al. "Nucleotide sequence and fine structural analysis of the Corynebacterium glutamicum hom-thrB operon," *Mol. Microbiol.*, 2(1):63-72 (1988)
Y08964	murC; ftsQ/divD; ftsZ	UPD-N-acetylmuramate-alanine ligase; division initiation protein or cell division protein; cell division protein	Honrubia, M.P. et al. "Identification, characterization, and chromosomal organization of the ftsZ gene from Brevibacterium lactofermentum," *Mol. Gen. Genet.*, 259(1):97-104 (1998)
Y09163	putP	High affinity proline transport system	Peter, H. et al. "Isolation of the putP gene of Corynebacterium glutamicumproline and characterization of a low-affinity uptake system for compatible solutes," *Arch. Microbiol.*, 168(2):143-151 (1997)
Y09548	pyc	Pyruvate carboxylase	Peters-Wendisch, P.G. et al. "Pyruvate carboxylase from Corynebacterium glutamicum: characterization, expression and inactivation of the pyc gene," *Microbiology,* 144:915-927 (1998)
Y09578	leuB	3-isopropylmalate dehydrogenase	Patek, M. et al. "Analysis of the leuB gene from Corynebacterium glutamicum," *Appl. Microbiol. Biotechnol.*, 50(1):42-47 (1998)
Y12472		Attachment site bacteriophage Phi-16	Moreau, S. et al. "Site-specific integration of corynephage Phi-16: The construction of an integration vector," *Microbiol.*, 145:539-548 (1999)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
Y12537	proP	Proline/ectoine uptake system protein	Peter, H. et al. "Corynebacterium glutamicum is equipped with four secondary carriers for compatible solutes: Identification, sequencing, and characterization of the proline/ectoine uptake system, ProP, and the ectoine/proline/glycine betaine carrier, EctP," *J. Bacteriol.,* 180(22):6005-6012 (1998)
Y13221	glnA	Glutamine synthetase I	Jakoby, M. et al. "Isolation of Corynebacterium glutamicum glnA gene encoding glutamine synthetase I," *FEMS Microbiol. Lett.,* 154(1):81-88 (1997)
Y16642	lpd	Dihydrolipoamide dehydrogenase	
Y18059		Attachment site Corynephage 304L	Moreau, S. et al. "Analysis of the integration functions of φ304L: An integrase module among corynephages," *Virology*, 255(1):150-159 (1999)
Z21501	argS; lysA	Arginyl-tRNA synthetase; diaminopimelate decarboxylase (partial)	Oguiza, J.A. et al. "A gene encoding arginyl-tRNA synthetase is located in the upstream region of the lysA gene in Brevibacterium lactofermentum: Regulation of argS-lysA cluster expression by arginine," *J. Bacteriol.,*175(22):7356-7362 (1993)
Z21502	dapA; dapB	Dihydrodipicolinate synthase; dihydrodipicolinate reductase	Pisabarro, A. et al. "A cluster of three genes (dapA, orf2, and dapB) of Brevibacterium lactofermentum encodes dihydrodipicolinate reductase, and a third polypeptide of unknown function," *J. Bacteriol.,* 175(9):2743-2749 (1993)
Z29563	thrC	Threonine synthase	Malumbres, M. et al. "Analysis and expression of the thrC gene of the encoded threonine synthase," *Appl. Environ. Microbiol.,* 60(7)2209-2219 (1994)
Z46753	16S rDNA	Gene for 16S ribosomal RNA	
Z49822	sigA	SigA sigma factor	Oguiza, J.A. et al "Multiple sigma factor genes in Brevibacterium lactofermentum: Characterization of sigA and sigB," *J. Bacteriol.,* 178(2):550-553 (1996)
Z49823	galE; dtxR	Catalytic activity UDP-galactose 4-epimerase; diphtheria toxin regulatory protein	Oguiza, J.A. et al "The galE gene encoding the UDP-galactose 4-epimerase of Brevibacterium lactofermentum is coupled transcriptionally to the dmdR gene," *Gene,* 177:103-107 (1996)
Z49824	orf1; sigB	?; SigB sigma factor	Oguiza, J.A. et al "Multiple sigma factor genes in Brevibacterium lactofermentum: Characterization of sigA and sigB," *J. Bacteriol.,* 178(2):550-553 (1996)
Z66534		Transposase	Correia, A. et al. "Cloning and characterization of an IS-like element present in the genome of Brevibacterium lactofermentum ATCC 13869," *Gene,* 170(1):91-94 (1996)

[1] A sequence for this gene was published in the indicated reference. However, the sequence obtained by the inventors of the present application is significantly longer than the published version. It is believed that the published version relied on an incorrect start codon, and thus represents only a fragment of the actual coding region.

TABLE 3: Corynebacterium and Brevibacterium Strains Which May be Used in the Practice of the Invention

Genus	species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NCTC	DSMZ
Brevibacterium	ammoniagenes	21054							
Brevibacterium	ammoniagenes	19350							
Brevibacterium	ammoniagenes	19351							
Brevibacterium	ammoniagenes	19352							
Brevibacterium	ammoniagenes	19353							
Brevibacterium	ammoniagenes	19354							
Brevibacterium	ammoniagenes	19355							
Brevibacterium	ammoniagenes	19356							
Brevibacterium	ammoniagenes	21055							
Brevibacterium	ammoniagenes	21077							
Brevibacterium	ammoniagenes	21553							
Brevibacterium	ammoniagenes	21580							
Brevibacterium	ammoniagenes	39101							
Brevibacterium	butanicum	21196							
Brevibacterium	divaricatum	21792	P928						
Brevibacterium	flavum	21474							
Brevibacterium	flavum	21129							
Brevibacterium	flavum	21518							
Brevibacterium	flavum			B11474					
Brevibacterium	flavum			B11472					
Brevibacterium	flavum	21127							
Brevibacterium	flavum	21128							
Brevibacterium	flavum	21427							
Brevibacterium	flavum	21475							
Brevibacterium	flavum	21517							
Brevibacterium	flavum	21528							
Brevibacterium	flavum	21529							

Brevibacterium	flavum			B11477					
Brevibacterium	flavum			B11478					
Brevibacterium	flavum	21127							
Brevibacterium	flavum			B11474					
Brevibacterium	healii	15527							
Brevibacterium	ketoglutamicum	21004							
Brevibacterium	ketoglutamicum	21089							
Brevibacterium	ketosoreductum	21914							
Brevibacterium	lactofermentum				70				
Brevibacterium	lactofermentum				74				
Brevibacterium	lactofermentum				77				
Brevibacterium	lactofermentum	21798							
Brevibacterium	lactofermentum	21799							
Brevibacterium	lactofermentum	21800							
Brevibacterium	lactofermentum	21801							
Brevibacterium	lactofermentum			B11470					
Brevibacterium	lactofermentum			B11471					
Brevibacterium	lactofermentum	21086							
Brevibacterium	lactofermentum	21420							
Brevibacterium	lactofermentum	21086							
Brevibacterium	lactofermentum	31269							
Brevibacterium	linens	9174							
Brevibacterium	linens	19391							
Brevibacterium	linens	8377							
Brevibacterium	paraffinolyticum					11160			
Brevibacterium	spec.						717.73		
Brevibacterium	spec.						717.73		
Brevibacterium	spec.	14604							
Brevibacterium	spec.	21860							
Brevibacterium	spec.	21864							
Brevibacterium	spec.	21865							

Brevibacterium	spec.	21866							
Brevibacterium	spec.	19240							
Corynebacterium	acetoacidophilum	21476							
Corynebacterium	acetoacidophilum	13870							
Corynebacterium	acetoglutamicum			B11473					
Corynebacterium	acetoglutamicum			B11475					
Corynebacterium	acetoglutamicum	15806							
Corynebacterium	acetoglutamicum	21491							
Corynebacterium	acetoglutamicum	31270							
Corynebacterium	acetophilum			B3671					
Corynebacterium	ammoniagenes	6872						2399	
Corynebacterium	ammoniagenes	15511							
Corynebacterium	fujiokense	21496							
Corynebacterium	glutamicum	14067							
Corynebacterium	glutamicum	39137							
Corynebacterium	glutamicum	21254							
Corynebacterium	glutamicum	21255							
Corynebacterium	glutamicum	31830							
Corynebacterium	glutamicum	13032							
Corynebacterium	glutamicum	14305							
Corynebacterium	glutamicum	15455							
Corynebacterium	glutamicum	13058							
Corynebacterium	glutamicum	13059							
Corynebacterium	glutamicum	13060							
Corynebacterium	glutamicum	21492							
Corynebacterium	glutamicum	21513							
Corynebacterium	glutamicum	21526							
Corynebacterium	glutamicum	21543							
Corynebacterium	glutamicum	13287							
Corynebacterium	glutamicum	21851							
Corynebacterium	glutamicum	21253							

Corynebacterium	glutamicum	21514							
Corynebacterium	glutamicum	21516							
Corynebacterium	glutamicum	21299							
Corynebacterium	glutamicum	21300							
Corynebacterium	glutamicum	39684							
Corynebacterium	glutamicum	21488							
Corynebacterium	glutamicum	21649							
Corynebacterium	glutamicum	21650							
Corynebacterium	glutamicum	19223							
Corynebacterium	glutamicum	13869							
Corynebacterium	glutamicum	21157							
Corynebacterium	glutamicum	21158							
Corynebacterium	glutamicum	21159							
Corynebacterium	glutamicum	21355							
Corynebacterium	glutamicum	31808							
Corynebacterium	glutamicum	21674							
Corynebacterium	glutamicum	21562							
Corynebacterium	glutamicum	21563							
Corynebacterium	glutamicum	21564							
Corynebacterium	glutamicum	21565							
Corynebacterium	glutamicum	21566							
Corynebacterium	glutamicum	21567							
Corynebacterium	glutamicum	21568							
Corynebacterium	glutamicum	21569							
Corynebacterium	glutamicum	21570							
Corynebacterium	glutamicum	21571							
Corynebacterium	glutamicum	21572							
Corynebacterium	glutamicum	21573							
Corynebacterium	glutamicum	21579							
Corynebacterium	glutamicum	19049							
Corynebacterium	glutamicum	19050							

Corynebacterium	glutamicum	19051							
Corynebacterium	glutamicum	19052							
Corynebacterium	glutamicum	19053							
Corynebacterium	glutamicum	19054							
Corynebacterium	glutamicum	19055							
Corynebacterium	glutamicum	19056							
Corynebacterium	glutamicum	19057							
Corynebacterium	glutamicum	19058							
Corynebacterium	glutamicum	19059							
Corynebacterium	glutamicum	19060							
Corynebacterium	glutamicum	19185							
Corynebacterium	glutamicum	13286							
Corynebacterium	glutamicum	21515							
Corynebacterium	glutamicum	21527							
Corynebacterium	glutamicum	21544							
Corynebacterium	glutamicum	21492							
Corynebacterium	glutamicum			B8183					
Corynebacterium	glutamicum			B8182					
Corynebacterium	glutamicum			B12416					
Corynebacterium	glutamicum			B12417					
Corynebacterium	glutamicum			B12418					
Corynebacterium	glutamicum			B11476					
Corynebacterium	glutamicum	21608							
Corynebacterium	lilium		P973						
Corynebacterium	nitrilophilus	21419				11594			
Corynebacterium	spec.		P4445						
Corynebacterium	spec.		P4446						
Corynebacterium	spec.	31088							
Corynebacterium	spec.	31089							
Corynebacterium	spec.	31090							
Corynebacterium	spec.	31090							

Corynebacterium	spec.	31090							
Corynebacterium	spec.	15954							20145
Corynebacterium	spec.	21857							
Corynebacterium	spec.	21862							
Corynebacterium	spec.	21863							

ATCC: American Type Culture Collection, Rockville, MD, USA

FERM: Fermentation Research Institute, Chiba, Japan

NRRL: ARS Culture Collection, Northern Regional Research Laboratory, Peoria, IL, USA

CECT: Coleccion Espanola de Cultivos Tipo, Valencia, Spain

NCIMB: National Collection of Industrial and Marine Bacteria Ltd., Aberdeen, UK

CBS: Centraalbureau voor Schimmelcultures, Baarn, NL

NCTC: National Collection of Type Cultures, London, UK

DSMZ: Deutsche Sammlung von Mikroorganismen und Zellkulturen, Braunschweig, Germany

For reference see Sugawara, H. et al. (1993) World directory of collections of cultures of microorganisms: Bacteria, fungi and yeasts (4th edn), World federation for culture collections world data center on microorganisms, Saimata, Japen.

APPENDIX A: DNA SEQUENCES

>RXA00003-upstream
CATCCATTTCGCACAGAACATGGTAATCCTTCTCTAGGCCCCACTCGAAGCCGGCGATAT
AAGCGCCAAGAAGGCCACCCTTGCCTTCGCGGTGCAGCAC

>RXA00003
GTGCAGGTGAGAATCCTCAGCAGCGAGCTTGTCTGCAGCCTCTCCGGTGCCATCCGGGGC
GTGAACCTAGATATTGCAGCACCGAAGCCCAAGAAGTCAGGCCGCCGCACACTCACAAAA
CCCGAATGGGATGCCGTCATTAAGCATCTGTTAACGCGGGATACCGAGCCACTGTTAACC
CCCACCAAGCACAAGAACATCCGACAAAGCACCAAGAACATCCATGCCCGCATTGTGCGG
CTCACTCTCCTCCAAGCCGTTTCAGGGCTGAGAATTGCCGAAGCCAATCAATTGCAGTGG
AAGCACATCATCGACGGTGACGATGGCATGCTCATTAATGCCAGCGCCGATATTGTCAAG
GGGCGAAAAGGCAAGGAAAGAGGGCGGTATATCCCTATCCTGAGGGCCGACGTAGCGGAA
TACCTGCGTACACACCGCGAGGACGACGAGCATTTCATCGTAGGCTCACCGACGACGACC
GCGAGGCCCTGGGACGCGACGAACGCAGATGACAAGGTGCCCGAGCTATACCGGCAAATT
GCAGAAGCTACAGGCGTGAAGACTCTTCAAGACCTCCGAAGCCACTCCTGGCGTGCGACG
CTGCACGGTGTGTACGCGGACGTGATGGACCCAGCTACACGCGCCGCCATTTTCGGCCAC
ACCGAGCAGGTAGCTGAGGAGTACTACAACGACCGCCAAAATATTGAATCACTCATGAGA
CAAGTCAAGCGCGCCTACGCG

>RXA00003-downstream
TAACTACGCTTAAGACTACGCGT

>RXA00008-upstream
CATTGGCGTGGTGATCGCCGGCATTATCGCACAACTCACCCTGCGCTTCTACGTGAGGAA
ATAAGACTATTGAACTCCTTGCCGTAGACTTAGAAAGACT

>RXA00008
ATGGCCAAGAAGAAAAAGAAAGTCGACGAAAACAACTCAGTTCTCGCGACCAATCGCAAG
GCCCGCCATGACTACCACATCATTGATACGTGGGAGGCGGGCGTGGTGCTCTTAGGCACC
GAAATCAAATCACTGCGCGAAGGTAAGGTATCCCTCGTGGATTCCTTTGCCACCATTGAT
AACGGAGAAATCTGGCTTCAGCATCTCCACATCCCGCAGTATTCCATGGGCTCCTGGACA
AACCACACGCCCAAGCGCACCCGCAAACTTTTGCTGCACCGCAACGAGATTGATTCCCTG
ATGGGTAAAGTCCGCGACGGCAACCGCACGTTGGTTCCGCTCAAGCTTTACCTCAAAAAC
GGTCGCGTCAAACTCGAACTCGGACTCGCACAAGGTAAGCAGGATTACGACAAGCGCCAA
GATATCAAGCGTCGCACCGAAGAACGCGAAGTCACCCGTGAGCTCGGCCGTCGCATTAAG
GGAATCAACGCG

>RXA00008-downstream
TAAATGAGTATTCACATCGCAAA

>RXA00015-upstream
AAGACGCACAGAAGCTACACACATAGCTACATCGTCAGCACCAAAGCCGGAACAAGAACT
ACAGCAACCGACGACACTCAACGAGCGCGACCTCCAAGAC

>RXA00015
ATGATTGATATGTGCACCACTCCTCGACAAGAGATCATGATCCGCGAGCAATTTAAGGAG
ATCAACAACGGTAGGGTTGTACCTCATTACGATCAGCTTGAACAGCTCGCAGAGATTTTT
TCAACTAAAGACTCAATCGACATGGTCAACGAGATACTCAATCGCGATACGGATTTTCTC
AGTAATGAAGGCACAATTTTTATGGAATACATTTTCAACGGTGGATTCCATACGGACAAC
GGCTATCAACCGTTGTCCTATGCATATGTTGAACGAGGCTTAGCGATCCGCCCTCCACGC
ATAGTGCTC

>RXA00015-downstream
TAGATATGACACAAATCGGTATT

>RXA00018-upstream
CAACCCGCCCCACAAACACATACAATTAACTTCTATATTTAGTAAATAAATAACTAGTAT

TTTTAATGACTTACAAATATCAAGAAAGAATCTATTCCTT

>RXA00018
ATGTCCGCATTATCTAGACCGCACAAGATCGCCACCGGCGTTGCTGTCGCAACTCTTACC
CTCACCTTGTGTACCTCTGCTGCCGGCGTTGTCCATGCAGCGCAACAATCCATCAGCGGT
CCAGAATCCTCCTGTGCTTTTAATCAACAGCGTTGGGATGACAGCAAAGTTAAGCTTGAC
GACACCATCGCTACGGCCAAAAACTCATTGGTACAAACAGGCGAACTGCACCGCAACGAA
CAGGATCTACTTACTGGCTATCTTTTCCAGCAACCGCACAGCAGCAATTACCTTGCACTC
AACAACGCTTATGCCGATGCCGTAGCAATCAAAGACAGCTTTGTCCGCCCAACATGTGAC
GGTTCTAAAGAGTCCAAGATTGCCAGCGAACACGCCGTGTCTGAGGTTGTGGGTGCAGTG
AATGTACTCGCCCGAGCACAAAAAGCGCTGCAGATTAACTCCGACACCTACGAACAGCAA
CGTCGTTGTGATGCCCTTCGTCTAGCAAGCCGAGATGAATCAGATGTTCTTATGCGCATT
GATCGCACCATGCTGCAGCTTCGTCGCACACTAGCTGACATTGACCAGGCGTCCACAGAC
ATTCGCGATATTCGGGCTCAAACAACAAGCTTTGAACGTGATCTTGCCCGCGAGCAAAAA
GAGGCCGACGCAGCAGCACGTGCTCAAGCTGTAGACACTTCGACCACACCAACATCAAGC
ACAGAAGATCGTGTCAACGACATTCTTAAAGAGTCCCGTACCGATCACAGTGGCGACAGT
TACACGCGCTCAACGACAACGAGCGCACAAAGCACTGAGCCGGATTCTGCAACCAACACC
TCATATCTGTCACGTCGTCTCGACAGCCTGGAACGCAGTGCGCAGCATATTGATCTCAAT
ACCCAGTGCGACAACCTCGATGATCTTCGTGAACTCACCAACAATGACACGCGTGATCAC
ACCGGCTCCGTCATTTCCATTGCCGATCAACTCACAGACATCACCAATGAAATCAATGAA
TTACGCGATAGCACTTTTGCCACCAGAGACAGTGCCCAACAAGCACAGGATCAGGTAATT
GCTCAACGTGAAGAACTGCAACGAGCAAAGGAAGCACGACTAGAAGAACAGCGACTCGCC
AAAGAAGCAGAAGAGGGCGCTCGCAACGCAGCAATTCAGGAACGTGACGCGGCCGAAGCA
GCACTGCGTGAAGCACAAGACCTCCTCAGTCGCCTCGATGACACAGGCAACGCAACCAGT
GATGACACAGCAGCGCTAGTAGACGGTCTTCTCAATAAC

>RXA00018-downstream
TAACAATCAGCAACACCGCTCAC

>RXA00020-upstream
TAGGAGAACTACCTTTCTTGCTGGTGTTACCTAGCTTTAAGTTTGTTAGAGTAATTAATG
AATAACTAAGTAATGTAAGTAAAGGGACTTTTAAATAACT

>RXA00020
ATGACTGTGACCACCGCACAACGAATCGCTGACGAATTTCAACGTGGCATTAGTATCGGC
CCGTGGGATCTGTGCGAAGTACCAGCAGGCGATGACTATTTAGAGCACACCACCAAGGTC
AGGCGACGCCACAGCACGGCTGTAGAGATTCACACTGACTCTTTGATCATTTGTGCGCCT
GAAGGCAGTACGTACAGCCACAACCGCACTAAGGCTGGTCTTGCGTCCACGGGCACAGTC
ACTGTGCCAGTGAAGGGGCTTTCTGAGCCTGTGAAGCTTAGTCTCAATCTTCTTGCTGAT
TATGGAAACTCCTTTGACACTGTGCACGACGATCTGTGGCAACGAGAGCTGCGTGAGCAG
ACGCGGGGGCAGTTACTCACACTTAATGCAGTCTCCGGTCTTGGGGATGACAGCGTGGCG
ATTATGGGCACGCCATGGGGCGATGGTCTCACCGGGGAGGCCAACACCATTAAAGGTCGT
GAGCATTTTGTCATGTGGGCTGCAGGGTGCCGCTTTGAAGACGGTTATGGTCGTCACGCA
CTTCGAGAGGATCGCCATGTGCGACACCAGGCACGTGCGGGTGAGGATTCCACTGCACAT
CACGGTTGGTTGCTTAAAGGCACAGTGTTCGGGAAAGAACTCACCGGTGATGCTGTGACG
GCAGCCATGACAGTTTTTAGTGATGTGGTGGTCACTGTCGATGAGGGGCGTATCCCTGGC
ATGAAATCAGGACAACCGTTTTCTATGGCAACCCGTTTACGCGCATCATCTGCGCCTGTG

>RXA00020-downstream
TAGAGACTTTTTCAGACCTTAAC

>RXA00021-upstream
AAAAGCAACTCACTTCGTGCTTTTTTCACCGACCCCGGCTGTGTGGATGCCACCCACTTA
CACCGCACAATCGAAAATAAAAGTAAAGGATGTTCACCTT

>RXA00021
ATGTCTGACACCACAGACAGCCACGACCCAGCAACCTCCCCTACAGTCGATTCAGCCGCA
TCCGGTACTTCTGACCCCAACCAGCAACCCAAGAAGAAATTCACCATCATTAAGCAGGTG
AACATGATTGCGCGTACTGCCATTGATGACTGCATTAATCGACTAGGCCCAGATGTTGTC

ACCATGTCCAGCGAAGACATTGCTGATCAAGTGGTCAACTCCATTAACGTTGCTATTGCC
AGAGAAAACACACGTGCCCAAGATGCCAATGCTGCGGTGCGTTACACACCTATCTTTAAG
CTCGATTTCTCCCATGTCGCTGTCCTTATGCGCAGACTGCATGTGATTATCAACATCGCG
CCATCGCATAACTCTGATCCTGACAGCGATATGTTGGCTATTTACGACCCCAACCCACGC
AGCGAGCATTACGGGATCTATCGCACCTCAGAGGCTGAAATACGCCGCGTAGCCCGTGAA
TACTGCCCTGACCTCACCTCAGCGCAGTTTAGAGAACTGCAGATGGCACTCTCAGATGCT
GCACCTCGTAAAGTCCGCCACAAGCAGCGTGACTTGATTCCCGTGAAAAACGGCATCTTT
AATTACTCGACTAAACAACTAGAACCGTTTTCTCAAGAGTTTGTCTTTCTTGCTAAATCT
GCAGTGAACTACAACCCAAATGCACAAAACCCTGTCATCACTCATCCCCAGGATGGCTCT
GTCTGGGATGTTGAATCATGGATGAACGATCTCTCCGATGACCCTGAAGTCGTTAACCTG
CTGTGGGAGATTATCGGCGCTATCGTGCGCCCCTATGTGTCCTGGAACAAGTCTGCCTGG
TTCTACTCAGAGGCCGGCAACAACGGTAAAGGCACGCTCGTTGAGCTCATGCGCAACATC
TTGGGCGCAGAGGCCTATACCAGTATCCAGCTCTCGGACTTCTCTAAAGAGTTCCACCTT
GAATCACTGACTCGTGCACAAGCAATCCTTGTTGATGAGAACGATGTCGGCGCCTTCTTA
GAAAAGTCAGCAAACCTTAAAGCGATTGTCACCAATGACGTCATCTCCATTAACCGCAAG
CACAAAACCATGCTCAGCTATCAGTTTTATGGCTTTATGGTGCAGTGTATTAACGGCTTC
CCCAAGGTCAAAGACCAGTCGGAGTCATTTTTCAGGCGCCAACTCTTTGTGCCGTTTGAG
AAAAGCTTCACCGGTGCCGAGCGCAAGTACATCAAAGACGACTACATGTCGCGCACTGAT
GTCCTCGAATATGTACTGCACCGCGTACTGCATATGAACTACGACAATCTCTCCACCCCT
GCTGCAGCTCTCGCTGTGCTGGATGAATACAAAGAGTTTGTCGATCCTGTGCGCGCATTC
TGGAATGAATTCAGCGATCAATTTGTCTGGGATCTTCTTCCCCTGCAATTCCTCTACGAG
TTTTATCGCAAGTGGTTTGACCGTGACAGCCCATCCGGGTCTGTGCTCGGCAAACGCAGC
TTCATTCAAAAAATCACCACCATCGCCGTTGATAGCGGTCAGTGGGAGTATCCGCTGACA
GCACAGCGTCCCGGTGGCGATATGGCCGTTCCTGAGCCATTAGTCATTGATTATGACCTC
ACCGAGTGGCAAAACGCCACTGTACCTAAAGGTCACGTCAACAAGGGGCTCCCTCTACCA
CTCAAGGCTAATTATCGAGGACTGCTCCGCAAACCTCTAACAACACCTGCTACTCCCCCT
GCAGCGCCGGTCAACCCCACACCACCCACCCCT

>RXA00021-downstream
TAACAACCACAAGAAAGATTTAT

>RXA00022-upstream
AGGACTGCTCCGCAAACCTCTAACAACACCTGCTACTCCCCCTGCAGCGCCGGTCAACCC
CACACCACCCACCCCTTAACAACCACAAGAAAGATTTATC

>RXA00022
ATGTCCGCTCCAACCATCTACCCCGGCACCAAAACATCTATTGATCCGATCACCATGGAT
GACGCTCGCATCATCTTTTTCGATATTGAGTCGCTCCACAATATTTTCACGGTAGCAACC
TACGATTCTCTGTCCCACCACGTCGATGTCTTTTACCTGCTCGATCACACAACCAGCCCT
CAGATCACGGTGCTGCCGCACTCAATGGATTATTTCGATCAAACGCGCAGCGATGCTGTT
ATGGCTGCCATCATTGAGCAAAACCCTGCGTTCGCAGAAATTAAAGGCTCACCCATTACA
ACCGCAGATGTAGCCCTCCACAATCTCGGTGACACCAACGCCAACCGACGCTGGCAGTCT
AACGTGCTGCTTGCCCGGCTACTCGGGGGTATTAGTGTGCGCGGAGAGGTACCTGAGCAC
CAGAGCCACAACCATCTCGCCAAGCAGTTTGCCGAGGCAACCTTGGTCACCAGGGACTTC
GATGTGAATTATGATCCAACAAGCGCTCACCCTTTTACTGCTGGCTTCAACTCGATCAAC
TATGACACCACCTTGCTCAGCCTGTACTTCGCAATGTTGACCTCAAATATCGGAAGTACA
CCGACGTATTTCCCGGTGATCACCGCACAAGAACTTCGTGCGCATAACGACAAGCTCTTT
AGCCCTGAGTTCATCAAAAACATGCCAAAGTATTTCTGGGATCGCGACAGCGGTGCTGGA
CTCAGAGCTGCATCG

>RXA00025-upstream
TAAATTTCTCAATGGTGTGGAAACACTTGGAAACAAGCTGCCCACACCATTTACGCTTTT
CTTGATACTTTTCCTGATCACGGCGCTGGCTTCATCGATC

>RXA00025
ATGGCGTGGATGAACGTATCCGTGATTGTTCCAGGCTCTGATGAGGAACTATTTGTAAAA
GGCCTGTTCACCGGTGAAGGCCTAACCTGGTTGACTACGAATCTCGGGGCAAACTACATC
GGGTTCCCGCCGTTGCTCACCGTGTTGCCAATTCTGTTGGCAGTGGGTGTTGCTGAACGT
TCCGGCATGTTGGCTGCGCTGATTAGGAAACTTTTTGGTTCGGCGAAAAAGATCGTTTTG

CCATATGCAGTCGGTGTGATTGGCGTGACCGCGTCGATCATGGCGGACGCTGCCTTCGTG
GTGGTGCCACCTTTGGCCGCGATGGTGTTTAAAGCTGCTGGTCGGCACCCTGTGGCTGGG
CTATTGGGTTCGTTTGCAGCTGTGGGTGCAGGATATTCCACAGCGATTGTGCCCACCAGC
CTTGATGCACTTTTTGCGGGAATTACCAACGCCGTGATGGAGACACTTCCAGGCATTGCG
ACAACTGAAGTCAATCCGGTTTCTAACTATTACTTCAATATTGCATCCTCGATTGTGTTG
GGTCTGTTATGTGGTTTCCTCATTGATAAGGTGCTGGAACCTCGGATGTGGCGTCAGAAA
ATCGCTACGGAGTATGCAGAAAGCATTGAACCCACCAGCGCAGCAGATGATGAGGAAATC
TCTGCAACCCTAACCGCACAGGAAAACCGCGCGCTGACAATTTCCATGTGGACCACCCTG
GCGACGGCCATCATCGTGCTGGTTGTGGTGCTGATTCCGGGATCCCCATGGAGAAATGAG
GATGGTGGATTCTTGCCTACCTCGCCACTGCTGAGCTCTGTGGTGTTTATTGTATTTTTG
TTTTTCATGGTGATGGGCCTGGCCTACGGCATGGTGGTGGGCACGATCAAGAACATGGAT
GATGTCGTGAACATGATGGGCGAAGCAATCAAGGACATGATTGGTTTCTTGGTTTTGGCC
TTCATTTTGGGACAGTTTGTGGCGCTGTTTAACTGGACGGGCATCGGTACCTGGACTGCT
GTTCAGGGTGCTGCGGGATTGGAAGCGATCGGGCTTACCGGATTCCCTGCGATCATTGCA
TTTATTATTTTGGCGTCATGTTTGAACCTGCTGATTATTTCCGGCTCTGCGATGTGGACG
CTGATGGCTGCGGTGTTCGTCCCGATGTTCGCTCTGCTTGGCTATGAACCATCATTCATT
CAGGCAGCATTCCGCGTGGGTGACTCGGCAACTCAGGTGATCACACCGCTGAATCCGTAC
ATGATTGTGATCCTCGGTTTGCTCCGTCGATACGAACCGGATGCAGGTTTAGGCACCTTG
ATGTCAAGGCTTATCCCATTTGTGATCCCTTTCTGGCTAGCCTGGGCTACATTGTTGGCA
ATTTGGTTCTACGCCGATTTGCCGCTTGGACCTGGCTCTGCGATCTTCCTCGAAGGA

>RXA00025-downstream
TAAGTTTTCATGAGTACTGACAA

>RXA00027-upstream
TTAGGCAACGACTCCGAAACCTTCAAGAACGTGTGGCACTAACAATTGCGGACTATCCTT
GGGAACTGTTTTAGATTTTATTCAGGGTAGGGAGATTGTT

>RXA00027
GTGGATGAACGAAGCCGGTTTGCGCGCAGCGTTTTCCCGGACGGTGAAGAACCAGATCCA
CGTTTCACTTTGGCCAATGAGCGCACGTTTCTAGCATGGACGCGTACGTCTTTGGCGTTT
CTTGCCGGTGGTATTGCTTTTGAGGCGTTCCAGATCAGTGGACTATCGGATACTGTCCGT
ACAACAATCGCGGTTTTTATCATTGCGGTTGGCATGATCATTGCCGCTGGTGCTGCGGTG
AGGTGGATGAATGTGGAGCGTGCAATGCGTAAACAGAAGCCACTTCCCGTACCTGCGATT
ATTCCGTTTCTGTCTATTGCGGCTTTGGTGGCCTCTGCGGCTGTCTTGGTTCTGATTATT
GTTCAG

>RXA00027-downstream
TAGCTATGCGCATTCATGAGGAT

>RXA00028-upstream
AAAAGTCCTGGCCAGAAAACTCTCTATACTGTGCAGCATGGCACCAACGATCACCGACAT
CCATGTTCTGCTTCGTCGCGGTGAGCGACAATCAGTGATC

>RXA00028
ATGACCCTCACTGCCTCTTCCTTGGAGGCCGGGAAAATGTCTTTTAGTGGCGGGTATATC
GTGGGCGAGACGATGATCTTCCTCGTCGATCCCGATGAAGTCGAGATACGACGCAGCCCT
AACAGCCTCCACGTCCTGCGTAACGGTAGCGATATTCTGCGCCGCAACGAGCATCATTGC
TGGGTATTTGAGAATTTCAATAAACCCATTGACCCACCTGTTCGATTGGGTCCTCGGGAT
ATCATCTGCCCGAGCGCCTTGGCCTGGGTTCTTCAACAGCATTCCATCTCCCGGTCCTTA
TCCCACCACCTTCACGCGGATAAGATCACTGCGGGAGAGATTGCTGGACGCCCCACCTGG
ATCCTCCGTGAGGAACCTACTTCAGGAGGGCAGGACCCAAGTCGATTGGTCAGTCTTGAA
ATCGACCAGGAACACGGTGTCATCCTTGCAGTGGAGACTGGACAAGAACGACTCGAAGCC
ACGGAGATTTCTTTTCCTGACACTCTTCCTAATCCTTCCTGGGACGGAGCCTGGGAACCA
TTCCATTATCCAGATTCGACACCACACACTGCCCCTGATGTTGCTGAAATACCCGGTTAC
ATTCAGTCACTGCCGCCGCAGTCTGAAGATCCTCGCAGACTACGAGTCTTCGTCAATGAG
ATAGCACTCGAAGGTGATTTCCCTGACTACCGTCAAGGACAATCTGTGCGACTTACTTTG
GGAATTAGCTCCTCCCCTGTGCCACTCGAAGGAATGACAACCAGACGCCGGGGCCGGGTA
CGCAACCTTGGGGAAGAAGCTAGTCCAGGCGATGACGGTATGCCCCAGTGGCCAATCCTG

CTCACTGGTGATGGGTGGACGGCGCTGGCCTACACTCCCATCCCAAAACGTGGAGATGCA
GAGATCCAGGGGTGGTTTTATTATTCCGCCTACGGAATTGTTGATGTTCCCACAGATCTA
CGGGTAGAGCGTATTTTCGCTGGTATCGGCACAAGTGGCACCAACGAGCGTTTGTGGCAG
GAGATAGACAATACTTCTTCGGCTTATCACTCGGAAGATTGGTGGATCCGCGATGTCGTT
TTAGACGTCACGTTGGATGGAGCTGTTCCGCCTCCGCTTAGACGTGACGTCTTCACTGCT
GTCGATCCTATTGTGGCGGGTGACAAATTGTGGCTGTGTGACGTGCACTTTCCGGTAGCC
CGCTGCTGGGAGACCACGACCGGCCGATACTTGGGGCAGACTTTAKTCCCAGCACCACTG
CGAGATCGATCGTACGTCCTTGAGCTGCACAGCGACCAACAATTAGGAGCCGTAGCGGCA
AGTGGGAAGAGTGGTTGGATTCTCACACCTGGTCAAGCAGTAGCCACTAAAGCTCCTGAT
TGGACTCCTCCCACCCGGGCAACCGATCTGCCTCAGGTCCCCTCCCCCTGGGAGATCGTC
GCTGTCCGTGGCCAAGGTCTGTTTGAGCTGCAGGTGGAAACTAGTAGACGCACCGCCCTC
GGTCGAGTTAATGCGACCGGTGGCGTCGACATCGGTGAACTCCCGCCCAACGGCTATACC
ATCAGTTCTGTGGTTCAGATCGGTGATGAATACATCGTGGGCAGGTGGGTAGAGGAATAC
CGGCTCAACTCCAAACTGGAGGTCATTTCTACCAAAGAGCTAGATATCTCCGCATCCGGA
TGGAAGAGCAAGGGGACGGTTGCTTATCTGTCGGAAGACACTCACATATGTTTCTTCGAC
CAGGTCAGCGGGGCCGAGCTTCCCAGCCTGGGTATCGCCGAGGGACACCAGGGCGAGGTT
ATGTCAGCAACTTCTTCAGAGAGCATCGTGCTTATCTACCGGCGCAACCCGAACAATTCA
ATGTCGATTGTCCCGACTTCCGTTGCCACCTATGACAATGGCACCTGGACGACTATGCCG
CTACAGGAAGCTCCAGCGGAACTGTCC

>RXA00028-downstream
TAAACTGCTCATAGACTGCTGAG

>RXA00031-upstream
CACACATCGCCTCGTCATCCTTAGACACGCCAAATCTTCCTGGTCCACCGGAGTACTCGA
CCATAAACGCCCACTTAATCAACGTGGGCTTCGCGATGGC

>RXA00031
GTGGCAGCTGGCCAATGGCTAGCTGGCAACATCGGCGAAATTGATCATGTGCTGTGTTCA
GATGCCACCCGCACACAATTAACGTGGGAACGCGTCCAGCTTGGTGGCGCAACCGCCAAA
GGCTCTAGCTTCCACAATGACATCTATGAAAACCAAGTGTCTGAATTTAAACATTTAATA
ACAGGGCTCCCAGATGTAGTTGGTACCGCCCTACTCATCGGGCACTGGCCAGGCGTGGAA
GAACTAGCCCATTATTTTGGCATCCGCGATGAACATCCCGGTTGGGATCAGATGGAAGAA
AAGTTTCCCACCAGCGCCATTGCGGTGTTGGAATTTAACACCCCTTGGTCAAAACTTGAG
AGAAACTCTGCTCGGTTGACAGATTTTGTCATTCCACGGGGT

>RXA00031-downstream
TAGTTCTGCTTCAATTGAACAAT

>RXA00036-upstream
CTCTACCCACTTAAAATGGACGCATATTCGCAAGATAAGGCATGCTTGGATGAATAGATT
TTAACTCAACGTTTACTAAACAGAATCGGAATTAGGAGCC

>RXA00036
ATGCTTGAACGCACACAGGTATTCGTGGATACGTCCTACCTGCTCGCAAGCTTTTACAAC
TCTTGGGAGACAGGGGCACGTGCCCAATTAGAAATCGACCTCCCCGAAGTAGTCGGGGTA
TTAGGAAGGATGATTGAACAACAACTTAAACAGCCAGTACAACGCCAAATGTGGTACGAC
GGAATCCCCGATTCCGGCCCCCACCGCTATCAACGAGCACTACGCACCTGCGATGGTGTG
CAACTTCGTGCTGGCCAATTAATTGAATGGGGCGAACGCCGCACACAAAAGGCAGTAGAT
ACCCGCCTTGTTGCAGACCTCGTTCTCGCAGGTGTTCGCGGACAATGCTCCGATATCGTG
CTCGTCAGTGGCGACGCCGACATGATCCCCGGTGTTCAAGAAGCTGCCAATGCAGGCCTT
CGCGTTCACCTCTACGGCTTCGGCTGGGATTCCATGTCCTCCCAACTGCGCCACTGCTGT
GACACCACCACCATTTTGGATCCTCGAGAAGATTTTGCTGAATGCATGCAGCTGCAGGTT
CTCGAAGGTCCACTACCCCCTGTCGTTCGGGTAAAGCCCATCAACGATGCAGAACCCATC
GAGGATTTGGATTTCACTCCAGTTCCAGGCGTCGCCTCACCATTTGAAGAGGTCAGCGCG
AAAGATGAGAAATTCTCTCCACGCCCAAGTGAACCTGCCGAAGCTTTGTCGGAACAGGTC
TGTGAAGCGCAGTATGAGATCTCCAAACACGAAGGTCAAACCGCTGATTCAGGAGAAATC
ACCGAGTCTTTCGAGGCCGCTGAAATCAAGGTAACTGAGTTTTTTGGAGAACCAGCTGCT
CCAGTAGCGGAATCAGGCGTAGAAGCTCCCACTCCGGAAGCTCCCACGGTTCCTGAAGCA
GCTAAGCCCACTCCGGCGAAACCTAAGACTCCAAAGGCAGAGCCCCAAAAGCAAGAATCC

CCCAAGCCGGGAACTCCAAAACCAAAAGCTCCAAGCCCTGCGGATATTCCACCGAAAGCC
CCAGCTGACACTGAGGAACATTCGGAAGTCGAAGCTGAAATCGAGGACTCACGTCCAAAG
ATCCCCAGCCCTTCGATGATGGCTCCCCGCCGCAAGCTTCGTTCCCGCTACGTTCCGCTT
CCCAACGAAGTGTGGGCAACAGCAGGATTCCAAACTCCTTACGATGTCGGGCAACAGTAC
GCATCGTGGTGGTTTGAAAACGCAGCTACCAGCACTCAAAGAGATCAGGCTCATCTATTG
TCTGGTGGCGGACTTCCACCAGAGATCGATCGCCCGCTTCTGCAGTTTGCTTGTGAAACT
CTCCACGAATACACCCTGACTGAAGCGCAGCGCGTAGCTTTACGCGATGGCTTTCACTCC
GGAATCCGTGGTGTATTGCTCAACCAGCGAGATAGC

>RXA00036-downstream
TAGAATCACAAAAAACTGGGGCT

>RXA00037-upstream
AGCGAATCGGATTCAGTGATTTGCTTGCGGGCGCAGAAATGATTTTTCAATTAGACACAC
TTAGACACACGTAACTAAAACCTCAGGGAAGTGACTGATA

>RXA00037
ATGGCTAATCCGCTCAGCAAGGGCTGGAAGTATCTCATGGCATCGTTCGACAACAAGATC
GATGAGAATGCAGATCCAAAGATCCAAATTCAGCAAGCTACAGAAGCTGCCCAGAAGCAG
CACCAGCAGATTATGCAGCACGCTTCTCAGATTATCGGTCAGCAGAAGCAGCTTGAGATG
AAATTGAACCGCTTGGTTACTGACCGCGATAAGTTGCAGGAACAGGCTCGTCAGGCAATT
CAGTTGGCAGATAAGTCCGCAAACGAAGGCGACAGTGTTAAGGCTCAGGAGTTCAACAAC
ACTGCTGAGGTTTTTGCTTCCCAGTTGGTAGCTGTGGAACAGCAGTTGGAGCAGACTACT
GCGCTTCATCAGCAGGCTGAGGTTGCGGCGAAGGATGCTGTTGCGAAGTCTAAAGAGTCT
GAGATGCGCCTGAAAGAGCAGATGTCTCAGATTGATGCTCTACGTGCGCAGGCTGATCAG
GCGAAGATGCAGGAAAGTGTCACTAAGTCTATGGATTCTTTGAATCAGTTTGGCACTCAG
GATTCTTCTGTTCCTACCCTTGATGCGGTGCGTGAGAAGATCGAGCGTCGATACGCAGAT
GCTTTGGGCGCGCAGGAACTTACCCAGAACACTGTTAGTGATCGCATGGCTGAGATTGCG
CAGTCCGGCACCGATATGCGGGCGTCAGCTCGTTTGGCTGAACTTCGCGCGGAGGCGCTG
GGCACGTCCGCAACGCCTAAGGGCCAGCTAGAGGCAGGTGTCGAGGATGCGGAAGAACTT
ATCGACGAAACCTCCACCCCTTCAGCTACCCCAGAAACCGCAAGCCCAGAAGCTGATGCT
CCAGAAGCATCCGCAGACGAGTCCGAGAAGAAA

>RXA00037-downstream
TAACCTAAACACAAAAAACTGGG

>RXA00049-upstream
CTGAATCATGATTCATAAATGAACAAGGGTTCAGATTTTACAATACCCCCATTCCACCCC
CTTATATTTAAGTCACCGCAGATCAGCTAAGGTTTTCCCT

>RXA00049
ATGCCCACGCCTTCGCAGCACAAGGACGCTTCAACAGCACAAACCGACAACCAGGTACCA
ACTGGCCGCCGTGCACAAAAACGCGAACAAACCCGCGCGCGCCTGATCACTTCCGCTCGC
ACACTCATGGCAGAACGGGGTGTCGACAATGTAGGAATAGCTGAAATCACCGAAGGCGCA
AACATCGGAACGGGAACCTTCTACAACTACTTCCCAGACCGTGAACAACTACTCCAAGCT
GTCGCAGAAGATGCCTTTGAATCCGTGGGAATTGCCCTCGACCAGGTGCTAACCAAATTA
GACGATCCGGCTGAAGTATTTGCAGGGTCGCTTCGACATCTAGTACGGCACTCGTTAGAA
GATCGGATTTGGGGCGGATTTTTCATACAAATGGGTGCTGCTCATCCCGTACTCATGCGC
ATCCTAGGACCCCGCGCACGCCGAGATCTACTTCATGGTTTAGAAACTGGCCGATTCACC
ATCGAAGATCTGGACCTAGCAACCACATGCACTTTTGGTTCACTCATCGCAGCGATCCAA
ATGGCGCTTTCTGCAGATCAAGATTCCAACGATGACAAAGATCAGATTTTCGCAGCCGCG
ATGCTCCGGATGGTGGGTGTTCAAGCAGCAGAAGCCCGGGAGATCGCTTCGCGTCCACTC
CCCGAAATATCCCCAGTCAAACCGCAG

>RXA00049-downstream
TAGTGATCGGGCCTCAAATAAAC

>RXA00052-upstream
AGCTAAAGTTCTAATTTCCTAAATTGGTAAAGATCGGAACTCAAAAATGTCGCTTCGAAA

GCTCACAAGCTTAATTGGCATACTGGCTGTTGTTGGCCTA

>RXA00052
GTGGCGTTTATCCTTTTCAACTTCGTGAAAACAAACGACGAAACATCGAATGTCTCTCAG
AGCGAGTCAACTGCAGAGACAGTCAGCGAAACAAATGGCGTGCTCTCCGACGGCGCAGAA
AACATCGCTTCTCAATCTGATGAGAGTAAATCGGGTGTAGAGATTATTGATTCTGGATTT
GGGCAGAGCTCAAATTCGGCGATGGCAATTGTTATTGCCAAAACTTCTGGTGGAAGCCTC
GCAGGGGAATTTGTTACGGCGACGGTGAATTTCCTCGATGAAAGTGGCGCCGTTGTAGCG
ACTGAAGATCAAGTAGAAACACTCAGTTGGGAAGACCAGGAATTGGTATTGCCAGTATCT
CACTACAAGGAGGATTCAAGCCGCCCAGAAATTACAAGCATTGAGGCTTTTCTTTCAGTA
ACGGATTACGGTTCAGGACAACCAGATGAAACTGCATTGCCGGTGTTGGAAACCACCGAT
ATTTCCAACCCATACGCTGGTAGTTACAATGCCTCATTTGCGTTGAAAAATGACTCCTCA
GATGATTTTAAGAACCTGAGAGTTGGTATTGTTTGCTACAACGAGCAAACTGACATCATT
GGTGGTGGTTTCAAATTTCCGAACCTGGTTCCAGCGGGTGGGAGTATTCGAATGGACGCT
AGTGTGACGGTCTCCGAAATGCCAGCTTCTTGTAAGGCATATTTAAATCAC

>RXA00052-downstream
TAATAGATTCTTAAAAGGCAGCA

>RXA00054-upstream
ATGCTGAGATCCGCTGGGTGGCACCACACGAATTGGAATCTTTGGAGTGGGCACCTGCTG
ATATTCCTGCGGTGAAACTTCTCGTCGAGCAGCTTGCTTA

>RXA00054
ATGAGCCCATTCGATTCAAAGCTTGGTCGCGATACCCATTTTGGATTCCTCGATAAGACC
ACTGCTTCGCAACAACTGCTGAATCCTTCATTGATTTCTAATGAGGATCCGCACACCATG
TTGCAGGCGATCAAGTTAGAGCTTCGTACCGCACAGTCTTTTACATTTTCAGTCGCTTTT
ATTTCCAGTCGCGGTATCGCGTTGTTGAAACAGGCATTGTTGGACTTCAAGGGTAAAGGA
CGAATTATCACGTCCCGCTACCTGGATTTCAATGATCCAACGATGTTTCGTGAGCTTCTT
ACTTTGGAGAACGTGGAAGTCCTCATACATCAAGGCGATGGTTTCCACTCCAAGGGCTAC
GTTTTCCATCACGACGTGGGAATCACCGCAGTAGTGGGTAGTTCCAACCTCACAGATAAT
GCTCTGTTGGTAAACCGGGAATGGAATCTGAAGTTCTCTGCCAGCAAGAATGGCGACATT
GCTTTTCAACTTGATGATGCGATTAATCGCCAAATTGAACGATCCACGCCACTGACGCCT
GAATGGATCTCAGAGTATGAGGCAACCAGACGTGTACCTGAGCGTTTGGTGTCTCAGAAT
ATTCCTCTCGAGGATCAAAGTAACGCCGGAACAATTGTTCCAAACGTCATGCAGGAAGAG
GCCCTCGACGCTCTACTTTCTTTGACGGAGAAGGGAGAGAAACGTGGTGTCATTATTTCT
GCGACAGGAACTGGCAAGACTATCCTGGCTGCTCTAGCTACAAGAATGCTCAAGCCTGAA
CGAGTTTTGTTTGTCGTGCACCGCGAACAAATTCTGGATAAGGCGCGATCCGAGTTCATC
AAAGTTCTTGAACGTCCCGCTGTTGATTTCGGAAAAATGTCTGGCTCGACCAAGGAGCTA
GATAAGCCGTTTGTGTTTGGCACCATCCAAACGCTGACAAAGGAAGCTACACTTTCCCAG
ATCTCCCCTACTGACTTTGATTTAGTCATCGTCGATGAAGTCCATCGCGCCGGTGCCGAA
TCCTATTTGGCATTGCTCAATCATCTGCAGCCACAGTTTTTATTGGGCCTGACTGCTACC
CCAGAGCGAACTGATGGATTCAATATTTATGAGTTGTTCGATTTCAACGTGCCATATGAG
ATCCGACTTCAAGCTGCTTTAGAATCCAACATGCTCGTACCGTTTCACTATTACGGTGTC
ACAGACTTCACGCTTGATTCTGAAACAACGGTGACTGATACCTCCAAACTAAGTGCCTTG
GTGAGCGAAGAGAGAGTCCATCACATTCTGGAGGCCCTCAAAACTTATGGTCATCCAGAA
AATGTTCGTGGACTGATCTTCTGTTCCAAGACTGAAGAGGCTGAGGAGCTGTCAAAACTT
CTCGACCAGTCGTTGTTTAATGGCAGCTTGCTTAAAACCAAGGCGCTCTCTGCGAAGGAC
TCAATTCCCTACCGCGAAGAGGTTGTAGCTGAGCTGGAGTCCGGCGACCTGGACTACATC
TTGACGGTTGACATCTTCAATGAAGGCATTGATATTCCTTCGGTGAATCAAATCGTAATG
ATTCGTAGTACTCAATCAAGCATTGTGTTTACGCAGCAGCTCGGGCGTGGACTCCGAAAA
GCTGCTGGCAAAGACCATCTGCGCGTTATTGATTTCATTGGCAACTACGCGAACAACTAT
CTCATTCCCATCGCATTGTTTGGCGATAATTCTCGCAATAAGAACAGCATCAGACGCCGC
CTGATTGAGAGCGATATTGATGGAACAATCTCAGGTGTTTCAAGTGTTAACTTTGATCCC
ATCGCGCAGGAGAGAATTTTTGCTGCGTTGAAGGCTGCGAAGTTGGACTCAAAAGCACAA
TTCAAGCAGGATATTGTTCAGCTTCAAGATCGACTCAATCATGTGCCAGCACTGTTAGAC
TTCGCTCGCTTCAATACTGTTGATCCGTTTATCCTTGCCACGCATTCTGGCAACTACTGG
TCGCTGCTCAGTTCAGTGAAGTTTGTCGATCACGCTCCCAGCGAATCGGAGAAGTACTTT
CTGGATTTCCTTACCGGAGAGCTTCTTAACGGCAAGCGACCTCATGAGCTGTTGCTGATC
CAGGAACTAATGAAACAGCCTGAAACTTCTACTGAAGAATTCCGTAAGCTCTTGCAGGCC

CAATCGACTAGTTCAGATGAGCAAACAATCAACTCGGTTGAAAGGATTTTGAGCCAAGAA
TTCTATACGGGACCAAACCGCAAGAAGTTTGGCGAACATCCGATCCTCTCTGTTCAAAAC
CGCACCTACTCTTTTACTCCCGAGTTCCGACGTGCCCTCGACGAAAGCCTAGAAGTGACG
GACCGAGATGAGGCTGCTCAGAATTTTAAGTTTCACGTCCAAGACATCATCGACACTGGT
TTGTTTATCGCCAGAAACAATGGATTTTGGCAAGGAAACCTCGTTGTTGGCGAGAGATAC
TCCCGACGAGATGTCTGCCGAATTCTCAATTGGGAACGAAACAACGAGAGCACGATTTAT
GGATACAAAGTGGACAGTTACACATCTACTTGCCCAATCTTTGTGACCTATCACAAGGCT
GATGATGTATCCGAAAGTACTCGTTACCAGGATGAACTCGTCGATCCGAATACCCTTCAT
TGGTATTCCCGCGGCAACCGAAAGATCACGTCTAATGAGATCAAGCCCATCGCTGCGAAT
GCTGTGGATCTTCATGTTTTTGTGAAGAAGGACGATGCCGAAGGCCTTGATTTCTTCTAC
CTTGGTCAAGCGCATTCAGAAAACAGCAAACAGTCATCGATGCCCGGAAACAAAGGAGTT
GTGCAACCGGTGGTCACAATGGATCTACAGTTCGACACACCCGTCGAACAAAGCCTGTTT
GAGTACCTGAGCACAAATCTCGCCGTAACGGAG

>RXA00054-downstream
TAACCACCGCAACCAAGCGTCGA

>RXA00056-upstream
ATATGAATTTAATAATAGATTCCGAACGAAATCGGTGTTAGCGTCTGTGCTGAAACAATC
TAATCGCGTTTCAGGACACCTACATGATCAGGAGCTCTTT

>RXA00056
TTGTTAAACAGAGTCAGTCGTATTGCAGGCGCTTCTGCAATCACACTATGCATCGGCTTA
ACCACAATACTAAGCCCTACTTCCACTGCACAAAGCCTCGAACAGATCACCCCTTTACCT
GAATCTGCAATCGACCTCAACGCCGAGATTCACGTAAACACAAGCGACATTTCAGCTGAA
CAGATCCTTGGTGCTCAAGATGAAATCACAACTATGTACGATTCTCATGACCCCTACGAG
TACTTCGATACCCTCACCGACATCGAACAGCGTTCAATAATAGCAGCGCTTAAACGGGAT
CCGAGTTCACTCCAACAACGCCAAGAAACCCGTCTCGCGGCACAGTCCGACCCCTACAAA
ATTTACATATCAGGCCTCGAAATGCTTTCATGCATCAATCTAGTTGATGTTGTATCATGC
GGGATTGCAAACCAAGCAGCAACCAAAGCAAATAATGAGGCTGTCGCACGATACCCAGGC
GATTCCCTTCGCAACGGCAAAGGCGATGCATTTCGGCATTGCTCATGGAACGCTCTGATG
ACGATACGAATCGGGAGCAATGGAGCTGAAAGAATTGCAACAAACCACGAGACAATCGGG
GACGGTCCGGCCGATGAAAATGCAATGGACCTATTCAATAATGCACAAGGCCGACAGATC
GGAGCCGGATTCATTAATAGTAAGGATGAAACTAGCGCGCTCGCGATATGCGCGCTGTGG
ACAAATCTCGGTAGACTAAAAACTCTAAAA

>RXA00056-downstream
TAAGCAAGGTGCCCTCTGATGCT

>RXA00058-upstream
ATCACTAGGCTATCTTCCGGTTCACCTGAAGTTAGTAACACACCGGTCACAGAAGTTCCG
GCTCGTGTAATCTCCGCTTATCTAGCTCAAAGGAATACTT

>RXA00058
ATGAAGTTCTTCGGGTTTTATCGTCCTATTGCTTTAATTGCTGGCATTACCGTTTCAGCA
TCTATTCTCACATCCGTAGCTACTGCAGCTGAATCTCCAACTAGCTTTCAAGCGATTACA
CCTGCATTCTCTTCATCATCGGCTCCAGAAGCAGACGCAGAAGCAAACACCAGTGAAGCT
ACCGCAGACCTGCTTTACGTGGCAGAAAACCAACTACTTATTAAGCTTTCTAACGCCGTC
GTCGAAGATGTTAACGGCGAAATCTTAATGAAAGATAATAAGGGCACTCTTCTGGAGAAT
TTGACAGCTGAACTTCAAGCCCAACCAGGCTTCTCAATCGAGAAAGTCGATTCCCATACT
GCTTTGTTGACCATGAATCCAGATGAGGTGCCAGATTTACAGGACTGGCGATGCGGAGTC
GGCGCTTTGTCAGGCGGGGTAGCAGGTGTGGTGGCAACTGGTCTAGCTCTCGCCGCTTTG
GGAGTTGCCACAGGTGGCACGGGGTTTGCTGTGCTTGCAGCAGGGGGACTTGCTGGATAT
GGCACTGGCGCTGTCGCCAACTGC

>RXA00058-downstream
TAAGGAGAAATAATGGGAATTGT

>RXA00059-upstream
CTGGCAGGCGATTGTTCTCTTACTACTTGCGCTAGGTACAGGTGGTGCCTATCTGCTGGC
CGGTGGTGATGTCACTCAAACTGCCCGACTGGTGTTGTGG

>RXA00059
GTGTTGACCGGAATCTTACTGGCTATGGTCTCTACCGCCCTACGAATCCGCTTCGGATCA
GGGGTAGCTATCGCTGCAACCGTGCTGTGGACAGTTATCTCAATAACCTTGGGCGGAGAT
GTGCTAGCCGAGACCATGCTCTGGCTTGTAGCAGTACCATCCTGGCCAGAAACAGCGGAT
ACTACTACCCGCTTCCTTATTGCGATGCTACTGCAGGCAGTTCTTATCACCGGCAGCACT
ATCTGGGCTATCCGAGAGATCCGGGATTCAGAGCGCCGTGGC

>RXA00059-downstream
TAAGTTCAGCACCTCCGACAACG

>RXA00063-upstream
CCTGGTCATAGGATACTTAGCTCAACCACACGGTCAGGGCCAGCAATTCCTCACGTTTTA
CCAACTCCGTAAGCACACCATCATGGCCTGGTGCGCCGCT

>RXA00063
ATGACCGACGGGGACTTAGACGCTGATATCTCACCCCGCCAGATCGGGTTGATGACCACC
CGAACCGTGGTCGAAATCGTTCGACTACGCCACATGATTGCCCAACAACTAGAAAGAGCC
ACGATCATGGAAAACGAGTACCTCAAAGAAATCGCAGCGCTGAAGAAAGAACTCGCGCAC
TACAAGCAAAAAGACCATCAGAATCAAATGGTGATCGATATCTTGGGAAAAGCTATTGGG
ACCAGGCCCAATCCTGGCGAGGGCTTAGACGAGGAGGACGCCACC

>RXA00063-downstream
TAAACGTGGATGAGCAACGCGCC

>RXA00065-upstream
ATGCTTCTCAGACGCCTCCCTCTCCTTCAAATCCGCCACCGATTCCAGCGTCACTCCCAT
GCATGCCCAACCGGGACAGATCTTGCCGTGCGTAGGAATT

>RXA00065
ATGGCGAATCTTCCCCAAGAGGGTTTTTCTGTGGTGCACGGAATTTTGGCGGATCCCCGC
ATTTGGGGCCCGGAGATTCCGTATGTTCGTGAAGAAGCAGGTCAAGTAAATGTGGAAGCA
CCCGACGAGGCTGGCGATCTAGCCCGATTGACGTTGCCTCTGCAGTTGATCCTGCTCACG
GAGGAAGAGTTTGCCATCGCTCTCAACGAGGGCAGCGACGTCATGTTCGAACGAATGGCG
GAGCAAGAAGTCGATCTTCTGGATCTGAAACGT

>RXA00065-downstream
TAAGACGGTAGGCTCAATTCCGT

>RXA00067-upstream
GGAATCCCGCATGTTGGGCTCCAGTTGGGGACTGACTCTGTTTTTGATCATTTTGACGCC
AATCATTATTTTCCTCACTTTCAGCTAAAAGGACCATGCA

>RXA00067
ATGGTAGACGCTCAGCGCCCCAAAGCAGGCATCTTCGGTAGCCACACAGAAGAAACATGG
GTGTGGCTCGGTAATGAACTTTTCGACGAGTCCGGCGAGGTCATCGCCGACGTTCGCTCC
GACGTCCTCTACGTGGATCGCGAACGACTACTCATCGAATCCACCCCCGGCACCATGCGT
TTTCGTTGCCGCGCAACACTGTCCGGGGGTGAGGTCTATACGATGACTCAGAATTCTTTC
ACTGTGGGGGATCTCACTGCGGTGTGCGGGCGCCGGACGTATTCACTAAAAAGGGTGTCG
CCGTGGCGTAAAGAACGCCTGATCACCAACAATGGGGGTGGAAGTGGCGCGGCTTCGCCCG
ATGACCAGCGGTAAAGTCGAATTCATTGTGGGCACCGCGGGCAGCGAGGCGTTGCCGTTC
GTCGACGCAGTATTTTTGAGCTGGGCGTGCGTCCTGGTGGATTCGGCCGTGCGCCGGCCG
AAAATT

>RXA00067-downstream
TAAAAGCTTTTTGCTTATCGACG

>RXA00068-upstream
GGCTGCTAAACGGCAACCAATAGAGCGATAATTCGCTAAGGCGAATGTAATCGCAGCAAC
ATATAGCACCGGCTTAACAGGCCGGTGCTATTCTGTTCGC

>RXA00068
ATGACTTCGAAGGATCTGATTGTGACCTCCTATACGTCTTGGGGCAAGCGTTTCAAGAAT
GACGGGAAGCTTTTTATTAACCTACTTCGCAGCACCACTGATAGTGCTGATGAAAAGGTT
TTAGCCACTTTCGGTGAAGTTCCCAGCAAATCATTTGAAACCACCGCAACGGTTGATGAG
CAGCAGTGGGAACTGTCCTTCAGTATTGATGGAACGGCAACTGCCAAGCTTCCTGATGGT
CGTGTGTTCAGCGCGAATGCAGGTGAGAAGACCTTTACCAAGTCCAAGCGGATTGAAATC
GACATGGACGGCACCGCGATGGCTGCTGTTAATGAAGATAAAAACAATTGGATTATCGAC
GATTCTGAAGAGAATAAAGTCGCTCAGTTTACCGGTATGAACAACGGTGTGCGTCGCGCG
ATTGTGGAGTTTGAGCCTGACGTAGAAGTCACCCAGGAGCAGGAAATTTTCTTGTCGTGG
GTTGCTCGGAAAACTCTGGAATCCCGCATGTTGGGCTCCAGTTGGGGACTGACTCTGTTT
TTGATCATTTTGACGCCAATCATTATTTTCCTCACTTTCAGC

>RXA00068-downstream
TAAAAGGACCATGCAATGGTAGA

>RXA00071-upstream
GCTTTTCTATTTCGAAAAATAGCCTTGTATTCGAAAATTTGATCGGGTATGGTGGTTGGT
AKWRKSRSWGGKAACWAMACGGGGAAAGGGGGAAGACACC

>RXA00071
ATGAGCATCACCACACACGTCCAAGCACTCACCACAGCACTCAACGCCATCGACAACCAT
TTGGCCAGCATGCTYGACCATGGTGTCACCCCAGACCAATACAAGGCCATCGAGCCCGAC
CTCATCGCCCTAGAACACACCATCAACCACCACGCCACCATCGCCGCCCAAACCACMGCC
CTCGCCGAACGCACCAAYGCYGCSCASWCSATTGGCTCCACCCACCTCATCGACTACCTC
ACCACCACCTTCGGCCTATCTAAAGCACGCGCCCACCACCGCATCAATCTCGCCCACTCC
CTCTACCCCATACCGAAGCCAAACTCTGGATCTGGCAACGGCGGTAATGGTGGCAATCCC
GACGGCGGTCCTGATGGTGGCGACTCGGGTGATGACGACTCCGGCGATGATGACCCCGAC
CCCGAACCGGACAAGCCTGAAGACGGCAAACCTGATAGTGATAAGCCCCGTAGGCCACGG
ATCAGCGCGGAAAAACACGCCATCATCACCGACGAACTCGCCCGCCTCAACCCGAATACC
ACACCCAGCGCCGAGGAACTRCGCAMCCAAGCCCTGAGTCARGCGATCTGGCGCACCCCA
GAAGACCTCCGCACGTGGCTACGCCACCAGGTCACCACCGCGAACAAAAACAACCCCAAC
CCCATCACCGCCATGAAAAGGCGCTACCTCTCAGTAGGTAAACCCGATGCCGACAACATG
GTCCGCATCAGCGGCCTCGTGCCCGCAGCCACCGCAGCACTGATCACCGCGAACACCGCA
CCGTTAACCAAACGTGGCAACCTCGTGGATCTACCAGCAGCAGAAGATATGCGCACCCGC
GGGCAACGCCATGCGGATGCGTTGCATCACATCATGGAGATCTACAACCACGGTATTGTC
ACCCCAGCTCGTGGTGGAACAGCCAGCATCATCATCTCCATGACCACCGATGATCTTGAC
GAGATCAACCACGGTGATCATGGCGATGGCAGTCTACTTAACAACCTGTACCCCACGAAC
ACGGGTTACTCATTGAACTTGGCGGAGATCATGAACCTCATCGCTGCGAAATACGACTTC
GCTGTGCTCCTCGATGGTGAGACGGGGCAGCCGTTGAACGTCAATAGGATGCAGCGCTCA
GCGAACCTGACTCAACGCATCGCGTTGTTTGCTTCTGAGTTGGTGTGCTCGGCACCCAAT
TGTGACAGGCCGCAGTTAGAGTGCGAGGTTCATCATTTAGATCCCTGGATGAGAGGTGGG
CTGACCAACCTGGTCAATCTCACGCATCAGTGCTTTAATCACCACCCACGCAACGATGAT
TCCAGGAGTGGGGTCAATGGTAAAGGGTTTATGGACCGCGATCCCGTCACTGGCAGAGTA
GGTCACTACTCAGCAAGTGGTGAGGGGCCGGTGTTTAACCGGTCGGCTGCTGCTGATCGT
TCCGGTGGTGCA

>RXA00071-downstream
TAGTCCAGACGTAAGCATTATGG

>RXA00077-upstream
CTAAATTGTTTTAACGCGTGAAGCAGTCCCCGCCCGATTTATTCGAGGCGGGGACTTTCG
CTTTCCGGGATAAAAATTGCAACGCACTACACTGAGCAGT

>RXA00077
ATGAATGATGAGAATATTCAAAGCTCCAACTATCAGCCATTCCCGAGTTTTGACGATTGG
AAACAGATCGAGGTGTCGCTCTTAGATGTCATCGAATCCTCACGCCATTTTTCTGATTTG
AAAGATAGCACTGATCGTTCTGCGTTAGATGCTGCGCTAGAGAGAGCAAAAAGAGCTGCC
GCAGTTGATACCAATGCCATAGAAGGAATCTTCCAAACTGATCGCGGTTTTACCCATACA
GTTGCAACGCAGGTAGGGGCTTGGGAGCAACAAATGGCGATGAAAGGCAAACATGTTAAG
CCTGCGTTTGACGATACTCTAGAAGGCTTTGAGTATGTTCTCGATGCAGTAACTGGTAGA
ACTCCAATCTCTCAGCAATGGATTAGAAATTTGCACGCCGTCATTCTGCGGAGCCAAGAA
AGCCACGAGGTTTTTACAGCCGTTGGAGTCCAAAATCAGGCGCTTCAGAAAGGCGAGTAT
AAAACTCAGCCAAATAGTCCACAGCGCTCAGATGGATCTGTACATGCATACGCCCCAGTT
GAAGATACTCCTGCTGAAATGGCTAGATTTATTTCAGAACTTGAATCTAAGGAATTCTTA
GCAGCCGAGAAGGTTATTCAAGCTGCCTATGCCCACTATGCTTTCGTATGTATTCATCCT
TTTGCAGATGGGAATGGACGAGTTGCACGAGCCTTGGCTAGTGTTTTTCTATACAAAGAT
CCTGGTGTCCCTCTCGTAATCTACCAAGATCAACGCAGAGATTACATCCATGCTCTAGAA
GCAGCGGACAAGAATAACCCGCTCCTGCTGATTAGATTCTTTGCTGAACGAGTGACCGAT
ACTATTAACTCTATTATCGTTGATCTCACTACCCCGATCGCGGGTAAATCTGGTTCGGCT
AAGCTTTCGGATGCGCTACGCCCCACTCGCGTATTACCAGAATTACATGATGCTGCACAT
AGGCTCCAAGAAAGTTTATTTACAGAAATCCGATCTCGATTGGATGAAGAAGGAAAAAGG
AATGGGTTGGAGTTTCTACTTCAACGGATTTTTATCGGTTCCCCATTCAATCTGCCAGAG
GGCTATAACGCTTTCCCTGATAGCTATTGTCTGACCTTAGCTTTCAATAGCAACTCTCCA
AAACAAATCTTCCACCCGCTATCCATAGTAATAGCAGCTCGAGATGGGAAAAGAGCGAGC
AGCGACCTCGTGGCAGCTACTTCTATTGGATACAACTTTCACGCTTACGGACGTGAAGTC
GAGCCTGTTGTTACTGAAAGCTTTCGAGAACGTGTGAAAATTTACGCCGACGGGATTGTA
GATCACTTCTTAACCGAACTGGCTAAAAAGTTTCAACAGAAT

>RXA00077-downstream
TAATTAGCCTATCTCGGCTTTCG

>RXA00079-upstream
GATAGCGCGCGATCTTCCTAGGCTGCCCGCTTGGGCTTCAGGTTTAGCAAGCGGGACGCT
TTCGCTTATCGACGCCAACTCCCTCCATTTGGAATCCCCC

>RXA00079
ATGGGCCTAGTTCACACCGAATTCACCCCAATAAACACCTACGGAATCCTCGACCACGTA
GTCACCCTCCCCGACGGAACTAAAGTGCTCAACCCTTTCCGAGTCATCCCCCACGACACC
GGCTCCGAACTCATTTTCACCGTCCGCCCCAACGAAAACTTCGAAGAAGATTGCCAAGCA
GTCGCAGCAGACCTCGAAAGGCTGGTCGCACTGGCCGAAAAA

>RXA00079-downstream
TGACCCCACAGAATGGTCTCTAA

>RXA00080-upstream
TTGGCAGCGTTCCGCCAGTACGGAATCCAGCCCGGACCACTACTCTTCGATCGCAACCCT
GAACTTGTCTGGGCACTTCTTGCCAGCTTCTTTCATCGCG

>RXA00080
ATGATCGTCCTGCTGTTCATCAACCTGCCGTTCGCACAGCTGTGGGCAAAGCTCCTGCTC
ATTCCAAACCACTACCTCTACTCCGGCATCGCATTGTTCTGTGGCCTGGGCATTTACGCC
ACCTCCGGCGCAGTGTTCGACCTGCTCATGCTGCTCGGCATCGGTGTCGTGGCTTTGATC
ATGCGTCGCTACGGTTACCCGCTGGCACCGCTGATGATCGGTATGGTTCTTGGACCTTTG
GCTGAAACCTCCCTCCGCGACGCACTACTGTCCTCGGTTGGCGATTTCTCCATCCTCGTC
TCCAGCCCCATCACCTGGTCTCTCTACGCAGTGCTCGCCATCTTCATCGCGGTCAGTGTC
ATCACTGCAATCCGCGGTCGTCGCAAGCACCTGACTTCTCAGCTCGAAACCATCGACGCT

>RXA00080-downstream
TAAAGTCCCCGTATAGAAACAGG

>RXA00082-upstream

CACTTGAAGGCGAAGAACTCGACCAGTTTGTTGAAGATGAAATTGACCGAATTGATCAGC
TATTCAAGAAGATGGGCTA

>RXA00082
GTGAACGTCACTGAACAATCCGGCGAGTCCCATATCGACATCCCGGAATCACACCAGCTG
CCCGGACCTCGTCCAGTTGGCGAGGGCACTTTCTGGGAAGGCCGCTCCGGGCTCATCATG
CCCGCAATTCTTACGGCATTTAGTTTGTATTTGCTCATCGGTGTTTTAAACATGGATGTG
GGCAATGCAGCATTCCCAGGACCTCGATTCTTCCCAACAATCCTCGGCATCGCGGGTTTG
TTGGTGGCAGTGGCATTGACCATTCAAACCATCAAGTACCCCATGCATCCAGAAAATGAA
TCTGGCCGAAGCTGGAAATTCCACTCTGATTACGTCTCACTCGCGTGGGCGATCGGTGGC
TTCTTCGCCTTTGCAGTCTTGCTTCCATATCTTGGCTGGGTCCTTGCTGGCTCCTTGTTG
TTCTGGACAATGACCAGGGCTTTCGGTTCCAAACGCCCAGGTTTCGATGTTCTTGTTTCC
CTCATGATGAGCTCCGTGGTCTACCTCGCATTCGATGTGGGCTTGGGACTTAATCTTCCT
TCCGGACTTTTGGGTGGTGGCTTT

>RXA00082-downstream
TAATGGATATTTTGTCCCTCTTG

>RXA00083-upstream
GAAGATACAGGGGGCCACGGTGGGGTGGTGAACAAGAGCAGGCACGAGGCCTGGTAGATA
CGGATTCGACCAAGAAAACGTACACCACTCAGGAGCACTC

>RXA00083
GTGCTTGCCCTTCCATCCTCTATCATCGACCCCCTCTGGTGCCAGTTCGCCGCGCTGATC
CCACCCGTGACCGACACCCACCCACTTCGGTGCCACCGCCCACGCATCCCGGACCGGATC
ATCTTCGACAAGCTCATCCAGGTCCTCGTCCTCGGCGCCTCCTATGCCAAGATCGCCGAC
ACGACATGCTCGGCCACCACCTTGCGCACCCGCCGGGACGAGTGGATCACCGCTGGCATC
TTCGAGCAGCTGGAACAGATCTGTTTGGAATTCTACGACCGTATCGTCGGACTCGATCTC

>RXA00083-downstream
TAAGTTCGGATTGGCTCGAATTG

>RXA00087-upstream
TCGTCAGTCAACAAACGTTTTCCCACCCGGAGGTCTCCCCGTGTCTACCGAAATCCACAA
CGCCCCACCCAAGGCCCCAACTTGGCTTGGCTGGGTGCTC

>RXA00087
ATGATCGGCGGAATAATCGGCCTCATTTTGTCGGTGATCATCATGGCCGAAAAACTTGCC
ATCCTCGAGGATCCCGGTCACATCACCAGCTGCGATTTCAATGCAGTCCTAGCTTGTGGC
GATGTCATGCGTTCCGGCCAAGCTAACGCGTTCGGCATCCCGAATCCGCTCATCGGCATC
GCCGGTTTCGCCGCTGTCGCCATCATCGGCGCCGGCATCCTCGCGGGCGGCGGGTTCCGC
GGTTGGTTCTGGTTCGGCGCCCAGGCCGGACTCACTTTTGCCATGATGTTCTGCCACTGG
CTCGCCTACCAATCCATGTCCGTCATCCGCGCGCTCTGCCCTTACTGCATGGGCGTGTGG
ACCGTATCGATCATCATGTTCGTGCTGGTCACTGCATGGAATGTGAAAACTTTCAGCGGC
TCCGACAGCACGTTCGTCAACGCACTGTACAAATACAAGTGGGTCATCGCGATCGTCTGG
CTGCTGCTCATCGCAGCCGCAGCTGTGTGGTCATTCCGCTACATGTTC

>RXA00087-downstream
TAGGCATTTAAGGCTTTCAGGCC

>RXA00093-upstream
AAAGAATCGATTCCGGTGCCGCAGGCCTCCTTGTCACCCACGAACCCCGCTTCGCCGCGT
GGGCAGACCGAACAATCATGCTTAGGGATGGTGAAATCCA

>RXA00093
GTGACCACACTTCTAGCAGCAACCCGCCCCACCCTGCGCGATGCCTTTAAACACCCATGG
CGATCGCTGGCAGCCATCTTGTTGGTGGCCGTACCGATGTTCCTGGTGAGTTTCTTTCTT

ACCTATGATCAATCAATCAACAATGCAGCTAGCTATCCTGGTTCCCAGGTACAAGCTCAC
TATGACGGAGAAGGAGCCTACCAACTCCTCCAAGAAAACCTTCCAGAAGACTTCCACCTG
GAACTCTTTGCCAATGGTTATCCAGAAGTCTCCTTCGGTGATGAAGAAGTCAATTTCTTT
GTTGTGCAATCAACAAACGTACAACAAGCCTCATTTCCCGCCGATGCACTCGATGTTTTA
GGTGCCACAATCGGTGATACCGTGACCATTCACGGCACCCCGGTGGAAGTTCAGTCGATT
TCTCCCACAAATATCTTATTGCCCGAAGGTACTCTGTTTTCTCTTGAGAATTTCTCCGAA
TCAGAAACTTTTTCCGGCACCTGGTACTTCCCCGGATCGAATTTCACCGAAGAAAACCGA
CAAGCACTAGAAGCAGTTGGCTTTGAAGTTAATGAATATCGGCGCGGCCCCATATCCGTC
GACCCAAATTTGATCCCAAGCTACATCATGGGATTTTTATCGACGACAATTCTCGCCGTC
GTTGCACTCATGCTGATCTCACCAGTATTTACAATTTCCGCCTCAAGGCAAACCAGAACT
TTCGCACTGCTCGCCTCACAGGGTGCCACACCTAGACACATTCGGTGGGCAGTGCTTACA
TATGGGCTCTTCGCAGGTCTTGTTGGGGCATCCATTGGTTTAGTTCTGGGGCAAATAGGC
ATCTACGGCTGGTGGAAATACACCTATCCTGAATTCTCCCTCACCACCCCCTGGCTAGTT
CTTGTAGGTTTTTGGGCGCTGGCAATCATCGCTTCAACGATTGCTGCATTCTTACCGGCA
GTTTTTGTCAGTAGATCAAGCATCATCAACGGAATCTACGGAGGAATCTCCGACAAAATC
ATCCGGTGGAGCCCTCGAATGCTCATCGGGCCAATCGTCTTAATTGCAGCTGCGGTAATC
GCCTTGTTTATCGGTGACGGAGAGTGGGGAGGCGTCGTCAAGCAATTATGCTTCCTGGCA
GCCGTCATCGCCCTGCCGGCCTCAGTGCCTGCGGTGTTGTGGGCGCTTGGGCGCCTGCCT
GGTTTGACATTCAAACTAGCTACGCGCGATATGCTGCGCCGATCAATGCACTCCATTCCT
GCGATTGGTGCGCTGGCGGCAGTGATTATGCTTGGTACATTTATGCAAACAACTGGACTT
GCAACCCAAGCCAGCGATAGAGAAGCTACCGCCTCGGTGTATCCTGAGGCCGTATTCTTA
CGCGGTGACACACAAATCCCTGGACTCATGGGGCAAAAAATCGATGTATACGGTGATAAC
CATGGCTTTGGTATCTATGAACTAGATGTAGATTTTTACTCGGCCAACTATGTGCCCGCA
CTGACCTCATTTTTTGGCGGACCAGTTATTGCCACGCCCAAGATTTTAGACATGTTCGGT
GTCCACGAACAAGCCGACATCTACGCGCCATCAACCTATAATTCCGGGCTGCAAGAATAC
GCAATATACCCCGGCGATGAAACCTACATGCTAGACACCGCTGCTGTTTTACCGCCGCTG
TACTCACATGTTTTATTAAGCCCAGAAACTTTTGAAGAAATCGGAGGACAAACAGAATTC
TTGGGAACAATCGTGCTTCCCCAAGAACTAGATGACCAAACTGTACAAGCAATCAATCGG
TCAAGAGATGCGCATTTCAGCCACGACGGCCATAATTCTTCACTTGCTTCCAGTGCTGCA
CTAACTGCGGTGGCAATTGTGGTCGTTTCCCTTGTGATCGTGCTGGCTAATCGCAAACTC
CAACAGCACGCATTGATTGCCATCGGAGCAACACCTGGAACAATCTACAAAGTCAATGCC
TTAAATGCAGCGTTGCTTGCCCTTGTCGGAGGCATCATGGGCCTTGTCTCCGGATGGATT
GCAGCGCTGCTGACAGGCACCACTGATGAAATTGTTGATGGAGCAATTTTGAACTACGGC
ACGCTTGAACACATGATGCTGCCGTGGCCTCTGTTGGTAAGCCTCCTCGTTGTGGCGCCG
CTGGTGTGCGCCGTGATTGGGGCTATAGCTTCTCCATCGGGACGCCACCAAGAAGCATCA
ATC

>RXA00093-downstream
TAACCTTGCCGGAGGAACCGAAA

>RXA00096-upstream
GGGGAACCTGGGGTAAAAGGAGAAGTATTCATTACCCCAATAACCTACTAGGTGGGGTGG
ACACGCATAGTCGACAGCCAGACGTGGCAGAATAGTGTGC

>RXA00096
ATGACTAATGCAGGTGACAACTTCGAGATCAGGATGCCTTCTGGCACGGATGACCCATTG
TCCGATGCGGAGATCCAAAAGTATCGCGAGGAGATCAACCGCTTGGACCGCGAAATCCTC
GATGCGGTGAAACGCCGCACGAAGATTTCCCAAACCATCGGAAAAACACGCATGAGCTCG
GGCGGAACACGTCTCGTGCACACCCGAGAAGTAGCAATCATCAACCAGTTCCGTGAAGAG
ATCGGCGAGGAAGGCCCTGCCCTCGCTGGAATTTTGCTGCGCATGGGACGCGGAAAACTC
GGA

>RXA00096-downstream
TAAGTTATCCACAGGTAGAAAAA

>RXA00097-upstream
TTGATGGGCAGAGTTATCCACAGGTTTTTAGCGAGCTGGTTTCCGACGAAGAAAATAGTG
GATAGGTTACAGGGCAGAATCCCGAATGGAGGTGCCTTCC

>RXA00097
TTGTTTACCAACTTCTTCGCAGTCAACAACCCAGACAGTCCGCCCGCACGACAAAAAACC
AAACTCAGAGAACTGGAACACCGCTTCTGGCAAGAACACCTGCCAGGCGACGACGATGAC
CATTCCACCGCAATCTCCAGCCTCGCCATCGTCACAGGTCTAACAAAAGCGCAGGTCTCC
CGCATATCCATCGCGTTTGCCACGCTCGCCGACTTGCCCGAACTCAAAGCCCTGCAACAA
AAGCTGTACCACCTCGACCTCTCCCGACTGATCACCATTAGCAACGAACTCGCCGGCATC
AACCCCGACAACCTCGCCGGCGCCGACGCAATCCTCACCGAATACCTCACCGCCACCAGC
CCCAACCAGATTCTGCCAAGCCCGGCGTCCATAGGACGCAAGATAAAAGAAATAAGAGAT
TTGCTTGACGACGCAAGAGCCACCGGTTCGCGCGGTACCCAAGACGACAGCTCTTTCGGA
GTGACCTTCTCCCCAGACGGAACCGCCGAAATCGGAGCCTCCGTCGATGCTGTGGACGGG
CACATCATCAACGACGCCGTCACCCAACACGCGAAGAAAAACGACCTCACCTACGGCGAA
GCTTTCAGCGACATCCTTCGGAACAATATCCAAGTCAAGGTAGTCCTCAACTTGTACACC
GCCAAAGACCTCGCCAACGCCCCAGTGTGGGCCAGCGGAATCGGCTGGTTGGATGCCAAG
ACTGGAACATTCTGGTCAGAGAAAGCCAACAAAGAACAAGACATGGATGCGGCTGCCAAA
ATCAGCACCGACAAACACGATCCTCCACCAGCGTTGCGTGACGCACTCATTGGTCGTGAT
GGCACCTGCCGATTCCCTGGCTGTTCAGTCCCAGCGCTCAAAACCCAAGCCGACCACCGC
ATCCCCTACGAAGAAGGCGGAGAAACTTGCCTAGGCGGAATCGGCTGCCTCTGTCAACAC
CACCACAACATGAAAACCGACGGCCGAGTCACCTACCTTCTCGATCCCTTCTCCGGCATC
ATCGTCTGGCTCATGGGAGACGGAACATGGGCAGTGTCAGAACCCAACGGGCCGCTCAAT
CCCAAAAATGCGAGATGGGCGCAAACAGTCGCCCAACACCGGGCACGCCACCACAAGCGT
TGGGTTAAGGAGGACGCCAAG

>RXA00097-downstream
TAGCCGGATGGCCACGTCGAAAA

>RXA00101-upstream
TAAACCGTGCAGGAGATGCCGAACCCCAATCGTGAAAGCCGAGTTGGGGGAGCGAATAAT
CTGGTGGTGTCCGCGCTGCCAACCGCTAAACTCGTGAAGC

>RXA00101
ATGAGACTAATACTCAACCTGATTTGGTTATTCTTCGGTGGCATTTGGCTCGCGTTGGGA
TACGTATTCTTCGGAATCATCGCATGTATCTTCATCGTGACGATTCCCGCCGGTATCGCA
AGCTTCCGCATGGCTAACTACGCGCTGTGGCCGTTTGGTAGGACGGTTGTTCGTAATCCT
AAAGCCGGAGGGTTTTCTGCCCTGAGCAACGGACTGTGGTTTATCATTGCTGGACTGTGG
CTGGCGATCGGGCACCTCACCACCGCGGCTGCCCAGGCGATCACCATCATCGGAATTCCA
CTGGCGATCGCAAACATCCGAATGATCCCCGTGACGTGTTTCCCGTTCGGCAAAGAAATC
TATGACAGCAACCGCATTCCCTTCGGCTACGAACCGATGGTTAAGTTT

>RXA00101-downstream
TAATTCGGCGACGGACTAAACCA

>RXA00108-upstream
GAATTGGGTTTTGAGCATCGTGGCGGTGCTTGTTGTTGCAAGTGCCATCGTCATGATGAT
TGCAAAGAATCGTAACCAGAAATAAGAGGGTTTATTCACC

>RXA00108
ATGAAGAAGTTTTTTGTCGCAGGTGCTGTACTGAGCAGTGCGTTGGTTATGGCGGCGTGT
TCGCCTGCTAATCAAAGTGATTCCACCTCCACGAGCGTGGAGACTACTTCCTCCAGCAGC
ACGCAGGTAAGCGATGCTGTGATCACCACGGAAAACGCTGTTGTTCGTGCGTCTGTGGAG
GACAGCGACATGACGGCAGTGTTCGCTACGTTGGTGAACAATTCTGATGATGAGATCAAC
GTTTCTGGCTTTACTGCTGATGTTGATGCTGCCAGCTTTGAGGTCCATGAGGTTGTTGAT
GGCGTCATGCAGGAAAAGCCAGGTGGTTTTGTGATCCCTGCAGGGGAGAGCATCGAGCTG
GCACCAGGTGGCGATCATTTGATGATCATGGGGCTTGCGAACCCAATCGAGGCTGGCGAT
GAAGTGACGGTCACTCTTGAATTGGCTGATGGTTCTGAAGTTAAGCTTGATCCGATCCCG
GCGCGCACCATTGCTGCTGGTGATGAGGATTATGGCGATCTGGGAACTGAAGGCCACGAG
GGC

>RXA00110-upstream

ATATCGAATGTCCAGTCACGCTAAACTTCACCCAAGATGAGATTTCGTGGCACGATTGGG
AATAACGAACGCTAATTTTAAACACTGGAGGAGCTTCCAC

>RXA00110
GTGAGCAACAAAGACGGCCTTTTTACTGACGGTAACAGCACGTTTGCACCTAAGGTGGAT
TCAATTCCCCTCAGCGATGTGGATACCAGCGTTAGCGGTGAAGCCTCCATCGGCACGCTG
ATCTCCAACGCAACCTCCCAAATGTCCAGCCTTTTCCGCGCAGAAGTTGAGCTGGCGAAG
ACTGAACTCGCAGGCGAAGCCAAGAAAGCTGCCATCGGCGGCGGCGCATTCAGCGTTGCT
GGCGTAATCGCACTGTACAGCTCCTTCTTCTTTTTCTTCTTCGTCGCAGCACTGCTGAGC
GAGTGGATTAAGCCTTGGGCAGCATTCCTCATCGTGTTCCTCTTCATGCTGGTCATCGCC
GCAGCTCTCGCACTGTTCGGCTGGCGCAAGGTGAAGAAGATGGGCGCTCCGAAGAACACC
ATCCAATCGGTCAACCAACTGAAGAACCTGGTCCCAGGTCAGGCATCCGAGAAGCTGGAG
AAGGCCAACAAGCGTGGCCTCTACACCTCCGCGTCCTTCCACAGCCCCGGCGCCATCACT
GGCGACCAC

>RXA00110-downstream
TAAAAAAGGAGACTTCGATGGCC

>RXA00114-upstream
TGCATTCCCTAACGGGAATGCAGCTTTTTGTGTTCCTAGTGCAAATCGAAATCTCATGTG
ATTTACTTAAAACCTAATTAAATCTACTATCGGAGATCTC

>RXA00114
ATGAAACTTCTCAAGTTTGCTGCAGCAGGAACCTTCGCACTAGCCCTGGCTGGCTGCACA
CAGACTGAGTCTCTCGTAGCAACAATCGAATCTGCAACCTCTGCAGCACAGGCATCCGGA
AACGACGTAGAAGGAGACCAAACCTCCGCGTTCGAACTCTCCGTTGGCGAATGCTTCAAC
GACACCTACGAAGAAGAAATCTCCGAAGTACCCATCGTCGACTGCGCAGAACCTCACGAC
AACGAGATCTACTACCTCTACGACATCGAAGGCGACGACTTCCCAACCGACATCACCACC
ACAGGCTACGAAGGCTGCCTCCCAACATTTGAAGGCTTCGTAGGAGCTCCTTACGAAACC
TCCATCTACGAGGTCTACCCAATGACCCCAACCTTTGGCTCCTGGACAAACGGCGACCGC
GAGGTAGTGTGCTCCGTGTACTTGGCCACCGGTGAGCAGATGACCGGAACCGCAGCAGGA
ACCGCGCAG

>RXA00114-downstream
TAGATTTTGGATAGGGAATTTTG

>RXA00117-upstream
GTTGATCCCACAGTATACCCCCACCCCTATCTTGAATACCCCCCAGGGTATATGGCACAC
TTGGAATCGCCCATCACTTTGAGATTGAAAAGGACAAGGT

>RXA00117
ATGACTTCCGCTCAACCGATTACTTCCGTAGATGCACAGACTCTAAAATCGTGGATCGAT
AAGCATGAAGGACTCACCGTCATTGACGTCCGCACTGCACATGAGTTTTCAAATTTGCAC
ATTAAAGGCTCTTACAACGTGCCTCTAACTACACTTGCTGAGCATTCCGAAGAGATTTCC
TCTCGTGTTGGAGAACATGTTGTTTTGGTGTGTCAATCCGGCATTCGAGCAGGTCAGGCA
CAACAAAAGCTGGCACCTTTGGGAATTTCCACCGTGGCTGTTTTGGAGGGTGGCATCAAT
AGTTTTGCTAAGGCTGACGGTGATGTGGTCCGCGGAACCCAGGTGTGGGATATCGAACGT
CAGGTGCGTTTTGCCGCTGGATCATTGGTGCTCGCAGGGCTTGCGGGAGGTAAATTCCTT
TCACCAAAAGTTCGCACCCTGTCGGGAATTATTGGTGCGGGTCTGACATTTTCTGGCGTT
TCCAACACCTGTGCCATGGGCAAAGCTCTGTCCGCCTTGCCGTGGAATAAAACTAAGCCA
GTTCCTACCGAAACCGAGACATTGAGCAAGCTTCCAAGCCCTAAGGAGAAC

>RXA00117-downstream
TAAATGTCTATCACCATTACTGA

>RXA00118-upstream
ATGGGCGATTCCAAGTGTGCCATATACCCTGGGGGGTATTCAAGATAGGGGTGGGGGTAT
ACTGTGGGATCAACGTTCCAGGGCAACAAAAGGAGAAAAA

>RXA00118
ATGCAACTCAATCCTGATGAGATCACCCCAGTGCTCAACCGACTCAAGCGCGCCCAAGGT
CAACTCACCGGAGTAATCCGAATGCTTGATGAAGGCGAAGACTGTAAAGCCGTAGTCACC
CAACTTGCCGCAGTCACAAAAGCGCTGGACAGGGCAGGCTTCGCCATCATTGCCACAGGT
TTGGAACAGTGCCTCACCAACCCTGATGGCGACATGGACAAAAAGGAACTAGAAAAACTG
TTCCTGTCGCTGGCT

>RXA00118-downstream
TAACTATGGCCTAGTTCAGGGCG

>RXA00119-upstream
ACTAATGAGAACTGTTTTTCAATTGGTGCAGGATTTCCACAAGGAAGCTAGGGGAGAGGG
GCTTCCAATCAAGTGGGGTCCATCGCGTGGAGAATTTGGC

>RXA00119
ATGCTGGAGTTTCCTGCAGATGTCATTCCCGAGAACATCAAACACATTGCGCAGACAAAG
TTCCAGACTGAAGCAACTTCGGTGGAGGATATTCGTCGTGCGATTAACCTGCTGAGTGAT
CAGGCGGAGCGTGCGGGTGCGTCCTTTAATCCTGGTTTCATTCTTGCGCAGGTGGGCTCC
ACCATCGTGGAGGTTTATGGCGGTGCTCCGGTTGCTTGGCTGGATGCGGTTGAGCTGTTG
ATTAGTCCTGATGTGGAGTGGGTTGGGGTTCATGGCTCAAGGAAGCTCGATATTAATGTC
AGCGGAGAATTGTCCGGGGTGATTTCTGCTGGTGACAAGTTGGGTGAACTGCTTGGCGAT
GATTGGACAATCAACATTGTTCACGGCGAGTACAAAATCCAGATCGAAGATGCTCGACCA
AGTACTGCATTCCTTGCGGACGCGACTGAACTGATTAATCAGGCAAACTCTGAGATTGTT
CCGTTCCATGTTCGGATGCTCAGCAACTCGAAAATTGTGATGTCTGGCTTTAGTGATTAT
TCACTAGCGGGTGATGCGATTACATCTGCGGGAAAACTGGCTGAATTGGCGAGGCCTTTT
GCCCACTGGAAAGAAAACGTCATTCCTACGATAGAAATAGCCATGGACTATGAACCATCA
CCGGTGGCAGATCTTTGGCAGGGAGATTCTTCGGAGACACCTGAGCCTTTCGACGATTTT
GAGCGCTTATTGCGGGAAGAAATGCTTATTCCTGAGATT

>RXA00119-downstream
TAGCTGGTCATAGACCTGCTGTT

>RXA00120-upstream
AATCAAATACTTGATTACAGAGCAAGATGTACCTGCACTCCGCGAGCAGTTGGCAACGAG
GATGAGCACGGATCCGCTTTCCCCACCCGGAGGCTACCGA

>RXA00120
GTGGAATCCCTTTACTTCGATTCAGCCGATTTACGGTGCTACACCGAAAAGATCGAGGGT
CTGAAATTCCGAAGGAAACTACGGATCCGTACCTACGGTGATGGAGTGCTCACTCCAGAA
TCCACCGTGTCGGTAGAGATCAAGCAGCGGGTTAACAAAGTAACTCAAAAGCGTCGGCTG
GATTTGCCCTTTATATATGCGCTCGCCCTGGGCGATAGCACGGGCGCCGCGGTAGGCGAG
CAGGTGGACGTCGAGAAGCTTCTTGAAATCTCTCCGGAAAACCAGCACGCTTTGATTCAC
GAAATGGCGTCGTTTGCTAAAAATTATCGGCTGCGACCCATCGCCACCACGAAGTATCAC
CGCGAGGCATTCGTCGGCGCTGATGCGGAGGAAAGTTCGCGAGTCACCATTGACCACGGT
GTTTCAGGCCGTGATCGTGATTTTCTGCTTGGCCAAGACCTTGAAGACCGCCCAACGGTG
GCGCAAGGATTGGCAGTCGTGGAAATCAAATGCGATGAACGCGTGCCGTTTTGGCTCACT
GATATGACTGCTCAACTGGAAATGTCCGTGATTCGGATGTCCAAATACTGCGAAACCATC
GAAGCGTTTCACAACCGTCCGGCATCAGCTTTCGGCGCTGTCGACCCCATCTTC

>RXA00120-downstream
TAAACAAGAAAGGCCCCTCCAAT

>RXA00121-upstream
GATGTCCAAATACTGCGAAACCATCGAAGCGTTTCACAACCGTCCGGCATCAGCTTTCGG
CGCTGTCGACCCCATCTTCTAAACAAGAAAGGCCCCTCCA

>RXA00121
ATGTTGAGCGATCTGAGCTCCATTTTTGACTTCCAAGACCTCTCCGGCACCTTCTCTGTC

GTCGACGTTCTCATCACTTTGGTCTTGTCCTTCGTCCTGACCTCCATCGTGGGTGTGGTG
TACCAAAAGACCCACCGCCACATCTCCTACAGCCAGTCATTCGTACAAACGTTGGTGCTG
GTGGGAATGGTCATTGCAATCATCATGCTGGTGGTCGGCTCCAACATTGCACGTGCATTC
GCCCTGGTTGGCGCGCTTTCGGTGATTCGATTCCGCAACGCAGTGAAAGAAACCCGAGAT
GTGGGCTTCCTTTTCCTTGCCATGGCAATCGGCATGACTTGCGGTACCCGCTTCTACGTT
CTGGCGATCGCTGCAACCATCGTTGTCTGTGGCGTTCTGTTCATCATGTACCGCTTCGAC
TGGTTCAAGGCTGATATCCAGCGCCAGGTCATCAAGGTGCAGGTCCCAGCCGATGGACAA
GCTGATTCCGGCAGGTCCTACGCAGAAGAAGTTGAACTGATCCTCGCACAGTACTGCACT
TCCTTTGAGATGATGTCCGCTGAATCTGTCCGCGGCGGAGCCCTGACCGAGTTCTCCTAC
ACCGCTCAAATGCGCAAGAACGTGAAGCCACATGAGCTGGTCGCCAAGATGCGCGATGTG
AACTACGGCCAAAAAGCGACTGTCCTGACCGGTCACGATCAAACGGATGTA

>RXA00121-downstream
TAGAAAATGCCTAGCTTTAAATC

>RXA00122-upstream
GATGCGCGATGTGAACTACGGCCAAAAAGCGACTGTCCTGACCGGTCACGATCAAACGGA
TGTATAGAAAATGCCTAGCTTTAAATCTGCTCGATGGAGG

>RXA00122
ATGAACAGACGCCTCTTCCTAGGAACTTCCGCAGCTATCATCGCTGTCGGTGGCGTGCTC
GGTGGAGTGCAGGTTGTACCTTATATTTCCTCTGGTGAAATCCAAACGTCAGCATCATCG
ACTGCCACGATCGATGTCGGTGCAGGCAATGTCGATATTTTTGATACCTCCGTTTCCCAT
GAAATCAGCCTGCAGGTTTCGCAGGAAAGCCTCGATGAGATGCTCGCGGACTATCAAGAA
GACGGTTCCAAAACCTGGGTGAAAGCAACCATCACGATTGATGGCGTGACCATTGAAAAC
GTCGGCATCCGCCTCAAGGGCAACTCCACGCTGTCCGGGTTGGGTCGAACATCTGAAGAA
GGCGGACCTCAGGCACCAGAAGGCGTCGAAGAGTTTACAGATCTCAGTGAAGAGGAAATC
GCCCAGTTTGAGGAACAGTTCGCGGCGCAGCAAGAGACTACTGACGCTTCAGAGACCGGT
GAAACTGCGGAAAATGAAGAGACTCGCGGCCCCGGCGGTGGCATGGGTGGTGGCGGCATG
GGTGGCATGACTTCGGTCGATGCCGACGATGTCAGCACCTGGCCACTTCTGATCAGCTTC
GACAAATACGAAGACGGCCGCGTCTACCAAGGCATGACCCAACTGGCACTACGCCCCGGC
ACCACCGTGGTCAACGAAGCAATGGCGCTGGCCCTGACCGCAGAAACCGGCCAGGTCTCG
CAGCAATCCAGCTTCACAACGTTTTCGCTTAACGACGAGCCCTCCACCACTCGACTCCTT
TTGAAGCACCCCGATGAAAATTATGCCGACGCGCTCGGCAACGGAGTCCTCTTCAAAGCA
GATTCCAACAGTTCCTTCACCTACCAAGGCGAAGACCAAACTGAATACGACGGACAGTTC
AAGCAGATCAACGGTGACGGCAACGGAGACATCCAACCGATCATCAACCTGCTGAAATGG
CTCGACACCGCAAGCGATGAAGAGTTTGCTGAACACCTCTCTGACTACGTCGATGTGGAA
AGCTTTGCTCGCTACGTTGCCACTCAAAACCTGTTGGTAAATTCCGACGACATGGCTGGT
CCCGGTAGTAATTACTACCTGTGGTACGACTACGACACCGGCCTGATCAGCGTGATCTCT
TGGGATTTGAACCTCGCAATGTCCGGCTCAACTGATGCTGGCCCAGATGATGAAATCTCC
ATGGGCGGAGGTGGCGGTGGCGGAATGCGTCCTGGTGGAACGACCGACACTGAAATTGAA
GGTACTGCGACCGAGGATATGCCTGACATGGGCAATATGCAGCAACGTGAACGCCCTGAA
GGAATGCCAGACATGGGTGAGATGCCTGATATGGGTGACCGGGAAGGCGGTGGATCGATG
GGAGGAAACCAGCTCAAGGAACGTTTCCTCGCTTCCGATGCATTCACGGAAATCTATGAG
CAGGTGTACTGGGAGCTGTATGAAGAAATGTATGGTTCCGGAACTGCCATCGAGTTGTTG
GATGAGATTGCAGCGTCAATTCCAGAAACTGATGCGGTGACTGCAGATGAGATCGCTACG
GAAGTGGCGTCAATGCGGGAATGGATCACTGCCCGCACAGAAGCGTTGGCTGCTTTGCAA
GAG

>RXA00122-downstream
TGATCAAACTAGAAAACCAACAA

>RXA00127-upstream
TTGTGGGGCGCCGGGGGCGTCGTTATGCAGTGACTGCCAGCGTGTGTGGAGGAAGCCGCC
AACATTGGCGCGGCTTGATTTAGATTTACCGGTGTGGACG

>RXA00127
TTGTCGCCGTATGACGGCCCGCATCGCAACGTGCTCATTGCGCTGAAGGAGCACGGCCGT
GCAGACCTTGTGGCGTTTGTGGGCGCGGTGGTGGGGGCGTCGATAAGCTATCTGGCGGCT

CAGGGGGAAATTGAGCACGACATCACGCTGGTTCCGGCGCCCACCCGCGCCACCTCGCGA
CGCCGGCGGGGCGGCGATCCGGTTGAGCGGGTGTGCAATGCATCACGCTTATCGACGTTT
CCCTGCCTTCAAATCTCATCCCGCACACCAGACTCCGTCGGTCAAACTGCGCAACAGCGA
AGACTCAATATGCGAGTGGAGTTAGTCCGACAACCTCGGGGTTCTGTCTTGATCATCGAC
GATGTGGTAACAACGGGGGCAACTATTTCCGCATCTGCAAACGTTCTTCGCGCAGCGGGT
GTGCAGGTCAGAGGAGCTTTAACTTATTGCCAAGCG

>RXA00127-downstream
TGATCTTGGATATAAAAGGGGCC

>RXA00128-upstream
CCATTTTCCGTTTGGTCTTGCCTAAAGAACCGCATGGAAATTATCGTGAAGCACCGATCC
CGTTGATCGCTCCAGAGACACCGTGGGAAGGGGAGCAGCA

>RXA00128
GTGAGTAAAATTTCGACGAAACTGAAGGCCCTCACCGCGGTGCTGTCTGTGACCACTCTG
GTGGCTGGGTGTTCCACGCTTCCGCAGAACACGGATCCGCAAGTGCTGCGCTCATTTTCC
GGGTCCCAAAGCACACAAGAGATAGCAGGGCCGACCCCGAATCAAGATCCGGATTTGTTG
ATCCGCGGCTTCTTCAGCGCAGGTGCGTATCCGACTCAGCAGTATGAAGCGGCGAAGGCG
TATCTGACGGAAGGGACGCGCAGCACGTGGAATCCGGCTGCGTCGACTCGTATTTTGGAT
CGCATTGATCTGAACACTCTGCCAGGTTCGACGAATGCGGAACGAACGATTGCGATCCGT
GGAACGCAGGTCGGAACGTTGCTCAGCGGTGGCGTGTATCAGCCGGAGAATGCGGAGTTT
GAAGCTGAGATCACGATGCGTCGGGAAGATGGGGAGTGGCGTATCGATGCTTTGCCGGAC
GGGATTTTATTAGAGAGAAACGATCTGCGGAACCATTACACTCCGCACGATGTGTATTTC
TTTGATCCTTCTGGCCAGGTGTTGGTGGGGGATCGGCGTTGGTTGTTCAATGAGTCGCAG
TCGATGTCCACGGTGCTGATGGCCCTTCTGGTTAATGGTCCTTCGCCGGCAATTTCTCCT
GGTGTGGTCAATCAGCTGTCCACGGATGCGTCGTTCGTGGGGTTCAATGATGGGGAGTAT
CAGTTCACTGGTTTGGGAAATTTGGATGATGATGCGCGTTTGCGTTTCGCCGCCCAGGCC
GTGTGGACGTTGGCGCATGCTGATGTCGCAGGCCCCTACACTTTGGTCGCTGACGGCGCG
CCGTTGCTGTCGGAGTTCCCAACGCTCACCACCGATGACCTCGCCGAATACAACCCAGAG
GCTTACACCAACACGGTGTCCACGTTGTTTGCGTTGCAGGATGGATCGTTGTCGAGGGTC
AGTTCCGGCAATGTGAGTCCACTACAGGGCATTTGGAGCGGTGGAGATATCGATTCTGCA
GCGATTTCCTCCTCCGCCAATGTGGTGGCAGCGGTACGCCACGAAAACAACGAGGCAGTG
CTTACTGTTGGCTCCATGGAAGGCGTGACTTCAGATGCGTTGAGGAGTGAAACGATCACT
CGTCCCACCTTTGAATACGCGTCGAGTGGGTTGTGGGCTGTGGTGGATGGGGAGACGCCT
GTCCGAGTCGCACGATCGGCAACAACCGGTGAGCTCGTCCAGACGGAGGCGGAGATTGTG
CTGCCAAGGGATGTGACGGGTCCGATCTCTGAATTCCAACTGTCACGAACTGGGGTCCGG
GCCGCCATGATCATTGAAGGCAAGGTGTACGTGGGCGTCGTAACGCGTCCTGGTCCGGGC
GAGCGGCGCGTGACAAATATCACGGAGGTGGCGCCGAGCTTGGGCGAGGCGGCGCTGTCG
ATCAACTGGCGCCCAGACGGCATTTTGCTTGTGGGCACGTCAATTCCAGAGACGCCGCTG
TGGCGCGTCGAGCAGGACGGATCGGCGATTTCGTCGATGCCGAGCGGGAATCTCAGCGCG
CCGGTGGTGGCGGTGGCAAGTTCCGCGACGACGGTCTACGTCACTGATTCGCATGCGATG
CTTCAGCTGCCGACTGCCGATAATGATATTTGGCGCGAGGTGCCCGGTTTGCTGGGCACG
CGTGCGGCGCCGGTGGTTGCGTAC

>RXA00128-downstream
TGATGGAGCTGTTCTTCCCGCGC

>RXA00134-upstream
GCAGCTGTGCTCCACCAGTGACTAAAAACTTGTCTTTCACGTGCCCCACCTTATCCGTGT
TCCCCACCCCTGTGCGTAACGACAGCTAGAATCTCAAGTT

>RXA00134
ATGGCCGTTCATTTAACCAAGATCTATACGCGAACCGGGGACGATGGAACCACGGGGCTC
TCAAATTTTGAGCGAGTTCCCAAGGACGATCCCCGCCTTATTGCATACGCCGACTCCGAT
GAAGCAAACTGTGCGATTGGCCAAGTGCTTGCACTCAGCAGCCCTACGGAAGATATGGCA
ACCTTATTGCGGACTATTCAAAATGAACTTTTTGATGTGGGCGCAGACTTAGCAACCCCG
ATTGAGGAGAATCCGAAGTATCCCCCACTTCGAGTTCTTCCGGAATATATCGAACGACTT
GAGAAGGAGTGCGATAAATGGAACGAGGATGTGCCGGCGTTGGATTCCTTCATTTTGCCG

GGTGGCACGCCAGCAGCGGCACTCTTGCACACCGCAAGGGTAATTACGAGGCGCGCGGAG
AGAGCAGCTTGGATAGCGGTGCGGGAATTTCCGAGCACCACCTCTACCTTGCCAGCCCAA
TACCTGAATCGTCTTAGCGATCTGCTGTTTATTCTTTCCCGTGTTGCCAACAATGGCAAT
GATGTGAAGTGGGTTCCGGGCGGAAAAAGA

>RXA00134-downstream
TGAAAACCACCCTGCGACCGTGA

>RXA00140-upstream
CTCAACGATATTCAGCTTTCCGCAATGCTGAAAAACGCCATCGATCACGTCCTCGCGATT
CAAGATGCCGTAGCCAATGCAGGCAAGGAAATCGGCTAAC

>RXA00140
ATGTCGGACGAGTCCATCGAAGAGCAGGAAAAAGAACTCGCGGCGCTGAAGGCTCAAATC
GATGAACTGGAAAAGAAAGACAAGCAGAACAAGCTAATCATCGAGATTTTGTCCAAGGCC
GTCGAAAAGAATGTGGCAGAGGCAGAAGCGAAAAGAGCCCGCAAATATCCGCCCAATCCC
CTGTGG

>RXA00140-downstream
TGAATTCTAAGGCGTCGAACTTT

>RXA00141-upstream
GTCGGCTCCTACGTTATGAGCTCCATCGAATCCGCTGTTCAGTGCTTCGAATGGCTTGAG
CAGCAATTCCCAGATCTAGTCACCTGGAAGGACGAACACC

>RXA00141
ATGACCACTGATTCCAATTCTGCGACAATCCCAACCCCAAAGCCGATTCCAGTGACCATC
GACCGAATCTCCCTCATCATGAAAGAATTCGGCATTGACCTATCCATCGCCGATGAACAA
GGCACCGGATCCCAAGTAGCCAGCGCCAACCTCAACGGCCATCACGTCATGTTCGCTGTC
ATCGGTTCAGTCCTGATCGTTCGTGCCGATCGCGCCACCGAAATGCCAGTCTCCGACGGC
AACCCCGCATGGCATCTCGCCTGCAACCAAGTCAACTGTTTCAACTTCGCTGCCAAGGCT
GTCGTAGTTGATCGCACCGACAACATCGTGATCCGCGCCGAGAAGGATGTCCCCATCGCC
GCTGGGCTCAACGATATTCAGCTTTCCGCAATGCTGAAAAACGCCATCGATCACGTCCTC
GCGATTCAAGATGCCGTAGCCAATGCAGGCAAGGAAATCGGC

>RXA00141-downstream
TAACATGTCGGACGAGTCCATCG

>RXA00142-upstream
ATCCTCAATTTCCGCCGTAAGCGCAACGACTAAAACCACCATCTGTAGTGTGGTGGAAAA
GTTACTTTTAAAAGGATTTTGGAAGGACTGAAACTCCCCA

>RXA00142
GTGCCTCAATCACCCACAGCACACGACCCCAACGACATCCAGGAATTTAACCTCGATGCC
GTTGCAGGGATTCTCCAGGACGAAAAACTGGACTACCGCATCGATGAACACGACGGCGAA
AAAGTAATCCGCACCGGATTCATCAACGCCGCCATCAGCTTCATCCTCTTAGACGGCAGC
TTAACCATGGAAGCCATGTGGCGAGGAGCCCCCTCCACCGATGCTGCCGCACAAGTTCTC
GCGGCCACCAACGAATGGAACCTCACCCAGTTCGCACCCACCATTCGATTCTTCGAACTC
AACGAAGGCACCCTCGCCATCAATGCACTGCGACACGTCGTTGTTTCCGCAGGCATGAGC
CACAACCAAGTCGGCTCCTACGTTATGAGCTCCATCGAATCCGCTGTTCAGTGCTTCGAA
TGGCTTGAGCAGCAATTCCCAGATCTAGTCACCTGGAAGGACGAACACCATGACCAC

>RXA00142-downstream
TGATTCCAATTCTGCGACAATCC

>RXA00150-upstream

AGCTGAGCAGGGATCGGCACTAGCTTCTACTACGATAACGAGAACTTTGTTTCAATACAT
TCAAAATGGCGGAATATTTTGATCACGGGGGTGCAACTGT

>RXA00150
ATGGTGTTTTCTATGCATGACAAAGGTGAGACCCAGGAGAATCCTGCGGACATGTCAGGA
CGCCTAAACACACCAATTTCCACGGTCTTTCACTTCTTTAGCTCACTTTTCCATGACGCT
CTGCGCAGTGTTGCCCAGTGGAGTGCGTGGAAGAAAATCGCTGTATCGGTTGTCATCGTC
GCAATTATTTCCGTAACTTTTCTTGTCGATGTCCCCCCGATTTCGGTTTATCGTGACTGG
GCAAACAACGCCGGCGACGCTTTTGTCTTAGTTTTTTGCGCCTTTTATATCCTCATTACT
CAGTTCCCTATCCCCCGCACAGTTCTCACACTGGCCTCCGGCGTGCTGTTCGGGCCGGTT
CTTGGATCAGTCGTGGCGCTGGGTTCCACCACAGTGTCAGCGGTAATCTCGCTCCTCATT
GTTCGGGGTCTGCTTGGCGATTGGATGGCGCCACGTTTAACGCACCCCGCAGTCTCACGC
ATCAATACCCGACTTGAGCAACGTGGATGGCTGGCGATTACCTCTTTAAGAATGATCGCC
GCTATCCCCTTTTCCATCCTCAACTATGTTGCAGCCTTGACTAGCGTTCCTGTTTTTTCT
TTTGCCATCGCTACCTTGATCGGATCTGCACCAGGAACCATCGTCACCGTCGTTTTGGGA
GATGCAGTCACAGGTTCTGGAAACTGGACTGCCGTTGCATTCACGGTATTTTTAGCGATT
TTGGGTGTTTTAGGTATCTTTTTAGATCAAAAGATGCCAGTCAAGCCTGGAAAG

>RXA00150-downstream
TAGACAATATAAGGTAGGGTTGG

>RXA00151-upstream
AAGTAGACAATATAAGGTAGGGTTGGAGAAGATTCTTTACTTCTTCACTCATTCGCCCTG
ACAGCGAATCCACTACAATAAACAAAGGGGGCAGCCACCC

>RXA00151
ATGTGGGCACTGCATGCCAGATACCGCGGCCGAGACACACGACGAGCCGAATTGGTTAAA
AGATTTGCAGAAGCTTTGTCCACCCTCGAAGGTGCTGGCCAGTTTGAAGTCATTGGTGTC
GAAGACATCCGAGCACACATCACCTCACCGTTAACCACATGTGATGTTGTCATGGCGCTA
CTCGCAGCTGGCGATTGGGCAATCGGAATTGGTGTTATCCCCACCGTTGACGGAACAGTC
GATGAATCGGATGAGGCCATCATCGAACAGGTAAAGAAAATTTCCTCTGATGCTCTGCGC
CCCACCGCCAAGGCGGGAACGGTCAAAGTTAGGATCGCCGGAACCAAACGGGACAATACT
CAAGCCTTCAACATCTCCGCTGCATTCACGTTGATTGGGCAAGTTCTGTCAAAGCGCACC
ATCGAAGGACGCGAAGCCACCGCACTCGTCCGTTCTGGACTGAATCAAAATGAGGCAGCC
CAAGAGCTCGGTATTTCCAAGCAGGCAATGTCGCAGCGATTGCAGGCGGCAGGTTGGCAG
GCGGAATCTGCTGGTTGGCAATTGGCCGTAAACCTCATCGAGCAGGCTGGCAAGCGC

>RXA00151-downstream
TAGCAGGCGATTTAAGAGCCTGA

>RXA00153-upstream
CCTCGATTTGAGTAAAGAGGACGTCCTCGCCTGATTTTTCGGGTGTGTTTTTGCGTGGCG
AGCCCTGCCTGGCCCTTCCAAATTATGTAGGGTGGCCTGC

>RXA00153
GTGGGAGCAATAATTTGGTTTATCGGAGCATTGGTTCTTGCTGGCTTGGAATTGGCAGTA
GGTGAGTTCACCTTATTGATGCTCGGCGGTGCAGCTTTGGCAACCGCCGGCGTGGCACTC
ATCGGTGTCCCAGTATGGGCTGAATTTGTCACCTTCGCGGTGGCCTCAGCTGCTCTACTG
ATGTTCATTAGGCCGGCCATTAGAAAGCGTCTGCTGAAACCAAAGGTTCTGGACTCTTCA
CCACGAGCACTTGTTGGCCACCGTGCTGAAGTGCTCGAAGATGTCGGAGCGACCAGCGGG
CAGGTCCGCCTGGATGGTTCAATTTGGTCCGCCCGCAGCATGGATCCCACACACACCTTC
GCGGAAGGTGAAATTGTCAGTGTCATTGATATCCAAGGCACGACCGCGATTGTATGGAAA
GAAGCC

>RXA00153-downstream
TAAATTTTTAACAATCAAATAGT

>RXA00154-upstream

TAGCCAGACGGCAGTATTTTGAAGCGGTGAATAAACGTTTGCTCGAATTTCCATAGTGTT
AGGGAAGTGTAGTGCAGTGCTTTGACTAGGGTGGTGAGCT

>RXA00154
ATGAGTTTTTCAGACCCCTATGCAGGCAATATTTTTGGTGGACACTCCCGCAACAAGCAG
CCGGAGTATCCCGATGTGCCCGCAAAACCAGGCCTTGTGGTGGAAGTTCGTGGAGATGGC
TTCGTCGGCGCTGTGACCGGTTTTGAACGCACCTACGATGGTGATTTTGTGCGTCTCGAG
GACCGCCGCGGACGCGATGCGCTGTACAAGCTGCGCAAGGGTGCGTTCATGATTGATGGG
CAGATCGTTAACCTCACCCGTTTCGTGGAAAAACAAGCACCACGTAAATCTAATTCTGGT
TCCAGGCGTGTAGAAAACGCGCAAGCAAAGGTCGCGGCGCCGTCACGCATCTGGGTAGAA
GGCATCCATGACGCCGCCATCGTGGAGAAAGTGTGGGGACACGACCTTCGCGTTGAGGGC
GTCGTGGTGGAGTACCTGGAAGGTCTAGACAACCTGGAGGAACGTCTCGCGGAATTTCAG
CCTGGGCCTGGACGACGCATCGGAGTGCTCGCTGATCACCTTGTTGAGGGATCTAAAGAA
ACTCGGATGACTAAATCACTACCCGCGGATGTCGCTGTCACCGGCCACCCCTACATCGAT
ATTTGGGCTGCTGTGAAACCAGAGCGTTTGGGGCTTAAGGCGTGGCCTGAGGTGCCATAC
GGGGAGGATTGGAAAACCGGCATCTGCAAACGAGTTGGCTGGTCAGACCCCAAAGAAGGC
TGGCACCGTGTGTATAACGCCGTGAATTCCTTCCGCGATTTGGACTACACCCTAATTGGG
GCAGTGGAACGTTTGGTGGATTTTGTGACCAACCTCGATTTGAGTAAAGAGGACGTCCTC
GCC

>RXA00154-downstream
TGATTTTTCGGGTGTGTTTTTGC

>RXA00155-upstream
GTTGCGGGAGTGTCCACCAAAAATATTGCCTGCATAGGGGTCTGAAAAACTCATAGCTCA
CCACCCTAGTCAAAGCACTGCACTACACTTCCCTAACACT

>RXA00155
ATGGAAATTCGAGCAAACGTTTATTCACCGCTTCAAAATACTGCCGTCTGGCTAGGTGCG
TGGCTCTATGAATTAGTGCCCACCGAAGATGTCATCGATGCGTTCGTCGATCTCGGCGGC
CCGCACACCTTCGGCGACGGCGGGCTGCTCGATATGCTGCGAACTTTAAAAGAATTAACA
AGCACGCTTATCGACGCCCCCTTCCACGGTCCGATTTTAACTCTCGCACTCAGCGGCCCA
GGCCAAGTGCCGGCGTTGCCGGCAGGTTCACGCGCTGCGGTCTTGGCCTCCGCCTCGAAG
GAGGGGGCGTTGGTGCTGGGCGGCGTCGATAAGCAGCATTCTTGGGCGCTTATTCCTACG
CGCGGTAAGGATGCCACTGAGTGGAATTTGGTGGAGGTGGAGGGCTTTTTGCCGGCGATT
GCGACTGTCTCGCCCGGTGAGGCGGATCAGCTGCTCCGTCAGGCGACAGATCAGGCGGCA
AATATCATTGAGTTAAGTGGCTACGCTTCACTTGCGCCGAAATCTTTGAAGAATCCGCGA
CTAACCGTGGGCATGCTGTCAGATTTTTACGACACCCCGGGGCTTCCCTATGCAGTCCCA
GAGAGGTCGGCGAAGCTTTTTGCGCGCGCAGATCGCGTGGCTGCCATCGCAGAGACCGTG
CAGGAAACCATCGGCGATCACAGCCTGGATCCACAGTTGATTTTCCTGTGGAGCCATATT
CGGACCGCGCGCATGGCTGGGGTGAGTTATGCCCTCGCAGAGTTTGCGAGGGACTATCAC
TCC

>RXA00155-downstream
TAGTTGGCAGCTGGCGCCGCTGA

>RXA00159-upstream
CTTAGGGGGTAACCCCACCCCTGTACAAGTTTTCGTGCTACCAAACACGCCGTGCTAGGG
GTGTCGCATGGTGCAATGATCCCCGCTAACCTGGGATTCC

>RXA00159
ATGGAGAATGTTAGTTCCGTCACGTCGGATGGTTCGGTAGCGGATGTGCATGCCGAACGG
TGGCAAGAATTGCTCGCACGTTTGGATGCCGATGCGCCGGATATTGCGGAGGGCACCGCC
GCAAAGTTGCTCGCTACGATCCCGGGCTATGAGCTCGTTGACGCGGGGCCGATCAGGGAG
TCGTCGATACGCAATACGGCCTTGATTATTCGCGTGATTAACGCGGGCACCGAGCCAAAG
GCCGAGGACTTGCCTGAGGCTTTAAGGCTTGCCGACGAACGTATAGCGCAAAATGTGCCG
CTGGGAAGTGTGCTGCACGGTTTTCGGATGTCTCTGGGGGAAATTCTGGAGCATTTGGTG
CAGTTGGGCCCGGAATACAATATTGATCCCGGCAGAATGCTGCGCTGGTCCACACTGATG

TGGGCGGTCAATGATGCCTTTTCTACGCGTGCCACAAGGGTGTACCGCGATCACGAGGTC
GCCACGGCGATCGCCGATTCGGTGCGAAGGTCAGAATGGATCGGCAAAGCGGTCTCGGAA
GGCTCTGAACTGTCAGAGCTTTTATGGGGTGCTGCGATGTATGACGTTCCCGCCGACACT
CCTCTAAGAGCATTGGCAGCCACCTCACCTGATCATGCGAAAGCTGAAACACAGATCCAG
AAGTGGACTCAGCGCGCCGGAGTGCGGGTGCTGGCATCGGTGCAGCCAAGCGTGATCGTG
GGGATCGTGATTGGGGAGCCGAAGCGAAACGTGGACGGCCCTGGTTTTGCTGTGGGTTTG
GGTAGGGCAGAGGTGCTCTCAAAGCTGGCGGACTCATATAAGGATGCATCCCTTGTATTG
AAGGCTGCCGATAATCTGAAACTTAATGAGGTGCAGCGGGCACAAGATTTGTCATGGAAG
TTGGCTATCCATGCAAGCCCACGGGTGACGGAGATTCTTGCGCAGAAATATGTGAAGCCA
CTAAGGGAATCTGGCGAGTTTGCTCATGAGATCGTGGAATCTTTGCGGGCATATGTGGAC
AACCAGATGAATATTCCTGCTGCTGCGCGCAGTATTCCTGTGCATGTGAATACGCTTCGC
TATCGGTTGCGCCGGTTTGAGGAGTTAACGGGCTGCTATTTGGAGGATACATCCACGGTC
ATTGAAGTGTCGTGGGTGCTGGAAGTCTTTGGCCGGGAGCTG

>RXA00159-downstream
TAGAAAATTGCACCTATATATAT

>RXA00161-upstream
TTACTATACATGGTGTAGTCCCAAATTAACTAATGCGGGTGACCAACTGCACCGTAAAAA
AAATTCGCTTATCGTAAATCAGCAGGTAGAATAACACTCT

>RXA00161
ATGAGCGAGCCAGGGCCATCCGGGGTTAAAGAAAAGAAGAAAGTAAAGGCAAGTCACATT
GTCTTTCTTCTCATTTGTTTTATCGCAGCCTGCGCGTTGGCGTGGTGGCAGTGGTCAAGA
TTCCAGTCCGGGTCTGGAACTTTCCAAAACCTTGGCTATGCCTTCCAGTGGCCTCTTATC
GGAGCATTCTTTGTTTATGCCTACCGCAAGTATTTGCAGTATGAGAATGAGTCCATTGAG
TTAGAAAACATGGAAGCCAAAATGATGGCGGAGCAAGGCAAAACACCAGTTGCGCAATCA
GAGCAGGAAGATAGCTTCGTTCAGCTCTCTCACCGTCCGAGCCTGGTGGAAGATGACAGC
GTCAAGGAAATCGACGAATCCTTCCTGCCGTCTCGCCCGACGATGGATGTGGAAGAGTTC
AACAGGTTGAATGATCCGCATGCACGGAGACGTCGAAAAGCA

>RXA00161-downstream
TAAACCTGGAACTTTTCCGGGCC

>RXA00162-upstream
GGAGACGTCGAAAAGCATAAACCTGGAACTTTTCCGGGCCCGCGCCCGACTGCTTTGCTG
AAGCCCTATCCCGCTATTTTATTTTTGAAGGAAGAGTTGC

>RXA00162
GTGTCTACCACCACCCCAATCCACCCTGAGCGCAAGAAACGCGTTCGTCAGGCCCTCACC
ATGTTCTCCATCGCTGCGTGGGTGACTGGTGTGTTTTTGCTGGCGCTGGTGGCGGAGATG
ATCATGAAGTACATAATTGGCATGGATCTTCCTGAGTGGGCACGATTCGTTCCGATTGCA
CATGGATGGGTTTACATTGTTTTCTTGATGACCACCCTGAACCTGGGTCTGAAGGCGCGT
TGGAATCCGACTCGTTGGGTGACCACCGCTATCGCAGGTGTGGTTCCGCTGCTGTCGTTT
TTTGTTGAGCACAACCGCCGCAAGGAAGTTACTCAGACATTCCAGCTGAACTCA

>RXA00162-downstream
TAGTTAAATACACAAAAACCTCC

>RXA00167-upstream
CCGACAATCCAGTGGAACTTCCCTATCGCTGTGATGCATTTTTACTTTCACGTTCCGGTA
CCCTGGCAGGCAGATCTTCCAATCTTTAGGAGCCCTCGCC

>RXA00167
ATGTACCTGTTGAATCCACCAGTCACTGAACCCGAGATCCTCACTGTCAACGAGATTCCG
ACCGTCGTCGCTGTCTTTGACAACCACCCCATGAACGACATGCCCGCAGCATTCGATCAA
ACCTACCAAGTGCTCTTCCCCACCTTGGGTGCCAAGGGCATCGCGCCAATTGGCCCCGGA
TTTGCTCTGTACACCTCCGAACCAACTGACACCGTCAGCTTTGAAGTGGGCATGCCAGTC

AGCCAACCACTTGAGGGAGAG

>RXA00169-upstream
TTTGCTGTGTCTAAGTGTGTGGGGTAATTGTAATATAATTGGTAGAATTTTCTCTAATTA
ATATTTTATTAACTTACGGAGAAAGTTTATGATAAATATG

>RXA00169
ATGTCGTTGGGTAATCCAGCAGCAATGCTCGCTGCGTACAACACCAGCACGCAGGTGGCA
CCGCAGCCACAGCTGGGACCACGTGCTGGAGAAGTTCAACTCAGTAGCGAACAGCAAGCC
ATGATTGATTATGTACTTGCTGGCAAAGATGTCATTGTTGATGCCACCGTAGGCTCGGGC
AAAACTACCGCTATTCAACGACTGTGTTCGATCATGGGTGCAGACCATGACGTGCTGTAT
TTGACGTATTCGAAGTTGTTGAAGGTCGATGCACAGCAGCGCGTTCGTGGCGCCAAGGTG
CAGAACTATCACGGCATTGTCTATCCGCATCTACTCAAGGCCGGCATCAAGTGTGGTATT
AGCGAGTCGATTCGGGAGTTTAACAAGAACTTCAAACACATTTCTCGCACGTTCCCCAGT
TACGACCTGCTGGTTATTGATGAGTACCAGGACATCAATGAGGACTATGCAGAACTGCTG
CGCAACATTAAGTCTGTGAATCCGCTTATGCAGATTGTCATGGTGGGTGATTTGGAACAA
AAAGTCCGGTCTGACACCACGTTAGATCCACAAGAATTTGCAGCACAATTGTGTGAAGAT
CCAGTCTTCGCGCCGTTTACACAGTCGTTTCGAATTGGCGAGGCTATGGCAGCGGGTTTG
GCTGATGCCTGGAATAAACCGATTGTGGGTGCCAATACCGCACAGCAGATTGAATATAGG
TCTTTCGCTGAGGCAGTGGTGTTGATCCAAAGCACCGAGCCGAGCAAACTGTTGTGTTTG
GGTAGCCGCAATGGGCAGATGTCAGATGCGCTTAATGTCGTGGAGAGGAAGTCGCCGGCA
AAGTTCAATAAGAAAACTGTGTTCGCCTCTATTCGCGATGGTGATTCCCAGATTGCACAC
CCTAATGACGCTGCGGTGTTTACCACCTTTGATTCCAGTAAAGGTCTAGAGCGCGATACC
TGCGTGGTCTTTGACTATGACGAAGAATTCTGGGACATGCGTCTTGGTTACCCCAATGTT
GATCCAGTGGTCATGCGCAATGTGTTTTTGGTGGCAGCATCACGCGGTAAAAACAAGGTT
GTTTTTGTACGTAGCGATTCTCTTCAAGCAGCGTATGAGGCTGGTGCGGACTGGGCTGCA
GGGCTCGCTGTGGGTGTGGTGGACAACAATACTGAGGTTGCACCTGAGGTAGATGCCCAT
ACGCCGGCAGAAGAAAGTAAGGGTGATGTGGGTGAGGTTCAGTCACAGATTGAGCGCATG
ATGGGTTTTATCCCTGTTTCAGTGTTTAAAGAACTACCTGAGTTGGCGCCGAGCGAATAT
GCGCGACCGATCTCTGTGACTGAAGCCTTTGATTTTAAGTACGCAGAGAATGTCGAAGCA
TGTTTTGACCTGCTTGATGTCAAGCGTCTCGACAACGGCAAGGGTGCAGCCATTGAGGTC
AATCGCAGTGACGGGCTTATTGATCTCTCACCCACAGTGGGAAACTTTCAGGAAGCAGTG
TTCTTCAAGGACTACAACGTTCATACAGCACTATCGGCGTACCCGAGTCAGTTCGCGAAA
AATCTTAAACGTTTGGTGAAGAAAAACAATAGCGTATGGCGTAACTGCCTTATTGTCACA
GCAGCGTCCACAGAGCAGATGCGGTATGTCGATCAGGTGCGCAGCTCTATCCCGGTTGCT
GCGGAGAAGGCATTGGTCTCACGGCTGAGTACGAGGCTGAATGCTGATTCACGTAATCAG
ATTCCACTGATCCTTGACGGCGAGGCAGTACAGAGCAAAGTAGTGCGCACGCCAATGTCT
TTTGCAGGTGTCGCAGATGCGGTGCACAAGGGTGTGCTTTATGAATTGAAATTCGTCTCT
GAGTTGACACATCCGATGTTTTTGCAGCTCGCAATGTATTTGGTCATGTCTGGGATGAAG
GACGGTATTTTGTGGAACACCCGGACAGATGAGGCGTGGCAGGTGCGTGTTCCTGACCCG
AAGCGTTTTCTTAATGCTGTGGTGTTGTGTGTCTCCAAGCAGGATTACCGGGTCGGTAAC
TTTGATCTGCCGAGCACTGGTGGAGGTGCGCGC

>RXA00169-downstream
TAAATGGTGTTGATGTGTGGGGT

>RXA00170-upstream
TAACTAATTCTTTACCTATCCTCAGTTTGTACATATTTTCCGACAGGTAAAGGTTTGATA
TAAGCGGTTGGTACGAAGACTAGTGGGTGTTTCTGCTGTC

>RXA00170
ATGTTGCTGGCCATCGGGGTTGCATCTCCGGTAGCTCAAGCACAAGTGGAAGATCAATTT
GAGCTTGTAAAAGAAATCAGTGATGAGCAGTTTGCTGATGATGGTGTTGACTATGTTCCC
AATAGGAATGCTCCGACTGTTAAGGAACAACTTGAGGATTTCGAATCAGCACATCCAGAA
GTAGTCATTGAGTATCACGAGCACGTCAACGATAGTAAAGACAATGTTGAGGAACTTCCG
CTACCTAAGCGGGACATCGTTGCAGGGGAAATGCGCTCAGATGTCATCGAGTTACCGGAG
GGGGTGAGCAAGGACGAAGCTGATCAGGTGGAGGTTGCGGAAGCGCGACTTAATGAGGGC
GCACGATTGATGGCTGCAACTGGGTGTGAGGCTATGTGGCCAACAGGTTTCTCAGTTTGT
GGCCGGATTCTTGACGCTTATCGGCAGGTTGGAGGTCAGTTGTCATGGCTTGGGCCACCA

AAGTCAAACGAGTTGACCAATCCCGACGGTGTTGGCAAAAGAAGTGAATTTGTTGGGGGT
GCCATCTATTGGCATCCAGACACAGGCGCTTATGCAGTGACCCTGGACGGTTTGAGGCAG
TGGGGGACCTTGAACTGGGAATCAGGGCCATTGGGGTACCCAACCTCTGGTCCGATGGAT
ACAAACTATCCCCTTACTCAGCGACAGACTTTTCAAGGTGGTGACAACTATTACAACCCA
TTGACTGGCGGTGCTGTGTGGGGCGATATTAAACAGCGCTACGAAGAACTTGGCGGCTCG
AATCATGCCATTGGCATCCCGATCACTAATGAGCTACCTAGCGGTACTGAGTATTTTTAC
AATAATTTCTTCAATGGAACAATTTCGTGGCGAAATGATCGTCAGACACGGTTTATGTAT
TTGGCTACGCAGCGGGTGTGGGATGCGTTGGGTCGGGAGACGGGTCGTTTAGGTTTTCCT
GAAGCAGATGAAACACCTGAGGTTTCTGGTCTATTCCATGTGGTGAATTTTGCGGAGCGC
GGGGTGATTGCGTGGAATGGAATCCTAGGCGCCAGAGAGCTGTATGGTGATGTTTACTCC
CTGTGGCTGCAATACCAAAATACCGATACTCCTTTAGGGTGGCCGATACCATCATTGACA
TCATTAAATGAGTCACTCGAACAAGAATTCACCAGAGGTGTTGTTTTAGGCTCAGGTGAT
GCACTGACATGGATTCCTGACGATGAAGAAAGAAGTTTGGAGGATTTCCTCCCAATTGGA
AGTAGCGGCTCATCCTCATCGAGCCAAGAGATGACCCTGTTTTCCCAGCGTGCACAATAC
GTGGATTGCAAGAATCTTCCCGATTTAGATGAGCAGAGAAAAACTGAAAACAACATTGAA
AAGAATGGTGGCCCGATCAAAAAAGAGTATAGTTCGCGAGGTTTCCCCACCGAGTTCAGA
TTTGTCGTGAGAAAAGGGCATTATGACCGTTACAGGAATGAAGGCTGGGGATATTTAAAA
AACTATTGCAAACACAACTTCGCCAACCACGCTATGGCTGAGGCCGTAGTAGATAAAGCG
GTGATTGATTATGGCTCATCGCCAGGAACCAGCTATTACAAGTTCGAGAAAACGGTGTAC
TTTCTAGATTGCAGAACTTATACATTCAATAAGAACTCAGGATGTAAAGAAATGCACGCT
CCGCAATGGGTGACTATTATTTACAATCCTCATACTTTCACTGGAGCAAATTCGAACAGA
CCCAAGGGGGTAATTTCAGCATGGTGTAATTCAACCCCACCTGGTGGAATCGAACACGAG
CCTGAAATTTCCCAATGTCCTGATCATGTGAATCTTTATAATAAGCTTCGCATA

>RXA00170-downstream
TGACAGAACCCCATCAACTGTGC

>RXA00171-upstream
CGATTAAGGTAGGGGCCTTAAAAAGGGGAATAAAGAATATTGGGCCCAGACGAAAACTGC
TGGCGAGATCATCAAAGATCAGCAGAAGCAGATTCATAAC

>RXA00171
TTGGCAGCTGAGGTAAAGCGTCTTCGTGAGCGTGACGATGCACGAGATCAGCAGCTAGGA
GTGCTTAATGAAGCCATGTTTTCACTACTAGGAGATGGACTTGACCGTTTTCGTGAATCT
GGCGATGAGGCATCCTTCAATGCTGCATTGAACTATCAGGCAGTGGTGGCACCAGAAATG
TTTAAGACCGTGTATGGTGTCGATCCGTCTACCGGAGAGCCTATTCCCACT

>RXA00171-downstream
TAAAGTACAACACAGTCTTTTCA

>RXA00173-upstream
TGCCCTGATCCACACACAACTGTGAAGAAAGAAGCCGCAATGTCCACCACATCCACCTAT
GAGAGCCGTAAGGCAGCTATTCGCGACGCTATTCTCGCCT

>RXA00173
ATGTCAACAACAATCAAGGCTGCTGCACCCTACAGCCTTCATGCCCATGATCTCGAACAG
CTTGCTGTAGATCTCACTTTAGTTACCACCTTTGATAGCAATGCTGCAGTTGATGTCACG
CCAACACATACAGAAGCACCTGGTTTTACCCTGCATGAGGGCACCGATACTGCGCCTATG
GCTCCAACCCTGGTCGTACCTATTTCCAGCGACATCTCCACAGCCGTTTCGGAAATATCT
ACATTAGTGCAGCAGGCTCGCACCGACGCAGCAAGCGCCATTCATGAAGCAGAAGCTGAA
TTTTACAACCAACTTGCTGCGGTCCTTGCTCAG

>RXA00173-downstream
TGATTTAATGTGGCCGACACACC

>RXA00174-upstream
GCGGTGTGGCTGTTACCAACAATCCCGATGGCACTGAACAAGGTGATGCACGCCGCTGGG
TAAGCCACTGGGAATCATAAAAAAGAAAGTAGCACTAGCT

>RXA00174
ATGCCTAATCACCCACCTATTTCCACCTTCGATGACCGTCGCTCTGCTATGCGCGAAGGC
ATTACTGATTACCTTGCCAATACAAATGCAAATGGGTTAGGCGGTTACAGCATCAGCGAC
ACCCACCTCGACAATCTTGCTGAGAAATTCACCCGCACACATGGTGAAGCACAGTACGAT
GCCGGCTTTGATCCCAATGATCTTGAACCAGAGACTTTTGTTCGTGACATTGAGATGAGC
TGGGATGAGCGTGCTATTGATCGTGCCCTGATCCACACACAACTG

>RXA00174-downstream
TGAAGAAAGAAGCCGCAATGTCC

>RXA00175-upstream
AGCTCGACAGCCGTAAAGAAGTTGTAGGTCTTTTTCGCTTGGGATACTGATGCTCTCCCA
AGCGAACATGGGCGGGAGCCCATGTCGGGGTGTTGTGCGA

>RXA00175
ATGGCTGTGTGTCAACTACCTCAGCCTGAGAAAACAACACTTATAAAGAAAGACCTTTTA
CTCATGACTTCTACAACTAACTCCACCGCCATGTTCAACGACCACCTTATCCCTATGGCA
GAGCTTGATGAACAAGCTCTGCGCGACAGCGTTGGTTCTTGGGCACAGTACAAGCACCCG
CTTGACCAGCGCAAAGAACCAGAGCTCGTCCTTATTCGTCGCGTCAACAGCTCAGAGCGT
GTGTGGGTCTTAAGTTTCACTGACCTGCGTGCTGATGCAGGTCTTGTGCCTCGTAGCACA
CCGAATGCTGACCCCTCCAATATCCGCAATACCATTTTCTCTGTCGCTGTCCGCGATCTT
GTCCTTGATCGCTCACTTCCCCGGCTGCTTAACCTCAACGGGCAACCACCAGCAGGTGAA
TGGGAAGAAGGCTTTGTCTACGTCGATTATGACCAGAGCGACACCGTAGATGGCTACCTC
ATTGAGCACAGCGAACCTGTCTCCATTGAAAGTCAAACCACCGGTGAAATGCACTATTTC
GATAAGGTGCCAGGCGGTGTGGCTGTTACCAACAATCCCGATGGCACTGAACAAGGTGAT
GCACGCCGCTGGGTAAGCCACTGGGAATCA

>RXA00175-downstream
TAAAAAAGAAAGTAGCACTAGCT

>RXA00176
CAGCTGATGTACTCGACATCATCATTTACCACCGTGAAGCAGACCATCGGCATTGATCTT
GCTGAACTGATTCAGGGCCGTGCACTCGGCCAGGCTCAAGGTGAGGCACAAGGCAAAGCT
AGTGCAGCAGCCCTTGAGCAGGCACCTCATAATGAGCAG

>RXA00176-downstream
TAAATAACACACACCACATGTGC

>RXA00179-upstream
GCGGGTTCGCCAAACCTTGGTGATCTCGTTAGTGTATGTATCAAGCATTTTCTTTTTGCC
CAACCATAATTGAAAGGTCCACCAGCCCGTGACCACCATC

>RXA00179
ATGATCGCTATTCACGCTATTGCAGCAATCCTGTTCCTAGGACCAGCAACAGTAGCTAAC
TCTCAGTTCCACGTCCGCGCGTACGATGCACACAACGGCAACACCCAAGCCGCTGGCTCC
GCAAAAACCCTTTTCAAGATTTCCCAGTCCTACGGCATGCTGTCCCTGCTCGTGCCTTTG
CTGGGTATCGCCATCATGCTTCTCGATTGGTCTTTCTACAAGTCTGAAGGCCAGTTCCAC
GCAGCAATCGCTCTCAGTGTTATCACCTGGGCGCTGCTTCTCTTCGTTATCTTCCCACGC
CAGAAGAAGATGATGGGTGCTCTTGACCTTCTGGAGGACGATGAGCAGGCTGCAAAGACT
TACGAGATCGAAAACTGGGACAAGGCGAAGAGCCAGCTGTCCATGTTCGGCGGCATCTGG
GCTCTGCTGTGGGTCATCATCGCTGTGCTGATGTTCATC

>RXA00179-downstream
TAACACATCTCAAATTGCCAAAA

>RXA00180-upstream

AAACGAGGATGTTGATTTCGCTGACGCAGCTCAGAAGCTTTCGAAAGAAAGTTAAGCCTT
AGAGGGAACCAAACGCCAAGGCGATGAGTCTAACCCGAGT

>RXA00180
ATGAAGAACTTTATTCGGGTACTCATCGCCTTTAGTGTTTTCCTCTGTATATATACCGTT
GCTCCCCACATTGGCCGAGGTCCTGGAGACCTCGCACCAGTTACAGCAATCCCCCAACGA
GCCACAGTCCTAGGCTATGACAGAGCCTCCATGTTTGGCGGATGGTTGGGTGGCGTGCGG
GAAGGCATCGTGGATGAAGCCGGCGACACTGATCCATACTCCGGGAATCGATTAGACCTC
TCTAGTGCCGAGGTGGATCATATTCTCCCGCTCAGCGCCGCCTGGGATCTAGGCGCACAC
CGGTGGAGCGCTGGCGAGAGAATCAGCTTTGCCAACGACCCCCTCAACCTCGTGCTCGTC
TCAAAAGCTGAGAACCAAGAAAAATCCGATCAACTTCCCAGCGAGTGGCTCCCCTCTGAT
CGAAGTGCACGATGTTGGTACGTGGAACGCCTTTTCGCCGTGGCCAACGCATACGAACTT
CCGTTACCAGAAAACGACATTCGGGTTGGACGAAAACAGTGCGGGTTCGCCAAACCTTGG

>RXA00180-downstream
TGATCTCGTTAGTGTATGTATCA

>RXA00183-upstream
CTGGCCAGCGCCATCGTGGGCGAGGGCGAAGGCTGGATCACCGAACTCAACCCAGAAGAA
TTGGCTATGCTGATGAGTTACCGCGAAAAGGAGGGTGCAG

>RXA00183
ATGACTGAATCACGCCGCGTGAAAATGGATAACGTTATTTACGCCAATTTTGGCAGCAAA
CAGCGCGTATCTACTCCTGATGACCGCACCCAGGTGATTAATAAATCACGACACAAACAA
TTCAGCCCAGCGGGTACTCGTACCGTGATGTTGACGGAGAAAAACGCCGACAGCGGACGA
CGGTCCCGCGGTGAGCAGTACTACCGAAACGGCAATGTCACCGGCATGACTGTGCTGGAA
GGCCGCGTGGAATGCACTGTCGCGGGCTCCCAAAACGAGCCGTTTGTTACCACAGTGACC
TTCCCATACCGAAGCTCGGAAAAACTCCGCGAAGCCTACGCAGCTATTGCGGATACTCCC
AATGGCCTGCGGCTTGTGCGTGATGGCCATCTGACCTCCTCCATGCTGGATCACTTGGTG
GGAAGTCCTGATGAGTCGATTTATTTTGACTGCACCTGCCCCGACCGATCGCTTGTGTGT
AAACATGCCGTTGCCAGCGCGTATCACGTTGCCGAGAAGATGACCGCGAACCCCGGTCTG
ATCTTGGATATTCGTGGTCAAGGGATGGCTGGATTAGAAGCACTGATTCGGACCTATCAC
ACCAAGGTTGAAACTGAACCTGAAGACAATGACAGTTTTTGGAACGGCAGGGAACTTCCT
GCTTTGCCTGATCCAAAGATTGCCCCTGCTATCGACGATTCCGATATCAACTACCTCCAC
AAGGCTTTAAGGATGGTCTCATACACCTCCCTGGAGCAGCTTCGTGCGGTCAGTGATATT
GAAGATATGTACGAGATTTTGGTAGCCAACCACCCTGATAACCAGCAAGTGTATGAGGAA
GAAGACACTGAT

>RXA00183-downstream
TAACCAGGGCTTATGGTTGTGGT

>RXA00185-upstream
ATTGCGAGAGCTCGCTGACTCTGTGGTCAATGGTGCAGCGCCGGAAGAAGACCGCGATGC
GCTCAACCTATTGTTCCGACTAAGCCGGGAGGTCTAAGAC

>RXA00185
ATGCGTATTCATGAAATCATCATTGACAATTTCCGAGCCATCGAACATCTAGAACTTCGT
GACATTCCTGACCAGGGCGTTATCGTGATCCACGGTGACAATGAGCAAGGCAAATCTTCA
ATCCTTGAAGCCATAAAAACAGTTCTGAATAGTAAACACAGAACCACCAGCAAGACGATC
AAGGCCATTCAGCCTGTTGACCGTGATGTTCCCATCAGCATCACCCTCGAGGCAACCGTA
GGCACGGTTCGATTCCGCATACACAAACGCTTCCTAAAATCCACAGCCGCAGAACTGCAA
GTCATCGAGCCACGTCCATCCAACCACCGTGGACTAGAAGCCGAAGCTGCACTGGCAGAA
ATACTGGAAAGCCATTTGGACACCTCTTTGCTTGACGCATTGTTTATGAAACAGGGTGAA
GTAGAAGCAGGTATCAGCGCTGTAGGAATTCCTACCCTGACCAGCGCTTTGAACGCTCAA
AATGGCAATACCGAAGATGCCACCGAAGACACCGCACTCATGGAGGCTGTAGAAAAGGAA
TACCTAAAGTTCTACACCAACTCCGGAAAGGCGAATACGAGGTTCCTACAGTTTTCCAAA
CAGGTGGAAACCCTTCGTACTGATTTGGATGAGGCTAACGCTGAAGTAGCAAAGCTCTCC
TCCCATGTTGACCGAGTTAAACGATTGGAAATTGATCGGGATCAGGCCACAGCACAGTTA
CCCAAGGCAGAGGAAGAACTCGCAGGGAGGAAAGCAGAACTGGAGGAAGCCCAAAAGGTT

AAGGCTCAAGCCACGGAAATCCTTGCGCAGTTTTCCCGGGCGGAAGAACAGTTAGAGCAG
GCAACAGGAGCTCAGAAACGACGTAAAGAACTCCGCAATAAGCTGGAATTAGCACAGACA
GAAGTCGAAAAGGCTGAAGCAGGGCAAGAGAACCTGGCGCAAGAAGCTTCCCGTGAAGCA
GAAGAATTCCTAGCCTTAAGTGAAAAGTTCGAGGCAGCGCGCGCAGCTGAAACTCTGGCC
GTTGAAAAGGTGAAAGCAGCACGTCAATCGGTTGCTGGAATCAAAAACCGTGACCGTAAA
GAACACCTCACGGTTATGCTTGGTGAACTTGATCGAATTGGGCAGCGCCTCTACGAATTG
CGCAGCGTCCAGCACTCATCGGTGCGTGTGAGCCAGCGTGATATTGATGCTCTGCAAAAG
GCGATCACCGAGGTCGATATCCAAAGGACGCTCGTTGAAGCGCAGCAGGGAAGTATTACC
CTCAGTGCTTCCACACCCACCGACATTCAACTAGGTGATGACACCGTTTCAGCTACCGAC
GCTGGAACCACAGTTGCCCTCGACCGAGAACTCACCGTCGTGGTCGGCGATGTCACCTTG
GTGATTAACCCAGGAAAAACAGCAGCGGAAAGTCGCACCGATTTTGAATCCGCCGAGGCA
GCATTGGCGGAGCTGCTTGATCAACTCGACGTCTCAGACTTGGACCAGCTCAGGGAACGT
TTCACTGCCCAAGAGCAACGAGACGCGGATATTGCAGAACTGGTTCGCGAACAACAGCGC
ATGAGCGGTGGGACAGAAACAACAGTTTTACGTGCCGAGCTAGAAGGCCTGCACGTCCCA
GAGGATCTAGACCCATCAATTTCTGTGGATGATGCGCAAACTCAGTTGAATGAGGCAGAA
GAGTCCAGAGAGCTCGCTGCGGAGGCGCATAAACACGCAAATGCAGCACTTGATGGATTG
CGTTCGCGTCCCGTAGATAAAGCTCTGACAGTTTTCAACGCTCAGCTCGCAGCACTGCAG
AGAAACCTCTCTTCCGCACAAGTTGAATTAGACCGTGCAGTGGCAGAAACCTCGGATGAC
GAAGTTGATGCTGCTGTACAGCGGTGCGCTGAAGCTCTAGCTGGGGTGCGGGTACAGAAG
CAGGAGATTGAACAGGTCTTGGCAAAAACCAACCCAGACATGGCTCAACGCTTATGTGAT
GCTGCTGAAGCAAATGTGCGATCGTATAAAACGGCAGTGTCTGATGCCACCACAGAGTTG
GTGCGCCTGGAAGGCCTCATCGGTGTAGCTGCAGGTGCGAAAGAACGACTAGATAAAGTT
AAGTCTGCGCTGACAGCAGCTGAAAACCGGTTTGAATCAGAACAACGTCGCGCCCACGCT
GCACGTCGCCTCTATGCCCTCATGGTGTTCTACCGTGATGAATCCCGAAAGCGCTACGCA
GCACCCTTCGCGGACAAACTATCCAGGCTGGCAGCATCCGTATTTGGAGAATCAGCAGAC
TTTGATCTTGATGATGAGCTGAAGATCTCCAGTCGTTCCATAGGACCACGAACAGTGGAC
CTTGCCAATCTTTCTGGCGGCGCAAAGGAACAGCTGGCAATCCTCACCCGCTTTGCTATC
GCAGAATTGGTAGCAGAATCCTCCGCGCAAGGTGCTGTGCCTGTGTTTATTGATGATGCA
TTGGGGAGCACAGACCCAGAGCGACTGACCCGCATATCTACTCTGTTTAGTGATGCAGGC
AAGGACTCTCAGGTGTTTGTTCTCACCTGTGTTCCAGACCGGTACAACTATGTAGAGGTC
ACCCAAAAGCACAGCATCGAGTCATTGAAAACTGCCAACGCTCTGCTG

>RXA00185-downstream
TAGCTGAGCAAAAAGCCAAGCAA

>RXA00194-upstream
AAATATGAGAACATAGTGAGAGTTAAACCAAGTTCTGTAGGTGCTTGTTGCAGCGGGCGC
GAAGGCGTACCACTGCAACTTGCGAATAAAGGAGTAAAAC

>RXA00194
GTGGCTGGTTCCTCCCACACGATTGAGCCTGAGATCTACCGCGGTGTATCCACCCTTGAT
GAGCCTTCGGCTGCATGGGGATGGCACGGTCTCAAGCGCAACACCATCCAACTCGCTGGC
TGGATTTCCGTTCTGTTCATGCTTGGATACAACTTCGGTAACCACAAGGGCCACGTTGAA
ACCATCTGGCTTCTCGTCATCACCGCCCTTCTGGTCATCGGCCTGCTGATCCACCTGTTC
GAGCCAAAAGCTCTTCCAGGTTCGCACCATCACTTCTCGCAACAA

>RXA00197-upstream
GTCGATGATATTTTGGCAACCGAATCTGAGGCACGCGCGCGTGCGAATGCTTTGATCAAC
CGGTTGGCAACCAACTTGTAAGCTAAGGAGCTTCCGCCTC

>RXA00197
GTGGCAGCCTATCTTCTTGGTGTCGTATTATTTTTCCTCGGCATCGCAGTAACCATCGCG
CTTCACGAGTGGGGGCACTTCATCACAGCGCGCATTTTCGGAATGAAAGTGCGGCGTTTC
TTCATCGGTTTCGGCCCGACGGTGTTTGCCAAAAGACGCGGCGAAACCGTGTACGGCCTT
AAAGCGATTCCGGTCGGCGGTTTTTGTGACATCGCGGGGATGACTGCCCAAGATGAACTT
GATCCGGAAGACCTGCCGCGCGCCATGTATCTAAAGCCCTGGTGGCAGCGCATAATTGTG
CTTTCCGGCGGCGTGATCATGAATCTGATCGTCGGCTTTTTGGTGCTTTACGGCGTGGCG
GTGAGCTCCGGAATCCCGAATCCGGATGTGGATACCACCGCGACAGTCGACACCGTTCAG
TGCGTGCCGGAAACCCAAATTTCCGCAACTGAACTGTCCTCCTGCGTAGGTTCAGGCCCA

GCGGGCGACGCCGGCATTGAGCACGGCGATAAGATTTTGGCCGTCAACGGCCAAGAGATG
GCAAGCTTCACCGCCATCCGCGATGCGATCCTCGAGCTCCCAGGCGAAACGGCAACGCTG
ACGATTGAACGGGAGGGAACGCTTTTCGACGTCGACCTCCAGGTTGCCTCTGTCACCCGT
CTCGCCTCTGACGGTTCAGAAATTACCGTCGGCGCGGTGGGCATGTCGAGCCTTCCACCG
ACCGATGTGTACAAAAAATACGGCCCAATCGAGGGTGTGGGAGCAACTGCACGTTTCACC
GGCGACATGATCAGCGCCACGTGGGATGGCCTCAAAGCCTTCCCGGCGAAAATCCCAGGG
GTCGTCGCATCCATCTTCGGTGCAGAACGAGATGTAGAAAGCCCCATGAGTGTGGTGGGC
GCGTCACGCATCGGCGGCGAATTTGTCGAACGTTCCATGTGGGACATGTTCATGATGATG
CTGGCCAGCCTGAACTTCTTCCTCGCGCTGTTTAACCTCGTGCCGCTGCCA

>RXA00199-upstream
ACCCAGCACCATTTTTTGTGGTTTGCTCTAAGTTATGGGCGAATCAGTAAGTACTGACAG
GTACACTCCGCAGCAGCGCACGCGTTATCGCCAGCTGCTC

>RXA00199
ATGGAAGATCTTGAGATTTTTGATCGGCATTTGCAGCATTCCGATTTTGAGGATCAGGGT
TCCATCGGCCTCGAGTTGGAACTCAACCTCGTGGATAAGCATATGCAACCTGCTTTGGCA
GGCCACGCGGTGCTTTCCCATTTAGACGATGAGTACCAGTCGGAGATCGGTAACTTTAAT
GTTGAAATGAACCACCCGCCACTATCCGTTAAAGGCGATGCTTTACGACGCCTCGAGCAA
GGCATCACCTCGCGTCTAGGTCGCGTGCGCGCGGCCGCCACATCGGAGAACGTGAACGTG
GCGATGATCGGCACGCTGCCCACCATCACCCCAGAATTCCTCGAAGATCCGGCATGGATG
ACCCAAGAAAACCGCTACCGTGCGCTGAGCAATGCGGTGATGGAATCGCGTGGCGAGTTA
GTGCACATCAACATCGCCGACCGTGAACAAATCATCCACGATTTCACTGATCTCGCCCCC
GAATCAACTTGCACGTCTATTCAGTTGCACCTGCAATTAGCACCCAATAAGTTTGCTGCA
GCGTGGAATGCGTCGCAAGCAATAGCTGGTGTTCAAGCAGCTCTTTCCGCCAACTCCCCA
CTTTTCCTAGGCCGTCGGGTGTGGCATGAAAGCCGCATTCCAGTGTTTCAACAAGCTATC
GATACGCGTACTCCTGAACTTGTGAATCAAGGAGTCCGCCCCAGAGTATGGTTCGGCGAA
CGATGGATCACCAGTGTTTTTGATCTTTTCGAAGAAAACGTACGCTACTTCTCCCCTCTC
ATCGCAGAATCCCGCGCCCTGTCTGGCACACCAATGATGAAGGGAAAATCCCCCGCACTC
CACTACCTCAATCTCCACAACGGAACGGTGTGGCGCTGGAACCGACCCATTTACGCACCG
GGGGAAGAGCGCTCTCATCTGCGTTTGGAAAACCGTCTCCTACCTGCAGGTCCCACCCCC
ATCGACATCACCGCCGATGCCGCTTTCTACTACGGTTTGGTTAAATATCTGGCCGAGGAA
AACCGCCCTGTCTGGTCACGTCTCCTATTCCCTGATGCGGAAAAGAACTTCCAATCCGGT
GCACGTTCAGGGCTGTTCGCCCGCATGACCTGGCCAACCCTCGGACAAGTCAACGTTGCG
AATCTGGTCCAAGAGCACCTCATCCCTCAAGCCAGAATCGGACTGGAACGACTCGAAGTA
AACAAAGACCTTATCGACCAATACCTGGGCATCATCACCGAACGCGCGAAGTCCCGCCAA
AACGGTGCCACCTGGCAGTTGCGTAGCCTCAACAAGCTGGAAGCACACGGAAGCATGCCG
GGTTCCGATGCTCGAAAAGCAGGTCTTGCAGCAATGTTGCAACAGTATTTACAGAATCAA
GAAAGCGGCCAACCTGTCCACACATGGGCTATTGGTTCG

>RXA00199-downstream
TAAAACGGCAAGGAAAGATAATA

>RXA00200
CACTACGCCGGAGTCACCGAGATTCCTGAATACCGAATCTCCCCAGACCACGGCGGAAAA
TCCACCCTCTCCCCATTCCAAGACTGGGCAGGCGGCGGATCCATGGGCACGGCCGAAGCA
GTAAACAACGCCTACGAAATCCCGTCCTACCTCCGCAACGACTGGGGCCGCGACTGGGGT
TCCATCGAACGCTACTCGCTGCGCACCAACTCCAACGGCGATGCACCTAAGGTTGCAGAC
ATCAACCTTGAAACCATCCAACGTTCCGGACTCTGGAATCCAGGGCATATGAAGGTAGAT
GAA

>RXA00200-downstream
TAAGACCTTCAGTACTGGAAGTT

>RXA00207-upstream
CTGCACAATTTTTGGTCGGACACATTTTTGCCCCCATTGGGTTGTCGGATCAGATCAAGA
AAACCCCCGCGGAAAAATTTTGTCTCTAGACTGGCTCACC

>RXA00207
ATGGAAATGAAATTGAAAAAGGCATCCCAGGTCAGCACTGCCACCGTCGTCGCAGCAGGT
TTGATCGGCGGTTGGTTGACTGCCCGTGAATCCGGCATTCGCCCACTGGGCACCATTCCA
TTGGCAGCATCCGGAGCGCTTGCTGCACGAAGCTGGAATGAAAAGAAGGGTCCTGCAGTA
GCTACTGGCCTGCTGGCAACCTACGTTGGTGCATTTGGCCTGTCCCACCCACTTGCCAAG
AAGATTGGCGCGTGGCCTGCAGTTCTTACTGTGACCGCTGGCGCTGCTGCGATTGCTTAC
GCAGTATCTGACTCCCAG

>RXA00207-downstream
TAATAATTACGGTAAAAAAACTT

>RXA00211-upstream
TGAGCCAAAATCAATAAGGTGTTTTTCAGCCTGAGGTAAAAATACGGTGGTACTGTCGAA
ACCAATCATCCCCTAGTTTTGAAAAGAAGGAAGCGAGCCA

>RXA00211
ATGTCATTCCTGATCCGCGTCCTGTTGTCCGACACCCCAGGCAGCCTCGCGTTACTCGCT
GAAGCCCTTGGGATTGTAGAGGCCAATATTCAATCCGTGGACGTGGTGGAACGCTTCCCC
AATGGCACGGTCATGGACGATCTGGTGATCTCCATCCCTCGCGATGTCATGGCAGACACC
ATCATCACCGCAGCTGAAGAAGTCGACGGCGTGGAGATTGATTCCATCCGCCCATTCTCC
GGGACTGTTGACCGCCGCGGACAGATCCAAATGCTGGCTGCTGTTGCTCACCAACGCCGC
GATATCACCGCAGCGATGGAAGAAATGGTCGATGTCATCCCCCGCACCATGACCTCTGGT
TGGGCTTTGGTCATTGATCTAAAAGGACCCATCACTCGCATCGCTGGTTCCCTAGCAGCG
CCCGAAGATGACGGCACCGTTCCGGAGAACATCGTTCTCAAAGAAGCTCGCATGCTCAAC
CCGGAAAACGATCCGTGGATTCCAGAGTCCTGGACACTGCTTGATTCTTCCCTTGCCATC
GCTCCGATCGGCAAGCACGGCCTGGCTCTGATTATCGGTCGCCCTGGTGGCCCTGATTTC
TTGGCCAGCGAAGTGGAGCACTTAGGCCAAGTCGGTGACATTATCGGAGCAATGCTTCAA
AAA

>RXA00211-downstream
TAATCTGAGCTGTTTAAAAAATG

>RXA00218-upstream
TCTAAACTCACGCTAGACTTCTAAAAGATCTAAAGTTCAGTTCCAACACAAGCCAGCACT
GCATTCCGCAAACCCGACTAGACCATCCAAGGTGTCTTCT

>RXA00218
ATGTCAGCTCGCAATCCGTTCCGCCCCACTTTCGGAGTTTCCCCCACCGTACTTGCAGGC
CGAGACTCACTTCTACAGTCTTTCAAACTTGGTCTCGCGGAAGGCCCCGGAAGCCCCTTT
AGAGCATTGCTGATTTCGGGATCTCGTGGCATGGGTAAAACTGTGTTGCTCAATGAATTT
GAAGATGCAGCTGCGTCTCAAGGGTGGATCACGCTGCGCGCCTATCCGGATAATTCCATG
GTGGATGGCTTAGTTAATTCCGCCATCCCGGAGGCGCTACAGAATCTTGACGGACCGCAG
TCCAAAAGAATGCTCAGTGGTGTGGCCATTCCTGGTATCGCTACGGTGACGGCCATTGCT
GATCCAACCAAGAAGGATCCCACTCCCACGCTGATTTCCAGGCTCCGCGAGTTGGCTACT
CGTTTGCAAAAGCACGGCTCCGGAATTTTGATCACCCTTGATGAACTCCAAAGCGCCAAT
GTGGATCTTTTGCATGTGTTGGCCACTGCGGTCCAGGATCTCCTACGGGATGATTTCGAT
ATCGCATTGGTAGCAGCGGGTCTGCCAGAGGGAATCGATCGTCTTCTCCAGCATGAGGGC
ACAACCTTTATCCGCCGAGCCGAAAGAATCCTGCTCAATCCTGTCAACCATGAAGATTCG
GTGGAGATGTTCCTGGATACCGCTGCGGAAGGCCAACGCCACATGACTTCCGAGGCCGCC
GAACTCGCGGCGCAGATCAGCAAGGGCTACCCCTACTCCATGCAGCTGACTGGTTCTCTG
GCATGGGCGCGAAGTACTCTTGACAACTCCGATACCATCCAGGCCGAACAAGTAGATGCT
GTCCGCGACGAGGTTGTGCGCCGCATGGGCATGCAAGTCCACGAGCCAAGCCTGCACCAG
GTCCCTGATGGTGAGCTGACCATTTTGTACGCGATTGCCCAACTGTCAAAAAACGGCGAG
ATGGTGTCTACTGGAGATATCGCACACCTCATGGGCGTCAAGCCCAACGCCTTGTCGATG
CAGAGAAAGCAACTTCTCAGCAGAGGTCTCGTAGAGGTTCCCAAGTACGGTTTCCTCAAT
TTCACTTTGCCGTACATGCGCGAGCACCTCCTCAACAGCCCGCACCACCGACCAATCACA

>RXA00218-downstream
TAAGACACAAGCACTAAAACAGC

>RXA00220-upstream
AGATCGTGCCGAGTTTCCGGTTTGGATGGGGTTTGGGATGTTAATGGGAGAGGATCGGCG
TGATCGTGCCGGTTTTCCTTGCGTTGGTAGTCTTGGGGCT

>RXA00220
ATGAGCGCATTCCACATCCGAGCGGAACAATCGCACGATATCAGCGCGATTCATGATGTT
ACTGAAGCGGCCTTTACAGGAATTGAGCATTCAGATGGAACAGAGCAAGATCTCGTCGAT
AAGCTTCGTGCTGCAAAGGCGCTGAGCCTTTCGCTCGTCGCTGAGGCGGATGGCGAGGTC
ATTGGGCATATTGCTGCCTCTGAGGTGCTGATTGGCGGTGGGGTGCAGGGCTGGTTTGGC
ATTGGGCCTGTCAGTGTTCGGCCCGATAAGCAGCAGCAAGGCGTGGGTATTGCGCTGATG
GGCAGCGCGCTTGATCAGTTGCGTGCGGAGGGTGCTGGCGGCATCGTGTTGCTGGGGGAT
CCGGGCTATTATCGACGCTTCGGTTTTGAGGTCGTGCCCGGGCTGGTCTATCCGGACGCG
CCAGCGGAATTTTTTATGGCTGTGTGTTTGAATGCTCCGGCGTTTCCGCAGGGTGTTGTG
GAGTATCACTCGGCATTTGGAGGG

>RXA00220-downstream
TAGAGACCCCATCGTGGCGGGCC

>RXA00222-upstream
AGGGAAAAACTACCGTCCGCCTGGACAAAGTCATCGATGTACTCCGCGTCCTTGGACTCG
AGCTTTCTGTTGGAATTCACGATCCCCTCAAGGTTAATCA

>RXA00222
ATGACCCCCACTGCCGATATCTGGTTTAAAGATACTTTGGCTGCTCATTTCACACGCGAC
GGCGACCAGACCACATTCTCCTACACAGCTGATTACGCAGGTCCACCGATTGCCACGTCC
CTGCCCATCAATTCTGAACCCGTGATTACGCGCTCTGGAGCGATCCCACCATTTTTCGCG
GGATTACTCCCCGAAGGTCGTCGCTTAAGTTCACTCCGGAGAAACATTAAAGCCTCTGCC
GATGATGAACTTTCACTCCTTCTAGCAGTGGGAGCTGATCCTGTTGGTGCAGTCGCTATC
TTCCCCCATGGTGAAAATACACAACCTGCACCACCCACAGTTGATTTTGACGATGAACTT
GATTTCTCGGCTGCACTAACCGAGTCCGGGATTGCGGATCCCGTTGCACTGGCCGGTGTC
CAAGACAAAGCCTCTGCACGCACCATCGCGGTCCCCGTTGCAAGCGATGCCATCTTGAAA
CTCTCCCCGCCTGAATACCCTTACTTGGTGGAAAACGAAGCAGCTTGTTACCAGTTGCTG
ACCAAAAATAAGCTTCGCATTGAACTGTCCAAAGTAGAAGTTCTCCATGACAAACACGGC
AGGTCCGGACTCTTAGTTCACCGCTTTGACCGCACACCCAAAGGCAAAATCCCCGTCGAG
GATGCAGGACAGGTCTTGGGAATCTGGCCTGCAGATAAATACTTAGTGAGCTACGAGGAC
ATCGCACAAGCCCTCACTAAAGTGTGCGCCTCCCCCATCTTGGCGATGCGCAATCTCGCC
TTCCAAATCGCAGTCGCGTGGCTCAGCGGCAATGGTGATCTTCATGCCAAGAACATCTCC
ATTATCAACAAAGGCCGCGGATTTGAGATCAGCCCCATCTATGACATCCCTGCCACCGCA
GTATATGGCGACACCACGATGGCATTAGAAATCCAGGGATCCAAAAAGGATCTCAGCCAA
AAGAAATTCCTAAAATTCTGTACATCCATCGGACTACCAGAAAAAACAGCCATGTCGGTT
GCGAACGCTGCACTGTTGGCAACAGAAAATGCCGCAGAGACAATTCTTGCTTCGGGAAAT
TTTGATACACGGATGAATCGAGATCTGGCCAGGGTTCTCAAACATCGACGAAGCGCATGG
GGAGCT

>RXA00222-downstream
TAATTCGCCTGTTTAAGAGGTCG

>RXA00230-upstream
AGGTCTTACCGCCCCTCAAATCCTGCAGATTTTCCGTCGTCAATCAGGGACGAAAGTACA
TCCTATCTATCTAGCTCCACTAGCACAGATAGGAACTCCG

>RXA00230
TTGATTCATGAGCAAGACGTTCAGAAGCTGTTAAACTACATCACTTCACACTTTGGTGTT
GACCCTGAAAGATGGTTTCATCCTGAAGGCTACCAAAGCATTGCCCTAGCGATTCTTGAC
TCCATTTACTCGACTGGTAATCGCTATACAGGTGTACTCAACCTTGTCAATCGATACTGC
GGGCTGCGCGCAAATGAAGGATCACACCCTGAAGCCGATACTGCCACTGATCTCATCGAG
ACATTCTACCGGTGGGGAGGGGTCGACGAATTTGTTCTCAAAACGAATAATCGGTGGAGA

ACTTCCTCCAAGATTCACGCACCCTATAAGGCATACGCAGCTTTGGAAGCAGCAAAGGTA
CTTGCGGGTCATTCCATCGAATCCATCAGCGATGTTGTCGGCAGGTTCGATTCGCGCGAA
AGCCGTGAACACTCAGATATCGCGAGAGAATGGTTGATGATAACCGGCCAAAGTAGTGCG
TTGACCTGGAGTTACTTCCTTATGCTCGTAGGTGTCCCAGGAGTGAAAGCAGACCGAATG
ATCGTCCGTTTCGTCACTCACGTGCTCGAGCGTCCGAAAGAGATTTCCAGGCACGAAGCT
TCACGGTTGATTGAGGAAGTTGCGGACATTATGTGCGTCAACTACATCTACCTCGACCAC
ACCATCTGGCGGTTCCAATCAGGGCGCCCCTACCTCCAAGAAGACTCCTCCCCTTTCGAA

>RXA00230-downstream
TAAATCCATCACATTTCACAGTC

>RXA00232-upstream
GCTGAAAAAACTCCCATTTGGACAATGAACACTTGTCAAAATGGGAGTTTTGGATTTTCG
CACCACCGGCAGCACTCGAAAACGTGTTTATACTTGAACT

>RXA00232
ATGAACGACAGGGCTCACCAACGAATAGGCGACATCGAGCGATCCCAAGCCCTCGACCGA
CTTGGGTCATATTTTGCAGACGGATACCTCGACATCGACGAATTCGATACCCGAACCGGC
GCCGCAGCAATCGCACGCACAGCCGGTGAAATAGATGTCTTGTTCACAGATCTTCCCGAA
CAACAGGCAAGCACCGCCGTGACACCCGTGCAAGACGATACCGAGAAAGAATTAGACCTG
GTCCTACAGCGAGGAAAGAAGCTCAAGCAGATCGACTCCGCCATTTGGGCTGTCGTGATG
GTCTCGTTCTTCCTAGGCTTGTTTGTTTTCAACGTGCCATATTTCTGGGTTGTGTTCATC
CTTGGCGGAGCGGCCTCCGCGGGTGCGCGATTCTTGCTCAAAGTAGATGACGCCGATGAA
AAACTCTTTGAGGAACTCCACAGCAAGGAACAAAGCGAACGCGAAGCACGCCTACGCATT
GCGGCACAACGTCGACGCGAGTTGGAACAA

>RXA00232-downstream
TAGCCACAAAAGCTATC

>RXA00233-upstream
CGCCTCCAGCAGTTGAGGGAGAAGTTCCAACACTTGCACCAACTGAGGAAGCAACTGTGC
AATAGCGCTTTAGACACAGACTCATGACAGAATAGAAGAC

>RXA00233
ATGAGTGTGAATGAAGCAGATCTGAACGCTGTCGAAGAGCAATTGGGAAGGGCCCCACGA
GGTGTCCTCGATATTTCTTACCGCAGCCCTGATGGAGTACCCGGTGTGGTGATGACCGCA
CCAAAACTGGATGACGGAACCCCATTCCCAACCCTGTACTACTTGACAGATCCACGCCTG
ACCACCGAGGCATCCCGCCTCGAGGTCGCATTGGTAATGAAGTGGATGACTGATCGCCTT
TCCACCGACGAAGAGCTTCGTGCCGACTACCAGCGCGCCCACGAGCACTTCCTGGCAAAG
CGCAACGCAATTGAAGATCTCGGCACGGATTTTTCCGGCGGTGGCATGCCTGACCGAGTG
AAGTGCCTTCACGTCCTCATTGACTATGCACTGGCAGAAGGCCCACACCATTTCCTT

>RXA00234-upstream
TTCAGGGCTAAATAAAAGCGCTTTTCGACGCCCGGTAACCTCAAGGTTGCCGGGCGTCGT
TGCCTTACTACTGTTACTGGTGTGACTATGATCGAGGATT

>RXA00234
ATGGCAAAGCAGAAGAAAACTCATAAAGGCCTTGTTCCTGTCTCAAGCAGGGAACGTGCT
TCAGAGTCAGTTTCTGCTACCCGCGCCCCATTTAGATTGGGTGCCGTCGGCATCGGTGCA
ATCGCACTCGTAGTTCTTCTCATCCTGTTTGTCATCGCGATTCCTGTGCGTAACTATTTT
CAGCTGCGCTCCGACATCGCCCAAACAGAGGCTTCCATTGAAGCCAAAGAACAACAGATC
AAACAACTGGAATCTGACCTCAACAGGTACCAATCAGAGGCGTACATCCGCGAACAAGCA
CGCCTGCGCCTAGGCGTCATTGAACCTGGAGAAACCGCGTTCAGAATCGTGGACCCAGCA
CTAGATACCGACACCTCAGTCACCTCTGACGGCAACGAAGAGAAACCACTGGGAGCTTGG
TATGAAAACCTCTGGGACTCAGTCACCAAGCCAGAAGCACTCGGCGAAGAGGAAATTGCG
CCTCCAGCAGTTGAGGGAGAAGTTCCAACACTTGCACCAACTGAGGAAGCAACTGTGCAA

>RXA00234-downstream

TAGCGCTTTAGACACAGACTCAT

>RXA00236-upstream
AATGCGAGAGTTCTAAAACGAGCCGGTAACATCGACCCCCATGAGTTCAGGGGTTAGAAA
AGCAATGGGATTTGGATGCGGTTCGGTTTTGGCCGTCATC

>RXA00236
ATGGTGATCTCATTTGTTGGATGGGCGCTCAGCTTCATGGATGGAACGGCACCTATTCGC
CAACTCCAGCAAATCCCTGAAGATGTTCCGCCGGCGCGTGGTGTAGAAGTTCCGCAAATT
GATACAGAGGCAGATGGACGCACATCCAACCATTTGCGTTTTTGGGCGGAACCAATTGCT
CAAGATACTGGTGTGTCCGCTCAAGCGATTGCGGCTTATGGAAACGCAGAGCTCATCGCG
AGTACTGCGTGGCCTGGCTGCAATCTGGGGTGGAATACCTTGGCAGGTATCGGCCAGGTG
GAAACCCGTCACGGTACCTACAACGGCAAAATGTTCGGGGGCAGTTCCCTGGATGAAAAT
GGAGTTGCAACCCCTCCAATCATCGGCGTTCCACTTGATGGTTCACCGGGGTTTGCGGAA
ATTCCCGACACTGATGGTGGGGAATTAGATGGCGATACTGAATATGATCGCGCGGTAGGT
CCCATGCAGTTCATTCCGGAAACGTGGCGACTTATGGGATTGGATGCAAACGGTGATGGG
GTAGCGGACCCCAACCAAATTGATGACGCAGCATTGAGTGCCGCAAACCTGTTGTGTTCC
AACGATCGTGACTTGTCCACTCCTGAAGGATGGACCGCAGCTGTTCATTCTTACAACATG
TCTAATCAGTATTTGATGGACGTTCGAGATGCTGCCGCGTCCTACGCTTTACGACAGCCG
GCGATC

>RXA00236-downstream
TAAAACTTAACAAGCGCAACCCC

>RXA00237-upstream
ACTGGTAGAAGCTTTGATGATCTACATCACAAATTTACAATGTGTGGTGAGTTATTCATA
TTACCCAAGGACTTAAACCTTAAAAGGAGCCCTAAAAATC

>RXA00237
ATGAAGCTTTCACACCGCATCGCAGCAATGGCAGCAACCGCAGGCATCACAGTGGCAGCA
TTCGCAGCACCTGCTTCCGCATCCGACTTCGCAAACCTATCCTCCACCAACAAAGAACTG
TCCCCTCAGTACAACTGGGTTGCTTGCGGCATCCTTGAGGGTGGCCTCAAAGCAGCTGGC
GTCCTTGAAGAAGGCCAGTACAACCGCGAGCTCGCAGAAGCAATCGCCGCAAAGGGTGAA
GGCTTCTGGACCACTCAGTTCCCACAAATCGGTGATTGGAACGAAGATCAGGCAGCAGCA
CTTGCCGACCGCGCACAAACCTGTGGCCTAGTTAAGGCTGACACCTACCTTTCTGAGCTG
TCCTCCAACTTCTCTTCC

>RXA00237-downstream
TAAAAGGTTCGGGGGTAACCCCA

>RXA00238-upstream
AACAGTCACATAAATCACTTCAGTAACGTATGATTTTGGACTGTTGTGGCTTTTGCCATA
TTTATTTCATTTCCATCTCAGTGATCTCTTAAGGAAACCC

>RXA00238
ATGAAGAAACTACGTTTCGCCACCATCGCTGCCGCTACCGTTGCCCTGACTGCGAGCCTT
ACCCCCTCAGCTTCCGCACAGGATTTCAACCAAATCATCGACAACTTTGATTGCGGCATC
CTTCAGACCGCTATCTACACCACCGGCCTGGCTCACGAGAACTCCACTCGCTCAGAGCTC
GCCGCTAATCTGCGCAACTCCGCAGCTGTCGGCCAACTAGACTTCCCATTGAATATCGCG
GCTACCGGCTACTCCGAGCGCATCGCTAACCGCGCACTGACCTGCGGAATCGTGAAGGAA
GATCCACAGGACTTCCTCTCCCAGCTGCAGCTTCTGTCCTCTAACCTATCTTCTTCCTTC
TTCACTGCT

>RXA00238-downstream
TAGTTTCTCTTGGGCTTTTCCTT

>RXA00239-upstream

ACAAAGCGGATCAGATTAACAAGGTCCGTGACGCTGTCGATGAGCGCATTGGCAAAAACA
ACGGCGGCGAAGAGAATCCAGCCAACTAGTATTAGGCGTC

>RXA00239
ATGCGCGTCGTAGTTGTTGATCCTAAACACCCCGTCCTTCCAGTCTCTTTCCTCGAGGCT
GTTCTTGGGCGGGGTGAACCTGTTTCTATCGATCCCGATTTTCCATTTGATATTGAAAAA
TGGGGGATCAAGACGTCGACAAGCGCCTCCTGGTTTATCATCGCAAAACCGCAAAGCACG
CTGCTTATCGACGCGCCCCTCAACCCTTTGCATGAGGCCGTCGGCGTCATGCGGGCGGCC
GTGGGCCGCGGCGAGTGGGAACGCACGCAAACCCATGAGAGTTTGATTCCGTATCTGGAA
GAAGAATCGCAGGAGTTTATTGAAGCGATTCATGGTGGCGATGATGAGCACATGAAAAGC
GAACTGGGGGATGTTTTGCTGCAGGTGCTTTTTCATGCAGAAATCGCCGCCCGTCAGGGT
CGATTCGACATTTTTGACGTGGCGGCGAGTTTCGTAGCCAAGATGCAATCTCGTTCGCCG
TACCTGTTCGACGGCTCTACCGGAATTGTGGACACCGACGAGCAGCAGCGGCTGTGGGCT
CAAGGAAAAGCCCAAGAGAAACTAAGCAGTGAAGAAGGAAGAAGA

>RXA00239-downstream
TAGGTTAGAGGACAGAAGCTGCA

>RXA00240-upstream
TCATTTAACGTAGTTGACGTACGGCGAAGTCGCTAAACTTCGCGTAATCTTGGGGCCAAT
TAATCAAGTGCAGATGAATTGTTTAGAAAGGCTGGAGACC

>RXA00240
ATGGGTATTTTTGACGAAGCTAAGAAGAAGGCAACCGAATTCCTCGACTCTGATTCAGGC
GAGCAGAAGTCCGATGGACTGCTGGATAAGGCCGCAGACAAAGCTAAGGGTCTCCTCGGT
GAAGACAAAGCGGATCAGATTAACAAGGTCCGTGACGCTGTCGATGAGCGCATTGGCAAA
AACAACGGCGGCGAAGAGAATCCAGCCAAC

>RXA00240-downstream
TAGTATTAGGCGTCATGCGCGTC

>RXA00242-upstream
GGATCACTATCGCTTTAAACACCGAAACCTTCCTGCTAGTTCACCAAGATTTTTAAGTTT
TACCGCAATTTCTTGAGAGCTTTGGGAGGATAATGGCGGT

>RXA00242
GTGAATGAATGGCGAACAGTCTCGCTTGTAGATTCCACGGCGCTGACCGTGATCATCAGT
GTGGCCGTGTTTACTTCTGCTGTGGCTCTGCTCGGAGTTGTGAAAAAGCGCTCTCGGTGG
CGGGTTCTCGGAGCTCTCATCTCCTCAGCAGTTCTCACCAGTGGCGCATGGGTGGTTATT
GAAAAGCTGTGGAAGCCTTTCCCCGACCCCAATCCGTGGACCATCTATCTTTCCGCTGGT
TTGGCGGTTTTTCCTCTGTTGAGCATCTTGTTCCGCACTGGTCGTACAAGAATACTGATG
GCTACACTCACCGTGATTGCACTGGTTAATACGGCCGCAGTCATCAATGTCATCTACCAG
CCATACCCGACGTTGGGTTCTTTCAATCCCGTGCCAACGGCTGTGTCCATGTCGTATGCA
GATTTTGAATCTCAGACCACTGCCCCGACGATGGATGACCGTGAAGTCGGTGCCCTTGTG
CAGGTGCCGCTAGCTGGAACAACAGATGATTCCACCTCCGGCTTTGATGCGCGCGATGCC
TACGCCTATATTCCGCCTGCGTATTGGGATAATCCTTCCCTACAACTGCCAGTTTTGGTT
CTCATGCCCGGAAACCCCGGCCAGCCAGATCAGTGGTTTAGCAGTGGAAATGCCGATCAA
ACAGCAGATAATTTCCAAGCAACCCACGATGGCATCAGCCCCATTGTCATCAGCGTGGAT
GGCACAGGATCATTCAGCGGAAACCCTGCTTGCGTGGATTCTGATGCCCAAAGCGTGATG
ACATATCTATCCCACGATGTCCCCATGTTGATCAAACAGAAATTCCGAGTCAATCAGGAT
CAGCGCACCTGGACAATTGGTGGTTTAAGTTACGGCGGCACCTGTGCTTTGCAGATCATG
ACCAATCACCCCGAAGCGTATGGTTCTTTCCTTGACTTCTCGGGCCAGGAAGAACCAACA
CTTGGCACACGCCAGCAAACTGTTGATCAGCTTTTCGGCGGCGATGAAGACGCATTCAAA
GCCGTTAATCCGGAAGATCTGCTCAATCAAGCAATCAGCTCAGGAGCGCATACCTACAGC
GGGATTTCGGGCAGGTTTATTGCTGGTAGCAACGATAAAAGTGCAGTGAGCGCGCTGTCT
CATCTTGATAATTTGAGCAATCAGGCGGGCATGTCCACCACCTTTGATACCGTGGCCGGT
GGA

>RXA00244-upstream
AGTGGGAAAGTGATGATGCCACACACCGCCGGCGGATTACAGGATGGCAGTTCATCAGGG
GTTTAAACAGTGAAGATTTGGCAGAAAGCGAGATGGATAA

>RXA00244
ATGAATGATCAGCTGTGGGAAGGCGACACTGGAACGCTGACTTTTGGGTCCAGGAAAGCT
CTGGTGCAATTACTCAAAGGTCCCATGGTGAATGCTTTGCAGCATGTTGAAGTGTGGCGG
GCTATCACCACAGATCAAGATGCGCTCAATGCTGTGCTTAACAATTTGTTCCTCGAGTTG
GTTCTTGATGAGGATGCGGGTGTTGCATTTACTCGGCCTGCCAATGGTAGACAAGAAGTA
TTGGTTGGAAATAACAAAACTGAAGCGATGCCCAAAGTGCTGCGCACGGAGACGCTGTCG
CATTTTGATACGTTGATCATTTTGATTCTGCGCCAAGAACTCACCATGGCGCCACCGGGG
GAACGAGTCATTGTGGATCGTGAAGAAATCCGCGAACAAGTGTTGCTCTACCGCGTTGAT
GAAGAGCGAGATGAAGCCAAACTAGCTAAGCGATTCGACGCTGCATTTAGGCGCATCGTG
GATTATTCATTAGCTAAAAAGACAGAGACACCTGAACGTTTTGAGGTCTCACCAGCACTG
CGCCAGATTTTTGATGCCGACACTGTGGCAGGTGTGCGCGCTGAGTACGAAAAATTTAAC
AAAGCAGCCCATGATGGAAATGAAGAGGAACAGAAG

>RXA00244-downstream
TGACCAGCGAACAAGCTTTAGAT

>RXA00245-upstream
ATGACCTTTGTTTGAAGTTGGTGCGGTGATGGGGGAGTGTGACCGGATTCGAACAGGAAT
GTACGACACGTGTCCACCCCTTCTGGAATAGTCAATTGGC

>RXA00245
ATGACCGTTGTATCGCACGCGCTTGGGTTTAAGCGATTTAGGCAGGAATCCCTGGAGCTG
TCTTTGTTGCGCAGTGACAACTTTCCGGTGGTGCTCGCCGTGGTAGCGCAGTATTTTCCG
CAGGGGGCTATCGCTAAGCCGGCCTCAGAGCTGTATCAGCTGCTCAGCGATGATTTTCGG
GTGCTGCGTGAAGAAGGATTTGAGCTGCCGAAAAGCCCGTCGGATTATGTGAGTGATTGG
GTGAAGTCCCGGTGGTTTGTGCGTCGTCCGGGTAGTTCGCAGACTGGTGAGACCGTGGAA
CCGAGTGAAGAGCTGTTGGCGGTGCTGGATTCGGTGCAGCGGTGGGATAACCCGCATCGA
AGCATTTCGGCGTCTCGAATTGAATCGTTGACGCAGGCGTTGCAGACTTTGGCGTTGGAA
TCGGACCCCAGCACAGCGAAACGTTTAGCTGAGTTAGAGCGTGAACGCGACAGGATTGAA
CGCCAGATTGAAGCGGTCCACGCTGGTGAATTTGAAGTCCTCACCACCGTGCAGATTGGT
GATCGGGTAGCAGATATTTTGGATCTAGCAGCATCTATTCCTGCAGATTTCGCCAGGGTA
AGGCATGAGCTGAGCGATCTGAACCGGAAGCTGCGCAGGCAGTTGCTTGATCCTGAAGAT
TCCCGTGGTGATGTTTTGGAAGAGATCTTCAGGGGAGTTGATCTGATTGGGGATTCCGAT
GCGGGGCGCAGCTTCAATAGTTTCTTTGATGTTTTGCTCGATCGGGAACGCTCAAGTCTG
ATTGATCGATGGATCAGAGAAGTTCTGGGACGCGATGAGGCTATTGATCTGGATTCAAAA
TTAAGGACAGGGCTGTACCGAATTTTCCGGGATATGGAGGATGCCAGCTTCGAGGTCAAC
GGGGAAATGACAGGGCTGGCTCGAAGTTTGCGTCACTATGTCACTACCGAGGAGTTCGCA
GAGAGCCGACGCATGATTCAGTTGCTTCGCGATACCCGCAGTGCCGCTGCTAAGGCCGCC
GAGGCTGGTGAAGTGACCTCACTCAATCACATGGACACACCACTCGTGCGCATTGGTATG
GATGTTCGCTCGATTGCGGGGTTGAAACTGAAGAACCCAGGTGAAGAACGCGTCGAAGAT
TTGCCTGAGCCAGTTGAAGAACAAGAACTAGACACTGAAGTCTTGATGGAACAAATTCGG
GCAAGCGAGATTGATTTTGAGGAATTGGAAGAGGCTGTTTCTTTAGTTCTTGCCGAGCAA
TCGCACGCCACGATCACCGAGGTACTAGAACATTTCCCGGCAACGCAAGGTCTCGCCAGC
ATTGTTGGATTGTTATACCTGGCGATGCGTGATGGTGTTCCCACAGGTCGCGCGCAAATA
GTGGAGTGGGAAAGTGATGATGCCACACACCGCCGGCGGATTACAGGATGGCAGTTCATC
AGGGGTTTAAACAGTGAAGATTTGGCAGAAAGCGAGATGGATAAA

>RXA00245-downstream
TGAATGATCAGCTGTGGGAAGGC

>RXA00247-upstream
AACCCCTAACTACTGACCTCGCACCACTTGTTGCAGCCCGTTACCACGCTGCATTGAGCG
CACTGCTGGCACATATCTAAGACCGCTAAGGAAATCAGCT

>RXA00247

ATGCAGACATTAATCTTTATCGCCATTGCAGGCGTCGCAGCACAGCTTGTTGATGGCGGC
CTCGGCATGGGGTTCGGCGTCACCTCAACCACCATCCTCATCATGCTCGCAGGTTTAGGC
CCTGCGCAGGCATCCGCCGTCGTGCACACCGCAGAGGTTGGAACCACCTTAGTTTCTGGT
TTAAGCCACTGGAAATTTGGCAACGTGGATTGGAAAGTAGTTGTCCGGCTCGGTATCCCC
GGCGCTATCGGCGCATTTGCTGGCGCTACCTTCTTGTCCAATATTTCCACCGAAGCAGCA
GCACCGATCACCTCCCTGATTCTTGCCCTGATCGGCATGAACCTAGTCTGGCGATTCAGC
AAGGGACGCATCCGCCGCGACTATTCCGATCGCCCGCACAGCAGGGGATTCCTCGGCGGA
CTCGGTATTGTCGGTGGTTTCGTTGACGCATCCGGTGGCGGCGGATGGGGTCCAGTGACC
ACCTCTACGCTGCTGTCTTTGGGACGCACCGAACCCCGCAAAGTAGTCGGCACCGTCAAC
ACCGCAGAATTCTTAGTCTCCCTAGCCGCAACATTGGGCTTCGTCGTGGGACTGTGGGAT
GACCTAGTAGCTAACCTCTCTGCAGTTCTCGCGTTGCTCATCGGCGGCGCAATCGCAGCA
CCAATCGGCGCCTGGATGATCTCTCGCGTTAATGCAACCGTCCTCGGTGGCTTCGTGGGC
ACCCTGATTGTCACACTGAACCTGCCAAAGGTGCTCAACGTGGTTGGCCTTGATTTCATC
CCCACCGGCCTCATCCAGGTCACCGTCCTCCTCATCGGCCTGCCGCTGACGTACCTCGGC
TTCCGCCGCTACCGCAAAAATCTCCTCAACGAGACCATCTCCAGCGAAGTTGTCTCCGAA
CCAAAGGGCCAAAAGATTAAAAGCACT

>RXA00247-downstream
TAAAACACGCTTTTCGACGCCCA

>RXA00248-upstream
TCCGGCGATACCCTCGCAGCTGGCTTGGTTGGCCACCGCCTACGCAATAACTGGTCGATC
TAGACCAGTGTCTTAGGCAAGACCCCATTTAGGACACCTC

>RXA00248
ATGATTCCCCTGATTACGCTTTCCCACGGTTCCCGCAAAAAGTCCGCAGCTGCAGGCATT
ACTGCGCTGACTCATGAGGCCGGACGAATGCTGGAAACACCAGCCGTGGAAGCGCATTTA
GAGCTTGCTGAACCTTCCCTTGATCAGGTTGTGGCAACGCTCAGTGCGGAAGGTGTAACC
AGGGCAGCGTTGGTTCCTTTGCTGTTTAGCAATGCGTATCACGCAAAGATTGACGTTCCT
GAGGCAGTAAAAGATGCTTCAGAAAAGTATGGTGTGGAACTTCTCGTGGGTCCGCATTTG
GGCACTGGCTCCGATGTAGCCAGCGTGCTTGCGCAGCGGTTGAGTGCGGACGCCCCCACA
GATGCCCATGTGATTTTGTATTCCGTTGGCAGCTCACACGTGTCCGCCAATGAATCAGTC
ATCGATCTTGCCCACACCATTGCTCTCCTCACTGGCTTTTCGGTTGAGGTGGTGCCCGCT
ACCGGTGGGCCAGGTGCCGGCGGCGCCGGAGTAATAGAGGTGGCCTCGAAACACAAGGCC
GTCCACATCCTGCCGCTGTTTGTTACGGAAGGTTTGCTGCTGGATCGGGCTATTGATCAA
TCCGCCAACATCGCAGCTGCCACCGGCACAAACTTCACCTATTCCGAACCCCTAACTACT
GACCTCGCACCACTTGTTGCAGCCCGTTACCACGCTGCATTGAGCGCACTGCTGGCACAT
ATC

>RXA00248-downstream
TAAGACCGCTAAGGAAATCAGCT

>RXA00250
GCTTTGGGTGCTGCGTTGGGTCAGTTCGATTTCGTCCGCAACAATATTGATCTGATTTTC
TTGCTGATCGTGTTCATTTCGGTGGTTCCTGGTTTGGTCGGCATGGCCCGCAAGCTGGCT
GACGGCCACAAGCAAGCCAACACCGAGCCACAAGAAAACCCCGCAGTCCAGACAGCCCCA
GTAAAAACCCAGGAAGCCCAGGAAGCCCCCCAGAAC

>RXA00250-downstream
TAATCTTTCCGGTCCGCCAGTTC

>RXA00252-upstream
GCAGCATGGGGGTGTTGGTGGGGCCGGGGCTGACAGTGCTGACGCGGATGCCGTTGTTGG
CTTCTTCTTTGCGGAAGGCGTCGGCGAGTCCGCGGAGGGC

>RXA00252
GTGTTTGCTGGCGGCGTAGATGGTGTTGCCGGGGTGTGGTCCGTTGCCGGCGCCGGAGTT
GATGTAGATGACGCAGCCGGATGCCGCGCGGAGGGCGGGCAAGAGTTGGCGACTCAACTC

GGCCGGGACAATGACGTTGAGATCAAGGTGTGCGTGCCATTCGGCCACACTGCCGGCTTC
GATGGTCGTGTCACGCGCCACCGCCGCGGCGTGCACCAGCGTATCCACGTGGTCGAGGTT
TTT

>RXA00252-downstream
TAGCTTGTCGACGCCTCCCTCTT

>RXA00256-upstream
AATTAATCAATCAGAAAAACATATTGAATACTTATAAATTTCTGACATACTCATTAATGA
GATATTCGAAGTCTTTATCAAAATGATTAACAAAAGGAGT

>RXA00256
ATGTTTATGTCGCTAAAAACTCGCCGAATATTCGGCGCACTTGCTGTTTCGCTATCAATC
TCTTTCTCAGCCATTGCTACACCTGCAGCATCCGCACAAGAACTAGTGGTGAGCACATCA
GCAGTAAACGAATTTGGTGTAGTTACCAGTGACATCACGGCTGAGCAAATTCTTCAGGCG
CAAGATCTAATCGCTGAGATGAAACAGTCAGAGGACATATATGAGTATTTCGGTGCCTTG
TCTGACGTTGAACAGAGATCCATCATTGCAGCTGTAAAGGAAAATCCATATCTCATTGAG
AACGAATCACCCCGTATGAGAGTCCAAAGTGAAACACCCGACGAGGAAACACCTGATAAG
AAAAAGCCGAGCAAAACCTACAAGCTCTATATGAGCATTCTCGAAATGATGTCATGTATC
AATCTTGTTGATGTTCCGTCATGTGCCCAAGCCCTTAAAGCGGCAAATATAGCTGAACGC
GAGGCCAAGGCCCGTTACCCCGATTCGGTCACTAATGGTAAAGGCGATGCCCTTCGTCAT
TGTGCATGGAGCGCTCTCATGACTATTCGAATCGGAAAAGATGCAGCCGAAAGAATTGGT
AACGCTCATGAAACCGTTGTGAGAGGTGAACCCGAAGAAAGAGAAATGGATCTCATCAAT
AACGCGCTGGGTAGAGACATCGGCGAAAGATTCATCATCAATGGCGATGAAACGGGTGCG
CTCAGTACTTGTGTATCCATGGCTAATATCGGGCTACTTCATACTCTGTTG

>RXA00256-downstream
TAAACAAAGGAAGTTTCTATCAT

>RXA00257-upstream
CATCATCAATGGCGATGAAACGGGTGCGCTCAGTACTTGTGTATCCATGGCTAATATCGG
GCTACTTCATACTCTGTTGTAAACAAAGGAAGTTTCTATC

>RXA00257
ATGAAAATCAAGAAATTCAGCATCACAGCGCTAGCCTCAGTTCTAATGCTCACGGGTTGC
GCGACCAATCACAGCTCACCTCTGTACAGTTATCTGAATGCGTCAACATCAACCACTGTT
GAACAAGTACGTCTCAGCGATCTTTACGGTGAGCAGTGGACCGAGTTCGCTCTTGTCTGC
CCCTACACCACAAAAGACGAGGTAAAAGAAGAGCTTGGTATAAAAATAAACACCTACCTC
ACCGATTCGACCGATGACAGTAGTAACGATATTGTGCTCAGGGATAAAGACGGTTCATAT
GATTGGATCTATTTCAACAGATTCGACATTGTGTACCTCTGCAACGGCTCAGCGGAAAAT
CTAAAAATCTACCCCATTGATTCAGTTCTAGAATTTGAGCATAGAGACGACTACGGTACC
TGGAAACTGAGCGCTATCACAGAGCCGGGTAATCAA

>RXA00257-downstream
TAATAACGCGGACACTTAAGTAC

>RXA00258-upstream
TAATTAATATAATTAATGTAGTTTATTAACCTATTATGCAATGACATTTTTTAATAATTA
ACCACGTCACAACATTCTCTCAGATCACAGAGGTTCGCTC

>RXA00258
ATGCGCCACACCACGTCAGCCACATCAACTACATCTATTATTAAGCGTGCTATGACCATT
AGTGCCGCTGTTCTTATTGCCAGCGCTGTTGGTCTCACAACCAGCGCAAGTTCGCTCAAT
ACTCTCAGCGCTACATCACCTGAATCACCCGATCAGGCAGCCACTGTGTCACAGGCTGAA
TCAGATAGTGAATTAGATGACGGCATGAAAAAGCTTGCAACCAAGATCCTTAATCGCGCT
GACAACGCTGAAAATAATGATGACACCGGCAAAAACCTCAACAATGATGATAAGAAGCTC
AACACGAAGCAGCCGCAGCGCCCTGCTGAAAAAGTTGCCCAGGCGATCGAGCTAAGCCTT

GATACCACCACGAATGCAGAAAAGCCTGATAAAAGTTTTCACCATGAAAAACCCGTAAAC
GCCTATGTCACAAGTGTCAGCTACAACAAAAGCAATGACACCTGGACTATCAAACCATCA
GACAGCGCGGTGAATACACCGACCAATGATGCTGAGCGCATCAGCAATATCATCCAAGAA
GCTCGCGACCTCGGTCTCAGCGACGATGAATCCTTGACGCAACAGATCGCATTTCACGCT
CATGCTGCTAATTATTTAGTCACCGAATGGGTACTTCGCGGCTATCAGCTTGCTAACCCG
AAGGTGCTTCCA

>RXA00258-downstream
TGAGAAAACAACGACGCATGATG

>RXA00260-upstream
GCAACAGCGGCTTGCAGATCAGAAGGCGCGAGAGGCGCGACAGCTGCTAGATATTGAACG
TCAGCAGGTGATTGCAGATCGCTATGGGCCGTTGGTGAAT

>RXA00260
ATGCATAGCGACGCTGTGCTAGCGGGTGCTTCAATAAGAGCAAAAATAGGTGCTCTCGCA
ACTATTTACGGTGCTCAAAACTTAGAGAATGTCATTCACTCAGTTAGTTTTACTGACAGA
CGTATTTCTCCCGATGGACAACTGTCGAAAGAATTATTTCGCGAAGCTTGGAGCGCAAAC
CTTCTTATCCCTGATCCATCTTCTGATGTGGAAGCGTTTGCGTGGAGCGAAAAGAATTCC
ACTGAGCTAGCGGGAGGCATATTCGTTGAGAAAATGCTATTTACTGTCCCGGACACAGGC
CGCTCCAATAACCGTGTCCAGAGCTTCTCAGAAGAACTTCGTAACCACATTTCTTTGAAA
GATATGTATTCTACACAACGTGAAGAGCTATTAGACCTTGCCTACGAGCTCATGGTGGGG
GAAGCAGTACGTTTTGCTAACTTCCGCCTTTATGATCAGAATCTCCCACCACTTACTGAA
GCAAATATAGACAAATTGAGAGCCCATCTACGTGAGGCCGCAGCTAGTGCGTCACTAGGA
GTGTTATATCTAATGGTGTGGCGATCTGTAAAAGACGCAGCTGCAGCGCACACTAAACAT
ACAAGAATGAGCAAAGAAAATGCGACAACGCATAGTGTTACAAAAGTTTCTATCTTTGTT
GACCAATTATTAAGCGGAACATTCCCTTGTTCAAAGCCTTTTCACGAATCTTCACAAGTC
CCACTGAGTGAAGCCACCAAGATAGTTTTTAATTTGATTATGGAGTCACCGCCGATGGAA
ACTGAGCCGAGTGTGCTGCGAAATTCCCTCCAAGAACACTCGGATTGGGAGCTATTGCAA
CAGTGTGATGAGAAGATTCCTGATCGGGAGTTTCTGATGGAGTGGTTATATCAAGAACAG
ACGTGGACTGCAGAGCAATTTTTTGATGCTCTAGCTATGGTTTCTTCTAGCGAGTTTCGT
ATATGTGCACCTGGATGTGCGCATCAAGTAAGTGCAGACATCGCTACACAAGTCTTAGAA
TTCCACGATCGAGTGTCTTTCCATGACGATCGTAAAAGCGCCATGCTTGCTGCTGAAGCA
ACTATTATTGGTAACAAAATTGGTTCACAAGCACGGGCCGGAGACTTTGTTTTAGGTGAA
GTAATCACCAAGCTGCAGAACATACCTGGTGAGGTA

>RXA00260-downstream
TAACTTCTGCGTCGTCCAATTAG

>RXA00261-upstream
AAGGTCAGCCGTATTTCGGTCAGTCAGCAACTAATTACGCTTATCTTCCGTGTACGATAG
ACCGTAGTTAACATAAGGAATGGAATAGGAGAATTGCGGC

>RXA00261
ATGTATTCCGACAAGCTGATTCTCTTGTTCCTTTCTGAGCAGGATTCAAGCTATGAATGC
TGCGTAGGTTTATTAGATGGCTCAGATGGACGTGATTATATTGAAAAGCTTCTGAAGGGT
AGGAAGCTGAAGAACCATTTTCTTGAATGGGAAGATATTAACAAGGCTGATGTTGCTCGT
GAAGAAATATATAAAGGGCAATTGGTGCATCTGGTGTTTGTGACGGCTCTTTCCACGCCT
GGTGAAATTTCTTTTGTTTTTCCAGGTCAATCTCTCATGAGTGCAACACTCGAAGAAGAC
TTTGCTGCACTTGTGCTCGAAGAGGAGCGCACATCATTTAGACCTGATCTGTCTCACTTG
TGGTCACTCCCCGTAGGGTGGGTAGCTCCGGGGCTTGAGGGTTTCGTGGAGCGTAATTCA
GAGGCAGCT

>RXA00261-downstream
TGAACCACCGCTCTTTGAGCCGG

>RXA00264-upstream
AAACCGGAAGGGCCSGTTTACTCCCCTACTTGGCGCAGAAATCCACATCAATCCAGGTGA

AGCAGTCATCTTTGATGTTGATCCCACGTTTGAACACGGT

>RXA00264
TTGCTTGTCGATTCCGGCGACGTCCAACTAGAAGGCGTCACCGTCGAGCCCACCCAGCTG
GCCTACACCGGCATCAATGAAACCCAACTCCGAATCCGTAACATCGGCACCACACCGGCG
CGTACTGTACTGCTAGGTGGCGAACCATTTACCGAAGACATCGTGATGTGGTGGAACTTC
ATTGGCCGCAGCCATGAAGAAATTGCCGAGTACCGTAAACAGTGGCAGGCCGAAGCTGAT
CGTTTTGGTATCACCCACGGATATATCAGCCACCACAAAGATGGGCTCACCAGGCTTCCA
GCACCCGAGCTTCCCAACGCTGCTATCAAGGCACGTAAAAACCCAGCACCAACTGCACGA
CCAGAAACGAGAATTGAT

>RXA00264-downstream
TAAATGCGCTCCGCTCACGGCCC

>RXA00267-upstream
CGTAGCGTTGAGAACTATGCGAAACTCTAAGTCTGGCCTGGCCTTTTCCGCAGCTGCACT
ATTTT

>RXA00267
GTGTCTGTCGCGGTAATCACTCGTATTGCAAGTTCCCCATCATTTATCGCTATTGTGGCG
ATCATCGTGGCTGCGATCGCACTTTTTGTGGGTCTGAACAGTCGTGTGGGAACAAAGCTT
GTTGATCAGCCAGTGGTGTTCACCCAGGAACAAATTGATCAATTGAAAGAGTTGAAATCC
CGCGACCAGGAGGCGGCAGCGATCCGTCAGGCGCAGCTGTGGAGTAGGGGATCGTCCAGC
GAAGCGGTCGCAGAGGCTGTGAGGAAGCTC

>RXA00267-downstream
TAAGTCGACTTAAGTGCGCGAAG

>RXA00271-upstream
TAGTTTAAATCATGAGACATTTCACATATGGTTCTTTATCCGAGACATGTGTTGACGCTG
TCTGCCCCTTTTTGAAAATAACACTTTAAGGAGATGTGCC

>RXA00271
ATGTTTTCTTCCCGTTCGAAGGTACTCGCAAGCATCTTTACTGTTGGCGCCTTGGCGTTG
GCTTCGTGCTCAAGCGATTCCAGTGACAGCTCCACCTCCACTGATGCTGCAGGTGGCGAC
TCTTACCGAGTTGGCATCAACCAGCTTGTTCAGCACCCTGCACTTGATGCAGCGACCACT
GGTTTCAAGGAAGCTTTTGAAGAGGCAGGCGTTGACGTCACCTTTGATGAGCAAAACGCT
AACGGCGAGCAGGGCACTGCACTGACTATTTCTCAGCAGTTCGCTTCTGACAATTTGGAT
CTCGTGTTGGCTGTTGCAACTCCAGCAGCACAGGCAACTGCGCAGAATATCACTGATATC
CCAGTCCTGTTCACCGCAGTTACCGATGCAGTGTCGGCAGAGCTGGTGGATTCTAATGAA
GCACCTGGCGGAAACGTCACCGGTACTTCTGATATCGCACCGATTGAGCAGCAGTTGGAG
CTTTTGCAGCAGCTGGTTCCTGACGCAAAGTCCATCGGCATCGTCTACGCGTCTGGTGAG
GTCAACTCTCAGGTGCAGGTCGATGAGGTCACCAAGGCTGCTGAGCCACTGGGGCTGTCC
GTTAATACTCAGACTGTCACTACCGTGAACGAGATTCAGCAGGCTGTTGAAGCTCTCGGC
GATGTTGATGTCATCTACGTTCCAACTGACAACATGGTTGTTTCCGGTATTTCTTCTCTG
GTTCAGGTTGCTGAGCAGAAGCAGATCCCTGTGATCGGCGCTGAGTCCGGCACTGTTGAG
GGTGGCGCACTGGCAACCCTGGGTATCGATTACACCGAGCTTGGCCGCCAGACTGGTGAG
ATGGCTCTGCGTATTCTGCAGGACGGCGAAGACCCAGCAACCATGCCTGTGGAGACTGCA
ACTGAGTTCACCTACGTGATCAACGAAGATGCAGCAGAGCGCCAGGGCGTGGAGATCCCT
CAAGAGATTTTGGATAAGGCCGAACGCGTA

>RXA00271-downstream
TGATCGGCGCTTTTGAGTTCGGA

>RXA00272-upstream
ACCGATGCACCAGCCACCAACGCGTCCAAATCAATATCAGCCTGGCCCACAAGGTGGAAT
TCCAGTGGGTGGCCATCTGCCACAACCAGGTGCAGGGCAC

>RXA00272
ATGCCGGAACCAGAAACCTCCACGATGGGCTCCATCCAAAAGTCCGGTGAATGGCTCGTT
CCTGCATATTCGGCATACAAGCTCAACGGTGCTGACCTTTTCTTAGATATCCGCCATGCC
ACCGCGGCTGCTCCTGTCATTACCTTTGATGTCAACATGACCATGGGTTCTATGACGCTG
ATTGTTCCACCGGGTGTGTATGTGGAAGTGCAGATGGCTTCCAAGAACTGGTCGGATTTC
AAGGTTCAAACAACCAATCCTCTCCCCGGTGCTCCCCGAGTGTTCATCACTGGTGTTGCA
CGCGCATCAGGGTTGAAGGTTTTCACCAAGCATCCTCATGAGCCTTTTGGGTTCTGGCAG
AAAATGTTTGAG

>RXA00272-downstream
TAGCCTCGGGCCACGCCCGAACC

>RXA00273-upstream
TCGGTCTTGGTGGCGGCTCCGTCATTAGTTCCAGTAAGTAGTTTTTTCACTCCCTGTTTT
GAGTTTTTTTCTCACCTTTATATAGATAAGGAATATTCAC

>RXA00273
ATGTCTTTGAAGCTTAATTCTCGTCGTCTTGCATCCATTGCTGTCGCTGTTGCAGTCGGT
GTCTCTGGTGTTGCTGCTGTTGGTGCGGCACCAGCTACGGCTCAGCAGGTAGGTGCTGGT
ACCCCGATTCACGTTGTCAACCTTGATCGCACCGTTGTTGATCCAGTGACTGGTGACATC
ACCTTCCACTTCACCGACGGCACTTTTGTCACCCTCAAGGCGGGTGTTGATGGCAAGGAT
GGTACCGATGGCCAAGATGGTGTGATCGGCAAGGACGCAACCATTGTTGATGTCGCTACG
GAGTCCAATGGTGATGTCAAGCTCACCTTCTCTGATGGCACCGTCGTCACCATTCCTGCA
GCTAAGGACGGTGTGGATGGTGAAGATGGCAAGGATGGCGAGGACGCTACTGTGGTGTCT
ACTGCGACTGACGCCAACGGCAATATCGTCATTACGTTCTCTGATGGCTCTGTGCTTGTT
GTTGCTAACGGTAAGGACGGCAACGATGGCTCAGACGGCCAGGATGGTGCTGATGGTGAA
AATGGCAAGGATGGTGAGAACGGCGCTAACGCGACCATTGTCGATCAGATTGCCAATGAC
GATGGTTCCATTACCATTGTGTTCTCCGATGGTTCTGAGGTCACTATCCCAGCGCCAGCT
AAGGGTGCCACCGATGAGCTGGCACAGTGTCTGCTGAACCCGAAGATGTTGCTGCTGGCA
GCAATTCCTGCTGCAGGTGCTATTGCTAACGCTGTGGCACCGGCGATCCCACGTGTTGTT
GAAGATGTGCGTGCACAGTTCAATCTTCCAAGCCTCAACCCCCAGTTTGATCAGTGGCTC
TACAACGCGACCAAGGATATTGATGCAGGGTTGTTGATCTCTGGTGCTACCGGCCTTGCT
GTGCTGTCGGTGCTCGCTGATGATTTCTGTGGCGACATTGATGCCGATGACAACGCAGAT
GGTGACGTGGCGGCAGAAAAGCCAACTGGCTCTTCTGGGCTTGGATCATCTGAACAGAGT
GAAAAGGTTGATGGTGACGACGATAGTGTGATCGACACTGAAACTGATGCAGATCTCGAA
GTAGAAGAAGACCCTGAGCTTGTTAACGCAGGT

>RXA00273-downstream
TAACGCCAGTGTAATGCTGGATT

>RXA00274-upstream
AGTTTAAAAGTCATTAATTACTTTATGGGAAATAATAATTAAGTTTTCATCTTTTAACTA
GTTACAGCATGTTATTACCTTTTATGAAAGGCGTTTCACC

>RXA00274
TTGTCTCTTAATTTGAAGAAGAATTCTGCGCGTTCTATTACCGCGCTGACTGTTGCTGGT
CTGGGTCTGTCTATTGTTCCTGCGGCATCTGCACAGGATGTTGCGGATGACACTACCAAC
TCCGATTCCACCCGTGATGCCATTTGTGCTGCTGCACCGCTTGTTGCAGGCGCAGCAGTG
GGTGTTGGTCTGCTGTCTCAGCAGCCAGAATTCCAGCATATGGTGTCCCAGATTCAGTCT
GACGCACAGCGCATTGGGCAGGATCTCAGCAATCAGTTCAACAACTCTCTTGAATCGCTC
AACATTGGCCTCGGTAACGGCGTGCACGGCCCACAGCAGAACGCTGTGCAGGGTATTGAT
CTCACTGAAGCAGCACGAACCATGGCTGGATGGAATGACCTGGCGGCACAGGTGGGCCAG
ACTGCAGGCCCTGCTATCGGCGCTGTTGCTGGTACTGCCGGCCTGATCGCACTGGTTGAC
TACTGCTGGCTGGAAGGCTTCGACTTCGCGGGTGGCTCCAGTGGCACTGATGGTGAAAAT
GGTGTTGATGGTCAAGATGGTACCTCGATCACCATTACTGAGATTAAGACTGATGATGAC
GGCAATACCATTGTTGTCTTTTCCGATGGTTCTGAAATCACCATCACCAATGGTAAAGAC
GGCGCTGCTATCACCATTGTTAATACTTACCGCGACGATGAAGGTAATACTGTTGTTGAG
TTCTCTGACGGTTCCACCATTGTTATCGACAAGGGTGAAGACGGTAAAGATGGAGAAGAC
GGCAAGGACGGCGAAGACGGTAAGGACCTTACCGTAACTGATACCTACATCAACGATGAT

GGAGACACCGTTGTTGAGCTTTCCGATGGTTCCACGATCATTGTAAAGAAGGGTACCGAT
GGTAAGGACGGTGCTGACGGCTCTGACGGTGCTGATGGAGTCAGCATCACTGTGGAGAAC
TCTTATGTTGATGCGGACGGCAACACTGTTGTCGAATTCTCCGATGGCTCCAATGTGACC
ATCAACAAGGGTGAGAAGGGCGACAAGGGTGACGCTGGCGCCGATGGCGAAGACGGCGCA
GATGGTGAATCAATTACTGTTGTTAACACCAGCAACGATGCTGAAGGCAACACTCTTGTT
GAGCTCTCCGATGGCACTGTTATTACCATTAATAAGGGTGATAAGGGTGACGCTGGCGCC
GATGGTGAAGATGGAAGTAATGGCGCAGATGGCGAGTCCATTACGGTCATCGAAACCCGT
TTCGATGCGGACGGCAACACTGTTGTGGTGTTCTCGAACGGCACTGAAATCACCATCAAC
AAGGGTGAGAAGGGCGACAAGGGAGATACCGGCGAAGACGGTAAGGACGGACTGACCCCG
TACATCGGCCCAGATGGTAACTGGTGGATCGGTGAGAACAACACCTGTACTGCTGCACGT
GGCAATGACGGTAAAGACGGTGACACCCCACGCATCGGTGATAATGGTAATTGGTGGATC
GGCATCGTTGATACCGGCGTTCCTGCTCGTGGTCAGGATGGCGCCAACGGAGCCGATGGT
GCTAACACCGTTGAGATCATTAATGGCTACTGGTACATCAATGGTGAAAATACCGGTGTC
AAGGCAGTTGGTGAAAATGGCACCAACGGAGCCGATGGACAAGACGGTGAAAATGGAACC
AACGGTGCTAACACCGTTGAGATCATTAATGGCTACTGGTACATCAATGGTGAAAATACC
GGTGTCAAGGCGCAGGGTCCAAAGGGCGATAAGGGTGACACTGGTGACACGGGCGCTCCG
GGCGAGGGTTCCGGTAATGTGGACATTGAGATCCGAGAATCGAGTTATCCAGGTGGTGGC
CAGGCCACCATCATCATTCTTGATCAATTTGAATATGAAATCCCGCACACTGTTATTGGT
GACAACGGTAACTGGTACATCGGTGAAAAGGATACTGGTATCCCAGCTCAGGGTGGCACT
GGAACACCTGGTGAGGATGGCCTCACACCACACATTGGCGACAACGGTAACTGGTGGATC
GGTGATACCGATACAGGTGTCTCTGCAAGCCCGACCCCCGTTGGTGAGGCGGTAGCGGGT
GTCACTGATGTGGTCTTCAACACTAGTGATGAACCCAAGACCATTACTGCAACGATCAAT
GGTGAAGAATATGATTACACCCTTCCACCACATAGTGCTGTTGTGTTCTACGCTACAGGT
TCACCAATGGCATATTCTCTACCGAATGCATCGGGCCTCACTGTTATAGGTACTGAAGAG
ACTCCTGGTTTCACCACTATTCGATTCAGTGACCATTCCACTGTGACCATTCCACATGGA
CGAGATGGCACCAACGGTACTAACGAACTGACGGTAAGGATGGTCTCACCCCGCACATCG
GTGAGAACGGAAACTGGTGGATCGGCGAAAAGGACACTGGTATTTCGACAACCTTTGGCG
GTGGCGGCAACCCTGGTACCGGCAATGACTGCATCACGGTCCCAGGTGATGATCTTGGAT
TCCCAGATGATGCTGAGGCCGGTGCAGAGACCGGTGCAGATGCCGAAGGTACTATTGACT
AAAGGTCATAGAGCAACGACCATGACTGAT

>RXA00274-downstream
TAAAGTCGGAACACAACCCCTAG

>RXA00275-upstream
CTGACGCAGACGTTGCACAGCTCGCAACCGCTATTGACGAACAGAACCGCCCCACAAAGA
GCTGTTCCCTACGGCAGATCGCAAGGAACTATTCGCCTGG

>RXA00275
TTGGATAAGCGTCGCCCAGAATTAAGCGACGATTTCATCAAAGCTTTTGATGATTTCCTT
CATTCTTTTGCGTGCCTGGACAAAACAACGATCACCCTATTGGCGCAATCACCGGTGCGC
ACATCCACTGGCTATACAGGTACTTTTATCGGCATCCCCAATAATGAACCACTGTCCGAA
GAGCCCACCCCCACCATTTACATTGTGCACGATAATCACACAGGGATAATCCACAGTTAC
CCCGCACGAATGATTAATCTTAAATCTGAGCTCGGTTCCGCTGAGATGATTCACGAGGCA
ATCTGGGGGTCACCCCATCAACAGCAGTTAATCTCATGGTATGAGACTTACTACACCAAC
ATCTACTATGGTTTTAACCCACCCACTGAACCACATAAGAGTCTTGAGATTTTTGCTCAA
GACTTCTGTCTGACCCCACCAGAGAAACCTCCTTTTTTC

>RXA00275-downstream
TAAGGCAAGGCCCGTGGCACACA

>RXA00276-upstream
GGCACACTACCCTATGACTACACCGCAACCCAGCAAACCTGCGCCATGGTCGCTTGCCTA
TAAGTATCAAGCCATCAGCAATGATGATTTTGACAACCAT

>RXA00276
ATGGATGACCTCAGCAGTCGCCAAGACCATGAAGCCTACGGCACGTACAACCCCGATAAC
GGTGTCATGCCCGATCATGTCATCGTGCCTTCACCCTATGAACCATATGATGATGCTGCG
CCGATTGATCCTTTCGACTACGACGAAGATCTTCTCGATGAGATTAAAGAAGAGCGCGCT

GCACATGCGGTTGACGCACAAGTAACAGAAACAACTAAAGCTGACGCAGACGTTGCACAG
CTCGCAACCGCTATTGACGAACAGAACCGCCCCACAAAGAGCTGTTCCCTACGGCAGATC
GCAAGGAACTATTCGCCTGGTTGGATAAGCGTCGCCCAGAAT

>RXA00276-downstream
TAAGCGACGATTTCATCAAAGCT

>RXA00279-upstream
TGGGGAGCATTCAGAGGTGCCTAATCCTCTGGATGATTCTGCGGTGCAAAATTCAGCCCC
ACATTCAGCCCCACATTCAGCTCGGACCCGGTTGGAGTTT

>RXA00279
TTGGATACCGATGACTCGCCTGATCATTGGCTTGATCCGTTAACGGAGAAGGATACTTCT
AAGCGCACTCTCGTTAATTCGATTGTTCAGGAAACTTTCGGCCAGCCTATTTTTGTTGCC
CGCAAGATTTGGGCTTTCGTCAATACGTCGCCGGGCCGGATGACGTTGATGACGATTATC
ATTTCGATCGCCATTTTTGCTGCTGGTTACGCCATGTCGGTGTCTTCGGATACTAGGCAG
TCCAATTTGGATGATTTGATCACTAATGCGGAGCCTGTTTCCTATAACGCGCATGTGCTG
TATACATCATTGTCGGTTGCTGATACCACTGCTACCACTGGTTTTGTTCAGGCTGGTGTG
GAGGGCCCGGTGAATCGGGTGAAGTATCACACTGCTATTGATCGTGCTGCGGTTGCTGCT
ACTCATACTGCGGCGTCTGCGGATAGTAGTAATGAGCATTTGATGGAGTTGGTGCTGGAG
ATTCAGCGTCAGTTGCCGGTGTATACGGGGTTGGTGGAAACTGCTCGGACTAATAACCGT
GCGGGTAATCCCGTGGGTGTGGCCTATATGTCTGAGGCCAGCGCGATGATGCGTAATGAA
ATTTTGCCGATGGCGTCTGAGCTTTACAACCTGACGAGTCGTGCGGTGTCTGATCAGCAG
CGTTCGGTGACGGGTCCGCAGTGGTTTCCGCTGTCTGGATTGCTTGCGGCTCTTGCCATG
TTGATTGTTGCGCAGTGGTGGTTGATGCGGATTACGCGCAGGCGCATCAACAAGGGGTTT
GCCCTGGCCACGGTGATGATGATGACGGCAACGTTATGGGTGTCAGCTGCAAACTGGGCG
ACGTGGCAGGCTGGCACGAAGGGTTTTGAGGAAGCGTCGGGGCCGTTGAATTCCATGACT
ACGGCTCGTATTTATGCGCAGCAGACCCGCACGACGGAGACGTTGTCGTTGGTGCGTAGG
CAGTCGATTCAGGGCAGTGGCACTGGTTTTACCGCAACGATTAATCAGATTAAGCGTGCG
CTGGATGAGTATGAAACCACTGCGCAGTCACAGACTCCGGAGCATCAGCAGTTGATTACG
GCGATTCGTAATGCGATTGCTGCATGGACTGCCGATCACGATGAGTTCACGGTGTTGTTG
GCGTCTGGTGATTACAACGGTGCGGTCAATGCGGTGCTCAACAAAGATGAGGAGGGCCAG
ACCAGCTTTGATGAGCTCGATACTGCGCTGGCTGAGCTGATCGCGGATTCTCGCAGCTCC
ATGCGTTCCTATATCCAGTCGGGCCTGCAGGCCACGGAGTTGGTGTCCGTCATGGTGATG
ATTCTGTCTGTCGTTTCTGTGTTGGCTTTGTGGGTCGGCATCCGCCCCCGTTTGCAGGAG
TACTTA

>RXA00279-downstream
TAAATGCACGCTTTTCGACGCCC

>RXA00282
ATGAGCCGCGACGACCAGACGAACAACAACGGTGAGGGCGACGACACATCGCGCGAGCAG
TCCTGGGATCAATCCTGGCAGAACCTAAATAAGGATTCCCAGTACGGTCCGACCTCGCAT
CCGGAGGACGCGCCGGGAGGATTCCAGGGAAACGGCCAGGGTAACAGCCGGGGCAACGCT
CAGGGCAATGGTCAGGGCAATGGTCAGGGCTTTGGCCCGGGTAATGCTTCGGGATATGGA
GGCTACGGTCAGCCATACCCGCAGACTCCGTACCAGAATTCCTACCAAGGTTATGGCGCT
ACTTCACCGCAGAACGACGTGGCGCTGGAAGCGAGCAACGGCAAAGTCGACATCATGCGG
GCGATTCGCTTCGGATTCAAAGCCACGTTTGCCAATCCAGCAGTGTGGATTTTGGGCACC
GTCGGTCTTGGCCTTGCGTTCATGATTGTGAGTGGGTTGCTTGGCTACTTATCATTTTTG
ATCGACCCTAATGCGGGCACGACGACTTCTGGTTTTTCGGTTTCCGAGACCCTGTTGAAC
GTAGCTATCGGAATCATCACCTTCGCAATAACCATTTGCGTCATGCGCGGTGCACTGCTT
TCTGTTGATGGACACAAAGTTCGCTTCGGTGATTTCTTTAAACCCATCAATGTTGGTCAA
ACAGTGATTCTGATGGTGGGGCTGGGTATCTTCGGCATCATCCTGGGCACCTTCACCACT
TTTCTCACTCAAAATCTGGTGTCGTTTAATGACGCTGCCGGTACCGTTGAGGTCAATAAC
AGCGGTTTA

>RXA00283-upstream
GAAGCTCCGTTCATTTACGCCACTCTCTGGGCGGTGCGCAGGCTGATTCGGTGGAGTTCT

ACGGAAAACGTCCACAGACCTCATTACCTGTGGTTTTGCG

>RXA00283
TTGGCATTGGCGTTTTTAGCGCGCTATGACGCCCTCATCATGGCCTTCGTAGCCATGTGG
ACTGTCGGATTTATGACATGGCGCGCACGATACCGCCGTGGCTTCCGCGACCGCATCGGA
TTCGCACTTGTCGACATGCTGCTCCTCGTCTGGCCGATCGGCTTCGCCTTCGTCGCCTGG
ACTGGCGCCAGCTGGCTCACTACCGGCGAACTCTTTGCCCAATTCACCTCCACAGACGGC
AACGCTGCGATCATCGCAGCATCCGGCGGCGGCGCCATAGGGCCCCAAGCGCTTTTCGAC
GCCTCCGTCCGCACCTTCCTCATCTCCCCAGCTCTCCTACTCGTCGCAGTAGTTGCAGTC
TTTTTTGCTTATCGACGCCGCGACCCCGAACCCATCATCCCCTTAGCTCTCATCGGCTCT
GTGGTGTTCTTCCAAATCATTACCTACTCACTTGGATCTACCTTCGGCCTGCTGCGCTTT
TTCCTCACCGCCCTGCCGCTCACCATTATCTTGCTGTTCCAAATTATCCCGCCCCGCCAC
CGATTCCCCTCACTGCGACCAGGTGCGTGCTACCGCGATCGCGTCACCGGCAAGTACGTG
CCCAAAACAATCACCGGTGTTTTAGTTCTCGCGATCTTCGGCGGCACCGGCATCACCCTG
TACGGCATGAGCAGTGCTAACTGGGCGCCCCAGGAATATGCCATCCAAGAACTAGTTTTC
AACATGGGATCGCCATCGCAGGACGCCGTCCACACCCTGAACACCTTCTCCACTGAAATG
GATGTCGCCGATTTCGTCGACTCCCTAAACCTTGGAGACGGCGAAGTCCTTCTCTCCACC
ACCTACGGCTTCGCCGTCCTCACCGCATCAAACAACCAAAAGCAATTCATCATCCCCTCC
GACGAAGACTTCATCACCACCCTCAACGAACCCGCTGAGCACGGCGTTAAGTACATCCTC
GCCCTCCCACGCGAAGGTCGCGGCGCCACCGACCCGATCAACCTGCGCTACCCAGACATG
TATGAAACCGGCAGCCACATCGCCACGATGGAAATCGAATTCATCAATCAAGGCCAAGGA
CAACCAAATTGGCGCCTCTATCGGGTGCTCACCACACCTGAACAGTCG

>RXA00283-downstream
TAGACTCTTTGTAACTACCGTTG

>RXA00285
GGAACTGAATTGGGCGCATTGTTACTGCGTGTCCTCAACAGGGAAGAAATGATGGACAGA
TTCGCACGGGAGCTGGGTTTTTTCGTCGACAAGCAGCTTGAAGAGGTCGAGCGCATCAAC
TGTCACCATAACTACACGGTCCAGGAGGAGCACTACGGCGAGACCATTTGGCTCACCCGT
AAGGGTGCCGTGTTGGCGGACGAAGGCACGCCGGCGTTGATTCCGGGGTCGATGGGCACC
GCGTCGTACGTGGGCAGTGGCAAGGGCAACGCCGAGGCACTGCGGTCGGCGCCGCATGGG
GCGGGCCGGAGGATGTACCGCAACCAGGCTAAAAAGCGCTTCTCGACGGCCGACCTGGAT
TCTCGGATGGCGGGCATCGTCTACCGGCCCGGCAAGGAGTGGATCGATGAAATTCCCGAC
GCTTACAAAGACATCGATCAGGTGATGGCCGATGCTGCCGATTTGGTGACAATTCGCCAT
AAATTGCGCCAGATCGTCAACGTGAAAGGCACC

>RXA00285-downstream
TAAAGCGCATTACGGTAAAGTGC

>RXA00286-upstream
CCATAAATTGCGCCAGATCGTCAACGTGAAAGGCACCTAAAGCGCATTACGGTAAAGTGC
GAGAGGTATTTTGACGGGTTTAGATTGAGGGATGTGGATA

>RXA00286
GTGCTGAAAATCCCACGGCTGCTTCTACGCCGTGTGCTTCCGGTACTCATCACCTTGGCG
CTCCTGTGCGGACTGGTGCTTGCGTGGTTTATCTATCCTGCGAAGGCTGAGCCCAAAAAA
GATGATGTAGTTCTGGTGCTGGCCGGTTCCAGCGATGGTCGACACGAATATGGTGCCGAG
CTTGTTGAAGAAGGCTACGCCAGCAATTACGTCGTCTCCAACCCGAGTGGCTCCAAAGAC
AAAGTGGGATATGCCCACTGCGCAGGAAAGTCACGGCCAAAAAATGCGGAAAGTTTCTGC
ATGGATCCTTACCCCGTGATCACCTCCGGCGAAGCCCGCACGTTTAACGAGCTTGCCAAA
AAGGAAGGCTGGGAAAGCGTATTGGTAGTGACCAGCCGCACGCACACCCAACGCGTTCGC
ACCATGTTTGACCAGTGCTATACCGGTGATTCCACAGTGCTCAACGTCAACAGCCTAGGA
CGTACCGGGCTTCACAATGCAGTACTCCACGAGATTGGCGGCTTCATTAAATTTTGGATT
ACCGCTCCGTGCGCGGACACAAAC

>RXA00286-downstream
TAAGGACGTTCCAGCTCCAACAG

>RXA00294-upstream
TTGTTGGTGTGAGGTTGGGTTTTGTCATCCTGAATGCTTCATTTCTACCCTCGTGGGTAA
AGTTGGTGCCGAATCAACAATCTCTTTTGGAGGAACTTTA

>RXA00294
ATGAGCATTTCCAACGCAATCCTGCGTGGTGTGTCTGGCGCTTATATTCTGCAGTCCGGC
TACGGAAAACTTGGATTGCCTAATGAGGCCGCTGCTGGCATTCAGGGTCTAGCTGCAACG
GGTATCCCAGCGGTGGCTGATATGGATTCAGATACTTTCGGTAAGTTTGTTGCCTACTCG
GAGTTGGGTATCGGTGGAGCTTTGCTTGCTCCATTTATCCCTAGCCGTCTTGCAGGTTTG
GGTCTTGGTGCTTTCTCTACAGGTTTGTTGGCCATTTACTTCCGTAACCCAGCGATGACT
CAAGACGACGGAATCCGCCCTTCCCAGGATGGAACCGGATTGTCTAAGGATCTTTTCCTT
GCTGCTATTGCGGGTGCTTTGGTGTTCGCACCTGCTAAGAAGCGTAAGAAGGCGAAGAAC
AAGTCTAAG

>RXA00294-downstream
TAAGCTTGCTTGAACGGCGCTTG

>RXA00297-upstream
AACAAGGCACCGGAAAACAAGCAACGCACCTTGCAGAGGTGGTCTTAAGCATCTTGGAGC
AAAACAACATGGCACAATAACGATCATGCAACAGGTGCTC

>RXA00297
ATGGGTTTCACGGTGGTGTTCATCGTCATCGGAATAGGTTGGATTCTCGGTAGAAGAGAC
ACCTTGGGCACACATGCCCAGAAACCTTTGAGCCTGTTTGTCTATTACGTGGCCACCCCA
GCGTTGTTGTTTGATCGGGTCACCAAGTCAGATACCTCGACGATTTTCTCTCTGAACTTC
GTGGTCATTGCACTCTCTGCGTTGATCGTAGGTTTCCTGTTTTTCCTACTCATGCGGTTC
GTGATCAAAAGAACTGCCGCAGTATCGGTGATCGGCATGCTAGCTGCGTCCTACGCCAAC
GCCGGTAACCTGGGTATCCCTTTGGCAGCCTATATTTTGGATGATTTCACCGTGGTGATT
CCCGTGATTTTGTTCCAGGTGGCGTTCTACGCACCGATCACCATGACCATCATGGAGATG
CTGACCAACAAGAAATCCACCAACTTGGTGCGCAACCTCCTGGTCACGCCACTAACCAAC
ACCATGGTGCTCGCAGCGATTGCCGGTATTGCTGTGTCTTTGACTTCGATGAGCGTGCCC
GTGGTGATTGCTCAGCCAGTGGAAATGTTGGCGAATGCTTCAGTGCCACTGGCTTTGGTG
GTGTTCGGACTGTCCTTGTCCAAGAGCAAGATCCTGGAAAAGGGGCAGGTATCCAGGCGC
GATGTGTTTACGGCGGCACTGTTCAAGAATGTTCTGCACCCAATTGTTGCGGGACTTTTA
GCCTTAGCCTTTGGTATGGAAGGTACTGCCTTGTTGTCGGCGGTGATTCTCGGTGCACTG
CCAACAGCGCAGAATGTCTACACCTACGCGTTGCGATTTAGAACAGCTGAATCGATGGCG
AGAGACACAGGGGTGGTCACCACACTCATTTCCTTCCCCGTATTGGTGGCGGTCTCCATT
ATCTTTGGATCT

>RXA00297-downstream
TAGGGTTAGCATTAGTGGTCATG

>RXA00318-upstream
TCTTAGAAGGCGTAGTCACACCATTAACCTTGCCAGAATTTTTCAAGGCTTGGCTTGACT
TGGGAAACGAACATGCGGTACCAACCAGGGGAGGTAATGC

>RXA00318
GTGAGTGATGTAACCGTTGGCGATATTCTCCGCATTTTGGATGAGGCTTATCCGCCGGCG
TTGGCGGAAAGCTGGGACAAAGTGGTGCTGATCTGCGTTGATCCAACAGAGTCGGTGAAG
CGTGTTGGTTTAGCACTCGATTGCACCCAGGCACTGGCCGACAAGGCTGTGGACATGGGT
TTGGACATGCTGATCATTCACCACCCATTA

>RXA00320-upstream
AACAGACCCACTCTAGCCGTTGCGGGTTCTTATTGAGGTCTATAGTGGGGTGCTACACAC
TACAAACCGTGATTTGTTTCGTGATTGGAGCTGAGCCCAC

>RXA00320
ATGGCTAAAGAAGATTTGAAGTGGTTCTACGATCTGGCAACCGGCAAGGTTTTTCAAGGC

AAGGTTTCCGGCTTTGAAACCCGCATGGGCCCATATGACACTGAAGAGGAAGCCCATCAC
GCCATCTCCATTGCGGCAGCCCGAACCAAGGCAGCCGAAATTTGGGACGACAAGGAAGAC

>RXA00320-downstream
TAAAAAAAACTGGGGTCACACTT

>RXA00321-upstream
CAAAGACAACACAGGTTCCCTATGAAAACGGGGAACCTGTTTCACCTACTTTTTAATCAC
GCTTCACAATCACATAAGTCTTTAAAGGATGGATACAACA

>RXA00321
ATGGGCCAGCATCTAGAAGTGGAAACTAAGTTTTCCGTCAGTGAATCAACTCAGATTCCA
CAACTTGAGGCTATCGCAGAAGTCGACCACATTGATCGCACCGAAATCCACCAACTAAGC
GCTGTTTACTTTGACACCGTAGATTTGCGCCTCACCCGCGCAAAAATTACCCTCCGTCGC
CGCACCGGTGGAAACGATGCCGGCTGGCACATTAAGTTCCCCGGAACCATCGGTCGCCGT
GAAGTCCAAGCCCCACTTGATGGCGAAGGCGCAACAGAAACCCTCCCTCCACGTGAGCTC
TTGGGACACATCCGAGCGCTGATCCAAGGCCGTGAGCTGACCCCTATCGCCCAGGTGGAT
AATGAACGCCACATGTCTTACCTCGCGGATGAGGACGGCGCAGTCATCGCAGAATTCTGC
GACGATCATGTATCCACCGTGTCCCACCTTCCAGGTGGCGTGCGCAAGCAGTGGCGTGAG
TGGGAATTCGAACTCGCTGATGGCACCCTCGCCGAAGAAGCCATCTCAGTACTGCTGCAA
TCTGCACAGTCAGTCCTGACCGCAGCTGGAGCTTTTGTCTCCAACAGCCCATCCAAACTT
GTTTCGGCGCTGGACGAATCAGTCAACCACGCGCCAAAGCCTCCACAGATGGCGCAGCTG
GACAAGAATGACCCAGCACGTGGTGTTCTTGCAGCAATCGCAGCCAACGCCTCAAAGATC
GCCGAATACGATCCTCGAGTACGCGCCGATGAATATGATTCAGTCCACCAGATGCGCGTA
GCTACCCGAGAACTACGCAGCCACCTCCAAACCTTTGAGGGCATCCTCGGCGGCGAAGAC
TACCTCAACCTGGAAAAGGAACTGAAGGTTCTCGCCAACATCTTGGGTCGCGCACGCGAT
GCTGAAGTTGTGGAAGAGCGCCTCAGCAACCTGATTAACACTGAGGTTGGCGACTCCATC
GAGGAGGAGACTAAGAAGGAACTGCTTGAAGATCTTGGTGCAGAATACCGTCGTGAGCAT
GAGCGAGTAGTTCGTGCGCTGGATAATGATCGCTACACTGATCTTCTTCAGGCACTGGAA
AACCTCCTTGTTGATCCACCGCTGATCACAGAAGTCGAAGAACCCGAAGCTACCGAAGCC
CCTGAGTCCGCTGAGACTACCGAGTCCACTGACGTCTCTGAAGCAACCGAAGAAGCAGAC
GCAGAAGCTGAGTCTGTCGAAGAAGCTACTGAGCAGGAAGAATCAGCAGACGCGCCTGAA
TCTGCAGATCTGGACGCTCTCGATGAGGAGTACTCCCCTGGTTCCCAAGCGCCGGTGGAG
GAGCCGAAGGAACCGAAGAAGGTTGATGCTGCTCTCGTACTTCTAGAGCACCTTGATAAG
GCGCACGTGAAGCTCGTCAAGCTGGAAAAGAAGGCTCGCTCACAGTGGGATGATCTCAGC
ATTCCGATGCTGGAGCGGGAAGAAAACTTCCACAACCTGCGCAAGGCTGCCAAGAAGCTT
CGCTACAGTGCAGAGGCAGTGGGCAAAGCAACCACCGTTGAGACGAAGAAACTGTACAAG
GCGTGCAGTGGTTTGCAGTCAGTTCTTGGCGATTACCAAGATGCCATTACTTCCCGTAAT
GAGCTGTTGCGCCGAGCTCAGGTTGCCCGCCGCCAAGGCCGGGATACCTTCGCATACGGA
ATCCTCTACCAGCACGAACAAACCCTGTCGAGGGAATACCTGACTGGTTATTCCGATGCG
TTCAAGAGCGTAGAAAAAGCCTATGCAAAGCTGGCTGAAGATACCGCCAAGCGTTCAAAG
AAGAACAAGCGTAAG

>RXA00321-downstream
TAAACGCAGGCAATAAAAAACTG

>RXA00322-upstream
CGCGGTTTTTTGATGACACGGGGGTGGGAGGTGTCCAGCTTGGGTGGTTCACTGAGAACC
GCACCGAAATTAGAACACTCCTACGAATAAGGAAACCGCA

>RXA00322
ATGACTCTCTCCCACTTCTCCGACAACGTCACCGACGCACAAGACTCTTACCGTCAGATT
TTAGAAGAAAGCATCATCAGCCACCTAGGTTTCTGTGCGCTTCGTGGGTGGACTCCCGCC
GATCTCCGCCATGAGTTTTCCGCCGATATTGATCCACTCCTGTTTCACGCGCTACCTGAG
ATTGCTTACTCCTGCTCCGATGAGATGTACACACTGTGGGTGAACGGAACGCGTGCCGCC
GAAACTAGCCACTTGCCGGTGATGACCCTGGAGAAGATTCTCACCGAGCTACCGAAGCTA
AGTACCTTGCCTGACTGGGCAATGCTCGCAGAGCTCCACGCCTTAGACAATCAAGACACC
AGCCCAATGACCCCGGCACAGGCCAAAGCGCATCATCGTATCACCGCACTTTTGAAAAAG
GCAGAGTCCACCAACTTCGAAGAAGAAGCCGAAGCATTGATCCTTAAAGCAGAGACACTT

CGACAGCAGTACCGGATTGAATCACTGCTGATTAATTCCTATGACCAAGATGTCCAAGCT
CGATCTTCTACGATTCGTGCATCTCGGGTGTATCTGGAAGCTCCATGGATCCGACACCAA
TACAAACTGCTCAATGCCATTGCTCGGGTGCATTCCAGCGAAGCGCTGCTGATCACCAAA
TCTGGCATCTGCACCCTCTTCGGCGAGCAAGATGACGTAGCCCACATTATTGATCTGTTC
AACAGTCTTAATCGACAACGTGCCCACTTCATGAAAACGTCAGCAGGTGCCCGAATTGCC
CAATTAAATGGCGAAACAAGCTCATATCGCCGTAGTTTTATGATCTCCTACGCCAGCCAA
ATCTCTAGACTTCTCATCTCAGCAAAAGAGGATGCATTCAACGAACTAGCTGGTCAGGCA
CCACTAGCTCACAGCGCCATCGTTCCTGTCCTAGAGAACAGAAGTGTGAGGTCAAAGGAA
GCACTGAAGGAAACCTTCCCGAATATGCGGACAATGACCTTCAAATCGACCAACCGACGA
GGCATTATTGACGGATTTAATGCTGCCAATGAATCCCACCTTGGCGGGGAATCTGCCAGC
TTGGAAGACTCAACATTCATGTTC

>RXA00322-downstream
TAGAGCGGGTGAAAGCCCCATTT

>RXA00325-upstream
AGGATTTCTCTGAGGAATCTAGACGCAGATTAACTTCCGCTTGGCAGCGACCGGGATAAC
ACCGCGGTTGCGGCCACGCAGGCTCACAAAGGACACCACT

>RXA00325
ATGACAAGCATTATTGCAAGCAACAGCGACCTATCGGAGGCGCTGCGCACCCACACTGCG
CAGGCCCATGAAGAGGCCGAGCACTCAACGTTTATGAATGATCTGCTCACCGGGAAGCTC
GATGCGCAGGCATTTATCAAGTTGCAGGAGCAATCATGGTTGTTCTACACCGCTTTGGAA
GCTGCAGCTCGTGCATGTGCAGAGGATTCCCGTGCGGCTGGTCTGCTGGACCCACGCCTC
GAGCGCAAGGAAACGTTGGAAGCTGATCTGGATAAGCTGCACGAAAACACCACCTGGCGT
GACAACGTCACGGCCACTGCAGCGACAGCGTCTTATGTGGAACGTCTTGAAAGCATCGAA
GCGGCCAAGGATTTCCCTCGTTTGGTTGCTCATCACTATGTCCGCTACCTGGGTGATTTG
TCCGGTGGGCAGGTTATTGCACGTCTGGTGAACAGGGAATATGGAGTTTCGGAAGAGGCG
TTGAGCTTCTACTGCTTTGAAGATCTTGGCAAGCTCAAACCGTACAAGGATAATTACCGT
GCAGAGCTTGATGCTTTGGAATTAACAGCAGAGGAGCGTGCTGCGTTGCTGGATGAAGCA
TCTGATGCGTTCAGGTTTAATCAGCAAGTTTTTCAGGCTCTTGCT

>RXA00325-downstream
TAACCGAAGGTGAAGTCTTGGCG

>RXA00326-upstream
CCTGATCTTTGCCCCTAAGTGGTTTACGGGCTGGAAAATGGTACGTAGTCTCGGGTGTAA
AGCACACTTCGGTACTCGACAGGAAGTTAGGAATTCCACC

>RXA00326
ATGGCAATCAAGCTGTCCATTGACCTATCAGATGCAACATTCGCAGAACTTTCGGCAGTC
ATCGGTTACGCACATCAGTTGGGTGTTGATGCGGATGAGAAGCTCACCTTTGAAGGTACA
GTCCTTAACATTGAATTCGACGGCGACCTTCAGTTTGATGATGTTTTTGATGCCTTTGAT
GAGGCGGAAATTGAGCTCGACAACCCTCGCGAAGACGGCCCCATCTACGCAGATGATCTG
ATCGATGAGGATGAGGACTACCGCGCACAGACCAAGAGCCAGATCAACGACGAGGTTATC
AACGAGATCCGCGATGGTATTTCAAGCTTCGTTGATGGCATCGTAAATGGCCTTGGCCAG
GGTCGCCGCGGTGGACGTTACGGTGATTTCGGTGGGCCACGCGGCCCTCGCGGTCCACGC
AATGACGGTCCATTCGGCCCATTTGGACCATTCGGTCCGGGATACCGCGGTCCGCGTTTC

>RXA00326-downstream
TAGCGGTTACGGTCGGGTTTTAG

>RXA00334-upstream
ATAAGCCCCGCATGGGATATGAGAAAAGGAATGCACGATGAGTATTGAATTTCCGTTAGG
TAATCCAGCGCCTGCACAGTGGTTTTCTGGCGAGGTCCAT

>RXA00334
ATGGCCAAGCTTGATGACAACGTGCAGATTGAGACTGTGAACGTGTCTTTTGAGGCAGGC

GGTCGCACCAATTGGCACACTCACCCAGTCGGTCAAAACATAATTGTGCTGTCGGGCTTG
GGCATTTATGAGGCGGAGGGGGAGCCTGCTCGACTCCTGGAGCCTGGCGATGTTGTTTTC
GCAGCCGCCGGGGTTCGCCACTGGCACGGCGCCGTGTCTGGTGCACCGATGTTCCACGTG
GTGGTTAACCTCAAAGGCATCGACGGCGAGACCGTCGATTGGGAGGAGCCGGTCGACGAG
GAGCACTACCGCAGCGTGAGCGCGGAGCTACAAAGA

>RXA00334-downstream
TAAAAATGCTTTTCGACGTCCAC

>RXA00336-upstream
TTAGGATCTTAAAGGTAGGAAATTGCGCTTTGCGACGTCGAAAAGCAACGCCTTTTGACT
GCAGTATCCGCCCTCTACATGTTTGGATTTGATTGTAACA

>RXA00336
ATGGCAAAGCCGAAGAGAAGTTGGCTTGACGGACCCGAAATTCCAGCTGATTTTGACGAT
CCTGATGCACCCGGCAGGTGGCCTGGCGAAAAGTTGGGGCTTCCTCAAGAAGGGGCCGGC
TCTCTGTCCTCAGTGGCTCGTCGTATCGGCGGGGTCTGCGTGGACTGGGGTGTTTCCTGG
GTTATTGCTATTGTGCTGTCCAATTTCACGGATGTGCTGGGCGATGTAGCGACATCCACG
CTCATTATTTTCGTGATCCTGGGTTGGCTTACCGGTTGGATCTTTGCTCGCACCCCAGGT
CATGCCGTGTTTGGCATGGGCCTTGCGCGTGTGGATGCAGAGGAACGTGTGGGCTGGTGG
CGTGCGCTGGTTCGCCCACTGCTGACGATCTTGATTCTGCCTGCCGTGATGGTGGATGCT
GACGGCCGTGGGCTCCACGACAAGGCAACGGGAACTGCAGTTATCCGCGGG

>RXA00336-downstream
TAATTTGTCTTGAGTGAAATTTA

>RXA00337
GATGTGGAGGGAGGCGTCGAAAAGCATTCTTTAAGCACTGCGGACATTGCAGCTCGCGCA
CACGCCCATATGAAATCCCATGATGTTTTGGGGCGGCAGACTACGCCGCCTCAGCCGGAG
GGCGGCGTTGCTGCCCGGTTGGGCGGGATTGCGTGGACAATGATCCATAAGCAAATGCTT
TCGCGTGACACAAAAGGCCTGGATATCACCGTGTTGAGCACCATTCCTGAGGGGGTGGGG
CTGGGTGAAAATTCCGCCATGGATGTGGCGCTCGCATTGGCGCTGTATCGGGAAAATATT
GAGGAAGCCCCCACGAAGGCGCGCATTGCGGACATTTGTTCGCAGTCCGCATTCATGTTC
AGTGAGACTTCAGTGTTGCGTGCGCGGCACACCGAGGCGTTGCGGGGTGAAACTGGACAC
ATTTCGGTGGTTGATTACGCCGATGGTTCGGTCACTCAGGCGCCACATCCGGTGAGTCGT
TCCGCTGGTTTGTCGGCATTTGTTGCTGCTGCGCAAACTGAAACT

>RXA00338
GTCGGCATCACGGCCGGGCGACCCATCGCGACACGGCTTTTAGGCGGCATGGACAAATGG
GGCGTGCACGTTCTGCCCAAGGATGCAGCGTACCTAAAGAAGATGCTTTTCGACGCAGGT
GCCGGTGCGATCGGCGACTACCGAGAGTGTGCCTTTGAGATCGAAGGAACCGGGCAGTTT
AGGCCCGTGGAGGGGGCGAATCCGGCAGAGGGGGACGTCGATAAGCTTTTTAAATCCCTT
GAGCTGCGCATCGAGTTTGTTGCACCGCGCAACCTGCGCGCCCGGCTCACGTCGGTGCTG
CGGGAGGCTCATCCGTATGAGGAGCCTGCCTTCGATATTGTTGAAATGCACAGCGCTGAG
AGTTTAGAAAATGCGACCGGATTGGGTCGTGTGGGTGAATTGCCGGAGCCGATGCGCCTC
GCGGATTTCGTGCAACAAGTGGCCAACAACCTGCCTGTCACCGAATGGGGCGTGCGCGCT
ACCGGCGATCCTGAACAAATGGTGTCCCGTGTGGCGGTTTCATCAGGGTCGGGTGACAGT
TTCTTAAACGATGTGATTAAGCTCGGAGTGGACGTTTATGTCACTTCTGATCTGCGCCAC
CATCCAGTTGATGAATATCTCCGAGAAGGTGGCCCTGCAGTAATCGATACTGCACACTGG
GCCAGCGAATTTCCATGGACTTCCCAAGCCCAAGAAATTTTGCAGGACAAAGCCCCACAG
GTTGAAGTTGATGTGATTTCGATCCGCACAGACCCCTGGACCATGTCTGCGCGAGCAGTG
AAC

>RXA00338-downstream
TAAATTCTTGAGAACTAAAAAAG

>RXA00339-upstream

ACAGGTTGAAGTTGATGTGATTTCGATCCGCACAGACCCCTGGACCATGTCTGCGCGAGC
AGTGAACTAAATTCTTGAGAACTAAAAAAGGAGAACTTCA

>RXA00339
ATGAAGCTGGACCCATCTCTGCACAAAACCCTGCTGCAGCTCGCCACCACCCTGCGCACC
CAAAACGCCAACTCCGCACCGAAGACCACCCCGGAGCAGGAAGCTGTAGACAAGGCTGTC
GCTGAACTTTCCCGCAACCGCGACGCTGCATCCGCTGGACAAATGGCTGTCGATGACATG
GAAAACGAAATCCTGCGCATTCAGTCCGACGAACGCAAACTGCGCCGCCGCAAGAAAGAC
GGCCAGGACGCACTCGGTGCAGAAACTGACGAAGAGCGTCGCCGCGACCTCAACCACGAC
GTCTACACTGCGAAGTCCCGCATCGCTGACCTCATGAGCGAACTGCAAGAAGCTCACAAT
GAAATCCATGCGCTGCGCAACAACCGCGACCTCGCACAGTCTCGCGTCAAAGACACCGAA
CGCAAAGTTGCCGACGCCCGCGCAGCCGCAGAAGCCGCCGCAGCAGCAACCCCAGAAGGT
GAAGACCCAGCAGTAGTCATCGCACACCTGGAAGAGAAACTTCCCTCCGAAGCACTGGCA
GAATTCCATGCACAACGCCTCGAAAACGGCGTAGGCGCAGCACTCTTCAACGGCCGCTCC
TGCAGCGGATGCGCCATGGTTCTCCCTGCAACCGGTATCTCCGACATCCGCAACACCCCC
AAAGATGAGGTTCCACAGTGCCCAGAATGTGGCTCTTACCTCATCACTGACATCTCT

>RXA00339-downstream
TAGAAAGACCACCCAGTGAAATT

>RXA00342-upstream
TAGCCCCGCGGTTTCATGTTGAATCCATGTAATCGAAAACACATCGGGGCCCACACGAGG
AGAATTATTAAA

>RXA00342
GTGGCCGACGCTCCGGGCGCAGTCAAGCAAGGTGCCCAGGATTATGCTCAACTACTCGGC
ATTCAATCGGGTCATATCGTTCAAGAAATTGGATGGGATGAAGATTCCGACACGCTGATC
AGCGAGTCCATCGAAGATGCAATCGGTGAGGAACTACTCGATGAAGAAACCGACGAGCTG
TGCGATGTCGTGCTGCTCTGGTGGCGCGAGGATGACGGCGATCTCGTCGACGGACTTGTG
GATTCCATCCGCTCCCTCGCTGAGAATGGTCGTATCTGGGTGTTGACTCCTGGCATTGGT
AAAGAAGGAGCCCTGGCTCCTGGAGTTATCTCTGAATCAGCTCAACTGGCAGGTCTCGTG
CAGACCAAGGCAGAACGTCTCGGTAATTGGCAAGGTTCTTGCCTCGTCCAGCGTGGAAAC
AAGAAGCCT

>RXA00342-downstream
TAACAATCGCTAATTTCCACGGC

>RXA00344
ATGAGTTTCGGACTCGGTCTGTCCGTGCTGTTCATTCACCTCTACCCCGGCCGAAGCTCC
ACCGCGTTCTCCCTGCTCACAGGGCAAATCGTTGGTGTTTCCTCATCATCGCTGTGGATC
CTTGTGGCAGTCACCGTGATCGTGGTTAGCGCCGTGGTGATTTTCTGGCGCCCGCTGCTT
TTCGCCAGCGCCGATCCGATCATGGCGCAGGCCTCCGGAGTAAACGTCCGATTCATCGCC
GTTGCCTTCGCAGTTCTGGTTGGCCTCACCACGTCCCAGTCCGTGCAGATTGTCGGTGCG
CTGCTGGTCATGGCATTGCTGATCACTCCCGGCGCGGCCGCTGTGGCGGTGACCGCCAAT
CCAGTGAAAGCCGTGGTGCTGGCAGTCATCTTCGCGGAAGTATCGGCTGTCGGTGGCCTG
CTATTGTCGCTAGCGCCTGGTTTGCCGGTGAGTGTTTTTGTCACCACCATCTCTTTTGTG
ATTTACCTGGTCTGCCGCCTGATCGGTTGGCTCCGCGGCCGTGGAGCTCAGCGTGACGAA
GATGCTTATCGACGCCGCCAGCACGATCACCACCCTCAC

>RXA00344-downstream
TAGGCGTTTCGAAGT

>RXA00349
GAGAAAATCCTGGACGAGTTGGAGCAATCCCCTGCGTCTTATGGTTTCCCTGTTGCGTTG
CTTGGCTGGCCAATGATGGGTGGTGCTGTTGCTGTGCTGTTGGGTGGTGGATGCCAGGTT
TCCCTAATTGCTTTTATTACCGCGTTCACGATCATTGCCACGACGTCATTTTTGGGAAAG
AAGGGTTTGCCTACTTTCTTCCAAAATGTTGTTGGTGGTTTTATTGCCACGCTGCCTGCA
TCGATTGCTTATTCTTTGGCGTTGCAATTTGGTCTTGAGATCAAACCGAGCCAGATCATC

GCATCTGGAATTGTTGTGCTGTTGGCAGGTTTGACACTCGTGCAATCTCTGCAGGACGGC
ATCACGGGCGCTCCGGTGACAGCAAGTGCACGATTTTTCGAAACACTCCTGTTTACCGGC
GGCATTGTTGCTGGCGTGGGTTTGGGCATTCAGCTTTCTGAAATCTTGCATGTCATGTTG
CCTGCCATGGAGTCCGCTGCAGCACCTAATTATTCGTCTACATTCGCCCGCATTATCGCT
GGTGGCGTCACCGCAGCGGCCTTCGCAGTGGGTTGTTACGCGGAGTGGTCCTCGGTGATT
ATTGCGGGGCTTACTGCGCTGATGGGTTCTGCGTTTTATTACCTCTTCGTTGTTTATTTA
GGCCCCGTCTCTGCCGCTGCGATTGCTGCAACAGCAGTTGGTTTCACTGGTGGTTTGCTT
GCCCGTCGATTCTTGATTCCACCGTTGATTGTGGCGATTGCCGGCATCACACCAATGCTT
CCAGGTCTAGCAATTTACCGCGGAATGTACGCCACCCTGAATGATCAAACACTCATGGGT
TTCACCAACATTGCGGTTGCTTTAGCCACTGCTTCATCACTTGCCGCTGGCGTGGTTTTG
GGTGAGTGGATTGCCCGCAGGCTACGTCGTCCACCACGCTTCAACCCATACCGTGCATTT
ACCAAGGCGAATGAGTTCTCCTTCCAGGAGGAAGCTGAGCAGAATCAGCGCCGGCAGAGA
AAACGTCCAAAGACTAATCAGAGATTCGGTAATAAAAGG

>RXA00349-downstream
TAAAAATCAACCTGCTTAGGCGT

>RXA00353-upstream
CTTTCATCAGGACCGAAAGCGAACGTTTCGTATTGTTGAGCCTTTTGGTTCCACCACGGA
TGCGCTGATCTATTTTCATGGCTCCCAGCAGTCAGGATCT

>RXA00353
GTGGGGCGCAGCTTCACCAACAGGACTTTTGATCCGTTGCCGTTCATGGTGGTTTATCCG
GATGGGGTGGATCAGCATTGGAATGATGCGCGGTTGGGTTTGGATGAAAATACCCGCCAT
TTAGGCATTGATGATGTGGGGTTCTTTGTAAAACTCGCCACGCACTTGGGCAACACGTAT
GGCATCAAGAGGATCTTTATTGTTGGCTATTCCAACGGTGGGCAGATGGTGTTGCGGCTC
ATGCATGAGGTTCCCAAGATGCTCAGTGGCGCTGCAACCATTGCATCCAACATGCCAGTT
GCAGAGAATACGCTGCCGCAGGTGAAAACCTTCAAGACACATCCGGTGCCTTATTTGGCG
ATGGCTGGAACTGCCGATACTTTTTCACCGTATGAGGGTGGCGATGCCGGTATTGGTCGC
GAACACCGCCGTGGCGTGGGCATGTCCGCCTTTGATTCAGCTGCCTATATTGCCGCCCGA
AACGGACTGACCGAACACCGCCACGACGTGATTGATGATGTGGTGTCGATCGATACCTGG
GATGGAGAAAATCCCGTTGAGTTTTGGACACTCAACGGGATCGGCCACTTGGTACCAAGT
GGGAAAACTTATCCAGAATTTCTAGGCCCCTCAACCACATCAGTGATAGCGGCTGAGGAG
ATTGGGAAGTTCTTTGATGGGGTCAGGCGTCGA

>RXA00353-downstream
TAAGCTCAAGCTTTAAAAACGCA

>RXA00355
ATCGCTTTCGGTCGCGCAGCTCACCGCATGAAGCAGCAGGGCCAAAGCGGAGCTTTCACC
GTCCTCGAAGTTGCTCCATACCTGCTCTCCCCAGAGAACTTGGACGATCTGATCGCACGC
GACGTC

>RXA00355-downstream
TAATTTAGCTCGAGGGGCAAGGA

>RXA00362
GATGAAAAGACGGGATGGACTGCTGAAAGGTCCGCAACGTTAGTCGCGGGCAACTCTGGC
CTTGGTGTTGCGTTGCCTCCCAATTCAACAATGTTCATCATTTTGGCATTGCCAGCTGCA
GCAGCTTCTTCGGCCTCTCAGGTGTACATTGCTTTGGCTTGTGGTGGTGCGTATGCAGTG
CTCTACCGCTTAGCGGTCGTCTTTTACTGGACACGTAAAGATAAAATTCCTGCCACCCCT
GATGATCAACGGGTGTCATTCGGTGAGGCAATGAAGACTGGATGGCGTTCACCGTTGATC
TTCCTTGGAATTTTGATCCCCGTAATCCTCACAATCGGCCCATTGTCTGAATGGTTAAAG
ACACATGGAGTTGGGGAGTCTGGTGTTAAATCGATGTCGATCATCGTGTGGGTGCCAATT
CTGATTACGGCAATTGCTCTGATTGAAGGGCGTAAACGAATTGCTAACAACATGGCACAC
TTTAGGGTTCAGATCTCCAAGGACTTGCCACAATTTGCCACCGTAGGAATTTCGTTGTTT
TCTGCGCTTGCAGCAGCGAACATCATGGAAGAACTGGGTGTTGGCCCGCAGTTGTCTAAC
TGGCTTGATTCCATGGACCTACCTAAGTCTGTCATGGTGATCATTGTCTGCATCATGTGC
ATTGTGGTGGCAACGCCACTGTCGTCAACAGCAACCGCGGCTGCGATTGGTGCTCCCGCT

GTCGCTGCGTTGGCTGCGGTAGGTATTGATCCAACTGTGGCGATCGTAGTGATCTTGCTG
TGCACTTCCACTGAAGGTGCATCCCCGCCGGTGGGCGCGCCGATTTACCTTTCTGCTGCG
ATCGCCGATGCAAACCCAACGAAAATGTTCGTACCACTGATTACGTACTTTGTTGTCCCC
ATGATTCTGCTTGCTTGGCTAGTTGGAATGGGATTCTTACCAGTGATTGTTCCTACGGGT

>RXA00362-downstream
TAAAGGGGTAAAAATGAACTCAA

>RXA00373-upstream
CACGTGGCGGATCTGCGCGCTAAGGGCGAGCTGCCGCCGCCGAGGAAGAAACGCAGGCGT
CGAAAAGCGTCTTAAAAGGTTTTTCACTAGGGTGTTGTCC

>RXA00373
ATGGACATCCAGCAGCTAGACGCCGAAACAACAGCATGGAAAGACAGCCTCCTGCGCGCC
GCACAGGAGGCTGGTTTTCATTTTGAGCCACCGAAACTCTTCGAGGATTTTGAGACCATG
GTGGAGCAGTACAAGCAGGCAGCTGCGAGCGACCCGGACATTGATGTCACTGATATTCAG
CAAATGTGGGGCATCGTGGTGGGGGAGTACCTGCGCGAAAAAATGGGCATGGAATGGGTC
GTCATCACCGATGACTACGGCACTGACCTCGCGATTCTAGCCACGGCACCCAACGGGGAC
CACGTATATTCCTGCCCCATCATCGTGGTGGGCAAGCGC

>RXA00375-upstream
CAGCCTGTCAAAATGCTCACCGACTACGCACCAGAAGACGCTAAACGGTAAGTACTGAAG
AATTTTTAAAGACGACGGAGATTTCACCACAATGCCAAGC

>RXA00375
ATGTTCCCATCACCCGCAACTGGCGGAGATGACATCAACCGACGCCCCCTGAATGAACCA
AACGCAGATGCAACCACCATCCCCACTGCACTAAAAGTGGTGTTCTGGATGCTGTTTGCC
ACTGCAGCGTTCATGATTTTTACAGGCCTGGTGATGTACACCGCCGGATACACGGGACCT
GATGATGTGGATGAGAGCTACAAAGCCGTTGTGGTGAACAACCAGGAGTTCATCGGTGGC
ATCAATGCCTTTGCTGGCGTCGTGATTGCTGCACTTACTTCACAACTGCCAAAGGGCGGC
AAGAATCCGCGCCGTCTTTTGTTGGCCATCATGTTGTTGGTATTGCTGACAGATCTGTTG
TCTTTTGCCACCCGCGCTGGAGGCTTCGCACTCGCAATCATCGCAGTCTTGTTGGCTTTG
GAAGCACTCTTGATGTTCCGCCCAGCAGTCAATGATCACATTGACCGAAATCATATGGCT
CGTGTAATGAATCGCGAGAAG

>RXA00375-downstream
TAGAACGGTTCGACCGTACTTTT

>RXA00380-upstream
CAGGCAATGCGACCTCGCCTCAGTGACATCCTTGGTGTTCCAAGACGATCAAATTGTCGG
CGTGCATTACAACGAACCAGCTCAGGAGATTTGATCACTC

>RXA00380
GTGCGTTTGACCAAACTAGCAGCAACAATCGGCTGCGTGACACTCAGCGGACTTGCGCTA
GTAGCCTGCAGCAGTGACAGTACCGCTGGTACTGACGCTGTTGCTGTCGGCGGAACCTTC
CAATTCCACTCCCCGGATGGAAAGATGGAAATTTTCTACGACGAGGCTGACCGTCAACAA
CTCCCCGACATTGGTGGAGATTCCCTCATGGAAGAGGGCACACAGATCAACCTGTCTGAT
TTCGAAAACCAAGTTGTCATCCTCAATGCGTGGGGGCAGTGGTGTGCACCGTGCCGCTCC
GAATCCGATGATCTCCAGATTATCCATGAGGAACTCCAAGCTGCCGGAAACGGCGACACC
CCTGGTGGCACCGTGTTGGGTATCAATGTGCGTGATTACTCCCGCGACATCGCCCAAGAC
TTTGTCACCGACAACGGCCTTGATTACCCAAGCATTTACGATCCACCATTTATGACAGCA
GCATCCCTCGGTGGTGTTCCCGCATCGGTGATCCCAACCACCATCGTGCTGGATAAACAG
CACCGCCCCGCAGCAGTGTTCTTGCGCGAAGTCACCTCCAAAGATGTGTTGGATGTTGCG
TTGCCATTGGTAGATGAGGCC

>RXA00380-downstream
TAAATGTCTGAGATTGTGGTAGC

>RXA00387
CAAAACGACCCAGAAACCTGGGAAGACTACGAACTTCGCGTCAACCACCCACTGCGCATC
GAAGGCGACCGCGTCTACCTTCAGGGCCACGGCTTCGCCCCAACATTCACCGTGACCTGG
CCAAATGGCGAGACCCGCACCCAGACCGTGCAGTGGCGCCCAGACGACCCGACCTTCTTC
CTGTCCTCAGGCGTGGTCCGTTTCGATCCACCCGCCGGCATGTACCCAGACCTTTACGAG
CGCCGCCAAAACCAGTTGGCCATCCAGGGACTTTTCGCACCGACCGCGGAATGGGAAGGC
GACAACAACGAACTGCTGACCTCCTCCTACCCGGCGATGCGTGACCCAGCCGTGGCGATC
GATATTTACCGCGGCGACAATGGCCTCGATACCGGCATCGGACAGTCATTGTTCAGCCTG
GACTCTAGTCTCATGCACAGCGGCGTGCTGCAAAAAATTGAGCGCGTCAACCTCCAAATC
GGCGACACCGTCACCCTGGATGATGGCACCACCGTCTCCTTCGACGGCGCGTCAGAATTT
GCCAACTACCAGATCAGCCGCGACCCCACACAAAACTGGGTGCTGGTCACCACCGTGATT
TCGCTGGTCTCCCTGGTTGGATCCCTGATGATCCGACGCCGCCGCATTTGGGTGCGTTTC
TATCCACAAGAAAACGGAACCACCCGCGTGGAAACCGGCGGACTTGCCCGCACCGACCGC
GCAGGCTGGGGTGGCGAATACGAGAAATTCCACCGCGAACTGCTGGGTCTGAAGGAGGAA
GATGAAGACGAAGAGTACTTCGACCACGACGAC

>RXA00387-downstream
TAACACCGCAATTTAAAGGCTTT

>RXA00390-upstream
GGAAATAGACCGTTAATAGCTGGTCTTTACATTTGCCAGAAAGCTCCGACGAAACCCCAA
TAGTTGACACGGAAACTAATTCATTCTAGCTTTAGTGACC

>RXA00390
ATGTCAACTACCAGGGAAATTGCATTCCTCATCGCACGTATCCTCTTGGGCGTCATCCTC
ATCGCCCACGGCTGGGACAAGTTCGCCATCACAGGACTTGAAGGCGTCACCGGCTTCTTC
GATTCACTCGGCATCCCAGCAGCCGGCATCGCCGCAATAGCTGCTGCAGTCGTCGAGCTC
CTAGGAGGAATCCTTATCATCCTAGGAGTATTTACCCGCATCGTTGCCGCCTTCGTTGCC
ATAGACATGCTCTTCGCAGCACTGTTTGCGCACGTCTCCTCCGGCATCTTTGTCACCAAC
AATGGTTGGGAACTCACCGGCGCAATCGGCGCTGGCGCGCTGCTTCTCATCGCAGTTGGC
GCAAGTGCATGGAGCATCGACGGGGTTCTGGCAAAACGCAAGGCC

>RXA00390-downstream
TAAATCTAGCGCCACAACTCCGA

>RXA00392-upstream
TGCTTGAAATACGTTCGGCAGGCTATGGGGGAGTGTGAAACGCTATTGTGAAATGAATAG
ATAGGTTCCATAGTCGATCGAGGAGGAGTCGCAGAAGTTT

>RXA00392
ATGTGGGTTGGTTATGCGGTTCGACAGATCGCCAGTGTTTTTCTTACTCTTTTGCGCATG
CTGCCACTAGCAGCGCGAAATCGAGTTGCCAGGGGACGCATCCCGGAAACCGGCGATGTG
GTGATCTCATTGACCACCCATGGGAAGCGAATTAACTACGTTCACTTCACCATCGAATCG
ATCGCACGCGGCCATGTGAAAGCACCAATTGTGCTGTGGTTGGACAAACCAGACTTTGAT
GCGCCGTGGCCTGCCACCATTAAGCGACTTGTCGCCCGCGGTCTGCAAGTACGGTGCAGC
GACGGCTTCTACGGCCCCCACACCAAATACTGGAACCAATTCCGAGAAATCCACGGCACC
GGCGTGCGTGTCGCCACCGTCGACGATGACATGATCTACCCCGAGTGGTTCCTGCAGCGC
TTGCTTTTTATTGGCGACCTGCGCATGGATGCGGTTGTCGCCTACCGGGCGCACAGAATT
GAGCTTCGCGACGACCGAATGCTCCCGTACGTTAAATGGAGTGCCGCAGACACCTCAAAA
GCGTCATTCCTGCACTTTGCCACGGGAGTGTCAGGCGTTTTGTACCCCGTGACCTTCATT
GATTATGTGGTCTCCCAGGGCGATGTATTCCTTGAGAACTGCAAGCGCGCCGATGACGTA
TGGCTGCATGCCTGCGCACTGCGCTCTGATCACCCTATTCGCCAGGTCTACGCTCAGCCC
CGACACTTCGCTGTCGTGCCCACCACCCAAGTGGGAGCACTAGTTGTTGGCAACACCCTC
ATGGGTGGAAATGATGAGCAGATCGCCAAAGTGTACACCGATGAAGATGTGGCAAAACTA
GTTGCAGCCAGCAAGAATGAAGAC

>RXA00392-downstream
TAAAACAGCTTCGCGATAGCACG

>RXA00394-upstream
ACCCACTTGAACCTCTCCTTAAATATTTGCTTCAACCTCCCACAATACGGAACTTTGAGG
CATTCTTGGGTATCGGTATGTATTGAGTAGGGTTGAATAT

>RXA00394
GTGAGTGAGTCCAATACCCCCAATCTCCAGACACACCAAGCGCCGGAATTAAACCCGGAA
CTACAAAAAGCTGCCCGGAAAAACGTGCTGATTTACGGTCTGGCACGTTTGCTTCTGTTC
GTCGTGCTGACCTTGATTATTCATAGCCTGGCTCTGCTGATTAGTGCGCCTGTGCCACTC
GTTATGTCTGCGATGCTGGCTCTGATTGTGGCGTTCCCATTGTCCATGCTGGTGTTCAGC
AAACTGCGCATGAATGCCACCCAGGCTGTTTCCCAGTGGGATGCACAGCGCAAGGCCCAC
AAGGAATGGGTTCGAAGCGAGCTGGCGGACCGC

>RXA00394-downstream
TAAAAAATTCCCCTCGTTCTTTG

>RXA00395-upstream
ACTCACATATTCAACCCTACTCAATACATACCGATACCCAAGAATGCCTCAAAGTTCCGT
ATTGTGGGAGGTTGAAGCAAATATTTAAGGAGAGGTTCAA

>RXA00395
GTGGGTAGGCTTTTGCTGATTATTTTGGTTATCGTCGCAATCGTCTTGCTGTGGAAGGCC
TTCAAGCCATCTACATGGAAGCGTAACGCGGAGATCAATCAGGGCCAGGCACCTCGTGCA
GTGAAAGGCCCCGACGATGATGAAGAATTCTTGTGGAATATTGAAAAGAATCGCTTCAAA
CAGCGTCGCGCCGACGAGGCTGCCCAATTAGAAGAGGAAGAACGTCTCAAACGGGCCAGG
GAACGCTACGCAAAGCCTGAAAGCTCAGAAGAAGGTCCAGAGAAGCCCACTGAGGATTCT

>RXA00395-downstream
TAAAAGGGCTTCTTTAAAAAGAT

>RXA00396-upstream
ATCCCTTGGCGCTACAACGGTGTAGCCATTGGTACCGAGGATCTGTGGTACATCGGCGCA
GACAAGACCTACATTTTGAGCCAGCGCTAAGGAGAACCCA

>RXA00396
GTGACAGAAATTGCAGAAAACCTTCAGCGCTTGGGTATTGAATTACCTGATCTACCAGCA
CCGCAGTATTCCTACGTACCGTTCAACCGCCAAGGAAACACCCTCTATGTATCGGGGCAG
ATTTCACGAACCGCAGCGGGAGACATCCTCGCCGGACGAGTTGGCGAAGACGCAACATTA
GAAGAAGGAATCCACGCCGCAGAGGTAGCCACCATCAATCTGCTGGCCAGAATCCACCAA
TCCATCGGTTTAGACAATGTGGCCCAAATTCTGAAACTGAATGTGTGGGTCAATAGCTCC
GATGACTTTATTCAGCAGCCTCAAGTGGCCGACGGTGCATCCCAGCTCCTTGAGGCAGTG
TTGGGTGAGGCCGGAAAACATGCACGCACAGCACTACCCACAAATACTCTCCCCCAGGGA
GCACTAGTGGAATTGGATGCTGTCGTTGCGGTCACCGAGGCCGCCGAAGTT

>RXA00396-downstream
TAGGACGCGTGGGCGAAAATTTC

>RXA00397
AACCTGCACTCCTCCAACAGAATGCTCTTCCCTGGACCTCCTGTGGATTTCCCGATCAAC
GCAGAAACCCGATGCATTCAGCTCGACGCCGGTGTTGCAGTAAAGAAGGACGGCGTGGTG
CTGGGTACCTCAGATATGGCGAGGTCCCTGCCTCGAACCGCCGCTGGCCAAGAAGCCTAT
GAGTACTTCTTCAAGGTGGTTCGTGAAGGCATCATCGGGCAGCTGCGCCCGGGCGTGATC
TGCGCTGACGTGCACGAAGCAACCCTTGATTACCTAAGCCCGCAGCTACCTCGCATGATT
GACATCGGAATGCTGGGTGCCGACACCGATTTCAACACCATCTACCGCAAGCGCAATGTT
GGCCACCTCATGGGCAAGCAGGAATCCTTTGCCAATGAGCTTCGCCCTGGATACAAGCAC
ATTCTTCACCACGGCTCCTATGGTGCCGCGGAGATCCCTTGGCGCTACAACGGTGTAGCC
ATTGGTACCGAGGATCTGTGGTACATCGGCGCAGACAAGACCTACATTTTGAGCCAGCGC

>RXA00397-downstream
TAAGGAGAACCCAGTGACAGAAA

>RXA00398
TACCTCCCCGAGCCTTTCACCGTGGAGGATTACACTGCGCGTGTTGAAGGCCTCGAAGTT
GCTGGCGGAGCGATTGTTTCCGGTTCTTTCCAGGCTTTCGACCAGGGCTACCTCAAAGAT
GCTCTCGCAGTGCTTGGCCCAGGCTATGTCGGTGTCACTCAGATCCCCGCAGATACCTCT
GATCAGGAGATTCTTGATCTGGACAAAGCTGGCGTGAAGGCTGTGCGTTTAAACTTGAAG
CGCGGTGGTTCGGCAGGTCTTGACGATCTCGAGACCTTGGCACGCCGAGTCCACGACCTA
GCCGGTTGGCACACCGAACTCTATGTGGATGCTCGCGAACTAGACGAGTTGGAATCAACC
TTGGCCTCCCTCCCTGCTGTCAGCATTGATCACTTAGGGCTCCACCGCGATGGACTTCCC
GCACTTCTTCGCTTGGTAGAAAATGGCATTAAAGTCAAAGCAACCGGATTCGGACGGGTA
GAACTAGATCCAACTGAAGTCATCCAGGCAATCATGGCTGTCGATCCCACTGCTTTGATG
ATCGGAACTGATCTTCCATCCACCCGCACTAAGCGACCTTTCGAAGACGCTGACCTAGAT
TTGATCGCTGAAACGGTTGGCGAAGATCATGTCGACAACGTCTTCTGGAACAACGCTGCA
GCGTTCTACCTCGGAGACCAG

>RXA00398-downstream
TAGTTTTAAGACCCGAAATGTCT

>RXA00399-upstream
GGACATTGCTATGTCGTGAGTTGTAGTAACCCCAAAGCCCACGGATTAATCAATAGTGAA
ATTCAATGATTTTCTTTTCCCACAGGCCTAAACTTAAATC

>RXA00399
ATGAGCCACAACGACAGCCCAAACTTTGCTCGCCGAGCGCTCAATTGGCTCCGCCAAGGT
TATCCAACCGGTGTTCCGCGGCACGATACTTTCGCTCTGTTTTACGTTTTGGAGCGCGAA
CTTACTGAGGAAGATCTCAATGAGCTCGCAGAGCTTCTCATCGCGGAAGGTGAGAACAAT
GGGCTGCACGATAATCCCATTACGCGTGAAAAAATCGGCAAGCTGATCACGCATGTTCAC
AGTCAGCCACCTGAGGATGAAGACATCGATCGAATTCAGAAAAAGCTGCAGGCTGAGGGC
TTCCCCACCCGCAAT

>RXA00399-downstream
TAATTAATTGGAGTTTTGTTGTT

>RXA00408-upstream
GGGGGAGTTTCTCAGCCGTGGCTCACGAGATTTTCGATAATTTGGCAAAGTGGACATTAT
GACAAATACGCACAGGCGAACCCCAGAACCACATGAGGGC

>RXA00408
ATGAATCCAGTGTCACCAAAACTGACCACGGCCAGGTACCTCACCCGCATTCCATGGCTG
CTGATCAGCGCGATTGTGTTTGGGGTGCTTGGAGTTTTTGTGTCTTCGTGGTTTTACGCC
GGTGTGATCGTAGTTGCCGTCATTCTTATCTGGCAGCTGTGGCTGATCCCGCAGCAGGTC
AAGCGACTGGGATGGCTGGAAACCTCCGATGAGCTGCTGATCACCAAGGGAAAACTGTGG
CACACCTTCACGGTTGTTCCCTATGGCCGCATCCAGTTTGTTGATGTCACCGCAGGTCCC
CTCGAGCGCGCGTTTGGCATGAAACAAGTGCAATTGCATACCGCGTCGGCGTCCTCTGAC
TCCACCATTCAAGGCCTGCCTGTCGCGGAAGCCGATGCCTTACGTGAGCGACTGGCTATT
AAGGCCCGGGAGAGGATGAGCGGACTA

>RXA00408-downstream
TGAGCAGCCTTGAAGGGTTTCGA

>RXA00409-upstream
CGGCGTCCTCTGACTCCACCATTCAAGGCCTGCCTGTCGCGGAAGCCGATGCCTTACGTG
AGCGACTGGCTATTAAGGCCCGGGAGAGGATGAGCGGACT

>RXA00409

ATGAGCAGCCTTGAAGGGTTTCGAAAAGTCCACCGCGCCACCCCATTCCTTCGCATCTGG
ACCATCATCGTCGCAGTTCTCGCGGCATTCGCATTCAATTCCGGCGCATCCGTTTTAAGT
TTCATCTGGGGTGTCGTCACCGGCGAATACGGATTCGCAGTGCTGCCGATTCTATTGACC
GTCGGTGGCGCCGTCATTGTGGTGGCACTGGCCTGGATTATCACCGGAATTTGGTGGAAA
GCCGTCGGATTCCGCATCACCAATGAAGAGGTGCAGCTGCAACGCGGAGTGATCAGCAAA
GACCTCCGCACCGCCCGATTTGACCGTATCCAAGCCGTTGACCTGGTGGAATCATTCATC
GCCCGTATCTTCCGACTGGCAGAAGTCCGCATCGAAACCGCCGGCGGCAGCGACTCCGCC
ATCAGCATTGGCTTTTTAAGAAAAAGCGAGGCCGAGGCCCTAAAAAGGGAGCTTCTCGAC
GCCTCCCAGCACTCAGTCGCCACCACCCCAGCCGGAGTTCCGGCTGAGCCTGGGGTAGGG
GAGACCGTTGTAGTTGAGAGCGCGGGCGATGTTCTGGTTCCACAAATCCCCGTGCAACGC
ACCCTCGCCAGCACCGCCTTATCACTAGCAACCATCATCACCGCGATCGGTATTGTGATT
TTGCTCTTCGTTCCTTTCGGAGTGAGCATTGCCGTGCCGTTCTTTGTAGGCATGGTGCCA
GCGGTCTGGAACTTGATCGATAAGTCGTGGCAATTCACCGCAACACAGCGCAACGATGTC
CTGCATGTCAGCTATGGACTTGCCAACCGCCGCAAACAATCAATCCCACTGGGACGCATC
CACGCAGTGAAACTAAAACAGCCATTGCTGTGGCGACTGGTTGGCTGGTGGACCGTGACC
GTGCCTGTAGTTGGCTACGGCGACACCACCCAAGGCGGAACCTCCAAAATCTTGCCCGTG
GGTTCCAAAGAACTCGCACTAAAAGTCCTTGAAGCGGTGGGGCCACTAAACAGCGCCGAC
ATCGCCGAATCTGCAGACCCATCACATATGAGCAGACCCCAGTACACACCACCAGTTGCT
GCACGCCTGCTCACACCAGTCGATCGGACCCGCCAAGGCGTCACGTTGATTGGTGTGGCT
GGTGCCCCTGGTGCGGTGGTCGTGCATGAAGGCAGATTCATGCCACGTATGTCTGTGATT
GATACCTCCCACATCCAAGAACTCACCCTTAAACACGGGCCGATCCAAAGAATACTGGGA
CTCTCCACCGTTGTGTTTAACCTGGTCCAAGGGCCAGTGGGAATGGCCGCATCGGATCTC
AGTGCAGCTGATGGAAAAGAACTTCTCAACATTCTCCGCAACAGAAAACTACCCGCACTG
GAATCAGCTCCGCTGGGACAAAACAGCCTGGAC

>RXA00409-downstream
TAAGGTGTAATCATGCACATCTC

>RXA00411-upstream
CATTTGGCAAAATGACTGTTCGACTCACCGGCAACACCGCTGCGATTGAAGAGTTCTATC
AAACCTTGACCAAGACCACGACCATCAAGGAGATCACCCG

>RXA00411
ATGAACGAGATGATCCTCGCAGCTGACTGGAACCGGCTAGGACCCACCTTCCAAACAGCC
ATCATTGACACCCTGTTGATGGTCATCATCACCATGGTGGTGGCTGGCTTACTGGGTCTT
GTCGTCGGCCTGCTGCTTTACACCACCCGCGCTGGTGGAATCTTGAAGAACAAGGTCATC
TACACCATTTTGAATGTGCTGGTGAACTTTGTTCGACCCATCCCATTCATTATTTTGATC
GCCGCCATCAAGCCACTAACGGTCGCCGTCATGGGCACCTCCATCGGCCGAGATGCCGGC
ATCTTCGTCATGGTTGTCGCAGCGATTTTCTCTGTGGCTCGAATCGTGGAGCAAAACTTG
GTCTCCATTGATCCTGGTGTCATCGAGGCAGCTCGCTCCATGGGTGCGTCCCCGATGCGC
ATCATCGCCACCGTGATCATTCCAGAAGCACTTGGACCATTGGTTCTGGGTTACACCTTC
CTGTTCATCGCGATCGTCGATATGTCCGCAATGGTCGGCTACATCGGTGGCGGTGGTCTT
GGTGACTTCGCCATTGTTTACGGCTACCGCGCCTTCGACAACGAAGTTATGTACGTTGCC
GTCCTGGTTATCGTCATCATCGTGCAGGCAGCCCAGCTTCTGGGCAATTGGCTGTCCAAG
AAGATCATGCGCCGC

>RXA00411-downstream
TAAACCTCTTGCATAGAAAAACC

>RXA00416
ACTTCCCACTACGCCAACCCGCTTGGTGAGTTCGGAAACAGGAACGCATTCATCGAAGAT
CTCGCGATCCGAAGCTGGAATGAGTTGGCTGATCCTCAACAATTCAGCGACGCCTTGAAC
ACCTCTCCATGGACGATCCCTGAGGTGTTCATCTTCCGTGGCTCCATCGATGATCCTGAC
GCCGGTTGGAAATACGATGTGGCTGAAGATCTGTACCCGAACAATCCAAACGTGCGCTTC
CGCGGCGTGTACTTTAACCCGGAGTCATTTGATCAGATGTGGCAGACCAAGCAAGTGGGA
CCTTTCGTGGTGGTAACGCACAATGAG

>RXA00416-downstream
TAATTCCTCACCAAACGACCCAA

>RXA00418
CTGGCGTCTTACTTAAGCCCAACTGCGCTGGTGGTTGCGGTGTTGGCTATTCCGCTGTCT
GCGACCCGCCTGTATTTGGACGGAATCAGCGTTGACCAGGGCTTTAGAACTCAGTTTTTA
ACCCGCATGGCTGACGATATCGGCTTGTCGGACATGAACTACATCGATATGCCTACCTTC
TACCCTGCTGGATGGTTCTGGCTCGGTGGTCGCTTGGCCAATCTTTTGGGGCTGCCCGGT
TGGGAAGCTTTCCAGCCATGGGCAATTGTGTCCATGGCAGTTGCTGCTTCTGTGTTAGTT
CCAGTGTGGCAGCGCATCACCGGTTCCCTGCCGGTGGCAACAGGCATTGCGTTGGTGACA
ACCTGCATTATCTTGGCGATGAATTCCGAAGAGCCCTACGCTGCAATCGTTGCGATGGGT
ATTCCAGCGATGCTCGTGCTGGCTTCCCGCATTGCCAAGGGCGATAAGTTTGCGCTTGCC
GGCGGCATTATTTACTTGGGTGTTTCGGCTACTTTCTATACTTTGTTCACCGGTGCTATC
GCGCTTTCTGCGGTCGCGGTGTGCATCGTGGTGGCGGCTATTGTGCAGCGCTCCATCAAA
CCACTGCTGTGGCTTGCAGTGCTGGGTGGTGGATCCATTGTCATTGCGTTGATTTCTTGG
GGTCCTTACCTTCTGGCCTCCATCAACGGAGCGGAGCGCTCTGGCGATTCCGCAACACAC
TACCTGCCTCTTGAAGGCACCCAATTCCCGGTTCCTTTCTTGGCATCAAGCGTTGTGGGA
CTGTTGTGTCTTGTTGGCCTGATCTATTTGGTGGTGCGTTTCCACAACAATGAGGTGCGC
GCGATGTGGGTCGGCATCGCAGTGTTTTATGCCTGGATGGGCATGTCCATGGCGATCACG
CTTTTGGGCAACACGTTGCTTGGATTCCGTCTTGATACGGTGCTGGTGCTTATTTTTGCC
ACGGCTGGAGTGTTGGGCATTGCAGATTTCCGCCTTGCCAGTGTGTATCAGCTCTACCCC
ACCCAAATCACAGAGCGCACGGCCACCCATCTGACCAATCTAATT

>RXA00422-upstream
AAGCGCCGGGCGCGGAAGGCGCTGGCTGAGGCCTTCGGCGCGGAGGTCCAGCCACTGCCG
CTTGACACCGAATAGGACAAATGGGTCTATCCTGGGGCGC

>RXA00422
ATGCCCACGAATTATGCACGCGACAACGTCATTTCCTTGGCGTCTGCCCGCGAGCAGCGT
TCCGGGAAACCCGAGCCCAAACCCGAACTAACACTCATCGTCCGCGCCACCAACGTGCAA
GCGGACGGCGAGGTCCACAGGCAAATTGGGTTGAACTCGGCGATGAGCCTGGACGAGCTG
CACAATGTACTCAACATCGTTTTCGGTGTTGGCGGCGAGCAGTCACCCTGGCGTTTCGAA
GACCAATTCCACCAACCCAGCGCCCCCGACACCAACCTCGGCGAACTCCTGCCCGAACCC
GGCGACTTCCTGTTTTACTTCTGGGGCCTGTGGCAATTCAACCTGCAATGCGTGGAAATG
TACCCGCGCGACAACGGCACCCCGCGCGCGCTGTGCATCGGCGGCTCCGGCGGCCTCGGC
GAC

>RXA00423-upstream
AGTTCTTTGAAAAACGTGGCGCTTCCAGGCCATTCACCTGCACTGGCATGGTGTACGCCG
CTTTTATTTACGCAATCTGTGAGCTGGAGGCCCGCACAAA

>RXA00423
ATGACCTATCCCGTGTTGAGTGTTTTGGATAATTCTGGCGATCACAACATCATCTGGCAT
GTGCAAACTTATCCCGCGGCGCTGCCCACCGGGGCGTGGATTGCCGATGAGCAACAACTG
ACTGACCTGCTGAAAGACACAGTAGTGTTCCTTACCCCTGGGAGCACCGCTCCGGAAAAT
GCCCCCGTGGCGACGATAGAAGGGGTGCGGGTTGACGTCGATAAGCAGGTGGCAGAGTAC
AACAAACATGGGATCCGCCTGCCCAGCTTGGGCGCGCGCACTGTGGAGGCGCAGTACCGC
GGCGAGCCGGAGGCAGAGGCTGCGTGGCGCACGGCGATGGAGCTCGTAGAGATCGCAGGC
GGCTGGCTAGAAATTGAAGCCAAGCGCCGGGCGCGGAAGGCGCTGGCTGAGGCCTTCGGC
GCGGAGGTCCAGCCACTGCCGCTTGACACCGAA

>RXA00423-downstream
TAGGACAAATGGGTCTATCCTGG

>RXA00424-upstream
GCGATGTGGACCTCGGGAGCCTTGGCTTTTTTGAATCTTTCAAACATGCCCACCACCTTA
ATCAGTGAGTAGTCTTGGCAACATGGATACCAGGATGAGA

>RXA00424

TTGCAGGTAGCAGCAGGTTCCGCGCTGATTGGTGCTGGGGTTGCGGTTAATGATTACGTA
CAAAGCCCAGTCCGCCGGGCCATCAGTTATGGTGCGTTGGCGCTTTCTGGGGCGACGGTG
ATTGCGATGGGTCAGGACCCGACTGGGGAGCGGTCCATCATTGCGAAAGATTCCGCGACG
ATGGTTGATCAAATCCGCCAGGAGATCGGCGATTTGGGTGTCACGCCTGGTCCAGAATCT
GATGTGGATGCCATCACGGAGCGAGGTCCGCTGGTGACGTGGCTGTTGCTTGCTGTTTTT
GTCGTGGCATTTTTCACCTTGGCGTATTTCTCCATGCGCATGGATGTGGCGGTGATGAGA
AGGATCGCTAAGTTCTTTGAAAAACGTGGCGCTTCCAGGCCATTCACCTGCACTGGCATG
GTGTACGCCGCTTTTATTTACGCAATCTGTGAGCTGGAGGCCCGCACAAAA

>RXA00424-downstream
TGACCTATCCCGTGTTGAGTGTT

>RXA00425-upstream
ACCGCAACCCCAGCACCAATCAGCGCGGAACCTGCTGCTACCTGCAATCTCATCCTGGTA
TCCATGTTGCCAAGACTACTCACTGATTAAGGTGGTGGGC

>RXA00425
ATGTTTGAAAGATTCAAAAAAGCCAAGGCTCCCGAGGTCCACATCGCGGCGGAACGCACC
AACCTTCCGCTTAACGATTTCATGACCCGCCTCTTCGCCCAGGAACTCCCCCTGCTCGAT
AGCACCTCACGTTCAGAGGTCTACCGCCTGCTTCGGGAATACGACGGCCCAACAATTAGC
TCCCAGGAAGAAATCCCCGCAGAGATTCGTGAACTCATGGATCTT

>RXA00425-downstream
TAGGCAATAAATGTGAGATTGGA

>RXA00428-upstream
AGCGTCGCAGGGATCGGCGCGATCTTCCTCCTTCCGATCGGCATCATCATGTGCCTCATC
GCCGGATTCAACCGCTACTACGCAGCCCTTAAGGTCTAAA

>RXA00428
ATGCCCGGTCTAGTTCTCTCCACAAACGTCGCCCATATCCAACAAGACCCAGGTGGCGAT
GACCGCATCAGCGGCATCAACAAACTCCCCGTCGCCACCGGCATCGATGTATTCATCCCC
GGACCCAACTACGGCGACGGCTCCGGCGTAGTCGGCGACGCCATCGGCGATTCCCTCCAC
CACGGCGGCGCCCACAAAGCCATCTACGCCTACAGCCGCGAAGAACTCGACTTCTTTGAC
CCCACCTACCGCAACGGATACTTCGGCGAAAACCTCACCACCAGCGGAATCGTGTTGGAA
GACCTCCTGATCAACCAACAAGTGCGCATCGGCACCACGCTGCTCGAAGTCTCCATTCCC
CGCCGACCCTGCCGCACGTTCGCCCACTGGCTCGACATCAAAGGCTGGCTAAAAACCTTC
ACCCAACGCGGCCTCCCCGGCAGCTACTTCCGAGTCATCGAAGAAGGCCACATCAACCCC
GGCGACCCCATTGAAGTTCTGCAGGCCCCCGACCACGACATCACCATGTCCATGGCCTTC
CGTGCAAAAATGGGAAACAAAGACCTCGCGCGCCGGGTTGTTGCAGCCAACTGTCTCCCA
GCGCGCTACCACGAGGAACTACTAAAACTGATC

>RXA00428-downstream
TAGGGCCTATTGAATTTCTCGTC

>RXA00429-upstream
CGATGGTGGTCGCCTTCGTGATCGCCCAAGGCACCCGGAACGGTCATCAACTTCATCGTC
CAAAGAACCATCATTTTCCGAGTGAAGTAAGGTACCCCTC

>RXA00429
ATGAAGACCTTCAATCCCACCATGATTGCCGGACTCATCGGCGTACTCTACTTCGTGCTG
CTCACCCTGATTTTCTCCATCCAAGACATGGAACTAGCAGCAGAAATCGCCTTCGGAATC
GTCACCATCGTCGGCCTGATCGCGGTGTGGGACAACTTCCGCGACCGCAACAACTCCACC
TGGAAAACCTGGACCGGCCTCGTCGGCGGACTGCTAATCGCCGTCCCCGGAATCTGCCTT
CTTGTGGGAAACCTCGTGCTCCTCGCAGTCGACGGCAACCCCTCAACCATGGTGAACACC
CTGCTCAGCGTCGCAGGGATCGGCGCGATCTTCCTCCTTCCGATCGGCATCATCATGTGC
CTCATCGCCGGATTCAACCGCTACTACGCAGCCCTTAAGGTC

>RXA00429-downstream
TAAAATGCCCGGTCTAGTTCTCT

>RXA00430-upstream
TGCCCCCGTGGATCGCCTGGACATTTATAGGGAGCTGCTGTGTTTCTAGGTATTGTGTAA
CCTCGTGTCCGAAAATCTTGATGTTACGATCGTCCGACCA

>RXA00430
ATGAGCCTGAAAACCCAAGCTTTCCGGTTCATCCTCACCGGTGGCCTCTCAGCCATCGTG
GACCTCGGCCTGCTGTCACTTTTGCAGCTAGTGTTCGGCCTTCCCGTACCTGTTGCCCGC
ACGATCTCCTTCATCGCCGGCACCACCACCGCCTACATGATCAACCGCCGGTGGACCTTC
CAAGCAGAAAGCTCCACCTCCAGGTTCCTTGCTGTGGTGGCCCTCTACGGCGTGACCTTC
CTGATCAACATTGGACTGCAAACCCTCTGCTCCGCATTGTTTGAGAATTGGGGCTGGAAC
GAAGCCGTCGCGATGGTGGTCGCCTTCGTGATCGCCCAAGGCACCCGGAACGGTCATCAA
CTTCATCGTCCAAAGAACCATCATTTTCCGAGTGAAGTAAGGTACCCCTCA

>RXA00430-downstream
TGAAGACCTTCAATCCCACCATG

>RXA00433-upstream
GTCTCCAGCGACTCAAACATCAAAAATTGATATTTGCGACAAGTTGAAATCATACCCGAT
AGTCTCGAACATACTAAATCACCTAATCAGGGGGAATTAC

>RXA00433
ATGGATGTGTTAAAGATCGCCATCATCGCTGCAGCCATGATTGGTGTGCCGGTTCTGGTG
GTTTTCCTCATTGTGTTTGCGGTGCACAAGTTGGCTAAGGAAGTGCCGCGGTCTGGTCGT
CGTCCGGGTATTGGGTTGGGGTTGTTGCTTGGTTTTGTTGCGGGGCTCATCGTGTGGTTT
GTGTGGTTGAGTTGGGGTGGTTATTACGAGAATGAGTTTGGGCAGATGCAAGGTCCGTAT
CGTCCGTGGCAGGTTGTTGCTTGTGGTGTCACGATGGTCGCGGTCACTGTGATTCTTGGT
CTGTGGACTAGGTGGACTGCGTCTGGTCCGTTTTATTCGGCGTTGGGTGGTGCGTCGGGG
TTTAGTTTCGCGTGGGCCATGGATGCCATTCCTCAGGATGAAACCGGATTGTCGGCGTTT
GGCTTAGTGATGGTCATTGTTGGTGTTGGTGCGGGGCTAAATGTGGTGGCAACTCTGACG
TCAATCGGCGCAACGATCTGGAATAACCGGCTACCCTCGAATGCA

>RXA00433-downstream
TGACTAAAACCACGCGCCAAACC

>RXA00447-upstream
GAGCACGGCATCGTGATTCGCGCGTTCCCCGAGGGTGCGCGCATTTCGGTGACCAACGCC
GAGGAAACTGACAAGCTGCTGCGCGCGTGGGAGGCCATCA

>RXA00447
ATGCTGGGTAGTCTTTGGCGTTTTGCGGTGCGCACCGCAGCAGGCGCGGTGGCGTTGTGG
GTGGTTATTAAGCTTATCGACGGCATCTCCCTGAGTTTTCCCACCACACCTCTCTATCAG
GACGGTCAGCACGACAATCTGCTGACATTCCTGGCGGTGGCAGCAATCATTGTCGTGTTG
AATGCCACGGTGAAACCCGTCTTGAAGCTGCTTGGTTTGCCGTTGACAATCATCACCTTG
GGTCTGTTCTCGCTGGTCATCAACGCGGTAATCATGCTGCTGGCGGAGTATGTGTCAGAT

>RXA00451-upstream
GGATCCGCCGATGAGGCCGAGGCCCAGGATGCATACTGGGCGGGAAATGTCTTTGGTAGT
CACCTGACAAGTGTGGCACATACCTACTACGGTTATCTCT

>RXA00451
ATGAACACTGAAGAGGATGGCCTGAGCTTTGCAGTTACGGCTACCTTAGTTGAAGGTAAA
TGGCAGGTACGCGAGTTTGAGGATCACTTCTCCAAGCTCTCTACCTCTATTAATGCGGTT
CGCTCGCTGCGTAGCGAGGGGCCGGCGTTTGCGCTGTTGTGCGTTGATGATGAATATTTT
GTGATGGTGCGTCCCACCCCAAGTAGGGTATTCCTTTTCCTTTCGGATGCGCCGATGGCT

GTCGACGATGATTTCGCCGCCGCGGTGATGGATGAACTCGATGCGGATCTTCCAGATATC
AACCCTGATGATTTGGACGACATCGATCCATGGCCAGAAGGTGATTTCGATATTTTGGCG
GATTTGGGGCTGTCTGAGGAGGTTCTTTCCGTGATTTGCGATGACATGGATTTGGATCCT
TCCGAACAATTGCTGCGCATCGCGGAAGAACTCGGTTTTGATAATGATCTGGCTCGGGTG
GTGGGATTCGAC

>RXA00451-downstream
TAGTGGGCGTTTTACCTGTGCAG

>RXA00455
ATTTTGCTGGCGCTGTTTGTTGCAGTCTTTCTAATTTCAAATATCACCGCAACCAAGGGC
GTAGAAATCGGCCCGTTGGTGACAGACGGTGCGTTCTTCCTCTTCCCCATCTCATATGTG
TTGGGCGATGTTCTAGCCGAATGTTACGGCTTCAAATCCACTCGTCGTGCCATTCTTACT
GGTTTTGGCATCACGATGCTCGCGGCGCTGTCTTTCTACATTTCCATCTGGCTGCCTGGC
GCAAGTTTCTGGGAAGGCCAAGAAGCTTTCGAAGCAACGCTCGGCCTTGTTCCACAGATC
ATCGTGGCATCACTGGCGGGCTATATTGTGGGTCAGCTGCTCAACGCCAAAGTTCTGGTG
GCTATCAAAAAGCGCACGGGTGAAAAGTCCCTGTGGGCGCGCCTGATTGGTTCCACCGTT
GTCGGAGAATTTGTCGATACCCTGCTGTTTTGCGCCATCGCAGCGCCAGTGATCGGTATT
GCCACCGCCCCGGATTTCATCAACTACGTTGTGGTGGGCTTCGTGTGGAAAACCCTTCTA
GAGGTCATCCTCATGCCCATCACCTACGCAGTCATTAGGTGGGTGAAACGCCGCGAAGGT
TATGAAACCTTCGACGCG

>RXA00455-downstream
TAGTACCGGCCTAAGAATTCTTC

>RXA00457-upstream
AAACTCTCATGTTGGTTTCATCGTGGTTTCATGAGGCGGGATTTAACTAGAGATTGTTAG
CCAATCGGCCAGACACTTCCTCCTAGAAAGGTCCCTCCTC

>RXA00457
ATGACCATTGCTCTTGAACACCCAGTACTGCACTCCACGGCGATCGCGTTGCCTGCTCGT
TTTCAGGCGAGCTATACGACGCGTTTGGTGGCGGTGGGCGTCGATAAGCGTCCTTCTGAT
TTTTGGTTGGAAACAGCCGGCACGCCGCAGGCGGGCGATGTGGTGATTGCGCGGGTGACG
GCGATTAATAATCACAAGCGGGTGGAGACGCCGGAGTCGCGCAAGGCCATTTTGTTTGAG
GGGGTGTTGGTGATGTTGGCGTATGGGCACCGGTATGCGGCGGATCAGTTTTTAGCGCAT
GTACCGGAGGATTTGGGGCCATGCCATTTGGTGGCGGCTGGTGGCATCGCGGGAACGGTG
ACGGCGCTGCACGATCGGGTGGATGAACCCACAGAGATTGAACCGTTGGGATTGCTCACC
AATGCGCGCGGAACTGTGAATGTACGGGACTTTGCGGCTTTTGATAATCCTTTGAAAGTG
GAGGCTCCCAACAAGCGTGCGCAGGTGATCGCGGTGCTGGGAACGTCGATGAACTCTGGA
AAATCCACCACGCTTGCCTGCTTGGTCAATGGTTTGGCTGCGGCGGGGCAGAAGGTGGCG
GCTGGAAAGATCACGGGCACTGGTGCTGGAAATGACCGCATGATTTATCACGATGCTGGT
GCTCACAGCGTTATTGATTTCACCGACTTTGGCTACCCAACTACGTTCAAGCTGAATTTC
GCGGAGATTCGTGCGCTGAGCGTCAACATGATTAATGTGCTGGCTGATTCTGGTGCGGAT
ACCGTGATCGTGGAAATCGCGGACGGAATTTATCAGGGCGAAACCTCGCGGCTGTTGCGC
GATCAAGTGTTCCAGGAAGCCGTGGATCATGTGGTGTTCTCCGCTGTTGATGCCTTGGGC
GCGAAGGCCGGTGTGCAGGAACTGCAGGCGGCGGGGCTTCATGTGGCTGCGGCCTCCGGA
GTGATGACGGCTTCGCCGCTGGCCACCGCGGAAGCTGCCGCTGTGCTTGAAGTTCCAGTG
GTGCCCACTTTTGATCTCACCAACCCGGAGATCGTCACAGCGGTGCTAACGGATCATGCC

>RXA00457-downstream
TAGCTTATGGCGTGCTCGTCGCA

>RXA00462-upstream
TGAAGCCTTGTCATTTTCTACATGTGCATCCGCTTTGACTACCGCCCTTTTCCGCCCAGT
CCTTTTAGAAACCAGCAACACAGAAAGCAAGTGATCATTT

>RXA00462
ATGGAAGCTATTGCCATACTATTTGTCATTGGGGCGATTCTTGTCGTCGCGGTCATTGTC

CTCGGTATTTTCTTCTTAACTTCACGCACCTGGATCAAGGTGGCTGCAGCTGATGAAGCG
CTCATTGTCTCTGCGAAGAAGAAGGGGGAATCGCAGGTCATTGTCCACGGCAAAGCTGTG
GTAATGCCTATTACCCAGACTCACCAGAAGATCTCTCTGCGTTCCCGTCAGGTAAATATG
CAGGTGACGGCACAAAGCGATGACAATGTCACGTTGAATGTCGAGGCTGTTGCGCTGGTG
AAGATCGGTTCCGAAGCTGAGTTTATTCGTCGCGCTGCCCAGCGCTTCGCTTCCAGTGAC
AAAGAAATTGTTCGGTTCACACAGGATCAGCTGGAAGGTGTGCTTCGTGGTGTCGTGGCG
CAGCAAACAGTCACGTCGCTCATGCGTGAGCGTAAAAAATTCTCCGAGCAGATCGCTGAA
ACAGTCATCCCCGAGCTAGAGAAGCAGGGTTTGATTCTTGACTCCTTCCAGATTCGTGGC
ATCACCGATGATGTGGGATACATCAAATCCCTCGGCGCACCGGAAATTCAGGCAAAGAAG
CAGGCTGCGGAAATTGCAGAAACTGAAGCTGCTCGTGCGATCGCTAAATCACGCATTGCT
AACCAAGAGGCAGATCTGGTTGAACAGACCCAACTTGATGCCAACAAGGCTGCCGCTGAT
GCTCAGGTCGGTGAAGCCCGTGCCCAGGCTATGCAGGCTGAACGCCTTGCCGATGAAAAA
GCTCGACTAGAGGTTCTTCGCCAACAGGCTGAAAATAAGCAGATCGAGCTGGAAGCCGAA
GTGAACAAGGTGGCCGACGCTGAACGCTACCGCCGCAAGCAGGAAGTCGAAGCCGATACT
TTCGAGCAAACCAGGCGCGCACAGGCTCAGGTCGAAATCGCAGAAGCCGAAGCTACCGCT
GCAAAGGTTCGTGCAATGGCTGAAGCCGAAGCTGTTCGATTGAAGGGACAGGCAGAGGCA
GACGCTATCAAGGCAAAGGCCGAGGCCTACCGCGAAAACCAAGAAGCACTACTCGCCCAG
CAAGCCATGGAAATCCTGCCGGAACTCATGAGCAACTTCGCCTCTGGATACGCAAACATT
GGATCCATGACAGTGCTCTCCGGTGGAGAAGGATCCGAGAATTCCGTGGGTTCACGTTTT
GCCGGTGAACAAGCACTTGGACTGAAATCCATTATTGAATCAGTCAAGCAAACCACCGGC
ATTGATCTAGCTGAGATCATCCAAGGCCGTGCTGCTGGACATGCACAGGGCTCCGCTCAG
GGTGCAGCGATTGCTGAAGCGCTTTCACGCGATGAAACTGTGGAAGATCGCTCTGAAAAA

>RXA00462-downstream
TAATCTAGCTGCCCAGCGCATCG

>RXA00463-upstream
TACCACGCTAGTCGCCAGCACTCTCGGATTAAGCGGATGTACCTCCGTAACTTCCAGTGC
TACGAGCTCCCCTGAACCGCCGACTAAAGTTGCGGCGGCA

>RXA00463
ATGCAGACAACGACTGGGGAGACGTCGATAAGCAATGAAACCTCGTTTAACGCCTCACGC
GAAACCTCGCTGACGGCGCTGGGTTTCTTGGACTATCTTGACGAGGAGCAACGCGCCGCC
TTGCTCGGTGAAGGCCTGGACATCAGCACGCTGACCTGGGCCAACCAGGTTACCGCGCTG
CGTGTGCTGGAATCCCTCTTCAATGAGCATGCATACGAGCTGGTTTCTGCAGTGATTCAG
CATGTAGCTCAAGAACCTGGCGATAATCCACACCACTTTCTGAAGTTCTCGCCTGAACCA
TCCACCGAGAATTCTTGGGAATTGACCCTGGATGGACCAACTGTCGGATTGAAAGTCACT
TTCGATCCGGACGGTCAGATCACTTTCAAGGATGCTCATTTGGGCCTGAGCCCAGCTGAG
GTCGTTAGTGTCACTGAGGCGTTAGATACCTCCTATTCGGAATCGCAAATCAAAAAAGCT
GCGGAACAACTGGTGGGAAGCCTCAATCCAACCCAGCAGGCAGCGCTCCAAGGATCCGGT
TTGCGAGGAGCACAGCTCACTGAAGAGCAAAAGACCCTGTTCTTAAAGATGACCTCCAAC
TGGATCGACCTTGCCAATGGCGATTCCGGCTCTGAACAGCAAGAAGAAATCGCTGATACG
TTCAGTGATACCTACATCATTTGGAATGAGCAGAAAGATGGCTCAGCATTCTTCCAGATG
AAAGGCCCTGAGCTCGACTTCAGCTATAAAGAGAGCGTGCCTGAAAACGCTGAACTCTCT
GCACGGGGAGTCCCCAATATTCAGACCTCTTTTCAGTCACCT

>RXA00463-downstream
TAACTGGCATTGGTTTAGTTTGG

>RXA00468-upstream
GGCAGAATTTTGCTCAAGTTGCCTAAATCAAGCACCCGTTCGAATAAGTGTCCACCCTTT
GGTTTATTCTTGAACTCACTTAAGTTTTGAATTTTTAGTT

>RXA00468
GTGAAAGTAGTTGATGCACAAGTGGTTATGGGGCCAACCCACGCTATGAGCGGTGCAGCC
GTGGGGCTTGCTGTTGCTCAAATTCTCCCAGCAGAATGGGGTGGGGTTACCACCGCCACG
GAGGCTTTTATTTATGCGGGTTTAGCGGCGGGTGCAGCGCTGCTCCCGGACCTTGATTCA
CCGCAGGCCACGGTGTCGCGTTCTTTTGGTCCGATTACCCAAGTGATTTCGCGTTTTACA

GAGAATATTTGCCAAACTTTCGTCAATGTCACCAGGGGCAGGAAAGACAAACACTGCAAC
AACGGGCACCGCACGTTGACACATACGGTGTGGAGCGCTGCTGCCACAGGCGCTGGTGCC
ACAGCGCTAATTGGCGCCTATGGAAAACCTGCGGTGATTGGTTTGCTGTTTTTCTTCCTC
GGGCTCGCCATTAGAGGTCTCATGCCTGAATGGTCAAAGAACGCAGATTGGCTTTTAGTT
ACTGGAGCTTCCGCTGCATTAGCAGTGGGAGTATGGAATTATGCTCCCGAAAGTTCATTC
GGCATTGTGTTAGGCTCCGCCATTACAGTTGGAAGCCTGACCCACTTGGCTGGCGATATG
GCCACTAAGGCCGGTATCCCAGCATTTGCCCCGGTCATTCCGCTGAAGGGCAAACGCTGG
TGGAACCTCAAATTGCCTAAGTTTTTAAGCATTCGTGCCAACGGTCCTGCCGATAAGTTC
TTACTGTTCGTATTCTCGGTGGCGGTCATCATTCAGATTGGTTTGGTCTCATCGGGAAAT
ATGAGCACCATTATGATGAATCTGCTTAGTCCTGCACTG

>RXA00468-downstream
TAATTAATGGCAGTTGCGTTTCG

>RXA00469-upstream
TGCCCCTGCGACACCAAACCATCAGGGAAGACCCTGAACGCCACCTTTTCAGGGCTTTCC
CCCATTCACTTATCAGCCTCAACACTCCACAATAGAGTCT

>RXA00469
ATGAGTACTTTTCAGGAGCCCCACCACAACCAGGGATTCATCCCTTTTGCCCAACCTGGT
TATGAAGCTCCAACACCACACCTTGCAACTGGTACTTTTCAGCAAATGTGGCAGACCCGC
CCCGCACGCATCCCTGCCAAGCAAGGTGGTCACGCCAAAGTAGCTGGTGTCTGTGAAGGC
ATTGGTGTGCGTTATCAAATCGACCCGGTGCTCATTCGTCTATTTTTCGTGGTCACTGGT
GTCTTCGGCGCCGGTGTCGCAGCCTATCTCATTGCATGGCTGTGCATGCCCCGCTACTCC
GTTCCGGTCTCCCCCATCGAAGCTCTCTGGACCCCGGGCCACACCAAAGACCGCAACCAC
GGCTGGTGGCTGGTCATCGCGTTCTTTATGTTCTCAGGTGTTTTATCCTCCGGCGCTGGA
GGAATATCCGGCCCAGCAGCAGCCATTACTTACCTTTGCCTTTTAGCCATGTGGTGGGCG
TTGCATAAGAAACAACCACTTCCACCCCGCGGACTACTCACCACTGAATTCACTGTTTCT
GAGGATGCCACCATGAAAAACGAAGATCTCTACCCACGACCCCAACCAGATCTAAGCACT
ATCACCCCCGTTGAGGGCTACTATGCACCCTTCGCGCAACAAACCCCCGAAGCGCCTCAT
TGGGATCCACTTGCCCAAAACCAATACAACACCTGGGATGTACAAGTCCCTCCACAAAAG
CCTCAGAAAAAGCGCCATGTGTGGCCATGGATTGTCGGCGGTGTAGTTGGTACCGGAGTT
GTCATGAGCGCCCTCGCAGGCCTGTTTATTTCAAATATCGATCCCATCTACTTTGAAGAC
GACCCTGGAATCGGCGATGTCAATCTCATCCCCACCAACGATGAACTCCTCAGCAGCTAC
ACCTCTGGTGTGGGCGAAATGAACCTAGATTTCAGCAACCTCACCCAACTTGATCAGGAA
CAAAACGTTCAAATCACCTCAGGTATCGGTGAAGTCATGGTGACCCTGCCTGATGACGTG
CCAGTAAGCTTGAGTTGCTCCGCCGGTGTGGGCACAGCGCGCTGTGATGTTGGAGACCTC
GCCGCCCACAATGCTGATTTGGAAGGTCCGATGTTGAATCTGGTTGTAAATTCTGGAATC
GGCGATGTGAAGGTGGAGTTCGCTGATCAGAATGAC

>RXA00469-downstream
TAGCCCGACCCTATGTGAGTAGT

>RXA00472-upstream
GTCTAAACGCTCCCGTGCTTTCGCCACAGCATTAATCGCCTTGGGCCTAGGGCTATCTTC
CTGCTCTACTACGGAAGATACCGCTATATCGGAGACGACA

>RXA00472
GTGTCTAGTGTTGCAACGAAAACAACCTCGACTCTGCCTGAAATGAACTCCGCAGTATCA
GCAGACGGCGTGACGATCACTATCGATTCTGCCTTCACGACAGACTCTGTAGAAATGGAA
TCCCTAGACAGACCTTCTGGCGACATCCAACCCGAGATGTCTAGAGAAGACGGAATCTTT
GTCGTAGTCGAAACCACTATAAAGAACGAGAGTGGAGCAGATATGGACATCACCTGTGCA
TCCACTGGTTCAACTGTCTATGCAGAAATCTCCACTAATCAAGAGGCCGTATACCAACCA
ATACGCGATTTATTCCTCATCCCAGGAAACCCGGAATGCAACCATAATCTAGGATCCGGT
TTCGACGCACCAATGACTTGGGTATTTCAAATCCCTAAAGATGCCACTGCGGAGCGATTT
GGATTCACACATAGTGAGCTCGGTGATGGGAAACTAACTTGGATTGCACTCAATGATTTG
AGTAATTCGGAGCCAGCTACTGAATCAACTATGCGAGACGAAGCAGCAATCGATCCGAGC
ACCCCTCAGCAAACTCCAGTACAGGAAACTGTGATCTCACAAAACACCATTGAAACTCCT
GTAGCCCCTGCTCCTGCGGTACCTGCTTATGGCGCTTCTTGCCCTGTCTCGATGCTCCAG
CAGCCAAGTCAAGCTGCAGATGGTTCAGCTTTGGTCTGCATTTATGCAGGAACCCCCAAC

CCAATCTGGGTCTACGGCCCAGAACCTCTCGGAGTCGGGACTGCTACACCGGGTGGGGCA
TGCGAAGGATACGAGGCCGGTGGGCAAGATGCTTCTGGAAATATAATGATGTGCTCAGGC
GGACAATGGGTCTATGGGCCA

>RXA00472-downstream
TAAATCTAAAATCAAAGAGTGCA

>RXA00473-upstream
CCACCCCTTTTCTCACACCAGCCCCGCATGAACAGGCTGGTTGCACACCGTTGAAAATGA
GTGTTTACTGGAACTCATGAGTGGAACAGGTGTTCGAAAG

>RXA00473
TTGTGGGGAGATGGCACTCCGGTGTCGCTCCCTGACCTTTCAGGATTAAGTAGAGCGGAG
CGCATTGATGCGTTGCGTTCACGCATGTCCACCATGGGTGCTGCGGTGCCAAAGTTTGAG
CCGTCGGTGGAAGAAAGTGCTGAACAAAAGCAGGATTCTCTCGCCGAAAAACAGGACATA
GTTGCAGTTCCTTCCGCTTTTTCTGATCTTTTCCCTGGGGATGGTTTGCCGCGTCGTGCG
GTTACTCAATTGGTTGAACAGCCACTTGTGGTGGTGGACTTCCTGGCTCATATTACTGCC
CAGGGTGGACACGCTGCGGTGATTGGGTGGAAGGATTTAGCCTACGCCGGGGTGATTGAT
TCCGGAGGTGTGTGCGAGAACATCATTGCTATTCCAAATCCTGGTACGGAGCCACTGAAT
GTGGCAGCGGTGCTGTGTGAGGGGTTGGATGTGGTCGTGTACAAAGGCCCGGAGATTTCC
CTGTCGCCAACCAGAGCGAGGCCGTTGCTGGGAAAGCTGAGGCAGGGGACTGCTGCCTTG
GTGATGGTTGGCACGAAAGTAAGCTCACCGGCGCTGTCGGTGGATGCAGAGATCACTGAT
TATGTTGGCATTGGTGCAGGTAGTGGGCGTATTCGTGGCGTTGAGATGCAGGTGCGGGCT
GTGTCGAAAACTCACGGTGTGCGCAGCGGAAAAGTCCTGATCAGTAGGCCTCAGGATGCA
GCATTGCTTGAGCCTGAACAGCCAACAACGTTGCGGGCGGTCCCA

>RXA00473-downstream
TGACGCGGGTGATGGCATTGTGG

>RXA00474-upstream
GTGTGCGCAGCGGAAAAGTCCTGATCAGTAGGCCTCAGGATGCAGCATTGCTTGAGCCTG
AACAGCCAACAACGTTGCGGGCGGTCCCATGACGCGGGTG

>RXA00474
ATGGCATTGTGGTTTCCGGATTGGCCTGTGCAGGCGGTTCATTTGGATGAAGATGCTCCC
GCGCACAATAAACCTGTGGCGATTGCTGCGCATTACCGCATCCAGGTGTGTGGCGTGGCT
GCGCGCAAGCGTGGGGTGCGTCGTGGGATGAAGGTTCGGCAGGCGCAGGCTGTGTGCCCT
GAGCTGGAGGTTGTTGACGCGGATGCAGATCGTGATGCCCGGATGTTTGAGGGCATCGTG
GCATCGCTCGGTGAGGTTGCCTCCAGCGTCGAGGTGCTTCGTCCGGGTCTGGTCGCGGTC
GATGCGGGAGCTGCCGCGCGCTATTACGGTTCAGAGGACATCGCTGCTCAGATGCTTATC
GACGCCGCCCTGCGCCAAGGCATCGACGTTTTCGCCGGGGTTGCGGATGAGATCACGACG
GCCGTCATCGCGGCGAGGGCGAATGGTGGGACTGTGGTGAAGAGGGAGGCGTCGAGAAGC
TTTTTACAGCAGCAACCCCTGGGCGTGCTGGCGGCCGAGGAAGCGCTGGGTTGTGAGGCG
GAGGTGGTGCGCGCGCTGGCGGATCTGGGCATGCGCACGCTTGGTGAGCTGGCGGAACTG
CCGGTAGAAGCCGTGGCGACGCGTTTCGGCAACGCTGGTCTGCGGTGTCACAACATTGCG
CGTGCCAGGCACGATCGTAAGGTCGCGCCACCGATCACGCATGCAGATTGGGAGGTTTCG
CATGTGCCGGAGGAGCCTATTTTGCGTGTCGACGCCGCCTCGTTTGTTGCGCGCAACCTT
GCCTCGCGCCTGCATCAACTGCTGAGCAAAGGTGGCGTGGTGTGCCAATTGCTCAAGGTC
ACAGCCGATTTCAGTACTGGTGATACGGTGAGCAGAATTTGGCGTACCGGTGAACCTTTA
ACGGAACAGGCAACTGCGGATCGGGTGCGTTGGCAGTTGGATGGGTGGTTGACTGCGCGC
GGTGTGCATTCCGATGATCCGAATGAGCACGATGGGATTACGGCGTTGTGGCTTATTCCT
TTGGAATGTGTGCCACCGGATATGGCCAGCGGCGGATTGTGGGATACCGGGCGCAGCCAG
CAGCATGTGGCCAGACAAGTCATTGAGCGTGTGCAATCAAGCTTGGGCGTGGATGCGGTG
CTGCAGCCTGTTCCGGCTGGTGGTCGGGGAGTAGAAGAACGCATTCATTTTGTTCCCTAT
GGTGAAAAACGTGATGCTATCCGCAATCCAGCGGGGTCGTGGCCAGGGAAAATACCAGGT
CCGCTGCCTGCTCGGTTGGGCGGTGGGATCAACCACCCGGCCTCGCAAGTGACCATGATT
GATACAGAAGGGCAGCGTATTTACGTCACCGCAGAGGCATTGCTCAGCTCGTCGCCGTAT
GCCTTGTCCTGGGGGCCGGCCCGCTATTTGATCACTGGCTGGGCTGGGCCATGGCCGGTG
GATGATCGATGGTGGGAGAAAAACGGCACAAAATATGCCCGCCTCCAAGTGGTGGGACGG

GCAGTATCTGAAGAAAGGCAGCTCAATGCGTGGCTGTTGATGTGGAAAGACAACAAGTGG
CGGATTGAGGCCACATAT

>RXA00474-downstream
TAGGAAACTACTGCGCTAAAACA

>RXA00475-upstream
GGGGTGTCTGTAATTTTCACGTCTCCTGGCGTTTTTAAGACGAATTACAACAATTCGTTC
ACGATTGAGCGAAATTGGGCGTCTTGCTTAGGTTTCGGGG

>RXA00475
GTGACCCAGGGTTACGGTGTGTGCATGATTGTGCAGCCAACTTCTCATTCAAAGCATCGT
GCCCGCCTGAAGACTCTAGCGATTGTCGGCGCTAGCGCGTTGACTCTTGCGGGTTGTGGA
ACCTCCAATTCCACCACCAACGATGCTTCTTCTGTAACCCAAACTATGTCCGCAACTGCG
GATGGCGCACAGTTGTCCAACGAAGCTTCCACCGGCCCAACCGCATTGGGCGAAGCCGAT
GTAGCAATGAAGACTCTCCGACCTGATGCGCCTGCACAGCTCATGGTCACCGATGTTCGG
ATTGGCTCTCACAGTGGCTTTGACCGCGTGGTATTTGATCTCACTGGCACCGGAACTCCT
GGTTGGTTCATTGATTACACCTCCAATCCCACCCAGCAGGGCAGCGGAAACACCATCAAC
TTCACGGGCGATACAGCGCTGAACGTAAATATTGACGGTACTGTTTATCCTTTCGATTTG
GGCCTTGAGGATCCAGAGATCGGCACCGTGGATGGCTCCGGCAGCATTGTCACCCAGGTC
GTCAGCGCAGGTACTTTTGAGGGACGCTCCCAGTTCGTCATCGGCCTCAACGGCAAGCAC
CGCTACTCGGTCACTGAGTTGCAGGATCCGCACCGTCTCGTTGTGGATGTTTTAGCGCAG

>RXA00475-downstream
TAGTTTCCTAATATGTGGCCTCA

>RXA00476-upstream
GTGAACGAATTGTTGTAATTCGTCTTAAAAACGCCAGGAGACGTGAAAATTACAGACACC
CCAGACATCAGATGGAGGCGGCGATACTAGGGTAGAGGAC

>RXA00476
ATGACTCTTCGCTGTTCTGACGTCAATGTTGAACCCCTGCCGGGAACGGCAAAAACAGGT
TCTGGGTTTGTTCTCCTTGAACATGCTGGCTCGTGGAGCCGTGATGTTTTAGACGGCGGA
ACATTTGATCCTGAGTTGACTGATCAATTGAAGAGGCACCTGAAAGCTTCCGGAATGGGT
CTGCAATTAATTAGGAAGCCGGGAAGGGAGGGTCGAAACGTCGAAAAGCATAATCTTTTT
CTCGTTTTTGCTGAGGCCTCAATTATTGAGCACCTGGTGGTGGACGCGCCGGCTGATGTT
TTGGATCTTGATTTAAGCGGGCCGGGCAAAAACAATGCGCAGCGCATGGATGATCCGATG
CTGCTGATTTGTACGCATTCGAAGCGCGATGTGTGCTGCGCGATCAAGGGGCGTCCGCTG
GCAGCTGCCGTGGAGCCACAATTTGGGCCGCTGCATGTGTGGGAGGCTTCGCACACCAAG
GGCCACCGTTTTGCGCCATCGATGCTGCTCATGCCGTGGAATTACTCTTATGGCCTACTT
GATGAGGCCGAAACCGTGCAGCTTTTCCAAGGCGCGTTGGACAACAAACTCTTCCTGCCG
GGCAACCGTGGCCGAGGAACCTTAGATGCTCGTGGCCAGGTTGCAGAAATTGCCGTGGCG
GAAGCTTTCGGCGAGGCGGTTGCTCCTGCGAGTTTGCAGGTTGAATTCGAAGATGATTCT
GTTTTGGTTACTCATCCCGATGGGCGCACGTGGGTTGTGGAGCTTGAACGCATCGAGGTC
GACGGCGTGGTGTCCTCGTGTGGTGATCAGCCGAAAACTGGAAAAGCGTGGGTGGCTAGG
CAAGTTACAGAACTGATCGGA

>RXA00476-downstream
TAAAAGCAGAGTTATATCTGATG

>RXA00481-upstream
GTCCATAAAAATAATGTGCCTACAAGAAATTTATAGTATCCCATGAGTTAATATTTTTAA
AAATAAACTTTATCTGACTTTGTAGAAAAAGGTGATTACT

>RXA00481
ATGCTGAATATGCAGGAACCAGATAAAATCCATCCGGCAGAACCTACACTTCGTAATATT
TATGACGTTAAAACTAGTGATCCCAAAAGTGAATTAGTTGATCGTTCTGGCATGTCGGAA
GAAGACATTGCGCAAATTGGGCGGCTAATGAAATCGTTGGCCAGTCTTCGCGATGTGGAA

CGTAGTATTGGTGAAGCCTCGGCACGTTATATGGAGCTAAGTGCCCCTGATATGCGAGCT
TTGCACTATTTGATTGTGGCGGGCAATGCGGGCGAAGTGGTGACTCCAGGAATGCTTGGA
GCTCACCTTAAGCTTTCCCCGGCATCTGTAACAAAGACGCTTAATAGGCTAGAAAAAGGT
GGGCATATTGTTCGTAATGTGCACCCCGTCGACCGCAGGGCTTTCGCCCTCATGGTCACT
GATGCCACTCGTGGAGAGGCGATGCGGACGCTTGGTAAGCATCAGGCGCGTCGTTTTGAT
GCTGCTAAACGATTAACTCCACAAGAGCGTGAAGTGGTTATCCGATTCCTTCAGGATATG
GCACAGGAGTTATCCCTTAATAATGCACCATGGCTCAACACGGAG

>RXA00481-downstream
TAGATGACCATCTACGTTAATTA

>RXA00485-upstream
TGCAGCCTCTGTAAAGCAATCAGACGGGATTTACGCCAGTACTTCAGTCCAGTCAATTTC
GGAAGGCCCACTGCAGTGGCGGCCAATCCTAGAAGGCCGA

>RXA00485
TTGCCCCAAGGACCTGGTGAGATTGCAGTAACAACGGCCCCGGGTGCGCCTGAAGTTGGT
GAGCACGTATCCATTCGCCTGTCCCAAAACACTGAGGACACTGAGGTTCTTGTGGTTGGC
GTGGTGGAGCCAGCGGCGCAGGAAACTTTAGGTGGCGCACCGTTCGTTGTGGCGTCTCCT
GATGCGCTGATGGAGTGGAATTCTTCCGGTGTGCGGGGTGAATTCCGAGTGGCAACTTCC
GATCCTGCCTCGCTAGAGGCTGCAAGCTTTAGCGACGCTACGGTGGTGGTTGCTTCGGCG
GAGGGGCACGTCGATAAGCTTGCTGATTCTTATTTGGGCCAGCGAGATCGCTATTTCTTG
CTGCTCGCAGCGTTTGTGGCAGTGGCTGCTGCCGTGGCGTTTTTGGTGGTCTTTTCTGCA
TATTCGGTGCTCACTGGTGAGCGAGTTCGCGAGTTCGGGCTGATTCGTTCAGTGGGCGCA
TCGACGCCGCAGATTTTGGGGTCAGTGATTTTTGAAGCCGGCATCCTCGGTGTGGTGGCT
GCTGGTTTTGGTGCGCCCGCCGGATTGATGGCGGCGCGTTTGTTGGCGGATAATGCCGCA
CGTTTTGGCATTCGTGTGCCCATTGATGTGATTGATCTGCCAAGTAGCACGATGTGGCTC
ATCGCTGGCGTCGGCGTGGTGATGTCCGTGATTGCGGCATTACCGGCAGTGTTCAGTGTG
TGCAGAAAATCCGCAGTGGAATCACTGAGTACGCCTGCTATTTCGAGGACTTCCCCCTGG
TTCGGTGCATTATGGTTGCTGCTCGCGGGCATTGTGGGCGCCGGCGGAATGTGGGCGTAT
GAGGCAACCTCGGACTACCGCGGCATGCGTTCAGTGGCTTTATCCATCGCCGGTTCAGGC
GCTTTGGTGTGTGCGTTGTTGATTGCCACGGCGGTGCTCGTGCCCTGGTTATTGCACGTA
TTCTCCAGGATTGTGGGCGGCACCGTCCCAACACTTCAGTTGGGATTGGCGTTTGCAGCA
AAGCAGAAATCTCGTTCGGCGGCGCTGATCGCTGTGATTCTTGCTGGTTCTGCATTAAGC
TCCGCTGTTCTGCATGGCCAGGCACATATCGGCACGCATTTGGTGGCCGTGGCTAAAGGC
ATGGGCGGCACAGACATGATGGTTACAGCGCTTGATGGGGAAATCCCCGCCGGAATGCTG
GAGGAAATCTCTAGCATCGACGGCGTGAAAACTGCCATCGCGCCAGCCACCACCGCTGTG
GAATTGGAAGATTCCGGCAATTTCTCTGTGCTCATGCTCGCTGAAGAAGACGGAGCCTCC
GTGATGCGCGCAGGCGATACTGGTGCACCAGCTGGTGGCCTTGTTTTGGGCAGAAACTCT
CCTGACCAGGATGCTTACCCGGCCGGCCAGGCTGCAAACATCATTGTCGCGGATACCCCA
ACGCAGGCGGAAATCTTCCACAGCGACAACTACTTCTCCATGATCGACCCAGCACTCGCC
ACCGGCCCCAGCACCACACGCAACGTACTGATCCTGCTCGACGGCGACTCCAACCAGGCC
CCCGACAACGCCACGGCGCAGGCGGTACGCAAGACCATTTCGCTTTTCGACGGACGATAC
TCCATCACCGAGGGTTTCTCCGCCCGCCAAAACACTTTTGAACTGGTTTCCCGCATCACC
ACCATGTCCACACTGCTTGCCATCGTGGCCTTAGCGATCGCTGCCGTTGGCCTGATCAAC
ACAGTGGCACTCACCATTTCTGAGCGTGCCCGCGATCGTTATTTGCTGCGCACCATTGGA
CTGACCTCAACTGGTCAGATTCTGGTGATGGCTATTGAAATGATCGCGCTCTCATTGCCG
GCTGCCATTGTTGGTGCAGTTTCGGGAGGATTCTTAGGCAGATTCGTTGCCAGTTCTGCC
ACCAACACCGCTGCGACGGCACCACTTCAAGTAGACATTCTCGGCGGAACGGTTCTCGCG
ATGGTCGCAGGATCTGTACTGTGCGCGCTCATCGTGCTGGCGAACAAACGACGTCGGGTG
GTT

>RXA00485-downstream
TGATTATAAAATCCAAAAATCGA

>RXA00486
CATGCGATCATGGCAGCAGTCGACCATGCCCGCGCAGCCGTTCTAGATTCGCTGTCTGAA
GTGTCCGGAACGTTGAAAGTCACCTCCTTCCAATCCCTGCTGTTCACCCTTGCCCCGAAA
GCCATCGCGCGCCTGACCGAGAAATACCCACACCTGCAAGTAGAAATCTCCCAACTAGAA

GTCACCGCAGCGCTCGAAGAACTCCGCGCCCGCCGCGTCGACGTCGCACTCGGCGAGGAA
TACCCCGTGGAAGTCCCCCTTGTTGAGGCCAGCATTCACCGCGAAGTCCTCTTCGAAGAC
CCCATGCTGCTCGTCACCCCAGCAAGCGGCCCATACTCTGGCCTCACCCTGCCAGAACTC
CGCGACATCCCCATCGCCATCGATCCACCCGACCTTCCCGCGGGCGAATGGGTCCATAGG
CTCTGCCGGCGCGCCGGGTTTGAGCCCCGCGTGACCTTTGAAACCAGCGATCCCATGCTC
CAAGCACACCTCGTGCGTAGCGGCTTGGCCGTGACATTTTCCCCCACACTGCTCACCCCG
ATGCTGGAAAGCGTGCACATCCAGCCGCTGCCCGGCAACCCCACGCGCACGCTCTACACC
GCGGTCAGGGAAGGGCGCCAGGGGCATCCAGCCATTAAAGCTTTTCGACGAGCCCTCGCC
CATGTGGCCAAAGAATCTTATTTGGAGGCTCGTCTAGTAGAG

>RXA00486-downstream
TGAGTTCTTGTGAGCCTTCAGAC

>RXA00490-upstream
GATTGAGCACGACACCTCCAAAATTGTTCAGTATTACTTAACTATAGTTGGCTGTTTTTC
GATCTAGTCCTTAAAGGTTTCTTTGGCAATAATCAAGGGC

>RXA00490
ATGAATAAACAGTCCGCTGCAGTGTTGATGGTGATGGGTTCCGCCCTATCCCTGCAATTT
GGTGCTGCCATTGGAACGCAGCTTTTCCCCCTCAACGGCCCCTGGGCTGTCACCTCTTTA
AGGCTGTTCATCGCAGGCTTGATCATGTGCCTGGTGATCCGCCCGCGACTTCGTTCCTGG
ACTAAAAAACAATGGATCGCCGTGCTGCTGTTGGGATTATCTCTTGGCGGAATGAACAGC
CTGTTTTACGCATCCATCGAACTCATCCCGCTGGGTACCGCCGTGACCATTGAGTTCCTC
GGCCCCCTGATTTTCTCCGCGGTGTTAGCCCGCACGCTGAAAAACGGATTGTGCGTGGCT
TTAGCGTTTCTCGGCATGGCACTACTGGGTATCGATTCCCTCAGCGGCGAAACCCTTGAC
CCACTCGGCGTCATTTTCGCAGCCGTCGCAGGAATCTTCTGGGTGTGCTACATCCTGGCA
TCAAAGAAAATCGGCCAACTCATCCCCGGAACAAGCGGCCTGGCCGTCGCACTGATTATC
GGCGCAGTGGCAGTATTTCCACTGGGTGCTACACACATGGGCCCGATTTTCCAGACCCCA
ACCCTACTCATCCTGGCGCTTGGCACAGCACTTCTCGGGTCGCTTATCCCCTATTCGCTG
GAATTATCGGCACTGCGCCGACTCCCCGCCCCCATTTTCAGTATTCTGCTCAGCCTCGAA
CCGGCATTCGCCGCCGCCGTCGGCTGGATCCTGCTTGATCAAACCCCCACCGCGCTCAAG
TGGGCCGCGATCATCCTTGTCATCGCGGCCAGCATCGGCGTCACGTGGGAGCCTAAAAAG
ATGCTTGTCGACGCGCCCCTCCACTCAAAATGCAACGCGAAGAGGCGAGTACACACACCT
AGT

>RXA00490-downstream
TAACGTGCAGGCTTACCTTTTGG

>RXA00491-upstream
TCCTCATAGTGTGTCCACAATTATCTAAACTTTAGTAGCTTGTCCTTAAATCGGATAACC
GCTGCAGCTCACACGCTATTCCACAACCGGAAATCTGGCA

>RXA00491
GTGTATTGGGTTTTAGCAACCTCTGCCAATAGGGTGGAAGATGTGAACTTTGATGCGATG
ATGCCCCGCGACCCGTTTGCCGATGATCCCAATGACCCGGCATCGTTTATTACCGACGAT
GACCCTTATGATCATCCCGAACCGCTTTCTGAAGAAGAGCGAATCCACGTGAGCCAAGAC
CTTCGCCTCGTGATGGAATTTAAAAAAGTTTTAGGTCCCCGAGGAATCGAAGGCGTGTTC
TTCATGTGCGAAGACTGCGAAGAGTTCCACTACTACGACTGGGACATCATGGCAGCAAAC
ATGCGCGCCACCTTGGCTGGGGAACTCAGCCCCGTGCATGAACCAAGTGCGCAACCCAAT
ATTGATGCCTATGTGCCGTGGGACTACTGCATTGGTTACCTAGACGGACTTGAAGCCAAA

>RXA00491-downstream
TAAAAACTGCTAGCAACTAAAGA

>RXA00493
TTCGAAGGCGACCAGAAGGTCGGCGTTCGCGCACTGGCTACTGCTTTGGGCAAGCCAGCG
TACTGGATCGCCTCCAACGCAGGTCTTGACGGCTCTGTTGTTGTTGCACGCACTGCTGCT
CTGCCAAACGGCGAGGGCTTCAACGCTGCAACTTTGGAATACGGAAACCTGATCAACGAC

GGTGTCATCGACCCAGTCAAGGTCACCCATTCCGCAGTAGTGAATGCAACCTCTGTTGCA
CGCATGGTTCTGACCACTGAGGCTTCTGTTGTTGAGAAGCCTGCAGAAGAAGCAGCCGAT
GCACATGCAGGACATCATCACCAC

>RXA00493-downstream
TAAAGTTCTGTGAAAAACACCGT

>RXA00496-upstream
CTGCAGAGATGGTGGGCAGCACCCCAGGTGCTGTACGAGTTGCCCAACACAGGGCACTCA
CGACACTTCGAAGCACACTTGAGCAGCAGGAGAACAAGTA

>RXA00496
ATGACTCGACGTCTACATGGTGGTGAGCAGGATGGCCAGGAACACGTTAAAGGACAGCTA
AAGCAGCTGTTCGACGACGACGCGTTCTTGACTGACCTGTCCCGCGGCGTTGATCCCTCA
GAGGGCGATGACGCCCTCGCTGGCCTCCTCCTCGATTTAACAAAGGAAGCTCAGGAGCCG
CCGGCAACAATGCCGGATTGGTCTACTTTGCTCCCTGGAATTTTGGATCAGGATCAGGAT
TTGCCAGTGGAATCCACTTCGGACACCACGGTTATGCAGGCATCAAACCCTGCAACCCAA
GAATTCGCACCTGTTTCTATTTCTGATACCCCCAACACTGCAACTAATTCAGCTGATGCA
GATGAGTCCGCAACTGTTGTTCCACTTGCAGCACGCCGTGAG

>RXA00504-upstream
AAGGTGGATTTGAAGCGAATTGTCTAGCTCTGCATGAATTCCGTATGAATTCTTTTCTTT
CAAGTGGCCGAGATGTGAAGCGCACGGTTAATTGAGAGGC

>RXA00504
ATGACCTACGGATTTCTTGTCAACACAGATCTCACCCACCGCGCGATTGACTTTGATTTA
GAAAACGCTGCGAAGTTCCTCGGCGGTGCCGATGATGGCCGCGTCGCTGTCGCTTTCCAA
GAGGATGGCACCTTGTACGCCGCTCTCTACAGCGCCAGCGCAAAAGATGAGGGTGCCGCA
GCAAACCCAGTAGCATCCCTTGGCCGCAACGCCGCTGCTACCGGTGATGGCTCCTTCTTC
TCTGAT

>RXA00505
GATCTGATCCACATGGATGCCTACCGATTGCTGGGCGAAGACAGCGAGGATGCTGATCCG
ATCGGTGCGCTGGACTCTTTGGATTTGGATACCGATTTGGACTTGGCTGTGGTTGTTGCG
GAATGGGGCGGTGGCTTGGTGGAGCAGATCGCTGACTCGTATCTTTTGATTACCATTGAT
CGAGAGACCGCTGTGCAGGAAGACCCGGAATCTGAGGCTCGAATTTTCCATTGGGAATGG
CGCGAAGGCCGC

>RXA00505-downstream
TGAGAAAGTTTTCCACGCTAAAA

>RXA00506-upstream
GTTGGATCTTGCATTGAAAAAATGAAAACCTCGTCGGGAATGCAACTTGGGATCACGTCT
CGGGCAAGAAACGTCCTTAAAAAAAGGGGAGTGATTGTGA

>RXA00506
GTGCTTGATTTCTTAGCTGCGAACCCGCTGATTGCGCTGGTGGTTATTTTGGCCGTTGGT
TTAGCAATTGGTCAGATTAGGGTCTTTGGCCTTTCTTTAGGTGCCGCCGCGGTGCTGTTT
GTGGCCCTGGTGGTTTCAACTGCAAATACCGACATCGTCATCCCCATGATTGTTTATCAG
CTGGGCTTGGCGATGTTCGTTTATGTCATCGGTTTGTCCGCCGGACCAGCATTTTTCAGT
GAGTTCGCTAAAAAGGGCTGGAAGCTCACCATCTTTATGCTCCTGCTGCTGGCAACACTG
ATTGGTTTGGCGTGGGTGCTTATTAAGTCACTGGGGCTTGATGCAGCGATCGGTACCGGT
ATGTTCACCGGCGCGCTGACCTCGACTCCCGGTATGGCAGCGGTCGTGGAATTGATTGAA
GGAATCGATCCAAGCCTTGCCAGTGAACCTGTTATTGGTTATTCCTTGGCATATCCGGGA
GCCGTGCTGGGATCCATTGTGGTGGCCGCGGTTGGAGCGAAACTGCTCAAAGTAAATCAC
CGGGAAGATGCTCGAAAAGAAGGCATGATCACCGCACCGCTGGTGTGGAAGGGTGTGCAG
CTCAAACCTGGAATCACAGGCAGGGTGGGAGATCTTCCACGCCTTGCAGGTGAAAGTATC

ATCGCAACCCGCATTGTGGATGATCCACATACACACCGCCTCGCGGATCCAGATCTGCCG
ATTACTGAAGGCATGGAACTGTTGATCAACGGCACTGAAGAAGCCGTGGATCGGGCAATT
AAGGCGTTGGGTGAAGAACGCGAAACCAAAATTGAGGACACAGAGCTGATCTACACCCGC
CTGACGGTATCTAGCCCTGAGGTTGCAGGTAGAACCGTTGCTGAGCTTGATACTGTAGCT
CACGGATTCATGATTGCCCGTATCCGCCAGGGCGATTCTGAGGTAGTGCCTAAACCTGAC
ACCGTGATCAACTACTCTGACCGCATCCGCGTGGTGGTTGCTCCTGGTCGTGTGGCTGAA
GTGCGACGATTCTTAGGGGACTCTGAAAAGTCCCTTGCTGATGTTAATCTGCTGCCTTTA
GCCATCGGATTATCTCTTGGCCTGTTGTTGGGCGCGATCCCGATTCCTCTTCCAGGCGGC
ACCACGATGTCCCTTGGCTTTGGTGGCGGCCCGATTATTGCCGGCCTGATTTTGGGAGCA
CTCAAGCACACAGGACCGCTGACGTGGCAGATGCCGTTCCACGCCAACCGCACGATCTCC
ACCTTGGGCCTGGCGCTGTTTTTGGCTGGTGTGGGTACCTCTGCAGGTGCAGGATTTAGA
GCTGCGCTTACCGATTCCTCC

>RXA00507-upstream
GTTCATGTTGAACTATTGTGCCACCAACCGCGGACAGAAATACGATTGGTGCCGGGGTTA
GTGCCAGTATTGCCCCACGCTTTCAACTATCCTTAAACAC

>RXA00507
GTGGCTGAGAATCTGAACAAACACCTGTCCAAACTGTCCAAGCGCGGACCGCACCGCGTG
CTGGTAGGCGATATGAACTACGCCGGCATCCCGGGCAAAATCTACACCCCAGCAGAAGGC
GACGGCATCCCAGGTGTAGCTTTCGGCCACGACTGGATGAAATCCATCAAGTACTACCAC
CAAACTTTGCGACACCTCGCGTCCTGGGGCATCGCTGTTGCCGCCCCAGACACCGAAAAT
GGCTTCATGCCAGACCACAAAGGTTTCGCCTCTGACCTCGAATCCTCCATTCAGATTCTC
GGCGGCGTAAAACTCGGCTCCGGAAACGTCACCGTCAACCCAGCCTGCCTCGGTGTAGTA
GGCCACGGCATGGGTGCTGGGGCTGCAGTACTATCCGCAGCAAACCGCGACCTCGTGCGC
GCAGTCGGAGCAATCTACCCAGCGAAAACCTCCCCCTCAGCAATCGACGCCGCCTTCGCT
GTCAAAGCCCCAGGCCTAGTCATCGGATCCTCCAGCCTCGGCCTCTTTGAATCCGGCGAG
CCAGCAAAACTCGCAGCCAACTGGGCCGGCGATGTCTGCTACCGCGAATCAGAAAAAGGC
AACCAACAGGGCTTCTCTGAAGACACCATGTTCAAACTTGTCGCAGGAATCGGCAGCCCA
CAAACCGGAGCTCAAGAAACCGTCCGCGGCCTCCTCACCGGATTCCTTCTCCACCAACTT
GCCGGAGAAAAGAAATACAAAGCATTCTCCGAACCAGACGCTGAAGCTAAGAAAGTTGTC
TCCTACTTCGGCCAGGAGCTGCAGGAACATGCCTTCCCTAAGGACACGTCCCCATTCGCG
TTCCTTAACGAGAAG

>RXA00507-downstream
TAGTTCGCTTTTCTTAGTGGGTG

RXA00509-upstream
CTTTTCTGGCGTCTTTTCAACCGGCTTCTCCACTGGTTTCTCGTCAGGTTTCTCAACGGC
AGCAGGTGTGGTCTTTTCCTTTTCAACACTGGATTCAGCA

>RXA00509
TTGGTCGACGTCGAACTATCCGCAGCACTGCTCGATCCGCCAGAACTCCCAGAGCTAGCA
GTGCTCGAGCTTGAACCACCTGAAGAGGCCGCAGCCGAAGAAGTCGCTCCACCAGATGAA
CCCCCAGAAGCTGCACTACACAACGGCTTTGGCTCAGTTTCACAAACTTGTTTTCCA

>RXA00509-downstream
TGATCGGTCAACGCGGAGAAACA

>RXA00510-upstream
GAGCAGTGCTGCGGATAGTTCGACGTCGACCAATGCTGAATCCAGTGTTGAAAAGGAAAA
GACCACACCTGCTGCCGTTGAGAAACCTGACGAGAAACCA

>RXA00510
GTGGAGAAGCCGGTTGAAAAGACGCCAGAAAAGCCGGTAGAAAAACCTGTCGAGAAGCAA
GAGTGTGAAGAAAAGCCTGACCCTGACCCGGAAAnAATGCAAAAnCAnGAGCCGGTCGAG
TGTGAGCCAACACCGAAACCTGAAACAGAGCCTGAACCAAAACCnGACACCCACGCCCAn
CnACCCGGAACACCAACACCAATACCTGnAGCTAGAGnACTGAGGATTGnTGnAnACnCT

GnGCAAGGAGAnCGnGGCACAGACTCAGnnAnATnCTnnnnnnnnGAATCGGAAGAGTGC
GCCCCCGAGCTCAATGACGTTCCAGAAGAGTCGGATCTGATTGGGCAACTCATCAAGGGA
GCAATCGGTATTGGGATTGTTGTTGTAGGCGTTGGGCTGTTGGTGAATTTCCTGGAGCAG
TGCGTCCCTGTGATTGAAGAAGTACCTGTGCCGGAGCCCGAGCCTATACCTGAACCCGCT
CCGCAGCCTGAGCCAACTTCAGTGAAACCACCAGAGTCTGAACTAGATAAG

>RXA00515
ATTGAAAGCTACATCGCCCAAGATGACAACGCCCCAACTGCTGCTGAACTGCAAGTACGC
CTCGATGCCATCGAATCCGGCGAAGGCCTAGCCATGCTCCTCCCAGACGATCCCACGCTG
GCAGACCCCAACGCCGAGGAAAGTTTCAAAACGGAGTACACATACGACGAAGCCAAAGAC
ATCATCAGCGGATTCTCCAGCGATCCAGCCAGCGATGTACTCAGCCAACTTCAACAAGCC
GCCACCACCGGCACCCGCACCGCAGAAATCCGCGCCGAAGTATTCGCCGACCGCACCGAT
GATTACAACGAATCCCAAACCGCTCTTAAAGAGGATTTCCAAAACTGCATCGATGCCATC
GATGACGCCCGCCCAATCCCACTGCAGTACATCCTGATTGGAGGCGCCATCGCTTTGGCG
GTCATCGTCCTCGGGATCAGGGCGTGGACTAACTCAAGGAAGCAGTCCAAGCACAGCCAG

>RXA00515-downstream
TAATACGCCAAGCAAAAAATTGC

>RXA00519
ATGGCTGGCGGCGGACTGTTCGAGACCGGTGCTGGTGGATCTGCTCCTAAGCACGTCCAG
CAGGTTCAGGAAGAAAACCACCTGCGTTGGGATTCCCTCGGTGAGTTCCTCGCACTGGCT
GAGTCCTTCCGCCACGAGCTCAACAACAACGGCAACACCAAGGCCGGCGTTCTGGCTGAC
GCTCTGGACAAGGCAACTGAGAAGCTGCTGAACGAAGAGAAGTCCCCATCCCGCAAGGTT
GGCGAGATCGACAACCGTGGCTCCCACTTCTGGCTGACCAAGTTCTGGGCTGACGAGCTC
GCTGCTCAGACCGAGGACGCAGATCTGGCTGCTACCTTCGCACCAGTCGCAGAAGCACTG
AACACAGGCGCTGCAGACATCGATGCTGCACTGCTCGCAGTTCAGGGTGGAGCAACTGAC
CTTGGTGGCTACTACTCCCCTAACGAGGAGAAGCTCACCAACATCATGCGCCCAGTCGCA
CAGTTCAACGAGATCGTTGACGCACTGAAGAAG

>RXA00519-downstream
TAAAGTCTCTTCACAAAAAGCGC

>RXA00520-upstream
GTTGACGCACTGAAGAAGTAAAGTCTCTTCACAAAAAGCGCTGTGCTTCCTCACATGGAA
GCACAGCGCTTTTTCATATTTTTATTGCCATAATGGGCAC

>RXA00520
ATGCGTTTTTCTCGAGTTCTTCCCGCACTTCTTATCACCACCGCCGTGAGCATCCCAACA
GCATCTGCTGCCACACTCACCGGCGACACCGACAAGGAATTGTGCATCGCCAGCAACACC
GACGATTCCGCGGTGGTTACCTTCTGGAACTCCATTGAAGACTCCGTGCGCGAACAACGC
CTCGACGAACTAGACGCC

>RXA00527-upstream
TTCCTTGGCCCCGAAGAAATTAATCATTGTGGCCGTGGTCCTGATTTTGATCATTGCGGC
TGCCTCGTTTTATTTTCTGCGTTCATCATCGAATGACCAG

>RXA00527
GTGATTGCCACTTCTGATGTTCGGGAGATTTCCTCCGAGGGAATCGTGGCGCGTGTGTCT
GTCAACGGAAATATTGAAGCTGCGCGAACCACCACCATTTACACCAGTCTGACTGTGCCG
GTCGCGAACTTGCCGGTTGCGGTTGGTGACCGTGTGGCAGCTGATCAGGTGTTGGCTGAG
TTGGATGCCTCTGCCCTGCAACGACAGTTGGATGAAACTGATGCCAACAATGCGCGTGCA
GCCATGGCGAACCGCAATTCCATCGCGCAGTCGCAGCAAGCATATGAGCAGTCCAGGGAA
CTTCTTGATAGTGGTTTGAGCCCGGAGATCAACTCGGCGCGGTCCTCGTTGCGGGCGTCC
TCACAGGCATATCAGGATGCGATCCGCAGTTTTGAAGCGAAGCAGCGAGATGTGGATGGC
GGATTGGATTCCACCATGGTCGCTCAATCGGATGCTCTCAAGGCAGCTCGTGAGCAAGCA
GATGCTGCTGAAATTGAACGACTGCGCGCGGACTTCGGACTGCTCAACAACGATCGCAGC

AACCTCAACGATGTCATTGGTCTGCTCGATGAGAGAGAATCTTTGGCTTCTGCGGAATCC
GAACTAGCTCAAGCCCGCGCTGCAGGTGACCTAGAGGCAGTCGCTGCAGCTGAAGCAAAG
GTTGCAGGCCTGGAACAATCAATTGCTTCCAAAACCTCCACGTGGCCTAGCCAAGATCAG
ACTTACTTGCAGTCCTACACCGCTTTGGAGGAAGCTGAGCGACGCGTCGCATCCACCACT
GAAGCTCTAGAAATAGCCGAGCGGATCTACATTGATTCACTCGGAAAAGTTGACTCAGAA
CTAGCCGCCGCACAGCGCGCCGTTGCCGAAGCCCACTCAGCACAACAAGACGCAGCACTT
GGCCTCGAGACCGCGCAGCTTTCCACCCAACACCAATTGGAAGCCCAATCAAGCGCCATC
GATGCAGCTTTAGGTTTGGCATCAGTAGATAATGAAGCCGCCACCAGATCCACGTCCCAG
CTGCGGATGGATATCAACAACACCACCGTTCGCTCCCCATACTCAGGCATTGTTTCATCC
GTGCAGGCAGCCCAAGGTCAACCAGCAGCCGGCGCACTGTTGAGTGTTGCTGATGATTCC
GAACTGAAGATCACCGCGAATGTAAAAGAAGCGGAGATCAGCAACGTCACCATCGGATCC
CGCGTCACCTTCACTACCCCATCGACCGGAACCAAAGAATTCGCCGGCCGAGTATCCAAA
GTCTCCCCCATTGCAGCTGCCGCCAGTGCCCCAGCTACAGGTGAAGGAGCTGCCGCAGGC
GCCACAACCACCAACACTGACGTCACCTTCCCCATCGAAATTTCCGTCACCGGCGACCGC
GAAGGCCTCAACCTCGGCGGATCCGCTCGAGTACGCATCGTCCATGAAATCGCACCACAC
GTACTGACCGTTCCTTTGGAAGCTGTGTACAAAAATGATGACGGCAAAGACGCTGTTTTG
ATCATCAGCGACGACAACAAAGTAGAAGAAGTAGAAGTAAAAACAGCTGAATCCGATGAC
TTTGATATCGCAGTCAGCGGTGCTGGAATTTCAGAAGACGCTCGAGTGCTCACCCAGCCT
GGAAACTACCGGGGCCTCATCGGAGAAACTGTGAAACTTCACGCAGATACGGTGGAGCAG
GCGGCGGCTCCTTTTAGTCCTGCGGCCCCTTTTGACCCTGCAGCCCCTGCCGTTTCTGCC
AAGCAAACCGTGGGCCAGGTGATT

>RXA00527-downstream
TAGCCTATGAGCCTCATCGAAAT

>RXA00528-upstream
TTCTGCTGGGAATCCCCACATTTTGGAACGTAGCGTCGATAAGCGTGCGGCGAAGCTTTT
TCGGTCGCGGCCGTTATCTTTTTAAGAGGAGAAATTTTAG

>RXA00528
ATGAGCACGTCCACCATCAGGGTTGCCATTGCCGGAGTCGGAAACTGCGCGACCTCCCTC
ATTCAGGGTGTGGAATATTACCGAAATGCGGATCCTTCCGAAACTGTCCCGGGTTTGATG
CACGTCAAATTCGGTGATTACCACGTTGGCGACATTGAATTCGTGGCCGCGTTCGACGTC
GACGCCGAAAAAGTAGGCATCGATCTTGCCGACGCCACCGAGGCTTCACAAAACTGCACT
ATCAAAATCGCCGATGTCCCACAGACCGGCATCAACGTGCTGCGTGGCCCGACTCTCGAC
GGCCTGGGCGATCATTACCGCGCGACCATCGACGAGTCCACCGCCGAGCCAGTCGACGTT
GTCCAGGCGCTTATCGACGCAAAAGCCGATGTTTTGGTGTCCTACCTCCCAGTGGGCTCC
GAAGAAGCCGACAAATTCTACGCACAAGCCGCCATCGATGCAGGCTGCGCCTTTGTCAAC
GCTCTCCCAGTATTCATCGCCTCCGACCCTGAGTGGGCTAAGAAGTTCACTGACGCTGGC
ATCCCAATTGTTGGCGATGACATCAAATCCCAGATCGGTGCAACCATCACCCACCGTGTC
CTCGCACGCCTTTTTGAAGAACGTGGCGTTCGCGTAGATCGCACCATGCAGCTCAACGTC
GGCGGCAACATGGACTTCAAAAACATGCTTGACCGCAATCGCTTGGAATCCAAGAAGGTC
TCCAAAACCCAAGCAGTGACCTCCAACATTCCAGATGGTCCACTGTCTGGAAAGGTGGAA
GACCGCAACGTCCACATCGGACCATCCGACCACGTCCAATGGCTCGATGACCGCAAGTGG
GCTTATGTCCGCCTCGAAGGCACCGCATTCGGTGGAGTTCCCCTCAACCTTGAGTACAAA
CTCGAGGTGTGGGATTCACCCAACTCTGCCGGCATCATCATCGACGCTGTTCGCGCCGCC
AAGATCGCCCTCGATCGCGGTATCGGCGGACCGATCATGCCAGCAAGCTCCTACCTGATG
AAGTCCCCACCTGAGCAGCTTCCAGACGATGTTGCTTGTGAACGCCTAGAGGCATTCATC
ATCGAGGCG

>RXA00528-downstream
TAAAATTAGGCTAAAAATTTGGG

>RXA00529-upstream
GCAAAGCTTTGTACCGGAAGCGTTAAGGCACTGGATTTTGTCGAGCAGTTTCAGGCTGTT
TAGCGGGCGAGTTCTTATAGAGATGTATAAGGTGAAGCTC

>RXA00529
ATGAAGTTGAAGTGGATTGCACCAATTCTTCCGGTTTTGGCCCTTGCAGGCTGCGGAAAC

TACGTCAACGTAGAGTCGCAAGGGAAATCTGGAATTTCCCATGATGAGGACGGAAATATA
AGCGTTCACATGTACATCTGTGGTGATAATGCGGTGGATGAACTGATACTTAGCGGTGGT
TTTTACGATGGCCCACCTGGGACAAACAACCCAGCCCTTGGGATGTTGAAAACTTCCAAC
CCTGAGTCGGGTTATGTTGTAGTCAACATCGCTGATCCAGCACCGTGGGAAGTTGTTGAG
CCAATCAATTTGCCCACGGAACAGGGAAAGTACATTATTGCCAATCCGAGGTTGGTAGAT
AAAGGTTGGCCGATTCCTTTCGCAAAAGAAAAGTATATGCCGAGTGTTTCCACATCAGTA
GGAATGCTTGAAGGAATAGATCCAGGTCTAGTCATGCGGGATATGTATACCGAGTCGACT
CATGTGTTCGGTACTGCCGAAGACTTTGTTGAAGCCGGTCAACAGTGGTGCGAGGATTAT
TTC

>RXA00529-downstream
TAAAACGTGAATCTGGCAAAAGA

>RXA00530-upstream
GGCGATAAGCCTCCTCCCTGGGGCCTTGCCCATTTCATAGGGTGTCCAGGTAATGTTTCA
GGGGTTAGATTTCAGCTGAAGCAACTGGGGAGTTGGCGCT

>RXA00530
ATGAGCATCGGATTCGACCGCGACCTTTATATTAAGATGCAGTCGCAGCACATCAATGAG
CGCCGCGAGCAGATCGGCGGCAAGCTGTATCTGGAAATGGGCGGCAAGCTTTTCGACGAC
ATGCACGCTTCCCGTGTGCTGCCAGGTTTCACGCCTGACAACAAGATCGCTATGCTCACT
GAGCTTAAAGATGAGCTGGAAATCCTCGTCGCAATCAATGCGAAGGATCTGGAGCGCAAG
AAAACCCGCGCCGACCTCGACATTTCTTATGAGGAAGATGTTTTACGCCTCATTGATGTG
TTCCGTGAGCTGGGCTTTTTGGCGGAGCATGTGGTGCTCACACAGTTGGAGGATGACAAC
TATCAGGCACTCGCGTTCAAGCAGCGCCTAGAGCGCCTTGGCCTGAAGGTTGCTGTTCAC
CGCGTGATTCCAGGTTACCCAACTGATGCTCGCCGCATTGTTAGCGAGGAAGGTTTCGGC
ATCAACGAGTATGTGGAAACCACCCGCAATTTGGTTGTTGTGACCGCACCGGGCCCAGGT
TCTGGAAAGCTCGCTACCTGCTTGAGCCAGATTTATGGCGATCACCAGCGCGGAATCAAG
TCCGGCTACGCAAAGTTTGAAACTTTCCCCATTTGGAACCTGCCTCTTGAGCACCCAGTT
AACTTGGCTTATGAGGCTGCCACGGCAGATCTCGATGACATCAACATCATCGATCCTTTC
CACCTCGCCGCCTATGACACCAAAGCCACCAGCTACAACCGCGACGTGGAAGTCTTCCCG
CTGCTGAAAACCATGCTGGAAATGCTGTCGGGCTCATCGCCGTACAAATCCCCCACCGAC
ATGGGTGTCAACATGGTCGGAAGCGCAATTATCGACGACGCCGCGTGCCAGGAAGCCGCC
CGCCAAGAAATTGTTCGGCGTTACTTCAAGGCGCTTGTCGACGAGCGTCGCGAGGAGCAG
GACGATACCATTTCAGCGCGCATCGCCATTGTCATGAGCAAGGCCGGTTGCACCGTTGAA
GACCGCCGCGTGGTTGCCCGAGCACTTGATGTTGAAGAATCCACCGGCGCGCCGGGTTGT
GCCATTGAACTTAACGATGGTCGACTCGTCACCGGCAAGACTTCAGAACTTCTCGGATGC
TCCGCAGCGATGGTGCTTAATGCACTGAAGGAACTCGCTGGCATTGATCGCAGCGTGGAT
CTCCTCTCCCCTGAATCCATCGAGCCAATCCAATCGCTGAAGACCCAGCACCTGGGATCC
CGCAACCCCTCGCCTGCACAC

>RXA00530-downstream
TGATGAAGTGCTTATTGCTTTGT

>RXA00535-upstream
AATCGCATGGGGCACCGTGGTCAGACACCGGATCGCGCTCCGCACCCCAAAAGATGGCTC
CCTAAGGAGCTCACCTTTACTCAATGCTCTGATGACACCG

>RXA00535
ATGTGGTGGGCAGGCATGAGTACCGCGATGCTGGCATATTTCTTACAAACAGTAGCACTT
GGTTTCGGCACCCTCTTGGTAGTGCAACCAGTGCTTGTCCTGTCGCTGATGTTCACGCTG
CCGCTCTCAGCACGATTCAATGGCTACCGACTACGCCGAACTGAAATCTTCTGGGCTACC
CTCCTCACCGTAGCCGTGGGCATCATGATCGTTTTGGGACGCCCCCTTCCCGGAAACCCC
CACCCCCCACTCGATCGATGGATTCCAGTACTTTTAGTCGGCGTTGCAGTAATGGGTGGA
ATGTGGCTGCTTGCGGAATACGTATTAAAGAAGGACAAAGCCCTCATCCTTGGTCTTGTG
ACGGGTGCATTGTTTGGCTACGTAGCAGTGATGTCCAAAGCCGCGGTGGATCTTTTTGTC
CATCAAGGCATAACGGGACTCATCTTGAACTGGGAAGGCTACGGCCTAATCCTCACCGCA
TTACTTGGAACAATCGTGCAGCAGTATTCCTTTAACGCTGGCGAACTACAAAAATCGCTA
CCCGCCATGACCATTGCCGAACCAATTGTTGCCTTCAGTTTGGGCTACTTGGTTCTGGGC

GAAAAATTCCAAGTCGTGGACTGGGAATGGATCGCCATGGGCATCGCACTACTGGTGATG
ATTGTTTCCACCATTGCACTGTCTCGTACAAGCACAATGCCGGCCGGATCGAAAAGG

>RXA00535-downstream
TAAAACTCCAAAGTTCCCCCCGA

>RXA00540-upstream
TCTCCCTATCTAAGGGCTGGCTAGGTTTGACCAGTGGCAACAGTTACACTTGTGCTCGTA
AAACATTGTCCTCCCCATTTCTTGAGTAAGGGAAAATACC

>RXA00540
GTGGCCCGTGTAGTTGTCAATGTCATGCCTAAGGCTGAGATTCTGGATCCCCAGGGGCAG
GCGGTACACCGCGCCCTCGGACGTATCGGAGTTTCTGGCGTTTCCGATGTCCGTCAGGGA
AAGCGCTTCGAGCTTGAGGTAGATGATTCCGTCACCGAAGCTGACCTAAAGAAAATTGCT
GAAACCCTCCTCGCAAACACCGTCATCGAAGACTTCGATGTGGTGGGAGTTGAGGTCGCG
AAG

>RXA00540-downstream
TGAGCGCCAAAATCGGTGTCATT

>RXA00546
CCGGTGTTGGGCGGAATTTTCCAGTGGATTTGTGGCATTATCACGCGGTTTTTGTACCCG
GTTGTTGATGTCATTCCGTTTCATACGCTGCCTGAATCTGGTCTTTATTTCATCGTCACC
GCGCTTGCGTTGGCGTTCTTTTGGGTGTTGGTCATCCGCATGATGGTGGAGCTCACTGGC
AATCGAGTGTGGGATACCGTCCTTGTTGCGGCGTCTCCCCTGGTTGCTGTGCATGCGTTT
ACCAACTGGGATACTCCAGCCATTGCGGCGGTGATTGGTGCGATGCTTGCGGTGAAACGC
GGAAACCCCTTGGTTGCGGGTGTGCTGATCGGCGCGGGTACGGCGTTCAAATTGTGGCCG
CTTTATCTTCTTGGTGCGTATTTGGTGCTGGCGGTCAAGAATAAGAATCTCAAGCCGTTT
ATCACCATGGCTGCAGCGGCTGCGGTGACATGGCTCGTGGTGAATGTGCCAGTGATGATC
GCGTACCCCAAGGCGTGGAATGAATTCTTGCGCCTGAACCGGGAGCGTGGTGCGGAGTGG
ACCACGATTTACCAGGTCATCGACCGTAATTTGCCGATCAATTTGAATGATCCAGTGCTG
CTTAATGTGCTGAGCTTCGGCTTGTTTGGTGCATCAGTGTGTGGCCATTTTGATCCTTGG
GCTCAAGGTGCAGCGCACTCCCCGAGTCGC

>RXA00546-downstream
TGAGCTGGCCTTTTTGATTGTCG

>RXA00547-upstream
ACCACGATTTACCAGGTCATCGACCGTAATTTGCCGATCAATTTGAATGATCCAGTGCTG
CTTAATGTGCTGAGCTTCGGCTTGTTTGGTGCATCAGTGT

>RXA00547
GTGGCCATTTTGATCCTTGGGCTCAAGGTGCAGCGCACTCCCCGAGTCGCTGAGCTGGCC
TTTTTGATTGTCGCGGCGTTTTTGCTGTTTAACAAGGTGTGGAGTCCTCAGTATTCACTG
TGGCTGGTCCCGTTGGCTGTTCTGGCATTTCCTCAGTGGAAAGTGCTGTTCCCGTGGATG
GTTACAGACGCCATGGTGTGGCCAATTTTGATGTGGCACATGCTCGGCACGGACAACAAG
GGACTCCCCCATGAAATGTTGGATCTCATCGTGATTTCCCGAGATGCCTTCATTGTGGTC
ATGATAAGTAGGTGTAATCCGGCAGATGCTCGGACGACGTGCAAATCCGGTGATGGATGC
GCACGCCGGGCGCGAATTGTTGGCCGGGCCCTTCGGCGCAAGCGAAGCGTCGAA

>RXA00549-upstream
ATTCGTTTGCAGCAGGATCTGGAAAATGGTTCACAGGATACTGCGGACATGGCGCATGCT
TTGGGTATCGCGAAGTCTTTGCCAACTATCCCTGAGACAC

>RXA00549
TTGACTGAAAACGGAGAGACCCCTTATGAGGGCATCATCTTGGGTCAGTATGAGTCCCGC
CCACTTGATATGGCTTCTGCGATGGCAACTATCGCTAATGAAGGTGTCTGGCACCGCCCG
CACTTCGTGTCCAAGGTGGAGACTGTCAGCGGTGAGGTTCTCTACGAGTTCGAGGATGGC

GACGGCGAGCGTCGTGTTTCTGAAAAGGTTGCACTGAATCTGCTCAAGGCCATGGGGCCA
ATCGCTGCATACTCCAACGGAAACGCTCTGGCTGATGGCCAGGTTTCTGCATCCAAGACT
GGTACCACTCAGCTTGGTGATACCGGTGCAAACAAGGATGCGTGGATGTTGGGTGCGGCA
CCTCAGCTAGCTACTGCGGTGTGGGTCGGAACTGCT

>RXA00549-downstream
TGATAACACTGCATTGTATAACA

>RXA00550-upstream
AAGGATGCGTGGATGTTGGGTGCGGCACCTCAGCTAGCTACTGCGGTGTGGGTCGGAACT
GCTTGATAACACTGCATTGTATAACACCTGGGGTGGCAGT

>RXA00550
ATGTATGGTTCTAACTCCCCTGCCACGATCTGGAAGCAGACCATGGATAACGCCCTCGAG
AACTCCCCTCTCGAAACTTGGGATATCGCTCCAGCATTGGGGTACGGTAACCCACCAGTT
CCGGAATATGTGTGGACTCCAAGTCCAAACATCGCGACTAATGATCCAGAAGGAGCAACC
GAGGAAGCTCCAGTGGAGGATCCAAATGCAGTAATCGATACCCCTGCTGTAGATCCCACT
GCACCTGCAGAGGAGACCGGTAACGGTCAGGTAGAAATCCTGCCGGGGCTGACTATCCCG
GGAGATCTCTTAGGGATCGGC

>RXA00550-downstream
TAAAATCCGGTCGTAGCCTAAAC

>RXA00552
TTTAAGTGGTCCGAGGGTGGCGCTGAGGATTTCCCAAAGCTCAGTGTCAAAGTCCGCGAT
GAGATCGTTGCCTTCGGCGCTCCAGATGAGCTCAAAGTGGATGAAAACGGCGTCGTCGGT
GGCGGCGTTCACCTGAAACCACAGCAGGTCAATGAGCTTGTGGAAGCCCGTGGCGATGAA
GTTGTGTTCTTTGACGGCCGCAACGCAATGGAAGCCCAGATCGGCAAGTTCAAGGACGCT
GTTGTCCCTGACGTAGAAACCACTCATGATTTCATCGCAGAAATTGAGTCTGGAAAATAC
GACGATCTCAAAGACAAGCCTGTGGTCACCTACTGCACCGGCGGAATTCGTTGTGAGATC
CTGAGTTCACTCATGATCAACCGTGGTTTCAAAGAGGTCTACCAAATCGATGGCGGCATC
GTTCGCTACGGCGAGCAGTTTGGCAACAAGGGCCTGTGGGAAGGCTCCCTCTACGTTTTC
GATAAGCGCATGCATATGGAATTCGGCGAGGATTACAAAGAGGTCGGACACTGCATCCAT
TGCGATACTCCCACCAACAAATTTGAGCACTGCCTCAACGAAGATGATTGCCGCGAGCTC
GTGTTGATGTGCCCTGATTGCTTCGCCAATGTTGAGACCCGTCATTGCAAGCGCGAACGC
TGTGCAGCAATTGCTGCGGATTTCGCTGAGCAAGGAATTGATCCGCTCGTTACTTCT

>RXA00552-downstream
TAAAAAGGGTATGGTGGCTGGGT

>RXA00553-upstream
GTCATTGCAAGCGCGAACGCTGTGCAGCAATTGCTGCGGATTTCGCTGAGCAAGGAATTG
ATCCGCTCGTTACTTCTTAAAAAGGGTATGGTGGCTGGGT

>RXA00553
ATGAGCATCGTTAAGATCAACGCAATTTCCGTACCCGAAGGCGCTGGTGAAGAGCTTGAG
AAGCGCTTCGCAGCCCGCCAAAATGCCGTGGATTCCGCTCCGGGATTTGAGGGCTTTCAA
CTGTTACGCCCTGTTTCCGGTGAAGACCGCTACTTTGTAGTCACCCAGTGGGCTGATGAA
GACAGCTATAACGCGTGGCGTGATGCCGAAAAGGCCAAGGGCGGTCATGGCCAGGGAGCC
CACGGCTCAGATAAGAAGCCTGTCGCTTCCGGCGCTTCCCTGCTGGAGTTCGAAGTAGTC
CTAGGATCTACCGGCGCTAAG

>RXA00553-downstream
TAGGGAAAGAGAAAAGTCGGAAC

>RXA00554-upstream
ATCCGAAACTCTCCTGTACCGACCATCATTTATCCCGGTCTTTAGGCTCTCCAACAGCAG

AGGACTAGACTTAAGTATGCCTGCAAAGGAGGACAACTTC

>RXA00554
ATGAACACCCAACCAGAGCATCCAGAAAATGATCTAGTCGACGAAGCCGATTTTTCTAAC
CGGCCCAGGATCTACTCGGACGATCCTGATTCCTTGGCTGATGCGCCAGACCCAGCGCTG
GAGCATGAGAAGAACAAGAAATCTTCACGCCAAGCACTCATTTATCTGTTGCAGGTTCCA
CTAGTTACATTCGTTTCTGCATACGTATTGGCCTGGGTGTCACGACTCCAGGGCGGTCCC
ATCTGTGACGCCGGTGAGGCTGTGTGGATTTGTTCCCGTGCTGCAGAACTGTGGTGGCCA
ATTACCACTAGCGTCATCGCATTTGGTGGCATGCTTGGATCTGCATGGATCCTCTATGAC
AAATACCGAAATTACCTACGCTGGCGTCCTTGGATGGGCGTGTTGTGGATTTTGATTCCA
TTCAGCATGCTGTGGGGAACCTCGGTGCTCACCTTGTCCATCTTGGGGCAC

>RXA00554-downstream
TAAAAACTTCACATAAATGACAA

>RXA00555
TCGGGTGGCAAACGTAGTGAACAAAATGATGCTGTTTTTGAGTTCGCCGCATGGCTAGCT
CGTACTTCAGACATCAATGTTCGTGGAATCACAACTTTCATACGCCCTTGGCCGTCTTCC
TCCATCAGTAAGCTCGGAGGAAAATATCATAAGTGGTATAAGAATTTAGATTCTTACTAC
CGCAGTCGCACGATCAAGGGACTCAAAGAGGCCGGAGTTGAGAAGTCCCAATGGGACGAT
GATGTTTCAGTTTTTGTAGATGGTCCTTCTGAATCCACGCTGCTCACCCATGCTGCTGAA
GAATTCGAAGCGGACCTCATTCTGCTTGGCTCTGATGCGACCGCACCAAAAGGCCGCTTT
CTGGCCAGCTCCACCGCAGATGCCCTCCTTCACTCCTCGCCCGTCCCACTAGGACTTGTG
CCGCGAGGGGTGAAGCTTTCCAAAAAGGGTGTCACCCGCGTCAACTACGCTTTCACCAAT
GAAAGCGATGACTTTGAGCAAGGTTTACGCTCTTCCGCGGAGCTCGCCACCAATTGGAAC
GTTCCTCTTCGGATCCTTGCTTTTTCACCCACAGGCATTACTTCCGCACCAACGTCGCGG
AGCTTGGATATTTCCACTGAGCTTTCCTCCGAGTGGCGTGAACTAACGCTCGCCATGCTT
GATCGAGCCCGTGATGGCGTCCTCACAGACCACCCAAACTTGAGCGTGAGCAGTGAAACC
GGTTCTGGCTGGGGTTGGAGCGGTGCAATTGATGCTTTGCGATGGAAGAAAGGTGACCTG
CTGTGCATGGGAAGCCATCGCACAGACACCCTTTCACGTGTCTTTGTCGGTTCGGAAACA
ATGGAAATTATCCGAAACTCTCCTGTACCGACCATCATTTATCCCGGTCTT

>RXA00555-downstream
TAGGCTCTCCAACAGCAGAGGAC

>RXA00560-upstream
AAGGACGACTTCTGGGGAGCGGTGTGGATTCTCACGGGGATTCTCATGCGGATTATCAGA
CATATGGACACTTTAACGGTTCGTACTAGGCTGATGCTTC

>RXA00560
ATGAGGATTGATCCGCTGGAAACCCGGCAAGCCGTATTGGCCGTCAAAGACTGGATTGAA
GGGGAGGGAGACGTCAAAAAGCCTGGTCGTGCGGCACTTGCCGCCGCAACTCGCCTGAGC
GTCCGACTGCTCGCGCAACACGCGCCGGGAAACAGCGTGGAGGTGCGGGTACCCCCATTT
GTTGCGGTGCAATGCATAGAGGGGCCAAAACATACACGCGGCACACCACCCAACGTG

>RXA00563
TTCTACAAGGATCTCTACGCACGTTCCGCACGCGGCACGGCAGCACTGTGGATCGTGGCG
GCTAACTTGAGCTCCTACTCAGACATCGACGCCATCATCAACTGGGTCGGATCCGAGCAG
ACCACCACCGTCAACGGCGCATCCAAGCTGGTCAAGCCAGCTTTGGTCCCTACCTTGCTG
TTCCCATTCGCGGCACCTCGCGTGTCCGGATCCATGGCAGATGCAGGCCCACAGGCAGAA
TCCCAGATGCGACTTCTGCTCTGGTCTGTTGAGCGCCTCATCGCAGGTCTTGCGCCATTG
GGCTCCTCCATCAACGTGGGTCACCGCCTGCACGTGGTCATCCCAGGTTCACCAAACCGT
GGACGCTTCGGTGGCGATGGTGCATACGGTGAATCCAAGGCAGCTCTCGACGCCGTGGTT
ACCCGTTGGAACGCAGAGCAAGCTGCATGGGGAGCACACACCTCCCTCGTGCACGCTCAC
ATCGGTTGGGTTCGCGGCACCGGCCTCATGGGCGGCAACGATCCTTTGGTCAAGGCAGCT
GAAGAAGCAGGCGTGGAAACCTACTCCACCCAAGAAATTGCAGAGAAACTGCTGTCCCAG
GCAACTTCCACTGTTCGCGAGCAGGCAGCATCCGCGCCAATCACCGTCGACTTCACTGGC
GGACTTGGTGAATCTGATCTGAACCTGGCGGAAATGGCACGTGCAGAAGCAGCTAAGGCA

GCTAACGCACCAGTGGTTGAGGCTCCACGCACAGTGGCAGCACTGCCAACTCCTTACCGA
CCAGTGGTTCAAACCACCCCTGATTTCGCAGGTCAAGTCACCCAAAACCTTGACGAGATG
GTCGTCATCGTTGGCGCCGGCGAGCTCGGCCCACTGGGTTCTGCACGTACGCGTTTCGAC
GCCGAACTCAACGGTTCCCTCTCCGCCGCGGGTGTCATCGAACTTGCATGGACGATGGGA
CTTATCCACTGGGATGAAGATCCAAAGCCAGGCTGGTACGACGACTCCGACGACGCAGTG
GCCGAAGAAGACATCTTCGACCGCTACCACGACGAAGTCATGGCACGCGTTGGTGTCCGC
AAGTACAATGACATGCCTGAGTACGGCATGATCGACAACTTTGCACCAGAGCTGACCACC
GTCTACCTCGACCAGGACCTCACCTTCAACGTGGGATCCCGCGAAGAGGCACTGACCTAC
GTCGACTCCGAGCCAGAACTCACCTTTGCTTCTTTCGACGAAGCAGCAGGGGAGTGGAAG
GTCACTCGCAAGGCAGGCTCCGCAATCCGCGTACCTCGCCGCATGGCGATGACCCGCTTC
GTTGGTGGACAGGTTCCTAAGGACTTCGACCCAGCTGTGTGGGGCATTCCAGCTGACATG
GTGGACAACCTGGACACCGTCGCGCTGTGGAACATTGTCTGTACTGTCGACGCCTTCCTG
TCCGCTGGATTCACCCCAGCAGAGCTGCTTGCTTCCGTTCACCCAGCACGCGTGTCCTCT
ACCCAAGGCACCGGCATGGGCGGCATGGAATCCCTCCGTGGCATCTACGTCGACCGCATT
CTGGCAGAGCCACGCGCCAACGACGTTCTGCAGGAAGCACTGCCCAACGTTGTTGCAGCT
CACGTCATGCAGTCCTACGTCGGTGGCTACGGACAGATGATCCACCCAGTCGCAGCTTGT
GCAACCGCAGCTGTTTCTGTGGAAGAAGCACTGGACAAGATCCGCATCGGCAAGTCCGAC
TTCGTTGTCGCAGGTGGCTTCGATGCCCTGTCCGTTGAAGGCATCACCGGCTTCGGCGAC
ATGGCAGCAACCGCCGACTCCGCAGAGATGGAAGGCAAGGGAATTGAGCACCGCTTCTTC
TCCCGCGCCAACGACCGGCGCCGCGGTGGATTCATCGAATCCGAAGGTGGCGGAACCGTC
CTTCTGGCACGCGGATCACTCGCAGCTGACCTGGGCCTTCCAGTACTCGGTGTCATCGGA
TTCGCAGAGTCCTTTGCAGATGGTGCCCACACCTCCATCCCAGCCCCAGGCCTCGGTGCC
CTTGGTGCTGCTCGCGATGGTGTGGAATCTCGCCTTGCAGTAGCACTGCGTTCCGTCGGT
GTCTCTGCTGATGAGATCTCCATTATCTCCAAGCACGACACCTCCACCAACGCGAATGAT
CCAAACGAGTCCGACCTGCACGAGCGCATCGCATCCGCTATCGGTCGTGCAGACGGCAAC
CCGATGTACGTGATTTCCCAGAAGTCACTCACCGGACACGCCAAGGGTGGTGCAGCAGCA
TTCCAGATGATCGGTCTCACCCAGGTCCTCCGATCCGGACTGGTGCCAGCCAACCGCGCA
CTCGACTGCGTTGACCCAGTACTGTCCAAGCATTCCCACCTCGTCTGGCTGCGCAAGCCA
CTAGACCTTCGTGCGAAGGCACCAAAGGCAGGTCTTGTTACCTCCCTTGGCTTCGGACAC
GTCTCCGCTCTGGTTGCGATTGTTCACCCAGACGCCTTCTATGAGGCAGTTCGTGTGGCA
CGTGGTGCTGAGGCAGCTGACGTATGGCGCGCATCCGCGATCGCTCGCGAAGAAGCAGGC
CTTCGTACCATCGTCGCCGGTATGCACGGTGGCGTACTGTACGAACGCCCAGTCGAGCGC
AACCTCGGTGTCCACGGAGACGCAGCTAAGGAAGTTGAAGCTGCAGTCCTCCTGGATTCC
CGCGCCCGCCTAGTTGACGGTGTCCTCCGCGCCGAAGGC

>RXA00563-downstream
TAGTTGGTTATTGCGTTGAGCCC

>RXA00564-upstream
CAACGATGGAGTGCTATTCGTAACGAGGTGACATTCCCACCGGCACCTTGATCCAGATAG
AAAAACGGATGGAACCAGTATTGGGAAAAGGATGGTTGCG

>RXA00564
ATGAAATACAACGTCGATGTCTCTCGTGAAAGCGAGGACTGGCTCGCCACCGTCACCAAT
CTCGAAGGCGTATCCACGTGGGCGACAACCTTCGCCAACCTTGATCGCAACGGCCGGGAA
GCCATTGCTCTAGCTGAAGATCTCCCCGAAGGTGCGGAAAGCTCACTGACCATCTCTTGG
TCGGTTCCTACAGATTCCCACCCCGAACTGGACACTGCAATTCAAATTGCTCAACAGCGT
CGCTATCTAGTGCAAGCCCAACAAGACTTAGAGCCCAAAGTTCGATCCGCTATTTCCGCT
CTCACCCAAGCTGCGCTGCTAGGTATGACTGCAGGTCGAGTATCCCCAACTCACAACCCG
GGTAGCAGAGCTATCTCATTGGATCAGGTGTCAGGAGTTTTAAAC

>RXA00564-downstream
TAGCGTGCGCAATTCCCGTGTGA

>RXA00573-upstream
GACGCCAACTCCATCTGTGTTCATGGGGATAATCCGCAAGCTCTCGCATTGGTGGAGAAA
ATCGTGACCACCCTTGCAGCTCATGAGGTTCAGGTTTCCC

>RXA00573

ATGCTCGTTAGGCCATGTGGTGAGCAAGCAGTCATCATCGATTTGCTTGCTGAAGATGCC
GAAGCCGTCCAAGGCAGCATCTTGGATGCTGTTCTTGCACTCAACCGCTCTTTGGTGGGC
ATGCAGGTCCCTGGAATCATCGATACTATTCCCGCTGCGCAAACACTGTTAGTGACGTTT
GACACCAAGCAGATCACCCCGAATCGTTTCGCAGAGATCGTTGATTCAATTGCGCTGACC
CCAGCCGCAAAGGGCGCAGCAGAGCTTACCGACACCATTGAGATTCCCGTGGTCTACGAC
GGCCCTGATCTAGAAACCGTAGCTCAACACACAGGTCTGAGCGTGGAGGAAGTTATCGCC
ACGCATTCTGGCACCGTGTGGACTGCTGCTTTCGGTGGATTTGCACCAGGTTTTTACTAT
CTGATCCCCCAGACTCCCCTGTGGGATATTCCCCGCTTGGAATCGCCACGCACCAAGATT
CCTGCAGGTTCTGTCGCAGTGGCCGGTGAATTCAGCGCTGTGTACCCGCAGCAGTCCCCT
GGTGGTTGGCAACTGCTGGGCACTACTGAGATTCCCATGTGGGATGTGGACCGGTGGCAA
CCATCGCTTCTCAAGCCCGGTGATTCAGTTCGATTTGTGCAGGTGAAGAAA

>RXA00573-downstream
TGAGCTTCAAAGTAATTTCCACT

>RXA00574-upstream
AACTGCTGGGCACTACTGAGATTCCCATGTGGGATGTGGACCGGTGGCAACCATCGCTTC
TCAAGCCCGGTGATTCAGTTCGATTTGTGCAGGTGAAGAA

>RXA00574
ATGAGCTTCAAAGTAATTTCCACTGGCCCCCAAGCCATCTTCCAAGACCGAGGTCGCTTC
GGTTTTGCCAGCGCTGGTGTTGGAACCTCAGGATCCTTTGATCGTTTATCCGCTGCTCGC
GCGAATCACGCTTTAGGTAATGATCCCAATGCAACCGTGGTAGAGATTCTGCTCGGTGGC
TTTGAGGTGGAGGCGTTGCACACCACCTCGATCGTGTTCACGGGAACTGAAGCTGAAGTG
ATGGTTCGAACGGCTGGTGGACAATCCAAAAATGCCACCACCAACACCATCATCGATGTT
GCAGCTGGTGAACGTATCCGCGTCGAGCCCGCAACCTATGGCATGCGTGCCTACTTTGCT
GCTCGCGGTGGATTTGCAGTAAAAAAAACTTTGGGATCTGCTTCAACCGATCTGATCTCC
CACATGGGCCCTTGCCCGATCGAGCCCGGGGATGTCATTGACGTAGCAACAGACATTGCA
GATTCTCAGTGGTGGCCAAAACTTCGGCAACTGCCCACCTTATGGAAACGCATGCCAACA
GAAACGCTTACCGTCATCCGAGGTCCACGTGACAAATGGTTCACGCAAGAATCCCTCAAC
AACTTTTTTACTCAGGTGTTTACGGTGAGCAATGACTCCAACCGGATTGGTTTGCGCATG
CACTCAAGCGAGCCGATCCAACATCGTGTGGAAGGCGAGCTGAAAAGTGAAGGAATGGTC
CGGGGGTCCATCCAGATTCCGCCTGGTGGAAACCCCGTGGTGTTTGGTCCCGATCATCCT
GTGACCGGTGGCTATCCAGTAATAGCAGTACTTACATCAAGGTCGTGTGATCGTTCGGCC
CAGCTGTTGCCGGGCGATAAAGTCAGATTTAAATTGCTT

>RXA00574-downstream
TAGGAACTTTGAGCTTGCTCTGG

>RXA00576-upstream
ACAGTCCGAGCTTCTTAGCGGCGGTCTGTGGCTTCATAGCCCTGCCCGATGGCTGGCGTA
CAGATTCTTCGTTCACGCCCACAACGGTAGCATTGTTTTC

>RXA00576
ATGCTGACCTTAAGTTTCATCACTGGCACGGAGCCAGGAAAGTGGTTTACCCGATTCCGA
GATCGGACTCATCACGGTGGACTTGAGACCCTTGATTCGGACGACGCCCTAGGCCTCATG
CTCGCTGGCCAGGCACAACTCGCCTTAACCAGGCTTCCAGATGCGCGTATCGACGCCTCC
CTCCACGTGGTCACTCTTTATCAGGAACAACCCGGAGTCGCTTTTCCAAAAGACTTTTTC
CTCAGTGCCGAAGAAGGCGCGGTGGACCTTGCGGACTTAGATGGGGAGATCATCAACTGG
TCCATGCCCGATAGTGGGGAAGTCGATGCCGCTGCTGTTCGCGATGCTCTGCAAATCGTG
GCAGCGAACGTCGGTGTGGTGATCGCCCCCAGGCCACTTCTCAAGGTGTTGAGCAAGAAA
TTGGTGGAGCACCGGGACATCAAGGGTGGAACTGAAACATCTATCGCCCTGGTATGGAAG
AAAGATGAGGATTCTGAAGAGATTCAAGACTTCGTCGGTATTGCTCGCGGTCGAACGCGG
AATTCCAGCAGGCAGCAAACGGTAAAGCTCAGTGCTCGTGAAAAAACACTGGCAAAACAA
GCCCGCAGGCAGGGGGAGAAACCAAAAACTCCGAAGCGTCCGCAGGCAAGAAAACGTCCC
GGAAAACGGCGA

>RXA00576-downstream
TAGGGGTCACCCGCGCATGTCCG

>RXA00577-upstream
CTGGCTCCGTGCCAGTGATGAAACTTAAGGTCAGCATGAAAACAATGCTACCGTTGTGGG
CGTGAACGAAGAATCTGTACGCCAGCCATCGGGCAGGGCT

>RXA00577
ATGAAGCCACAGACCGCCGCTAAGAAGCTCGGACTGTTTTTGCCCGCCACGCCAGAGGAG
TTCCAAACAGGTGCATTGACTCACCAAGAGTTCAAGAACCTGCAGGAAAACCCACCGGAG
TGGCTCCAAACCCTACGCCGCGAGGGCCCACACCCTCGTCCAGTGGTCGCCCAAAAATTG
GGCATCACCATCGCGGCTCTGAAAAAGAACGACATGGACAAACCACTGACCACCGCCGAG
ATCAAGGCACTTCTGGAAAACCAGCCAGAATGGTTGCGCACCGCACGCACACAGCTTGCT
GAAGGTCGCGAAACCGCAAAGAAAGAAACTGAAGAAACTACCGAAGAC

>RXA00577-downstream
TAAATCTTCACAAAGACTGCGCT

>RXA00578-upstream
TGGGCGGTGCACTTCTTGCTCTGTCTGATCCGGAGGCTGAGTGGGAGGAAATCCGCGTTA
AATCACGGCCTCTGCTGAATTTGTTTGGGGTTGAATTCCC

>RXA00578
ATGACGTACCTCGTGTGGGACGGTGCAACACTCGTAGAAGGCGCGCTGGAATCAACACCC
ACAGTTGTTGATTCCTACCTAGCCAAAGACCACCGCGTGGTGCGCTGGGATCTTCATGAA
CAGCGCTTCGCCACTAGCGTGGACGTGGACCCGTGGGATTTTCTCCACGCAGTAAGGGAA
GCAATTCCACGCCAGGGCTCATGGTTTCCCAAAGTTGAATGGCATGGCGATGATCTTTTC
GCAGTCAATATTCGCCCGGCACCAACACTGCGAAAGGCCACATCATTGTGGCTTTCCGAA
GACCCAGATCCACGCACACAGCCAACCATTAAAGGCCCAGACCTAGATGTGCTTGCTCAC
CTTCGCAGTCGCGCCAACGATAACGGCTGCGATGATGCGCTGTTGATCAGCGCGGATGGG
TTCATTCTGGAAGCTGCCAACGCCACCGTGGTGTTTTGGGCGGATCCACAGACGGTCATC
GTGCCCAGGGGAGATGTGCTCCCATCGGTGACACTCGCCGCAACCATTCCGCTGTGGGAA
AAAGCCGGAATCACATTGCGCTATCAAAACATTCGGCACATTGGTTTTCCCGCGTGGTGC
GGTAGTTCGCTGCATGGTTGGACACCTGTGGTCAGTTGGGGCAGGGGATTGGGCAAAATT
GCAGCAGCGAAAGCTCCATCGGTGAAGCCCTGGAATGAAAAATTGCGCCCAACCATTTTT
CTG

>RXA00578-downstream
TGAGGAAAAGGTTGAGCGCAGTC

>RXA00582-upstream
ACTGGCCAGCCTTCCGACGCATCGACTTCCTCCGCGCCATTCGCGACTACTCGCAGCGCA
GCAGAAGATTCGGTAAATAACTTATTCTCCAAGGAGAGAC

>RXA00582
ATGTCTGACTACATCGTCGCATTTGAATCCGCATACGGCTCTACCAAGCAGTACGCAGAA
TCTCTGGCGCAACGCCTCGGCGTAGATGCCTTAAATTTTGAACAAGCGTGTGCGGAACTC
GCGGCGAACCCGACCGCAGCAATCGTGGTTTTGAGCTTTGTTCACGGCCCATCCCATCCA
GGTGCGAAATTCATTACCGATACCGATCTCTCCGGCCACCGCGTCGCACTGTGCACCGTC
GGCATGACGCTTGATGATGTCGTGCAAAAGAAGGACGGCGCAGCTCGATCACTGGGAAAC
AAGGCAGACGATGTCACCCGTTTCTACCTTCCGGGACGCCTTAATTACTCAGAGCTCTCG
ACCGCGCACCGCACCACCATGTGGACGATCGTCAACATGCTGAAAGCGAAGCCGTTGAAG
AATGACAACGACAAAATGATGATCAACACTTTTGATACCGATGTTGACCGCGTCGATGAG
TCCCGCCTGGACGCAGTGGAGGAGTGGGCGAGGGGCCTC

>RXA00582-downstream
TAGAGTGGGCGTTGCAAAAACTC

>RXA00585-upstream

TGTGAAGACGTCGATCCCAGAAGATGACCTGTTTGCCGGAATCACACCCGATGCAGAATA
ATGCAGTTAGACCACATCCTTTAGGAAGGACCTTTTCGGC

>RXA00585
GTGATTGACCTCAGCCCTGTATTCAATACAGCTGCCGGCGTATACAACGACACCAACGCA
ATCATCTTGGCTCAGCAGCAGCAAGGTGGACCACTTGGACCTGAGTTTGGAAAGGCCTCG
CCGGTTGGTTTGCTACTGATCGTCGCGATGCTCGTTGCCATTCTTGTTCTCGGCTGGGCG
TTCCACCGACGCTGGTCACGGATGAATCGTCGTCGTATTTTCGCAGAGCGCAACGGCCTT
GATCCCTTCGATATTGAGGGTGTTCGCAAGGCAATGGCTGAGGCCGGCTTGAATGAAAAG
TCCAAAAAGGGCTTCCTT

>RXA00585-downstream
TAAAAAGAAAGTGTGTTAAGGTT

>RXA00586-upstream
TCATCCAAGGGGTAAATAGGTATGACGGCGGAAACGACTATCATGAATGCAATACACATC
AACTAAACCCTGCGGAAGCATATAAAGCTTCAAGGAAAGG

>RXA00586
ATGAAACACGTGAGTGGTCTACGCCTAATGGCGATCCACGCCCACCCTGACGACGAGTCA
AGCAAGGGCGCAGCAACCATGGCGCGCTATGCAGCTGAGGGCAATCAAGTAATGGTTGTT
ACCTGCACTGGTGGTGAGCGTGGAGACATTCTCAACCCTGCTATGGATAAGCCAGGAATC
CTGGACAATATTTTTGCTGTGCGTCAGGAAGAGATGGCGAAGGCCATGGAAATTCTTGGC
ACTGAGCACAGATGGCTAGGTTATGAGGACTCTGGGCTGCCCCAAGGTGATCCTTTGCCT
CCTCTGCCTGAGGGCTGTTTTGCTTTAGAAGACTCGGATAAAGTCACCCAAGATTTAGTG
AAGATTCTGCGCGAGTTCCGCCCACACGTCATCATTACCTATGATGAGAACGGCGGTTAC
CCACACCCGGATCACCTCAAGGTTCATGAGGTGTCGATGCTTGCATGGGAGAAGTCCGGC
GATGCAGCGTATGCACCTGAGTTGGGCGCACCGTGGGAGCCACTGAAGCTTTATTACACC
CACGGCTTTATCCGTCAGCGCATGGAAATGTTCCATGATCTGCTCATTGAACAGGGCAAG
CCCAGCCCATACACCCCGATGCTTGAGCGTTGGAAGGCAAATGAGGCTGATGTGATGGCT
CGAGTTACCACTCAGGTTCCTTGTGAGCGCTTCTTTGATCAGCGTGATGACGCCCTGCGT
GCGCACGCAACTCAGATTGATCCTGCGGGTGCTTTCTTTGGAACTCCCGTTGAGGTGCAG
CGTCGCCTGTGGCCGACTGAAGAGTTCGAATTAGCTAAAACTCGTGTGAAGACGTCGATC
CCAGAAGATGACCTGTTTGCCGGAATCACACCCGATGCAGAA

>RXA00586-downstream
TAATGCAGTTAGACCACATCCTT

>RXA00587-upstream
CCCTTGGATGACCTCGGTTAACAGTTTTTCCTGAGGTGACTAAGATGTATAGGTGACCAA
CTCGATTCGGCTTTGAAGAGGATGCAGACAGACTTCCATC

>RXA00587
ATGAGTACAAATTCCAACTCTCCATCCAACGCATCAGGCGCTTCGAACATTCCAAACACC
CAACGTCCGGCTAGCCGATACAATTCGCCTCGCCCGGAAGCTGCTGCAGGCAGGAACATC
AGCGGAAAAATCATCGCAGTCATTGGCGTGCTGCTGGTGATCGCCATTGTGATTGTTGGC
GCAAACTTCCTCAAAAACCGCGATGCACAAACAGTGTCCGGCCAAATGGGTTCATTTGAA
CGCATCGACGACGACACCTTCCGCTTTGAAGTTGACGTCACCCGCGATGACCCAAGCCAA
GTCGCCTACTGCATCGTGACCGCAAAGGACTACTCGCACGCAGAAGTCGGGCGTCGAGAA
GTGCTTGTGGAGCCCAGCGACCACTCAACGGTGCGTATCTCCACGCTGATCCCCACCCGC
GAACCAGCAGTTTCCGGTGGTGTTTACGGTTGTTCAACCGTGATCCCATCACATATGAAC
CTG

>RXA00587-downstream
TAAAACTAGAAAATTTTGCTGTG

>RXA00589-upstream
CCGTTATCTCCGTAACTGTTGTTTCTGCAGAACCATACAACTCAGCAAAAGCCGCGACAC

TCCGCGGCAAAAACTAACCAAGGATTTAAAAGTCTTCAAA

>RXA00589
ATGACAACTCTTTCACGTAAGTTCTTCGTTTCTGCTACCACAGCCCTGGCGGCAGTCGCA
CTGGTTGCGTGTTCCCCTAATGAGATTGATTCTGAACTGAAGGTGCCAACGGCAACTGGC
GTTTCTTTACCTTCGAAGAACGTTTCCGCGACCTCAACTGCTACTACAGATGAGGATGCG
CCTGGCTACATTGATTGCGTAGCCGCACCAACTCAGCAACCTGCTGAAATCTCACTAAAC
TGTGCAATGGATATTGATCGGCTCACGGATATTTCTTGGAGCGAATGGGATACTGATTCC
GCAACTGGAACCGGTACCCGCATCGTAACCGCTGCAAATGGTCAAGAGACCGAAACCGAA
GAT

>RXA00595
CGCAATATTGCAGCATGGATCGCAATCGCCGCCATCATCATCGCCAGCCTGGGCGCACTG
CTCTCGATGATCCGCGTGTGGCGTGAAGTCTTCTGGGGTGGCGCAATGCACCAGCGCGGC
GTCTCGCCGCAGCTGCGCATCAGCCCAGCAAAAATCGCCCCAGCGCTCAGCCTGATCATT
TTATCGGTAGGCATGTTCATCTTCGCGGGCCCGCTTATCGACGCGACCCTCACCGCCACC
GACGGCCTCTTGAACACCGATGCATACCAACAGGCTGTGCTCGGTGAAAATGCCATCGGA
GTGCCAAGCCCTAGCTACCAGGGAGGAAAC

>RXA00595-downstream
TAATGCTTAACGCCCTGAAATTC

>RXA00597-upstream
CAAGGAGATCCGCCCCAGCGATGCTGAGTGGCCAAGTCGCGAGATCGCTGACACCGCCCA
AAACACCGTCAGCCAAGACAAGAGGGAGTTTTAAAACAAC

>RXA00597
ATGACTGCTTTTGGAATTGTCACCACAGTTGGCATCTGCATGTTTGCGTTCTCCCTCTTA
TCTGCCCTGGTCCTTATTCTGCGCACCAAAGATTTCCTCACCCGCGTGGTGCTTTCCGAC
ATGGTTTTCTACTCTATGATCGCGATCTACCTCATCTGGGTGCTCAACAACCCAACCTCA
ATCGCCTTTGAGATTGCTCTTCTCGCAGCAGTCCTCGGCGGCGTACTTCCAACCCTGTCC
ATGGCTCGCATCATTTCGAAGGGACGCAGG

>RXA00597-downstream
TAAATGACCATTCCAGAGATCAT

>RXA00598-upstream
AACCTCAATCGCCTTTGAGATTGCTCTTCTCGCAGCAGTCCTCGGCGGCGTACTTCCAAC
CCTGTCCATGGCTCGCATCATTTCGAAGGGACGCAGGTAA

>RXA00598
ATGACCATTCCAGAGATCATCGTCTCCATCCTCGTGATCCTCGCAGGCCTGTTTTCTCTA
GGTACTGCAATCGCTTTGTGGCGCGCACCGGATCCGCTCACCCGAGCCAACCTGCTTGGC
ACCACCGTGGGTGTCTCCATACCGCTGCTCATCATTGCGCTGCTGATTCACACCTGGTCC
GTCGACGGATTTAACCCCAACAATTTCATCCGAGCGATCATCGCCATCATCGGCGTCTGG
GTCATCGGTTCCGTTGGTTCCTACTACATGGGACGCGCCATCTATGGTGTGACCGTAGTG
GATAACAGACGATCCAAA

>RXA00598-downstream
TAAACTGCTTTTAGAAAAAAAGG

>RXA00601-upstream
TAGATATAGAACACATTCTATTGCAGGGAATTATCAAGTTTCATACATTGTCCTCGTAGG
GGCAAGTATATTTCCCATGCAATATTTTTTAGGAGTCCCA

>RXA00601
ATGCGTTTCAAGTCAGTTGCAGCTATCGCACTTTCCACCGCAATGATCAGGGGTGGAACC

GCAAGCGTTGCTAATGCTCAGCAGGTTAGCCCTAGTTCCACGATTGAGATCCCTCAAGAA
TTCGTCCACACCGTGCAGAACTTCGTGCCAGGTATGACTTACGGCGATGCAGGGTCCGCT
ATCCAGAGCACCGCTGGTTCTGTGGCACTGAACAGTACCGCTGGAATCATCCTTCCAATC
GTTCTTCCATTCCTTGGTCTGGGAGCTGTTGGTTCTGCAGCGCTGTCTGCT

>RXA00601-downstream
TAAGCCTTTTCTAGGTTCCTTAA

>RXA00602-upstream
GCGCGATCAATGGAATCTAGCTTCATATATTGCACAATAGCCTAGTTGAGGTGCGCAAAC
TGGCAACAAAACTACCCGGCAATTGTGTGATGATTGTAGT

>RXA00602
GTGCAAAAAACGCAAGAGATTCATTCAAGCCTGGAGGTGTCGCCATCCAAGGCAGCCCTG
GAACCAGATGATAAAGGTTATCGGCGCTACGAAATCGCGCAAGGTCTAAAAACCTCCCTT
GCTGCAGGTTTGGGCATGTACCCGATTGGTATTGCGTTTGGTCTCTTGGTTATTCAATAC
GGCTACGAATGGTGGGCAGCCCCACTGTTTTCCGGCCTGATTTTCGCGGGCTCCACCGAA
ATGCTGGTCATCGCCCTCGTTGTGGGCGCAGCGCCCCTGGGCGCCATCGCGCTCACCACA
TTGCTGGTGAACTTCCGCCACGTATTCTATGCGTTTTCATTCCCGCTGCATGTGGTCAAA
AACCCCATTGCCCGTTTCTATTCGGTTTTCGCGCTTATCGACGAAGCCTACGCAGTCACT
GCGGCCAGGCCCGCAGGCTGGTCGGCGTGGCGACTTATCTCAATGCAAATAGCGTTTCAC
TCCTACTGGGTATTCGGCGGTCTCACCGGAGTGGCGATCGCAGAGTTGATTCCTTTTGAA
ATTAAGGGCCTCGAGTTCGCCCTTTGCTCTCTCTTTGTCACGCTGACTTTGGATTCCTGC
CGAACGAAAAAGCAGATCCCTTCTCTGCTGCTCGCAGGTTTGAGCTTCACCATTGCTCTT
GTGGTAATTCCAGGTCAGGCCCTATTTGCGGCGCTGCTGATCTTCTTGGGTCTGTTGACC
ATCCGGTACTTCTTCTTGGGAAAGGCTGCTAAA

>RXA00602-downstream
TGACAACTGATTTCTCCTGTATT

>RXA00604-upstream
ATCACGTTTTGCTATGAAAGTGGTGAAACCAGCTCGCCCCCAGGTGTGAAGCATGCATTT
TGAAGCATGAATCTTTTTCATCTAGTGAAGGACTGATCCC

>RXA00604
ATGCGTATGAAATCAATCGCAGCAATTGCAATCGCTACCGCCGCCCTGGCTGGTGGCACT
GGAGTCGCTAGCGCACAGGAAGCTGGCTCGACTGCTGGTTCCTCCAACCTCAGCTCTGGG
ATCCAGCTTCCACAAGAAGCCACCGATCTGTTGAGCTTCCTGCCTGCTGCTCAGGCTGCG
CAGGTTGAAGGAGCAATTCAGAGCACCGCTGGTTTCTTTGCCGTTGGACTCGGCTCGACC
GCCATTGGTTCCACTGCAGTGACCTTGGGAATTGCGGATCTGCTGTCTAGC

>RXA00604-downstream
TAATTTCCTCTCAATAGCTTCAA

>RXA00610-upstream
CAAGCACTCCCAGGGGAACGTTCATTCGAAAAACTCGACGCCTTATACGAGCTTCTAGAG
CCTCGGAACCAATTGCTCGAGATCGCAGTCTAACTAGAGT

>RXA00610
ATGGAACCGAAAAAACCTGTCACATATAAAGAACTTGCCCACGAATATTCAAGAAGAACG
TTTAACAAACTCTTCACCAAAATTACTGGCTTCGTCTATCTAAAAAACGATCTAATCAAC
GATCCCAACTTAGTGACCCAAGCACTGCTCAAAAGATGCCCAGAAGGAGTACTTCGCGGA
TATGCAGCATTAAAGCAACGTGGCTATCAGCTTTTAGACGATCAGTGGATGCCAATCATC
AGTGTTTCCGGAGATCTAAACAGGAGGGACTGCTCACGAGGTGAAATTCTCAGGCGGATT
GAACCAGAAAACACCCTGCTCAGTGGCAACATTAGGTTCGTTAATGATGTTCAAGCGATC
CAAGACGTCTTCGACCTGCATTCTCTCAACGACTTTGAAGACCAAGTAGCTCTCATCGAT
CATCTCATCAGGCAGCGCCCCGAATTATTCCAAGAACTCATACAAGAGCCAAAACTTAAG
AAACACACTCAATACGCCAATCCTTTTGCTGAATCTCCGCAAGAATCACGACTTCGGGTC

AGACTTCATTCACTGGGTTACCACGGCTTCATCCCACAGATTCATGTTGAATACGACGGT
CAATCCTATTTTCTAGATCTCGCAGATCCGCTGTGGCAGGTTGCCCTCGAATACAACGGC
GGATGGCACTACACCTCTGAGCAGCGAGAGAAAGATTCTCATCGGAAGAATGCTCTGAAA
AGTGCGGGATGGGATGTCCTAGAAGTGACATCAAAAACTCTGCAGAATCCGAATTCCTGG
AACAACCTGATACAACAGATCAATAGCTCTCTCCGCCGAAAGCAGGCTCAGCGACGCCGA
AGGTTACCCATGCAAACGGTGGGC

>RXA00610-downstream
TAACGGCATCACTGAAAAAGACC

>RXA00611-upstream
CTTTAAATTGACTATTTACAAAACTACTTGATGAGTTAGCAAGAGCACATTTCGGTGCGC
CTCCCTGCTAAACCTCGAAACAATAACTAGATTGCACACT

>RXA00611
ATGTCTGCCGCTGCTTCTCGATCAAGAAACATCTTGACTGCCCTCCTGCTATTGGTCCCG
CTCATCGCAGGTACCATCTACGCCTCCGCCATGGGCTTGGACGTCTCCCGCGCATGGTCC
TCAGCAGATGAAGTAACGGGGGCACCTGCAGCCTCCGTAGCCACCAACAACCAGGAGCTT
ATCGAAGCCCGTCGCGCCGCCGGAGAAGCCGGCGCCCAAGCGGGGTTCCTCACCTCAGGA
ACTGAAGAGCTAACCAGCGGAACACAAGAGCTTATCGACGGCGCAGCCCCACTCGAAGAA
GGCGTCTCAGCCGCGGCTGACGGTGCAGCGCAACTCCACGATGGCCTCATCCAACTCCAG
GCCGGCACTGGACAAATGGGAACCGGCGCCACCGAAATTGCCGACGGCGTCCAAAACGCA
GTCGAACAACTTGGCGGTCTTGTCGTTGTACAGCAGCAACTCTTAGGCGCCCTCAACGAA
GCAGACAAACAACTCGCCTCGAGCAAAATCCCCGAAGCCGAAGACCTGCGCAAACAAATC
ACCGAAGTCCGAGGACACCTCGAAAACTTCGGCATCTCCGTAGAAATGACCGACCAACTC
GATCAACTACGTTCCGGCACCCGCGACCTGGCTAACCAACTCGCAGTCCCCGGCTACGGA
TTCCACGATGGTATTTACAGCGCCACCAATGGAGCAGCCGAATTATCTGCAGGTTTGCAA
GAGCTAGAAGCAGGCGTTGGGACTGCCGTCGAAGGCTTCACCGCACTCGATGAAGGTGCA
AACCGATTAGACTCCATGGCCACCCTCAACGAAGAAAAAACCTCCGCAGTCCAACGAGCC
CTCCCGGTACCCCAAGTACCCGCCGGCACAATCGAAGGCACCGCAGACGAAGAACGCACC
AGCGCACTAGCGCCCATGTACGCCTTCTTAATTTCAGCATTGGTCATGCTGGCCGGTGCA
GCACTTGGATGGGCAACACTAAAAAACAAGTGGCTGATGGCCTTTGCTGTCATTGGTGTC
ACTGCAATCGGTGGCATTATCTTGTTCACCGTAGCTTTGGGCATATCCATTGGAGCTTTG
TTTGGAGCCTTAGGAATTTTGCTTCTTGCCACTGTTGTTGCCGGTATTCTCTCCCGGATT
TTGCTTGACGTGTTGGGAACTACCGGGGCTATTGTGGTTTCTGTTCTGGGATGGGTAGCC
CAAGCTGCAGTAATTGGCCATGTATGGAGTGTTACCGCTGTATCCGATATCGCACTTGTT
TGGCGAGTCGTCGCAGGCATGATGCCACTGCATTATCCAACCTTTGCAGTGACCTCCATT
GGTAATGGCGGATCAGCTGCAGCTATCTGGATGTCTGTTGCTGTCTTGTTGGCAATGGGA
GCGATCGGAGCTGTTGCGCTTCGGAAGCCAAAGGCGGTTGCGGTTGAGGTTGAAGAAGCT
GTTGATGCTGATGCAGACCAAGCAGCCTCGGAATCC

>RXA00611-downstream
TGATGGTTTTGGTCTGATTCGAC

>RXA00613-upstream
TGGCGATACCAGCTCCGAGTAGGGCTGCACTTGAAAAAGTGAGTGTTTTAGCGATAGTTG
ACACCTTATTCACCCTACCTGGGGAGTACTCTGGGCAAAC

>RXA00613
ATGAGTGAACTAAAAGACAAAATCCGCGCAGATCTGACCACCGCTATGAAGGCCCGCGAC
AAGGACACCACTGGTACCTTGCGCATGCTGCTTTCCGCATTGACCCAGGAAGAAACATCG
GGAACCAAGCACGAACTCAATGATGAAGAAGTGTTGAAGGTGATTGCTCGTGAGATTAAG
AAGCGTCGCGAGTCCGCTGAGGTGTACACCGAAAATGGTCGTCAGGAATTGGCTGACGTT
GAGCTTAAAGAGGCTGCCATTTTGGAGGGCTACCAGCCTGAGCAGCTTGATGATGATCAG
CTGAACGCGCTGATCGATGAGGCTATCGCTGAAGTCGGCGGCGAGGCCGATATGAAGAAG
ATGGGCCAGATCATGAAGGCTGCTACCGCTAAGGCTGCTGGCCGTGCAGATGGAAAACGA
CTCTCCACCGCAGTGAAGAGCCGTTTGAGCAAC

>RXA00613-downstream

TAGGTATTTCTAGCGGAAGAACT

>RXA00614-upstream
CAGTGGTGTCCTTGTCGCGGGCCTTCATAGCGGTGGTCAGATCTGCGCGGATTTTGTCTT
TTAGTTCACTCATGTTTGCCCAGAGTACTCCCCAGGTAGG

>RXA00614
GTGAATAAGGTGTCAACTATCGCTAAAACACTCACTTTTTCAAGTGCAGCCCTACTCGGA
GCTGGTATCGCCACCGCTGCATGGGGATACTCAGAGCTCAAAAAATTCGAGCTCAAAACA
GTAGAACTGCCAATTTTGAAGCCTGGAACGCTCCGTGGAAAGAAGGAATTCCGCCTTCTC
CACATCTCTGATCTCCACATGATCCCAGGCCAAGAAACCAAAAAAGCATGGGTCTCCGCA
CTCGATTCACTAAGCCCCGATTTGGTGATCAACACCGGTGACAACCTTAGCGATGAAAAA
GCAGTCCCCGACGTCCTCCGCGCACTCGGCCCACTGATGAACCGCCCCGGCGCGTTCGTC
TTCGGAACCAACGATTACTGGGCACCCCGCCCCGTCAATCCTTTCGGCTACCTCTTCGGT
AAAAAACGCGAAGTGAGCCACATCGACCTCCCCTGGCGAGCCATGCGAGCTGCTTTCATC
GAACACGGATGGCAAGACGCCAACCAAAAGCGACTCGAATTCCAAGTAGGTTCCGTCCGC
CTCGCCATCTCAGGTGTTGATGACCCCCACCATGACCTCGACGACTACACAGAGATCGCA
GGGGCACCAAACGTGGACGCTGATCTGTCCATAGCGTTGCTTCACGCACCAGAACCTCGA
GTCCTCGCTCAGTTCGAAGCCGACGGCTACCAGCTTTCCCTCTCCGGCCACACCCACGGC
GGTCAGCTTTGTCTTCCGGGCAGCAAGCCAATTGTCACCAACTGTGGAATCGACCGCAAA
CGCGCCACCGGCCTCAACAAATTTGGCGACATGTGGATGCACGTTTCCAACGGCCTCGGC
ACCTCAAAATTCGTCCCATTCCGCATCTTCTGCCGACCCAGCGCCACCCTAATAAAGATC
ACTGAACAGGCACTT

>RXA00614-downstream
TGACCTGAAAAACCCACAGGACT

>RXA00616-upstream
AACCGCAACCTCGCGCACTTGGAGTGAAAATTCTCATCTTCATTTCATCTTGGTGCCTAA
CAATGGAATACAGATTGAGTTGATCAAAGGAGAACCCCCA

>RXA00616
ATGAAATCACTCCCCCGTTTCGCCCCACTGATTACGATTCTGGCTCTGCTCGTACTCGTT
GCCATCGGAGGATCTGCACTGGCAAATAATCGTGCTACCCCTAATGTGGAAAGTGAACCC
GCCACGGTCAACCAGCGTTCCACTCCCACAACTTCCGCGTATGAGCCCCCTGCTACAGAA
TCTCCGGAAGAACCAACCACACAAATTCAAGAATCCCCAGTACAACCCCCAGTTCCTGCC
CCCGCTCAAATTCCTCAAGCCCCACAAGTTCCACTCAATTATCAGTACTATGACGATGAC
TGGGACGACGACGATGATGACTTCGACGACGACTGGGACGACGAC

>RXA00616-downstream
TAACTAACCCCTGAGGCACTTTC

>RXA00617-upstream
ACGACTGGGACGACGACTAACTAACCCCTGAGGCACTTTCTATTTCATGGCTAAATCAAC
TCCTTTGATTGCATCGCTACGCTGGCGAATTGTCCTGTGG

>RXA00617
ATGACAGCGGTTGTTTTCTTGACCCTAGCCAGCGTTGTGATCATTACCCGTTCGGTGCTG
CTTTCAGAGGTAACCAACACCGCGAACTCGGCAGTTGAGCAGGAAATTGAGGAGTTTCGT
CGCTTTGCAGCCGAAGGAATTGATCCAACAACTGCGCAGCCTTTTGAGTCAGGTCATCGC
CTGATGGAGGTTTACCTGTCGAGGCAGATTCCGGATGAAAATGAAGCCATTGTCGGCATT
TTCCCCGGAGAGCTCATTCAGGTTGATTACTCCCAGCTCAGTGGCGCCCATCCGCTTCCT
TTGGAACACTCCGATCCGTTGATTTCGGAAATCCGACAGACCACGCTGAATTCTGGAGTT
TTCAGCGATCTTGAACGCGGAACCACTCACTGGGGAAAGGTGAATTTCCAAACTGCTTCC
GGTGAGGCCGATGGTGAGTTCGTTGTCGCATTCTTCGCTGATAATCTTAAAGACCAGGTC
AACGGCCAGATCCAGATTCTTATTTTGATCGGCACAGGGGGTTTGATTGCCTCAATTCTG
ATTGCTTGGTTGATTGCGGGCCAGATCATTGCCCCGATCCGCAAATTGAGTTCCGTGTCC
GCAAAGATCAGTAATTCGGATCTCACCTGGCGCGTCCCTGTGGAGGGTCGTGATGAGATT

GCGCAGCTGGCCAGGACTTTTAATGCCATGTTGGATCGCATCGAAATCGCGTATAACGAT
CAGCGCCAGTTCGTTGATGATGCCGGCCACGAGCTGCGCACCCCGATCACAGTGGTGCGT
GGCCAGTTAGAGCTTCTCGCCACCACCCCGCCGGAGGAACAAGCGCGGTCGATTGAGCTG
GCCACCACTGAGTTGGATCGAATGTCGCGAATGGTCAATGATCTGCTCACCCTCGCAGTC
GCCGATTCTGGCACCTTCATCCACGCCCACCCCACGGATGTCACGGATTTAACAATCGAT
ATCGAAGACAAAGCCCGCACCATCAGCGACCGAATTTTGCTTGTCGACGCCGCCGAGGGC
CTCGTCAGCCTCGACGAGCAGCGGGTCACCGAGGCAGTGCTGGAGTTGTTCGGCAATGCG
TTG

>RXA00628-upstream
GGTTGAAAGTGGCGTCGAAAAGCGCCTTAAAATGACCGGCTCACCTGCATTATTTTATGC
AACCTCAATTTGGTTGCACGCCAAGTAGTAGTCTGTGCAT

>RXA00628
ATGGCTTCTGTATTCACGAAAATTATTAATGGCGAGCTCCCCGGCCGATTTGTGTATCGT
TCCGAGAATGTCGTGGCTTTTCTATCCATCGAACCCCTCACCTACGGCCACACCCTAGTC
GTACCCGTTGCAGAAGTTGACCGCTGGACCGACCTTCCTCAGAACATCTGGAGCGAAGTA
AACGAGGCCTCCCAGCTCATCGGAAATGCAATCCGCACAGCATTCGACGCCCCTCGATGT
GGTTACATCATCGCAGGATTCGATGTTCCCCACACTCACATCCACCTCTTCCCCACCGAC
AAAATGGCCGATTACGATTTCCGCAACGCCATGGCCGCAGACGCCACCGACCCTGCAAAA
ATGGATGAAGCTGCAGAGAAGATCCGCGAAGCGCTGGACGGTCTGGTC

>RXA00628-downstream
TAGTTCTTGTAGTTCTAATTGCT

>RXA00631-upstream
CCTACCTGCGCCGCAAGGTGGACACCCAGGATCCGCAGCTAATTCAGACTGTTCGTGGCG
TTGGATATGTTCTGCGCACCCCACGTAGCTAAATTCTCCT

>RXA00631
ATGGAAAATCCTTATGTTGCTGCGCTCGATGACGAAAACCAAGAAGTCGGCGTAAAAAAA
GAAGCAGAAAAAGAACCTGAAATAGGTCCCATCAGAGCTGCCGGACGAGCCATACCGCTG
CGCACCCGCATCATTTTGATCGTGGTGGGTATCGCCGGGCTTGGTTTGCTGGTCAACGCG
ATTGCTGTCTCCAGCCTCATGCGTGAAGTTTCCTATACCCGCATGGATCAAGAGCTAGAG
ACCTCGATGGGGACGTGGGCGCATAACGTTGAGCTGTTTAATTTCGATGGCGTCCGCCAA
GGGCCACCCAGCGATTATTATGTGGCCAAGGTTTTTCCTGATGGATCCAGCATCATCTTC
AACGATGCACAATCGGCACCCGATCTAGCTGAAACCACCATCGGTACTGGTCCACACACT
GTGGATGCTGCTAGCGGTTCTGCCTCCAACACTCCGTGGCGTGTGATGGCGGAAAAGAAC
GGTGACATTATCACCGTGGTGGGTAAAAGCATGGGGCGTGAAACAAACCTGCTGTACCGA
TTGGTGATGGTGCAGATGATCATCGGCGCGCTGATTCTGGTTGCTATTTTGATTACTTCA
CTCTTCCTAGTCAGACGCTCGTTGCGGCCGTTGAGAGAAGTTGAAGAGACCGCCACCAGG
ATTGCGGGCGGTGATTTGGATCGACGTGTCCCGCAGTGGCCAATGACCACAGAAGTCGGA
CAGCTGTCGAATGCCCTCAATATCATGTTGGAGCAGCTCCAAGCCTCAATTCTGACCGCC
CAGCAAAAAGAAGCTCAGATGCGCCGATTCGTTGGCGATGCCTCCCACGAGCTCCGCACA
CCACTGACCTCTGTGAAGGGCTTCACCGAGCTGTATTCATCAGGTGCAACAGATGATGCC
AACTGGGTCATGTCCAAGATCGGTGGCGAAGCCCAACGCATGAGTGTGCTTGTGGAAGAC
CTCCTGTCACTGACGCGTGCCGAAGGCCAGCAAATGGAGAAGCACCGCGTTGACGTGCTG
GAACTCGCCTTGGCAGTACGCGGATCCATGCGAGCAGCCTGGCCAGATCGCACAGTCAAT
GTATCCAACAAAGCTGAGTCCATTCCGGTTGTCAAAGGCGACCCAACTCGCCTCCACCAA
GTGCTTACCAACCTGGTTGCCAACGGACTAAACCACGGCGGACCGGACGCGGAAGTCAGC
ATTGAGATCAACACCGATGGACAAAACGTGAGGATTCTCGTGGCAGACAACGGTGTCGGA
ATGTCTGAAGAAGATGCTCAGCATATCTTCGAGCGTTTCTACCGCGCCGATTCCTCCCGC
TCACGCGCATCCGGCGGATCGGGCCTCGGCCTTGCGATCACGAAATCCCTGGTCGAAGGC
CACGGCGGCACAGTCACCGTCGACAGCGTGCAAGGCGAAGGCACGGTGTTCACGATCACC
TTGCCGGCGGTTTCT

>RXA00631-downstream
TAAAGGCATCAAGGGCCGGAAAA

>RXA00637-upstream
CCGATGGCACTTTCCGTACCTGGAAGGTAGTTGCCCGCGGCAGAAACAATTAGGGAAACC
TCTTGACCTTCACGCGACGTCAAGGATTTAACTAACAGTC

>RXA00637
ATGACAGATCGAACCATTGGCGAGGCTGCTGAACTACTCGGTGTCACCACCCGCACACTG
CGGCATTGGGACAGCATCGGGTTGCTTCAACCGAGCTGGCGAACCACAACGGATTATCGC
CTTTACACAGAAGACGATGTCGAGCGCGCCCTGCAGATTCTTATTTACAGGGCCGCCGGA
ATCGGGTTGAAGGATATTGCGGAGGTGCTTGATCAGCCGGATTCGGCCAATCAGCACCTG
CGCCGCCAGCGGGAACTCCTAGTGGAACAGATCGGTCAGCTGCATCGGATGGTCCGGGCA
GTAGATGAAATCCTTGGAAAGGATGCGATTAGCGTGAAGGAAAAGATTGAGATCTTCGGC
GAGGATCTGCCCAAGTACCAAGAGGAGGCTTTCCAGCGCTGGGGCGACACCCCGGAGTGG
AAAGAATCCCAAAAGATCCAGGAGAAGATGACCAAGGAGGATTTTCAGAGGGCGAAAGAT
GAACATGAGGGGTTCGTCGAAAAGCTTATCGACGCCTCCCTGCGCGGCATCGCGCCCGGC
TCTGCAGAGGGCAATGAGCTAGCGCTTGCGCACCGCGCAAGCATCGGTCAGTGGTACACC
GTGAGTGCAAACAAGCAAGTAATTTTGGCTCGGATGTACGTGGAAGACGAGCGTTTTAAC
GAAACTTACAAAGGACACGCCTCATATCTTTTAACACTTATTGAAGCATTGGCGCAGGTA
GAAGGCGTGGACTTGGAGAATGTGGAGTGGGAA

>RXA00637-downstream
TAATCCCAATTTCAACTCTTTCA

>RXA00646-upstream
AATGCAATCGGAACGGTTAACGCCAAGTGATCTGGTGGGATGTAGGTACCGTCAGGTCCA
GCGCATAAATTTCCCAGAAATCTCTCCTTTACCTGCAACA

>RXA00646
ATGCAGCGCAGGGCCCGCCGTGAGGTTGGGTTGACGGAAGTTTTGGATCGTCTCCCAGAG
CAGCCCAAAAAGCGGGGCCGAATTCCTTTCACCAGGGCAGATCTAGACAATGACGCTGAA
TTGGCGGAGTTTGAAACCCTCGAAGCAATTGCAGCCGGCGACACCTTGATTACCGGCGCA
GTGTTCACGGGCACCCTCGAAGGGGTGGCATGGGAAGTGCAAGTGGATGTCTTGGTGCGC
AACCCTGATGGAAGCTACATGCCCGTGATGGTGAGCAATCACCGTGTCGCCCGTCCGGAT
CCGCACAAAACTATGCAGGGCATTGCCGTCACCCGCCTCGGTTTGGGTCAGCCGCTAGAG
CTCAAGGCAACGCTGCGCCACCACACGATCGATGGCTATCGCCTCACCCTCGCGTTGATG
GGTTTGGAGGAAGCTGGAGCA

>RXA00647-upstream
TGCATTCTTCCCACAATGACATGAGCTTATTGCAACATCGTGGGTAAAGTTGAATCGAGA
AGTCGAGAAATAACCGACCGATGAAAGAGTTGAGACGATA

>RXA00647
ATGGGCATCTTCGAAGCCATCCGAGCCGCACGCGCGAAGACCAAAGCTGAGATCAAAGCA
GCCGAGGCAAAAGTAAAAACTGAGGCGAAAAACAAAGCAAAGCTAGATCTCAAGCGCGAG
AAGCTTCTTGTCCAGCAGGAAAAGAATCTGCTCAAGGTTGAAGAAAAGGGCCTGAAGAAG
CGCAACAAGCATGAGCTGAAGATGGCCAAAAATATCCTTGAGCAAAAGCGCCAAGGACGC
CTAAACAAAGACAAGGTGAAGCGCTGGGCTGGCACCGCACGTGTGCTCACTCCACTACTG
CTGCCTATTATTTATCGACTCTCCACCGAAGCACGCGATCAGGTTGTTAAGGGACGTGCC
CGTCGTGCAGGTGTCACCGCGGAGCAGCTTAGCCAATTCGCAGGTCACGCAGCAGCGCTG
AAGGCTCGTATTCAAGGTGTTCGCGAAACCGCAAAGAACTCCAGCCTCCCTGCTGGCTTT
GTACGCGATGTTGAAGAGCGTCTCAATGAGCTCGAGGCTGCTGCGAATAACTCTGAGTTC
ATGTCTCCACAGCAGAGGAACCGTGCGCACCAGTCGATCAGTCGTGATCTGAACCAGGTG
TCAGATCAGATTCAGGATCGACTACTGGACAAG

>RXA00647-downstream
TAGCTGCTGGTCGAGTCGCTGCC

>RXA00649-upstream

GTATTTGATCTGTGGTGTGGCTGATTCGGGAGGACTCGATGACATTATGTGTATGGTACA
CATTTTGTGCAAGATGCAATAGCTGGCAAACTGGAGAGCC

>RXA00649
ATGAGCACCGACCCCATCGCGGCCTTGGAATACGAATCCACCATCTTCGCCCGTCACCGG
AATCAATACACCGGCCAAGCAGGTACGAATGCTGGCGTCCTCGATTCCAGCGGCTACAAC
CTACTCACGCTGCTCCAGTTACGTGGCCCCTCCACCATCGGCGAACTCAGCGCCATCACC
GGCCTAGACGCATCTACCCTTAACCGTCAGACAAAAGCCCTACTAACCAAAGGATTTGTC
GAACGCATCCCAGATCCCGACGGTGGAATCGCTCGGAAATTCCACCCCACCGACCTCGGC
AATGAACTGCTCAACGAGGAACGCACATCCAGCCAAGAAAAATATGCCGAGTTACTTTCA
GACTGGCCCGAAGAGGATCTACGCACCTTCGTCAAACTTCTTGAAAAACTAAATAAAGCC
GTGGAGACACGCGTCGGAAAGCATTGGCCGCGCCCC

>RXA00649-downstream
TGACTCAGCCCAAGCCAGAGCCC

>RXA00652-upstream
GCGATAGCTCATCGCGCCCGGTTGATTCCCCTTCTTCACAAGGGTTTCAACATCGAGCTC
ATTGCGTCCGGTTTCCGACACACGATCTAGGCTTGACTGC

>RXA00652
ATGCGTCGTACATTACCTACTATCCTCGCTGCTTCCATCATGCTCACCGCTTGTACCCCG
GCGGAACCTGAAGCAACCCCAGAGACCACCACCGAGGCAGCCCCGGAAGTAATTACTGAC
GGCCTTCCCATCGACGCGATGCCCGCGGTCGAACGCACCGCACAAACCGCATGCCCCTAC
CTGGGCACCGACTGGGTCGCCGATACCAACGGCCAGCGCGTCACGGGTTACGGCACAGAC
GAACGCTTTTCGACGCCCTCCTGCGTTTTTTACTCCTACCCCGAAGAACCACAACTCACG
GTGATTGTCCGCGATATGGCCACCACGGATGACGCTATCGCGGTAGTGGATTGGGCAGCC
CCCATCGATTCCACTGAGCCCGCTGAGGAACCCGCAGGGTGGTCCGGTGGCCGCCGAGGT
GGAAACGATACTTCAGGCGCACTCTACGCGGTTCAAAACGGCCCCACCGCGGTCATCGTG
TTCACCAATCAGGATCAATCCCTCAAAGCGCAGTTAATCGCTGAGGAAGTAATCCAGAAT
CTTGGTCTC

>RXA00652-downstream
TAACTATTAGAAGGCCACATCGT

>RXA00653-upstream
GTTGAGATTCGCCTAACAAAGATTTTGGACGAAAACAGTAACGATGACAGCCACGTTAAG
CGCGGAATCTTCTCGCAATGGTAAAAAGCCGCGGCCTCGA

>RXA00653
GTGAGTGTTTCCCAGGTTGTTGGTGAAATCTTGCTCACCGTAGGCATTTTGGCCTTGTTA
TTCGCATACTATGAGGCCTATTGGACCAACGTGGAATCTGGGAAATTACAAGAATCGGCT
GGTCAAAAGCTTGATGAAGACTGGAATGAAGCTCGGGTGAATCCTCGACAAAAGCTCACC
CCGGAACTTGGTGAGGCATTTGCCCGGATGTATGTTCCAGCTTTCGGCTCTGACTTCAAC
TTCGCAGTGATTGAAGGAACCGATGAGGAAGACCTTCTTGCCGGTCCTGGCCGTTATGTG
GATTCCCAAATGCCTGGTGAAGCCGGAAACTTTGCAGTGGCAGGCCACCGAGTGGGCAAG
GGTGCGCCATTCAATGATCTAGGAAACCTGGAAGTCTGCGATGCGATCGTGGTGGAGACT
TACAATTCCTGGGATGTGTACCGCGTGATGCCGATGTCCACCAACGGTGCAGATCGTGCA
GCAGAAGCTGCGGATTGCTTCAACGAAAACCAGGTCAGCCGCATGGCTGAAGGTGACTAT
GTGAATGTGTCCGGACGAAGCATCACCACTCCGGATCGCATCGATGCCACCTACCCCACA
CCGGGCGTCTTCGACACTGCAGTGCGTGAAGGATCAGAAGCTCTGCTTACCTTGACCACG
TGTCACCCGCAGTTCTCCAACGCTGAGCGCATGATTGTGCACGCAATGTTGGTGGAAGAA
ATCGATAAATCAAGTGGCGAACGCCCTGCAGCTTTGGAGGAAAAC

>RXA00653-downstream
TAAATGTATTCACTTCTGTGGCA

>RXA00654-upstream

CAGCAATAGCGATTATTGCTTGATTGTGTGTTTTTAGATCTTCGGTTCTCTTCACTCAAC
TGCTGTGAAGTGCCACCTGTTTGGAAAGGCGAACACGATA

>RXA00654
GTGCTCGATATTTTGATTTACCCGGTGTCTGGAGTGATGAAGCTGTGGCACCTGCTTCTT
CACAACGTTGCGGGTTTGGACGATTCACTGGCGTGGTTCTTTTCCCTTTTCGGCCTTGTC
ATCACGATCCGTGCAATTATCGCGCCTTTCACCTGGCAGATGTATAAGTCGGGCCGCACT
GCCGCACATATTCGTCCTCACCGCGCTGCGCTCCGGGAAGAATACAAGGGAAAGTACGAT
GAAGCGTCCATTCGGGAGTTGCAGAAGCGCCAGAATGATTTGAATAAGGAATACGGCATT
AACCCGCTGGCAGGTTGTGTGCCTGGGCTGATCCAGATACCGATTGTCCTTGGTCTTTAC
TGGGCACTTCTCCGCATGGCTCGCCCTGAAGGTGGTTTGGAAAATCCCGTCTTCCAGTCG
ATCGGCTTCCTAACTCCTGAGGAAGTGGAATCTTTCCTCGCTGGTCGCGTGAGCAATGTG
CCTCTGCCCGCTTATGTTTCGATGCCCACTGAGCAGCTAAAATATTTGAGCACCACGCAG
GCGGAAGTTCTTAGTTTCGTTTTGCCACTGTTCATCACAGCCGCAATCCTCACCGCAATC
AACATGGCGATGTCCATGTACCGCAGCTTCCAAACCAACGATTACGCATCCGGATTCTCT
AACGGCATGCTGAAGTTCATGATCGTGATGTCGATCCTCGCGCCGATCTTCCCACTGTCC
CTTGGCCTCACAGGACCATTCCCCACAGCAATCGCACTCTATTGGGTCAGCAACAACCTG
TGGACGCTCCTCCAAACAATCATCATGATGGTCATTTTGGAACGCAAATACCCACTTACC
GACGATTTCAAAGTGCACCACCTAGAGCAGCGCGACATCTACCGCGCAAAACAAAAAGAA
AAGCGCATCTTCCTGTGGACACGACGCAAAAACCGCGCCCTGATGATTCTCACCCCATGG
AACGCCTCAACGCTTCACGCAACAAACGTGGAACTCACCAAAACCCGTACTGCCGAAATC
AACGAAGCAAAACAGGCCCGCAAAGAAATCGCGAACAAGAGGCGCGAAACGCAACGTGAA
ATGAACCGCGCCGCCATGCAGCGCTTAAAGCAGCGTCGCGCTGAGGTTAAAGCTAAAAAG
AAGGGGCTTATCGACGCCTCCCCCAACGAAGATACCCCTTCGGAAAATGAAGAAACTAAA
TTGAGTAGTCCGCAGGTGGAGCCGACAACAACTGCCGAGCCAAATCGCGAGCCGTCTCAA
GAGGAC

>RXA00654-downstream
TGATGTTGTGGACCAATCGAGAT

>RXA00656-upstream
CCTTTTAATAACAATACAATGAATAATTGGAATAGGTCGACACCTTTGGAGCGGAGCCGG
TTAAAATTGGCAGCATTCACCGAAAGAAAAGGAGAACCAC

>RXA00656
ATGCTTGCCCTAGGTTGGATTACATGGATCATTATTGGTGGTCTAGCTGGTTGGATTGCC
TCCAAGATTAAAGGCACTGATGCTCAGCAAGGAATTTTGCTGAACATAGTCGTCGGTATT
ATCGGTGGTTTGTTAGGCGGCTGGCTGCTTGGAATCTTCGGAGTGGATGTTGCCGGTGGC
GGCTTGATCTTCAGCTTCATCACATGTCTGATTGGTGCTGTCATTTTGCTGACGATCGTG
CAGTTCTTCACTCGGAAGAAG

>RXA00656-downstream
TAATCTGCTTTAAATCCGTAGGG

>RXA00657-upstream
GATCATGAGTTTCCACGAACTGTAACGCAGGATTCACCAATCAATGAAAGGTCGACCGAC

>RXA00657
ATGAGCACTGAAGACATTGTCGTCGTAGCAGTAGATGGCTCGGACGCCTCAAAACAAGCT
GTTCGGTGGGCTGCAAATACCGCCAACAAACGTGGCATTCCACTTCGCTTGGCTTCCAGC
TACACCATGCCTCAGTTCCTCTACGCAGAGGGAATGGTTCCACCACAAGAGCTTTTCGAT
GACCTCCAGGCCGAAGCCCTGGAAAAGATTAACGAAGCCCGTGACATCGCCCATGAGGTA
GCGCCAGAAATCAAGATCGGGCACACCATCGCTGAAGGCAGTCCCATCGACATGCTGTTG
GAAATGTCTCCCGATGCCACAATGATCGTCATGGGTTCCCGCGGACTCGGCGGACTCTCC
GGAATGGTCATGGGCTCCGTCTCCGGTGCAGTGGTCAGCCACGCAAAGTGTCCAGTCGTT
GTTGTCCGTGAAGACAGCGCAGTCAACGAAGACAGCAAGTACGGCCCAGTCGTCGTCGGT
GTGGATGGCTCCGAAGTCTCCCAACAGGCAACCGAATACGCATTTGCGGAAGCTGAAGCT
CGTGGCGCCGAACTCGTTGCAGTTCACACCTGGATGGACATGCAGGTACAGGCATCACTT
GCAGGTCTTGCAGCTGCTCAACAGCAGTGGGATGAAGTGGAACGTCAGCAAACCGACATG

CTGATCGAACGCCTCGCACCACTGGTGGAAAAGTACCCAAGTGTAACCGTCAAGAAGATC
ATCACCCGTGACCGCCCAGTTCGCGCACTTGCAGAAGCATCTGAAAACGCGCAGCTCCTA
GTCGTTGGTTCCCATGGTCGTGGCGGATTTAAGGGCATGCTCCTTGGCTCCACCTCCCGC
GCACTGCTGCAATCCGCACCGTGCCCAATGATGGTGGTTCGCCCACCTGAGAAGATTAAG
AAG

>RXA00657-downstream
TAGTTTCTTTTAAGTTTCGATGC

>RXA00661-upstream
CGGATGCAAGAGAACCGTGGTTTCGCTGATTTTTGGCGAACCCGGAATTAAGGCCCCGAG
GATTACATGCTTTTAAATCCTTTGAAAAGGGGACAAGATC

>RXA00661
ATGAATCCTATAACCGAATTATTAGACGCAACACTATGGATCGGCGGAGTTCCGATTCTG
TGGCGCGAAATCATCGGCAACGTTTTCGGATTATTTAGCGCGTGGGCAGGAATGCGACGC
ATCGTGTGGGCATGGCCCATCGGCATCATAGGCAACGCGCTGCTGTTCACAGTATTTATG
GGCGGCCTTTTCCACACTCCACAAAACCTCGATCTCTACGGCCAAGCGGGTCGCCAGATC
ATGTTCATCATCGTCAGTGGTTATGGCTGGTACCAATGGTCGGCCGCAAAACGTCGCGCA
CTCACCCCAGAAAATGCAGTAGCAGTGGTTCCTCGCTGGGCAAGCACCAAAGAACGCGCC
GGCATTGTGATTGCGGCGGTTGTGGGAACACTCAGCTTTGCCTGGATTTTCCAAGCACTC
GGCTCCTGGGGGCCATGGGCCGACGCGTGGATTTTCGTCGGCTCAATCCTGGCTACCTAC
GGAATGGCTCGCGGATGGACAGAGTTCTGGCTGATCTGGATCGCCGTCGACATAGTTGGC
GTTCCTCTACTTTTGACTGCTGGCTACTACCCATCCGCGGTGCTTTACCTGGTGTACGGT
GCGTTTGTCAGCTGGGGATTTGTCGTGTGGCTGCGGGTGCAAAAAGCAGACAAGGCTCGT
GCGCTGGAAGCTCAGGAGTCTGTGACAGTC

>RXA00661-downstream
TGAAAAGCGTTTACTAAATAGAA

>RXA00662-upstream
CCCTCATCATAGTTTTAAATCTGGGGCAGAGGCGGGAATTTAAACACCTCTGATACAGCG
TTTACTGGCTATAGTGTTGCGCGTGCCAAATCGAGTTCCT

>RXA00662
GTGTCAACCATTCCGCTGAATCGTCTAGCCGTTATCGCTGCCATCATTGGTGTCGGTACC
GGGCTGTTTGTTGCTGCACTGAACTGGTCTGCCATTGGCGTGGAGCGTTTAGTTTATGGC
GCTGACCATTTGCATAATTACAATCCGGTGGCCAATGTGTCGCCACTTCGCCTGTCCATC
ACGGTGATTGTGCTTAGCGTGGTGGCCTCCTGGGCGTGGTTTTTTGTGCACCGCACGGGG
CCGAAAGAGGTTTCGATTGTGGGTGCGATCCGGGGCGAGAAGATGCCGATTTTGGAGACC
ATAGCGTCCGCATTTTTGCAGGTCACCACGGTTGCTGCGGGTGCGCCGGTGGGTGCAGAG
AACGCTCCACGTATTGCTGGAGCCTTGGTGGGAGAGCGGTTTAGTCGGTGGTTGCAGCTC
GATATTGATGCAAAGCGCATCTTGGTGGCCTCTGCCGCGGGAGCTGGTTTGGGAGCAAGC
TTCCACCTTCCCCTAGCAGGCGTGCTGTTTGCCCTTGAGGTCCTACTGGTTGAGGCCTCC
ACTCGGACCGTGGTTATCGCAATTATCACCACGACCGCCGCCGTTGCCACCACTGGATTT
TTCGTGCAAACCCCAGATGTGTTCAGCACTGTCCCGCTGACGGAAAGCCCATGGATGCTG
CTTGCCGCGATGGTCACCGGAGTAGTCGCCGGCATGTGCGGGCACTGGTTTTCAGCGGCG
GCGCACAAAATGGCGCAGGCCTCGCCCAAGGGTGTGAAGATTTTGTGGCAGATGCCGTTG
GGTTTCGTGGTGATCGCTGCGGTGATTTATTTCTTCCCCGAAACCCTGGCGAATCCCCGT
TGGCTTGCCGATTCCATGCTCGGCGATGGCCTGATCCTCAGCACCATTTTATTGGTACTT
GTTCTGCGCACCGCCATGTTTTTGCTCGCCTTCCGCGTGGGCATGGTCGGCGGTAACCTG
ATCCCCGCATTCGCACTCGGATCCATGGTCGGTGGGGTAGTGGGTGCTGTATTGGAACCC
ATCACTAACGTCCCGATCGCCGCTTTTGCGCTGCTTGGCGCCGCCGCATTTTTGTCCACC
ACCATGGCAGCGCCACTGTTCGGGCTCATCGCCGCAGTGGAATTCACCGACATGGAAGCC
CAAGGCTACCTTCCGATTTTCCTCGCAGTAGCCTCCGCGGTCCTCGCCGTGCGCGTGTGG
TCTGTCATCGCCAAGCACGAGCTCCGCGCCATCCCGATCACGTACGCGAGCTGGACGGGC
GAGCTTAAA

>RXA00662-downstream

TAAGCTTGTCGACGCCTCCCTCC

>RXA00666-upstream
AGTGGTGAATGCTGGATAAGTTTTTAACATGTCTAGTGTAGTCGGGGAAGGCCCAAAACC
ACGATTGAGCGTGCTTGATCTCGTCGCGCTGAGTGAAGGG

>RXA00666
ATGACGGCCGGCGAGGCCATTGCACACAGTGTTCGCGCTGCGCAGATCGCCGAAGAGCAC
AATTATGCGCGTTTCTGGGTGGCGGAGCACCACAACTCGGAAGGCTTGGCATCTTCCGCG
ACGACGCTGCTCATGGGTCATATTGCAGGCCACACTTCACGCATTCGCGTTGGCTCCGGT
GGCATCATGATGCCCAACCACTCCGCGCTGCACGTCGCCGAAGAACTCGGCACCCTTGAG
GCCATTTACCCCGGCCGCATCGAGGCCGGCCTAGGGCGCGCACCAGGAACCGACCCCATG
ACGGCGCGGGAATTGGGTCGGGCAAGTTCGCTTGTCGACGACGTCCTCTCCACAATCGTC
TCCCTCCAGAATTATTTGGACACCCCC

>RXA00667-upstream
GGCATCAGTGTTTGAAGGGAAAAGCAGGTCAAACAAGGTGCGGCTGATTTGAGCGATCAC
AGCACCGAGATCTGTGCTGAAGAATTCAATGATTGGGTTG

>RXA00667
ATGATTGCGTTGAAGTCCATGTCTAACAGGGTAGTACAAAAGCCAAAAATGAAAGCGCCG
CTACCCATCCGCGACGGCCTCAACCCTTCCCGTGTGCGCTTGCCGCTCGACGCGGCGCCG
ATCCGCGCCATCGATTTTGTTGAATACCTCATTTCCACGCAGCGCCACCGCAATCCGGCC
GACAACGCCGAAGCGCTTCAAGCGCGTTTCGACGCCGACCTTGTTGTCAACCACTACGGC
GAGCCCTACGCCCCCGACACCATGGTTCAGCCCGACGACGACATTTGGTTCTACCGCATG
CCCGCCGCCGAACGGCCGATCCCTTACAAAATTCATGTCATTCACGAAGACGATGACATC
CTCGTCATTGACAAGCCACCCTACCTAGCAACCATGCCTCGTGGCCGCCACATCACCGAA
ACCGCTCTGGTGAAAATGCGTGTGCTGACTGGAAACAACGATCTCACCCCAGCTCACCGC
CTCGATCGCCTGACTTCCGGTGTGTTAGTCATGGTGAAAAAACCAGAACTCCGTGGCGCT
TACCAAACCTTGTTTGCCCGACGTGAGGCGTCCAAAACCTATGAG

>RXA00668-upstream
CTAAACTCGTCTCTCGTATCTTTCAGTCATTTATGTCTGATAAGCAGGCGCGTGCGCCAC
ACAATTGGCACAATCACAAGAAAGTGAAGTGGGAACCTAG

>RXA00668
ATGCTGACGACACTATGGATTGCGGTGTTGGTATTTACCGTTCCAGGATTGGTCGTCTCG
TGGGTTTCTGGCCTTAAAGTGCCCTGGGCTATCGCAGCCTCCATCCCAGCCACCTTCGGT
ATTTACGGCCTGTCCGCCTGGTTGCTGGGCTTGTGGGAGATGCGTTTTGATCTCCATTCT
GTAGTTATTTCCACATTGGTTTTCGCTGCGGTTGCTTTGGTATGGCGCTTGTTTTTTGTC
GGTGGTTGGCTTGTACGTCGGCGTAAAGCACGTATCCGCAGGCAGACGCTCGCGGATGAA
GAGCGGGCAGAAAATGCTGAGGTATCTGCAGGGGAGCCTGCCGAATCGAGCACAAACGAA
GCAGCCGAATCTGAATCTGAAACCTCGGAGCGTCGCGGAATCTGGCGCGTGATCTTTGAT
TACATGCGCGACGGTGGCATCTTGGATCACCGTTGGCTGCTGCCTGCCGCAGGTGCTATC
ACTGGTGCGTGGCTGATCATTGATCGTGCCGTTGATCTGCTCTTGAGCACCGAGCATGGT
TTGGGCGATATCGTCCAAGGCTGGGATGTCCATTGGCATGCTTCGACTGTCCGTTTTATA
GATGAGACCGGCATTGCGTCATCCACGATGATGGGGCAGCTGCGCAATATTGAAACGCAG
CAAGATCTGTTCTACCCAAGCGCATGGCATGCTGGTGCATGGGTGCTGTCGGATGTCGGA
AATCTGACGATTGTTGAAGCCACCAACCTCACTGGCATTGTGCTGTCCGGATTGTTGCTG
CCGTTAGCTGTT

>RXA00674
ATCTTTGCCGCAGCATTGGCGTTCATGGGTATGTTCCAGCTGCATCCAGCCCCATCCACC
ATCGTGATCATGGTGTTGCTGCTGTGGTGGCTGCTCAAACTCGTGGTGGTTCCAAGCCAG
AAAGTGAAGGGCTGGAAGGCGGGCATCGGTATCCGTTTGAAGGATGTCGGCATCCTGGCC
ATCACGGGCATCATCGGTGTGCTCTTCATGCTGCCTCAGGTGATTTCAGGTTCCGAACAA
ACCGAAGATGTGCTGTCATATTCTGCTGAGGAACAAGTCACCCGCAGCGAGTCCTGGTTG
GTGTCTATTTTCATGGAGACCCGCCATGTTGATTTCTTCGGAAATATTGACATCGTCCCA

GTGCTGGTATTCGCAGCAATCGGTGGCGTGGTTGCTTTGGTGTGGCGCGGAAACTTGTGG
GCGCCGGTGTTTTACTTCGCCAGCGTTGCGTTGACCGCTAACTCGCTGAAGCCTTTTGAA
GAGCCGTGGGGTGATTGGCTCAACATCGTGGGCGGTCTGCATTACTCCACAGGACACCGT
TTGATCATGCCTGTCGCCATGTTCACTTTTGCTGCCGCAGGTATCGGCGCTGCCGCAGTG
ATCCGTTTGATCTGCTTGGGACCAATAAAGAAGTTCACCACTGTTTCCGGTGTTGTTTCT
GTGGTGATGGCTCTTGTTGTGGCTGTGCCATTGCAGACTTGGGCGAAGGATTTTGTAGAG
GAAGGATCCGAAACCACAATCCTTGCGCCA

>RXA00676-upstream
GGTTTGCGACCTCCCCGGCGTGCCGCCAGGGGAGGAGGCGATAAAACTTTTTTACCTTTC
GAATATCAAAATCATAAAACAGCCTTATATACTTCAACGT

>RXA00676
ATGGCGAAGAATTCTCGAATCCGATACAGCGCGTCAATCAAGCGTGCCGCAGCTGCAATC
CTCACCGCAGCTGCTACCTCAGTCGCGTTGATCGCTGTGCCAGCAACTGCTTCAGCACAG
GACCTCGCAACCGGCAGCTCCCAGATCCAGACTGATGCTCGTGAAGGTGCGTGGGCAACC
CGCAACACCATCCAAGACCAACTTGCCTCCATTGGGCCAGCAGCCCTCCCAGTCCGCGCA
GCGGTAGACAATGCCATCAACGGCATGTTCCCAGGACTTGTTGATGAAAAGGTTGCAGCA
GAGCAGGAAGCTGCACGCGCAGAAGCTGAGCGCGAAGCAGCAGCTGCACGTGAAGCAGAA
GCAGCCCGCGTAGCCGCAGAAGAAGCCGCACGCTTTGACCGCGGCTCTTGCCCAGCAATC
GCTGATGTCTGCGTGGACATTGATGGTGGACGTACCTGGCTGCAGGAAAACGGTCAGGTC
ACCTACGGTGCAGTCCCAGTTTCCTCCGGCGGAGTTGGCCAGGAAACCCCTCGCGGAACG
TTCTACATCAACCGCAAGGTCAAGGATGAAATCTCTTACGAGTTCGGTAACGCCCCAATG
CCGTACGCCATGTACTTCACCTACAACGGCCACGCATTCCACCAGGGCAATGTTGCGACT
ACTTCCGCTGGTTGTGTTCGCCTAAACACTCAAGATGCCATCTACTACTTCAACAACGTT
GGCATCGGCGACATGGTGTACATCTAC

>RXA00676-downstream
TAAAACTCACCGTTGCTAGCAGG

>RXA00678-upstream
TGCGCAGTGCACTTTCCAGGAACCAAAATATCCCCGCCGACCTTGCTGCAGATATTTCGC
AGCCGCTGAAAAAACTAGCCGTTGACCTGGAGGTTACCCG

>RXA00678
ATGACTCGCAGTAATTTACCCGCTTGGGAGCAAGCAGACCCCAGCGTCCACGCCTCTGAT
CCCCGCGCCATCACTTTTGCGGAGGATTTTGGGATTCGTCCCATCCCGGCCGTAGGTCCA
ATTGATACCACCGCTATCTGTGCAACACCTTCAAATGGATTTGAGCAATTATGGAAAGCC
ATTGAGCCGGAAACCCGCACCCGCGCCAACGACATTCATCTTCCCATCGTCGTGGCGTAC
GCTGAACGTCTCTGCGACGCTTACCCACTGGCAGATAGAGAATTGGTTCTCGTAGCCGCA
ATCCTCCACGACACGGGCTGGGCACATGTCGATGAGAGCCGAATCATCTCCGAAGGATTC
TCCGGAAACTGGCGCAAAGCAGCAATCCGCTTCGAACACGAAACAGAAGGCTGCACTGTG
GCCCGCCGAGTGCTTCCATCCCTCGGATATACTGTCGATTTTGTCGAGCATGTCTGCGAC
ATCATCGACGGACACGACACCCGCCAAGTGGCCTACTCACTAGAAGACGCTCTTGTTCGC
GATTGCGACCGACTCTGGCGTTTCGACCGCGCCGGGATCACGGCTTCTAGCTCATGGTTC
GGGATGCCAGTCTCAGATTATGTCGACCGCCTGCACAGGGAAATCCTCCCAGAATTAATC
ACCGAAGCTGCACACCAGATGGCTACTGCAGACCTCAATCGTGCAAAGGCCCTGTTAAGA
ACGGATGCGATCCGA

>RXA00678-downstream
TGAATGCTGCAACCAGGCGTGCT

>RXA00691-upstream
TGCAGCTGCAGTCGCACTATGGATTGTTCTTGCCATATCGCCATGGGTTCCTTCTGCGCA
CGCCTTGACCACGCCTTGTGAAGACGACCAAGTGACAGTG

>RXA00691
ATGGTTGAGGGCAACACCATCGGCTGTGCTGACGCCGGCGGAAATGGCTATCAAACGCTT

CTTGATGCCGGATTTGATGTGGAAACCACCGTTCAGTTTCCAGAATTCTTGTGCCGAATC
AATGATTTCCCAGGTCCTGATGTGGACGATTGCATGACCGCATCACCTGCTGAAGCTTAT
TGGTCTTATTGGCATGCTCCCCTCGGCGGAGATGAATGGGAATACAGCAACCTTGGAGCT
TTCCTCTACTACCCCAAACCCGGCACTGTTGAAGCGTGGTATTGGGGAGATACTGATCGT
CCCGGCGCGATCCCGGTGAGTAAATCTCAGGCGGAGTTGGGGTTAGACTCCGCGGATCCG
GATTACAAAATTGATTTTGATCCAAATGATTTCATCACCACAACCCCAACCTCCGAGTCC
CCTATCGCCGATTTAGGGGGTGACGAAGAGCCCACTGAAACTACTGAAGCTCCTATCGCA
GGGGCTGGAGCTGGTTCGGCAAGAGGACAAGCAGCTGAACCCACTGTTGAGGTAAACCCT
GAGAACCCTAATGAGGTATTGGTGTATCAGGATTCTGAAGGAAACTCGATTACTAAAGGT
CAGTACGAGAACTTGGTTGCTGCAGCAGCCGCTAAGACCACTGCTGCTGTCCAAGCCCCA
GCTGGGGCTGGTGAAGCAAATAGCCAACCGCAGGCAACAGCGGTGGCAGAAGCTCCTGAA
GTTGATCCGATGACCACGCAGGTTCTTATGGCGCCTGCGGGCCAAGATGGAGACGTCATG
GCTGAGGGTTCGACGCAGCAGACGTACGCCACAGGCACGGTGGATTCTTCTGCTCAGGGA
TGGATCATTGGACTCACACTGGCTGTCATTTCCTTGGTTTCAGCGTCTGCTGTGGCGGCG
TGGGCGATTCGTCGTTCAGAGGTCCAGGGT

>RXA00691-downstream
TAAAGCTTCGTGAAATGGATTGA

>RXA00692-upstream
CCTTAAAGCGGGGTCAGAACATTTCTCCAATTCATTTTAAGGACATGTTTTCATGGCTCA
TCTACGTGGGAAGAGAACCATTCGCTGGTCTGCTGCAACC

>RXA00692
GTGGCTTTAGCAACCGGTGTTTCCCTGTTGGCTCCACAGGTCGTTGCTGCACAGGATGCA
TCATCGGATATTCAATTAGCTACCCAATTCATCGAAAAAGAATTTGCAACGAATGGCCTC
ATCCCTGGGCCTGTAGGTACTCCAGATATTGGGCTCAATCAGGATCTGTTGCTGTCCCTA
AATGCGCTTGCCCCTGATTCTCCAGAGATCGACGCTGCATATGCTGCAATTGCTCCGGAG
CTCGAGGGCTATGTCTCAGTTTCTGACTACATCTTCAGCGATCGTCTAGCCAAGACCGTA
GCTTTCCAAGATGCCCTCGGCGTCAGAGATGCTGATTTTATCGCGCAACTTGTCAGCGCT
GTTCAAGAAAACGGTCAGATCAAAAACTTAGATAATGGTGAAGCCACAACTGCAATTAAT
AACTTCAGCCAGGCCTGGGGCGTTCTAGCTCTGCACCGCGTCGGTGAAACCGAAGCAGCC
GAGCGCGCAACAGAATTCCTTAAAACTCAAGTGTGCTCCGACGGTGGTGTCCAATTAGCC
TCAGCAATCGAACCTACATGCAAAACCACGGATTCCGATGTCACTGCAATGGCTGCACAG
GCTTTGACTCTGGCAAATGGTGCGCAGGATCCAACCACACAAGCCACTCTCGATTACCTC
GTCACCACGATGGATGAGACCGGTGGTGTCAAAAATACTTGGACCGGTGTGAATTCCAAC
TCCACGGGAATTGTCGGATCCGCTTTTGCTCTTGCGGGCGATGAGGAAAACTACCTCAAG
GCTCGTGAATACCTGGCATCTGTTCAATTTGGCGAAGATGCAGACCCATCGATTCAGGGT
GGCTTTGCTTTCACCGTGAAGGCTAAGGAAACCAACACTGCGATTAGCGATCAGATTCGA
CGCGCAACTGGCCAAGCAGCATTAGGTTTTGCAGGCGGTAACTACGCCAACGATAAACTG
ATCACCATTGCGAACCCAGTAGATCCAACTCCAGATCCAGAAATTCCAACTCCCCCAGCT
GATTCAGAGGGATCCACCGGTGGAATTGGCGGCGCTGGAATTATCATCGCCATCTTGGCC
ATCCTTGCCGCCATCGCTGGTGTCATGGGACCAATGATGGCTAACCTGCAGTTT

>RXA00692-downstream
TAACATCTGAGAGAAGTACAGTG

>RXA00693-upstream
TCCATCAGCCCTCCCCCGCGTGCCCCACGCGGGGCACGGTTAGCGCTGCTAACCTGGCCC
GATGTACAAATTAATCTCACCGCATTTGTCAGGCCACGCC

>RXA00693
ATGTGGAAAGAGGCTTTGGAAGAATTCGGATCAGGCCCCATCCACGGCTCGGGTTATTTC
GAGAACTATCTTCCCATCGACTATTCCGAAGCAGGATTTCACCACTACCTCAAGGAGCGC
ACTGACGCGGCCGATCCTTCGGTTCCACCACCGGAAGGTTTTGTGCACTGCAGCTATTTC
TGGATCGTTGATGATGACGATGTTCTTGTCGGATTCTTAGCTTTAAGGCACGAGCTGAAC
CAACATCTCCTGGAAGTCGCGGGCCACATTGGTTACGGCGTGCGCCCGTCTGCGCGTCGA
AAAGGTGCTGCAACCGCAGCGCTGAAACTCGGTGTTCATGAAGCTCAGGCCTTGGGCATC
GACAAGGTTTTGCTGTGCGTCGCAGGAGATAACGAAGCGTCCAGGAACGTCATCGAAAAG

TGCGGTGGAGTTTATGAATCCACGATCCGTGGAATGCGACGCTATTGGATAGCCACAGAT
TCT

>RXA00693-downstream
TAAAAAATCTTCGCAAGAACTTA

>RXA00701-upstream
AAGAGACGATGGCGTATAGGACGATGATGAGCATTTCCTTTTTGCCGCGTACTTGGGGGA
GTAGGCCGGCGCCGAAGCTGACCCAGGCGGCTGCGAGCAT

>RXA00701
TTGGTAGGGGAGCCACGGTCCGATTCCTGCGGTGAGCAGCGCGGATGCGAACAGTCCGGT
GTTGCCGAGGATGAATCCGAAGCCGGGTCCGAAGGCTCGTCCGCCGAGGATGAGGACAAA
GAAGACTGCTTCAAAGCCTGCTGCGCCGGCACCGAATGGTCGGACTACGGCAACCATGGC
GGTGAGGACGCCGAGCATGGCTACGGCTTTAACGTCGAATCCGTTTTCACTGATTTCGGC
GATGACAGCGGCCAGCACGAGGGGAATGACGATCGCGATGTAGAGGGGCGCTTGGGCTTT
GTCGGACAGGAAGGATTCCGGGTTGACGATCAGCGGCCAGAAGAAAATCACGATGCTCAA
AACCGCAAGGAAGCT

>RXA00701-downstream
TAAGGTGAGGAAGGTTTTGGGCT

>RXA00704-upstream
TCAAATTCTGCGCACAAAGTGTTCTAAGACGACGTCTGCCCATCGGCGCTCTAATGCACA
TTACAGCGTTTACAGAATTGAAAATGAAAGGTTCAAAGCC

>RXA00704
TTGACCATTACTTTTAGCCGCGTTGCTCTGACCACCCTGGCAGTCACCGCAACCACTTTG
TCCCTGAGCACTGCTGCGAATGCACAGTCTTCCTTGTTGGATAAGACTCTTGATGCCCGT
CAGTGCATCGATGCAGACAACGTCTGGGTCTCAGTTGACTATGGTGCAGATTCCGAAAAA
GAACCAGAGGGCGCATGTGCCACCGAGTTCACTGATGGTGTTGTAGCTCTTGAATCTGCT
GGGTTCAAACTGACCTTTGACGAATCTGAAATGGGCAAATACATGACCGGTATCAACGGA
GTTGTTCCTGATTGGGTTGAAACTGGAACTTACTGGAGTTACTACTCTGGTGAAGTCGCA
GATGATTACAGCGTGGACTACACCTACTACGAGGTTGGTGCATCTAATTCTGAACCTGAA
GGTGGAACTGTTGAGGCTTGGGTTGTTGGCACCGGCGAGGAAACACCAGCACTCGAGACT
CTTTCTGAAACTTCAGCAGCAACCGGATCTTCT

>RXA00704-downstream
TAAGACGGCGGCTGGATTGCAGT

>RXA00707-upstream
TAGTTAAAAGCACTTACCTTAACTGGTAGGTGCTTTTTTCATGTCTACGCAGTGGGTAAC
TTTCAGAGGAAAATTACCCAACCAAAACAAAGGAACTTTC

>RXA00707
ATGAACGTGCAACGCAAACTGCTGGCGATCGTAGGGGCTTTCATGGCAGGGTCTTTAGCC
TTGGGAACACCAACTGCACAGGCCCAAAGCATTGGCAGCAGTGCCTCACAGAGAACTGAA
GTCTTACGTGGGCTGACCTCATCTGCCGGAATACCAGATGCCACAGCGCCGGAAGGCGGG
GCAAAAGTCGTGGTCTTTGGAGATTCACATGCATCAGGAACCAATGCACCATTTGATGTG
GATGAACGCGGCTGCCTCAAGGGGAACCAATCGTGGCCTGATCAATTGCAAGCACAACAA
GGATTGCAGCAGGGGGAGCTCATTGACCTTTCCTGCAACGGCGCCTCCATCAACTCGACG
GGTTTCCACTTTTCCGATGAAGTTCGGCATGCAGAAGCACTAGGGGCCATTGGACCAAAT
ACCGAGAACATCTTCATCCAATTTGGCAAGAATGATCAGTGGGGACACTCACCAATCAAT
TTGCGCTATTCCGTGATCAACTGCCTTTTTGATGCGGCCAACGGATGCGGTGAGAAAGCT
GTAGCGGCTGGAACCATGCAGGATCCCTCCTCGGTCACCGGCGAAAACTATGCTCAGCGG
ATGAAACCTGTCATCGACTACCTCAAGTACTACGCTCCAAATGCGCAGATCACGTTGCTG
GGATACCAGGAATACACCCCACGAAGCGGAAGCGAGATTTGTGTCCGCGTGGGAGGTACG
GAACTAAGGAAACCAGACGCCACCAACCTGGTGTCCTATATGAACAATCTTGAGTCGGCC

ATTTTTGAAGCCTCTGAGATTCTTGACGTCCAGCATGCCAATCTCCGTGAGGCCACTGCA
GGACACAGCAGCTGCTCAGCTGAACCGTGGGTCAACGGAGTGCTGGATATGCGGGTAAAC
GCTGTAGGAGGCACCTGGCACCCATCTCCAAAGGGAGATGAAGTGACCGCGGGCCTCCTC
GGAACCTTGATG

>RXA00707-downstream
TAACTATCTAGAATTCTTCATAG

>RXA00712
GCAGCAGAACCCACCACTAGAACGACTGTGCAAAGTGCTACAGAAGCCTCCACTACTGCA
CCAGTGCAATGCAATTTGGATCCCCGTACCTCGGATTTTGGGCCATATCTTGCACAATCT
CGCACCCCGGTTGGTGAGCTAGCTGGATCTGCAGATTCCGTCGTGCAGGTTCCTGACTGG
TTCTATCACTTCCAAATGGGCGACAACGGCTACGATTCCTGTTCCAAGCTCAGCTATGTG
GTTCTCAACGGTTCCAATGGAGACGCCGAACGTTCTACTGGAACGGGTGCTGCGATCGCC
GACGTGGTGGTGCTGTTTATCGACGGCCATATGGTTGCTCGTCCTGCTCCTTTTGAAATG
AAGACCGTGGAATCCGTCACCAGAGTGTCAGATTCAGAAATCCAAGTTGTTTACGGACAT
GCCGGCCGATCTACTGCCGAAGGTGTTACGGACTATTTCACCTTTAACTTCTTCGTTGAC
AACGGCGTTCTTTCAGGACGCGGCGATCTCCCAGAACACATCGATACTCACATGCGTCTA
TATCTGCTG

>RXA00712-downstream
TAGCCCCATCTAAAAACTCTTGA

>RXA00713-upstream
AACCACGCCTCCTTGTGCGGGCCTGTCAGTAACTGTTATCGCAGGTTCATGCGTTAAGGT
GTGGAAGACC

>RXA00713
ATGACAAAAGTAGCGGAGCTGGACCAAGAGTGGTCCGAAGTAGATGACGCGGAATTAGAC
GCGCAAAGCGCTGGCACTTCTGATAGTTCCAGCACAGACGACTTCGCTGACGCAGAAAAC
ACTTCTGAAAATCTGGGACCCATCGGCCCAGAACCACTCCCTGAACCAGATGGGGATGTT
CCGGCATCGGGTTTCCAAGTGCAGCTCGATAATTTTGAAGGTCCTTTTGACCTTCTCCTG
CAGCTGATTACCAAGAAGAAACTTGATGTCACTGAAGTTGCCTTGGCCCAGGTGACCGAC
GAGTTTATTGCTTACACCCGAAAACTGGGCGAAACCAGCGATTTGGATGAGACCACAGAG
TTCTTAGTGGTGGCCGCAACGCTGTTGGATCTTAAAACAGCTCGCCTGCTCCCGCGTGGT
GAAGTCGACGATGAAGATGATCTCGAATTGCTCGAAATAAAGGATCTCCTTTTCGCCAGG
TTGTTGCAGTATCGCGCTTACAAGCAAGTTGCGGAAATGTTTGCGCAATGGCAGCGAGAT
GCTCGACGCAGGTACCCGCGCGCTGTCTCATTAGAAACTCAGTTTGCCAACCTCTTGCCG
CCCGTTTCCTTGGGTCATTCCTTAAAAAGTTTCAGCGAGTTGGCTGCTGTGGTGTTTCGT
CCGAAACCCCCAGAGACGGTGAAAACAGATCACGTGCACCAAGTTGCGGTGTCAGTTCCA
GAGCAAGCGGGCAGGATTCTTAACACGTTGAAACTTGCCGGAATTGATCATTATTTGAGC
TTTCAGCTGCTCACACGTGATTGTACCGCGTCAATGGAAGTGATTGGCCGCTTCCTTGCC
TTGCTGGAATTGTATAAGGCACGCGCTATTGAAACCTTGCAAGAAGAGCCACTCGGCGAG
CTTAAAGTTTCGTGGACTGGCATTGATGTCGATCCAGCAGTCGTCGCGGCGAGTGACTGG
GAG

>RXA00713-downstream
TAATCAGTTTTTCTTAAGGAAAC

>RXA00714-upstream
CGTCAATCAAGCTGTCAAAAAAAATACAAGTTAGGTCACAAAATGATTTCAGTCGTGAGA
ACCATCACATATAAGACATCTCATGATCTAACATTTCTTC

>RXA00714
ATGGCTACGATTACACGCACCGACAGACTGATCCTCGTACCGCTCACTGTTGAGCTCGAA
GACGAGGCCCACCAGATTTACTCTGATTCTCGAATCTGGGAACACCGCCCCCAGGCGCGT
CACACCAACGTGCGTGTCACGCGCGACATCATCAAGCGCACCAATGAAAGCTGGGGCAAG
AAAGACCTTGGCCCCTGGGGTGTTTACCTCCGTGACCGCCCATCGGAATTCGTTGGCGTT

GGTGGCGTTGAACTCATCGACGGAAAAGTATGGGACCTCAAGTACCGCCTCCGCCCCGAC
CTATGGGGCAATGGATACGCCACGGAAATCTCCAACGCCGCAACACTGGCCACCAAGCGT
ATCGACGACAGCCTCCCACTCACGGCCAGGGTGACTACCAACCACCCTGCCTCATTCCGT
ATTTTGGAAAAACTGGGACTCACCCCCGTATGGGAAGGCCGACGAGTCGGAACGGAAGAT
GACCCCAACGAGCCTGATGTGAGAATTTATTCTGACCGTCCGCTATCGGATGAAATTCTT
GAAATGCTCAAGCAACGACCA

>RXA00714-downstream
TAGACCAGAAAATCTCACCCCTT

>RXA00716-upstream
AAAGCCGATTGCTTAACGCCCGCTATGATAACCACTCATGAATGATTTCGATCCAGCATT
GATTTCCGCGATGAGCCTTATCCCTCAGACGAGGTCTCGG

>RXA00716
ATGGAATCAATCTTGTTGGTGGTCGATACCCCAGTTTCAGCACGCACGCTGGCTGGGGTG
TTGGGCATTGACGTGCCTGCAACAGAGGCAATTTTGAAGGAAATGGCCTTTGAGCTTTCT
GAACGGGGCAGCGGCATTGATCTGCGGGAAACGGCAGAAGGATGGCGCTATTACACCCGC
CCGGAAAATGCGGACATCGTCGAGCAATTCCTCCTCGATGGAAACCAAACCAGACTGTCC
CGTGCAGCATTGGAAACACTCGCGGTGGTGGCATATCGGCAGCCGGTCACACGCTCCCAG
ATTTCAGCAGTGCGCGGAGTAAATGTCGACGGCGTCATGAGAACCTTGCAGCTTCGAGGC
CTAGTCAAAGAAGTCGATGTGGACGAATCAACGGGCGCACACCGCTATGGCACAACGGAA
TTGCTGCTTGAGCTGTTGGGTATTGATTCTTTGGATAAATTACCAGATCTAGCACCGCTT
TTGCCGGATGTTGACTCCATTGATGAAGACTTC

>RXA00716-downstream
TAAAGCATCAGTTAAAGCCCCGA

>RXA00719-upstream
CAGATGATGCACACATCGTGGACACCTCTGATATGACCATGGATCAAGTACTTGATCACC
TCATCCACCTAGTGGAAGCCTCCGCTGAAAGGAGCAACCA

>RXA00719
GTGACTGATAAACACACCATGCCTGGTGAAGAGGACGACACCGTATTCGTCTACCACACC
CACAAAGGCGAAATGGACGTCGAAGGTGCGTTTGCTGACGAAGAAGAACTAGCACCACAC
GGCGGTTGGGCTTCCGCAGATTTCGACCCAGCAGAATTCGGCTACGAAGACTCTGACGAT
GACTTCGATGCAGAGGACTTTGACGAAACAGAGTTCTCCAACCCTGATTTCGGCGAAGAC
TACTCTGATGAAGACTGGGAAGAAATCGAGACCGCATTCGGATTCGACCCAAGCCACCTT
GAAGAAGCTCTCTGCACGGTCGCTATCGTCGGACGCCCAAATGTTGGTAAATCAACCTTG
GTGAACCGCTTTATTGGACGTCGAGAAGCAGTCGTGGAAGATTTCCCCGGCGTAACCCGT
GACCGCATCTCCTACATCTCTGACTGGGGTGGACACCGTTTCTGGGTTCAGGACACAGGC
GGATGGGATCCTAACGTCAAGGGCATCCACGCATCGATCGCACAGCAAGCAGAAGTTGCT
ATGAGCACTGCCGATGTCATCGTATTCGTCGTGGACACCAAGGTGGGCATCACCGAAACT
GACTCAGTGATGGCAGCAAAACTGTTGCGCTCGGAAGTGCCAGTGATCTTGGTTGCGAAC
AAATTCGACTCCGACAGCCAGTGGGCTGACATGGCTGAGTTCTACAGCCTCGGCCTTGGC
GATCCATACCCAGTTTCAGCCCAGCATGGACGTGGTGGCGCTGACGTTTTGGACAAAGTC
CTTGAACTCTTCCCAGAAGAGCCTCGCTCCAAGTCCATCGTGGAAGGCCCTCGTCGTGTC
GCCCTTGTGGGTAAGCCAAACGTGGGTAAGTCTTCACTGCTCAACAAGTTTGCTGGCGAG
ACCCGCTCTGTCGTGGACAATGTTGCAGGAACCACCGTTGACCCCGTTGACTCCCTGATT
CAGCTGGATCAAAAACTGTGGAAATTCGTGGATACTGCTGGTCTTCGCAAAAAGGTCAAG
ACTGCATCTGGCCACGAGTACTACGCATCACTGCGTACCCACGGTGCCATCGATGCAGCT
GAGCTGTGTGTTTTGCTTATCGATTCCTCCGAACCCATCACCGAGCAGGATCAGCGCGTG
CTCGCAATGATCACCGATGCCGGTAAGGCACTGGTTATTGCGTTCAACAAGTGGGATCTC
ATGGATGAAGATCGCCGCATCGATTTGGATCGCGAACTTGATCTCCAGTTGGCACACGTG
CCTTGGGCAAAGCGCATCAACATCTCCGCCAAAACCGGTCGTGCACTGCAGCGCCTCGAG
CCAGCAATGTTGGAAGCGCTCGACAACTGGGATCGCCGTATCTCCACTGGTCAGCTGAAC
ACCTGGCTGCGTGAAGCAATTGCTGCGAACCCACCACCAATGCGTGGCGGACGTTTGCCT
CGAGTGCTGTTTGCCACCCAGGCATCTACTCAGCCACCAGTGATCGTACTGTTCACCACC
GGCTTCCTCGAAGCAGGTTACCGACGATACCTGGAGCGCAAGTTCCGTGAACGTTTCGGC

TTTGAAGGCACTCCAGTGCGAATCGCTGTGCGTGTTCGCGAGCGCCGCGGCAAGGGCGGA
AACAAGCAG

>RXA00719-downstream
TAAAGCTTGATTTTCCCTAAAAG

>RXA00720-upstream
CTGATCTATACGTCCTGTTGAAGTAGAGAAGCTTTCTGGTCAAGTTCCTTGAGTATGGTG
GTCGAAGACCAGCACTCCAGATTCAAGGAACTTATAAAAC

>RXA00720
ATGGCATCACCGCGCCGCCCACAGGTTGCAGCACCACGCATCAAAGAACTTCGCCTAACA
GGCCTTGACAACGCTGACCCTCAAGACATCGAATCGAATGAGCAGATAGAGTCATGCCGT
TTTAACGAGGCCGAGCTTTCCGAACGCGATCTTTCTGGTGCTGGTTTCATTGAATGTGAA
TTCCTTGGGCTGGAAGCACACGAAACCGAGCTACGCCGGGCTCAATTCGTGGAAACACGC
ATCGAAAGAGCCAATGCTCCATCTTTTAAGGCAGCCCGCTCCATCTGGCGCAACGCAACG
ATTTCCGACTCCCGCTTTGGTGCCGTCGAAATGTATGAAGCAACCGTCCAAGCTTTGAAA
ATCTCTGATTCTAAGCTGTCGTTTGTCAATCTGCGGGGTGCATCGTTACGGGATGTGCTC
TTTGAGAACTGTGTCATCGACGAGCTTGATCTTGGCCAAGCCAGAGCAGAACGCATCGCT
TTTAAAGACTGCACGGTGCATTCGCTCACCTTTGATCATGCCGTGCTCAGCAATGTGGAT
CTTCGCGGTTTAGATATCGAGCGCATCAGTGGCGTGGAGTCCATGTCCGGAACCGTGATC
TCATCCCTGCAGGCTGCTGACCTGTCGGGAGCATTTGCACGGCATTTAGGAATTACTGTA
AACGAT

>RXA00720-downstream
TAGAAATCCGCTCTTTTGAACAA

>RXA00722-upstream
CCCCCCCCGGTGATC

>RXA00722
TTGCTGCCCAACGGTCTTTTGACCAAGCGTGAGCTGGTTTCCATTGAGCGTTCCAGCCAT
GCTTTTGAGCAAAGTGTGGTTATTTTGCCTACTGCCACGTTGGTTGCAGGTCTTGCAGCG
GTGTCCGTTCATGAGCCAGCGCAACCCCTGGCGGTGGATTCCTATGCCATGGCAGAGGCC
GCCGGTTCCATGCGCACGGCCACGATCCGCGCCGCCACCAGCGCCGCGCTCACCCAGGCC
GGCGCATGCTCCAAGGGTGATCTATTAAGCTTCATCGGCCCGGAGATAGCTCTGGTCTCC
GAGGAGCTCAACGACGCGCTATCGCGCACCGCTTTAAGGCTTCTCGACGGCTCCAGCGAG
CAAATTACCCTTCTCATAGCGCAAGACCGTCAGTCCGCCTTCGACGAAGATGTTTTCCGC
CGTGGCCTGGGAACTCACACGGATGTGGAGATCACGGTCTATCCTGCTACTGGAATGGAG
AATCTGGTAGAGATCGGAGTGGAG

>RXA00722-downstream
TAGCCACATGTTGGGTTGGCATG

>RXA00724
ATCGGTGAGGAAGTCCTCGCCGGACGCCAAGCCTATGTGGTGTGTCCGCGCATTGAAGGC
GAAGGCGGCGTGCTGGAAATCCACGCCTATCTTTCCGAACAGGTATATCCAGGATTGAAT
GTTGGAATGCTGCACGGTCGCATGGACACGGATCTCAAAGATTCGGTCATGCAGGAATTC
GCCCAAGGTGAGATCGATATTTTGGTCGCCACCACGGTCATTGAGGTCGGTATTGACGTT
GCCAACGCCACCGTCATGCTCATCCGCGAGGCGGAACGCTTCGGCGTTTCCCAGATCCAC
CAGCTGCGCGGCCGTGTTGGCCGTGGGCAGCACGATTCCCTCTGCCTGCTGCACACCACC
TTCGACGAGGACTCCCCACAAGGCCAACGCCTCGCCGCAATTTCCACCACAACCGACGGT
TTTCAACTCTCTGAACTTGATTTGCAGGTACGCCAAGAAGGCGACGTGTTGGGCACCCGC
CAGTCCGGCAGCGACACCAAACTCCGTCACCTCTCGTTTATCAGCGACCAAAAAATCATC
GAGCGTGCGCTTATCGACGCCACCGAGCTGGTTGCCGCCAGCCGTTCCAGGGCGCTTGAG
CTGGTCAGCGACATCGCAATGATCAACCAGGAATACCTGGAAAAGAGC

>RXA00724-downstream
TGATATTGATAGGGTTTAAGTCA

>RXA00726
CACGAAATGGGCTTCGCCCACGAAGTCGCCGACCAGGTCGTGTTCATGGCCGATGGAGTT
GTCGTTGAAGCCGGAACCCCCGAACAAGTTCTGGACAATCCAAAGGAACAGCGCACCAAA
GACTTCCTGTCTTCTCTGCTC

>RXA00726-downstream
TAACCTTTTCGGGTCTTAAAAAA

>RXA00729
ACAGTTGTTGAGGACTACCAAGAGTTCACTCGCGGTCTGTTCCTTGGAATGGTTGCCGTG
TCTATCCTTGTTCCGTTGGGAATGATGGATATGCGGGATGCCAAGAAGCGCCTCGCAATC
GTCATCCCGCTATTTATAATCTGCGCCATGCTGGGATTCTTTGGAACATCCTTCACTAGT
GCGCCTCGCACCGATCCTTCACTGATCTTTGTCTTCATCTGTGCTGCGATCGCTGTGTGT
GCTCTTGTTCTTCCTGGTGTTTCAGGATCATTCTTCTTGCTGGCGGTCGGTATGTACGCG
CCAATCATGGAATCTCTGTCCAACCGTGACTTGTCGGTCATCGGCGTGTTCTTGCTTGGC
GCGCTCACCGGTGTGATCTTGTTTGTGAAGGTTTTGTCTTATGTTCTCGAGCACCACCGC
ACCATCACGCTGACCATCATGGCTGGTCTCATGCTGGGTTCACTTCGTGCGCTGTGGCCT
TGGCAGGACGGTGACGCTAATCTACTTGCTCCTGGCGATAACGCCGTGATGATTTTCAGC
ATCATCATTCTTGGTGGCGCGATTGTCGCTGCTTTGATGTTTGCTGAGCGTGTGTCTTCC
AAGAACATTGATTCTGAGACCGTGGCAGAAGAGCACCCGCGC

>RXA00729-downstream
TAAATAAGAACTCCACAAAGAAA

>RXA00730
CACTTTGTTGTATTCCAAAAGCAGCTTCAACAGGCAGATCCAAATGCAGAATATGATCTC
GATGTGCTCGCATTTGATATCGCACGCGTAGCCAACCTCCTTCGCTGGGCTGCTTATACA
GATCTGTTGCTCCCTGCAGAAGCCCGTTGGTTCCAAGACCAGCTGGGAATTGCGGCTGCT
GTGTCCTTTGGGAGCTGGGAAGAATACGGAGAGCGATACGTCCGTGGACTACAGAAGAAC
TTCAAGGGCGGAAACAAGCCATATATCGAAGGAGAACGCTGGCTCAACACTGAGGCTGAA
AGTCCATGGAAGACCCAAAAGTGGATTAGCGCC

>RXA00730-downstream
TAACTGCTCATGAGCTAAGCGGC

>RXA00731
TTATTATTCGGTCTGAGATGGCTGGGCAGGTCCCTGCGTTTCGCACCGTTAAGCCTGCTC
ATGATCGTTGTCATGCGGGGTTTGAGGGAAGTGTTTGGCGCCGAAGATCCCGCAAATAGC
TCTTTGGTAGACAACCTTGGGCTCACCCTGCCGTGGTCTCTTAATGATCCGCATTTTCTC
ACCGCAGGGTTTAGCGCTTCCACCACCACAGCAGCGCTCATGTCCACGTTGTGGATCATC
GTGTTTGCGGTGCCCTCTGAACGGATTCTGGGCAGCCTCAAATTCGCGATCACAGCAGCG
CTTATCCACATCACTTCCATTCCGCTGGGCATCGGCATCGCCCACCTCATCGAAGAAGCC
GATCTCAACCGCTGGGGCAACAACATGTTGGCCGATGTGCTGCTCACCCCAGATTTCTGG
GTCTTCGGCGTCGCCGCTTTCGCATCCGCCTCCATGCCACTGCTCTGGCGACGGCGCACC
CGATTGTTCCTCTTTACTATCACCTTGACGCTGCTGCTTTATACGGGCACGCTTGCCGAC
GTCACCATGCTCACCGCGACCATCATCGGCACCGTTGCCGGCGAGTTGAACAGGCATCGG
AAAACCCCAGGTGGCCGCTGGCTTCCCGGTTCCCTCACCGTGCGTGAAGCGCGCATTATG
ACGGCCATTTTGGTCACTGCCGTAGCAGCAGGTCCAGTGCTTGCTGCGCTTAATCCACTC
ACCCACGGCCCTTTTTCCAGTGCAACGAAATTGATCTGGCAGCCCCTTGTCACTGAAGAA
CACATGCATCACCTCTGCCACACAGACAGCACCTCTGATGCATGCCAAGGTGCGCTTGAT
CAGCTCCAACAGCACGGTGTTGGCCCTTCCGTTGCCAACCTGATTCCACTGATCCTCACC
GTGGTCCTTGCGATGGGGCTTAGCCGCGGACGTCGACTTGCATGGATTTTGGCGGTTTTG
GCCCAGCTCATTTCCATCGCAGTGTTGATGTTCCAGCTGACCAAACTATCGGCTGATTCC
ACCGATCTTCTATGGTCAGTCAATGCCTTTAGCGTGATCGTTCCTTGGCTGGTGGCGCTC
GCCGTCTTGGTGTTTTCCCGCCGTGCATTCCAGGTGAAGATTGATACCACCCGGATTTCT
AAATCCTTAGGCGCTCTCATGGTTACATGGTTGGCAACGGCAGCATTGTGGATCCTTGCC

ACATTGTTCCTGCCACACGCATTCCACCCACATCCAACATTGGGGCTGGCTTTCAAAGAA
CTCCCCTTCCGCTATCTCCCACCAACTATCGAAACGGTGTTAAGCCATCAACTCTTCCCC
AGAAGCCCTGCTGGGTGGGCAGTGTTTGAATGGACTGGAACGCTATTCTGGCTGGTCGTA
GCAGCAACTCTTTATCATCTGCTCATGGGTGTGCCCAGCAACAAAGCGCACGAGGACCAA
GAAAACGCAGCGACTCTCCTGCGCTCTGGCAGCGGCGATCACTTGTCCTGGATGACCATT
TGGGGTGGCAATACGTATTGGTGGGCACCAGAAAATGCAGGATATGTGGCCTACCGCGTG
AAAAGGGGCATCGCAATTACATTGGGTGAGCCTATTCTGGGTCCGGATTCATCCGTCTCT
AAAGCAGAGCTGGCCGCACAGTTTGAAGAATTTGCCAGCAACCAAGGCTGGATTGTTGCG
TGGTATTCCGTTTGTGAAGAATTCTCAAAGGAACGCATCAACGCTGGCCACCACACACTT
CGTGTGGCTGAGGAAGCAGTCTTAAGCTCAGCTAATGCGGATTTCAAAGGTAAGCACTTC
CAAAATGTCCGCACCGCCCGAAACCGCGCGGCCAAAGAGGGCGTAAGTTCCATCTGGACA
ACCTGGGCTGATTTGAGTGCCGAAATGCAGCACAAGATCATCACGCTGTCGGAAGAATGG
GTCTCTGATAAAGCTCTGCCGGAGATGGGCTTCACGCTTGGCACTGTCAACGAGCTCTCA
GATCCAGATACCTATCTTCTTCTCGCGATTGATGAGGAAGAGCATCTGCACGGTGTGACC
AGTTGGTTGCCGGTCTATGAAAAAGGACGCATCGTCGGCTACACACTTGATGTGATGCGC
CGTGATCCGCAAGGCTTTAAATCTGTCATCGAGTTTCTCATTTCCGAGGCCGTCGTTATC
GCAAGGGATCACGATCTGGAATGGATGTCGATGTCCGGCGCTCCTTTGAGTACGCCCCCA
GGTGTGGCCGACGACGGCACCATCGGACAAATTTTGGAGCTTTTGGGCCGAGCAATGGAG
CCGTTCTACGGTTTCCGTTCCCTCGCTGCGTCCAAGAACAAATTCCACCCAGAACACCAC
GGTTGGTACTTGTGTTACCGCGATGAATTATCGTTACCAAGCATTGGCCTTGCCGTTGCT
GCCTGCTACCTCAACGAGTTTCCGCTGCCGAATTGGCTGAAAAAGACCGCCACTTCCGCC
CCAAGCCACAGC

>RXA00731-downstream
TAGAAAAACGCGTAACCTTGGTG

>RXA00738-upstream
CATGCCCCTATTAGACGGATGGCTTTTTTGATTTTGGGCGCGATATGCGGCCCGGTGAGC
GCCGGTCGTATGGCACT

>RXA00738
TTGCTTAACGACGCCACGACGCAGGTGTCGCACATCCTCGGCAATGCCTTCACCCGATCT
GGGCTCAACGCTGAGTACGCGAATCTTTATGGTCAGGCGTTGGTGGGCATGGTGTCGATG
ACGGCGCAATGGTGGTTGGATGAGCGCACTCCGCCGAAGGAAGAAGTTGCCGCACATATT
GTTAATCTTTGTTGGAATGGTTTGACGGGGATGGAAGCCGATCCGAAGTTAACTCCCATC
AGTTCTGCTGAGGGTGCGATTTTTGGTCAAGAAAAGGAGAGTGAAGCG

>RXA00738-downstream
TGACACCTATGCTCGCGGGGCTG

>RXA00739-upstream
TTAAAGTTTCTATATTCCATTCTAAAATAACTTTGAATTGGGGATTAATGAAACTTTTTA
AGCAATTGTTTAAAACGAATATTGAGGGGGTGGCGGGCAA

>RXA00739
GTGACTGCGACAGTTTTAGAACCGCAACCTGTACAGCTTAGTGAGCAGGACGTAGATGCT
GAGATTGCGCGCATGGAGCTTAAACACAACCGACACAAGACGTGGCGACGCCGAACGATG
GCTGTTGTCATGACGCTCTTGATCTCAGTGGGTTTGAGCTTTGGTGCGTTTGGTAACAAG
GAACGTGAAGCTAATGCTTTCGCCAGCGCTATTATTGCCCAGGTTGTCGGTGCTATGGGC
GAGGTTGCCTTTGAAGCGATTTGTCCCAGTGATGGTGACACCGAGATGCTTCTTAAGTGC
ATCACCGAGAACTTAGGTGAAATGCACATTATCGAGAAGTGTCTCGAAGCAGAAGATGTC
TTGAAGTGCTTCTACGATGCGAAAAACGAAGAGCAACGTAAAGAACAGAACCTTGATAAA
GCCCCTGATTACTCCATGTACCGTATGGCCTCTGCGATGGCATCGTTCTATGGCAATGGT
CGGGCAGCTACTGCCGGTGTAGAGGAAGGCGGACCGAACGAGTTCCTCGATTCTGAGGAC
GCCGGTCTTAAGGTGTGGGAGGGCATTCTCAGTAAGGCCGCCAACGGAGGCAATGTCCTT
GGTTATGCTGACGCGAAACACAACGAGGACTCTGGTTGGTTCTTTGGTAATGGTGTTGCC
AACAACGAGAAAACGTACTCCTATGATTCTCTAGCTGATCATGCCTTTCAAGGGCCTTAT
CACTTTGCATTATTTGGCGCGACACTGAGTGGCTTAGGCTTTGATAGCTCAAAGGCGGAG
GATTCGCAGACTGATTTTGCTCAGCGTAAGGGCATG

>RXA00740-upstream
GTTATAAATATTAAAGTACGCTAACCATGGGTGCAGGGGGAGACTTCTACAGCAGTCATG
GTCCACACCACGACTGCTGTATATATTAAGGACGTAACTC

>RXA00740
ATGTTGAAGAATAAAACTCTTGCGCTGCTGGCTGTCAGTACGCTGATGTTTGGCTTATCT
GCTTGCTCTAGTGATGCTGACGGCCCGGACAGTAGCGGTGCTAGTAGTAGCAGTACTGGC
TCATCTTCTGCATCGGCTGACACAACAGATTCTGCAGCTGTTGATAAGGATGCTCAATTA
GACACCTTTATGCGTTCTGCTGTGGCTGATGGATCATCTGCTGCTGTGGCTGTGGACAAC
GCTGTAGGTAAGGGCTTTGATAAAGCTGATGCGCAGGCGGCTGCGGAGCGCTTGGGTGAT
GGTTTCCAATTCGCTGCGGATTACCAGGCTGTTGGCTATTTGGAATCTTGGTACTTTGGT
GGCGCGCGAAGCGAGAAGCTTGACGAGGTGCGTAGTGATGTCATCGCTCATTTGTCTGAA
TTGGGATTTACAGATTTAGAGGCTGAATCCTCGGCATCTCGTATTACATTAGGTGATTAC
TGTGATGGGGTCCCTGAGTATTGTGAGTTGTTTTTTGATGGCGAATCTCCTGACTTGTAT
GACATGGGTACGGAGCTTGACTCGTATAAGCCCACTGAA

>RXA00740-downstream
TAAAGCTATTTCACTTAAAGCAC

>RXA00741-upstream
TGGTGATCACTAGGTCCACCTCGTCTTGCATGGTGGTCACCTCAGTCCAGAACGCATTGA
TTGACACCGATCAAATGTTTGATGGATTATGATATTTAGC

>RXA00741
ATGACTGATTCTCTGCTTGTATCCATCAGAAAAGGCTTAATAGAAGAGCGTCCATTAACG
GAGCTTCTTCGGGCGTGTATCTTCCTTGGAAGTGATACTAACTCGGACTCTTTACAAGAG
TGGGCGAAAAATGAATTAAATGGTTATGGCTCCATTGATGGTATTCCGGAATATCGCAAA
TTGAAAGGACCTCCTGTATTCGCGAAAATTCAAGCTGGTAATTCAATAATGTCTAATATG
GTACTGGGGCCACATAATGTTCCTGAAAGAGCTCGTAAGTATTTCCCTGAAGAGCTGCAT
TTTGATCAGCCGATTCAAACGCTAATTGAATGGTCGACTAGGCAGGATGGGATTAATTTA
TCGCCCCCGAATTTACTTCGGGTCCGCGATCTTCATAATGATCAGTACGCGCCATTAAAT
CAAATTTTGAATTTAAATGTTTACTTAGATAACTCTTATTTTTCGGGAATTGTGGACCGC
ATCCGAACTCTAATGACTTCCATGATTGCCGACCTCACACACGCAACTCCTCTGGATGAA
CTACCAAGCAGCGAAAAGGTTAATGCCACGGTCATGAAGCACATTGAAAATAACTACGAA
ACTACAATCACTCAAGCCAATGGAGCTGTAGCCATTGGTAACAGCGCTAAAGCTGTGCAG
AAGGGATTGTCCGTGGATGACCTACTGAAGATTATGCAGACCATTAATCCTGAAAAGTTC
GACTTAGGGGAAGCTAGAGCTGAAGCCGAAGAAAGCATTCAATCCATCGCGGATGAGTTG
AAGAAGGAGTCTCCGAATAAAGGTTTTATCCAGAATGCTTTTGAAAAGTTGAAGGAACTC
AGCATAAAAGCCGGCGATAAAGCCTTCACTACAATGTTAAATCTTGTAGGTAAACAGATA
ATCGAAAACATCCCACAACTGGTTTCAGGTGGC

>RXA00741-downstream
TAGAGAAATTCAAGGCCGTCAGC

>RXA00742-upstream
AGAGGGGTTTTTTAGTGAAAATGATAAAACCACTTTTACAGATGGACACATAGATATTAG
TAATGATGCTTCTGGAGCTAAGCGTAGCTTTGGGGGTCGG

>RXA00742
GTGAATGTTCAGATTAAAGGGCGAAAGGTTAATGCCAAGGCTGCCGACTTAAATAGCTAT
CCGGTCTCAGTAGTTGATCTACGAGGCTTCGTGACACTGGCTGGTCTCTTATTTTTTGTG
GTTGATATTGATAAGAAATCAAATAAGAAATATCCAAAGTATGTTCTTTTGAAACCGTTT
TATATTCATGATCTACTGAGTAAAGCGAAGCCGGGCCAAAAGACAATTAGCGTCCGCTTA
AAACGGTTACCATCTGATGAAGATCGAATGGAAGCCATAATCGCATTAGCGCTCGCATCG
AGGCAAGAAAAGATAGTCGAGAACCCCAGTAACTATCTCTATGAAAATATGGAATCAATT
ACTGTTAAATCGGCTGAACCCCTTAATAGGGATAAGCTGGCTGTATATGATGGTAGTTCG
CCAGACCATTCGATCATTATTCGTACTGGGGATGGAATTGAACAGTTCGTCAATGCCACC

GTAGAAATAATACCCCCGAATATGCAGTTTCATCAAGCCAATTATAATGTTTCGTGTAAT
GGGGTCGTCTATGACAATGTTTTGCATCGAAACATTGATGATGAGCACATTGAATTGAAA
ATCGGAAAGGGGATTACTCTCCGCCTACAAAAGCTCGCCATTGATGCTCCGGGGAGCGTT
ACGGTTGAGTTTCAAGATAGTCTTCCTGAACGGTTAAAAGACATTGAGTTCTTCCTAGGA
GTGCTTCAGGCGAATACGTTTTTTATTAATGAAGAACCTGTTGTGTTGAAGATTAACTCG
AACCGGACTGTGGCTGACCTTAAGGATGAAGCGGGTGTTCTTCGTCAGTTGGTAGAAATA
GCTAACCATTTCAATATTGATCCGTCCCTTATTCGAATTGGTGAGATTACAGAAAAACAG
TTCTGGCAGTTGGATATTGTGTATCGAACAGCCGTTAAGGGAGAATACGTAAAGAATTTA
GAGGTTAAAGATGAGACTAGACTTATATTGCAGCCTTTTGGTCGTTGGAATCTTGCGTTG
ATAGCTCACCCTGGTGATGTTGCAGGGGAGTGGACTTATCATGAAGTAATTTCCAAGCGT
CATCATTTTGCTATGACACCTTCAACGGATCGGAGCGACTCCTCAATCGAGCGAGTGACG
CCGTACGAGCTCATTGATAATCGATGGCTTCCATCAGTATTGAATCTGCATTTGGATAAG
CTTGTTGATTTCTATTCAGCGCTTGAAGAAACTGTTGATGTTGATAATCTCGCCACATGG
ATGGTGCTTCGCCTAATTAAGGCAGCTGATTCTGAGCAGAGCAGGAAAACTGCATTTCTT
ATAGCAGCTCAAGCTCTCAATGATTGGCTCGTGGAACGAGATCGAGAAGAGTCGCCAATT
TACAGGCTTAATGGTTGGCAAATTTTGTATCGCCAAACTGGATTACTGGATTCACAAAGA
ACAGAAATTCGATCTTTTAGGCATAATCTTGATCAAACAATGCACCCAGACAACTATAGC
GAGATTATGATTGGTTGCGCTTTGCTTCTTGACGATAGAGAAGAGGCGAATTTTTTGCTT
ACTCAGCTTTCGGTTGATCGACGCGCAGTTTTTAATGAATGGCCGATAGCTCAATTGATG
ACGGGTGCCCTAAAAGAAGAGATTGAAAAA

>RXA00742-downstream
TGAGTTCTGAGATCTTGATTTAA

>RXA00743-upstream
ATTTTGGCGTAGTGTTTCGGGTTTTATAGGTTGAGATTGAAATACCAAGACAAGGATGGA
CATCATGTCAGCGCATCTACCTTCTCATCATGATGAGTTA

>RXA00743
GTGCAGCACTTAGTTCTTGCGGATGTAAAGTATCGGGAGCTCAGTGCGTTATCGGTCAAA
ATTGAGGAACCATCAGATCGTCCTGAGTTTAAACTTGGAGTTACTGTTAACGACAAGAGT
AAAGACGAAGAAGGTGTGCCGCGAATCATTGAGGTTTCATTGAGGGTGTCCATCGAGGTT
CCCGACGGAAAGATAACGGTAGAGCCTGAAGCAATCTATTTGATTCCTGAGAATAAGGTT
TATTTAACGGAATCTGATGCAATGGTGGATTATTTTAACAACCATGCGATTTTTACTCTG
GTGCCATATGCACGACAGGCCGTGTCTGATTTAGGGCAGCGTGCATTCCACACGCAGATC
CTCATGCCTGCGTTAGGTCCTGGTGATTTGGTTTTTAGTAAATCGACGGCCTCACGAGAA
TGG

>RXA00743-downstream
TAGAGAATTACCTGATAGTTGCA

>RXA00745-upstream
TTTGACGTGGGATGGCCACACCGGTGACGGGGTCAATGTGCAGAATCTGTGCAGTGGTGA
GTTCAGCATTGTTTTCCGCATCAGATAACGCGGTGGGCGA

>RXA00745
GTGGCTTATCTGTACGGATCTGCCGATGGGATGCTTAATACAGATGGTTTTAATATGTTT
CCGCGTGCGTCGTACACCATTCTTGGCCCTATGGATGCTGACGCGGTCGGTGTGTACCAA
CAGCTACTGAACAGCACGATTCCCATGGATTTGGCACGTCTTGTAACCACGCATAATTCC
GGTGCAAGTTATCTTCGCCGCGGTGCTACCAACGTAGTTTTTGAAACGAATCTTGCCCTC
GGTGTGAATCCGTATATGAAGAAACGCCGAGCAACAGAAGCACAACGTGGTAAGAAGCGT
TTTAAACGAGACAGTCATTACGGCGGTGGCACTGTGACCACAGGTACTGCTGATTTGGAT
GTGGTGGCGATGCAGGCGCGGGCAGAGCACCGGGAAGAAAGGTTGGGAGAAAAATCTACC
CGCAAGAAAGAGGAGCTTGCTGCAGTAGAGGCGAAAGAGTTAGCTGCGAAGAAGGGTCCG
CAGACTGTGGAAGAAGGTCTTGCTGCGGTGGAGAAGAAACACCTGGCGAAGCGG

>RXA00745-downstream
TAGGCGACGTGGTTGGCGGTGGG

>RXA00746-upstream
AAACTACGTTGGTAGCACCGCGGCGAAGATAACTTGCACCGGAATTATGCGTGGTTACAA
GACGTGCCAAATCCATGGGAATCGTGCTGTTCAGTAGCTG

>RXA00746
TTGGTACACACCGACCGCGTCAGCATCCATAGGGCCAAGAATGGTGTACGACGCACGCGG
AAACATATTAAAACCATCTGTATTAAGCATCCCATCGGCAGATCCGTACAGATAAGCCAC
TCGCCCACCGCGTTATCTGATGCGGAAAACAATGCTGAACTCACCACTGCACAGATTCTG
CACATTGACCCCGTCACCGGTGTGGCCATCCCACGTCAAAACATTCTGCTGGGTGAGGAT
TTTCAGACTATGGCCAGCTCTTTTAGTCAAATCCGCCATGGATGGGGTATCACCCAGCTC
ATCGGACAAGACCCCAACAGAAACCAACCAATCCGCTCTGCTGATACGTGGACAGTGACT
GGATCGACTGGACTCACCGGCTTTAATACTGCTACGCATAATACAGATGACACAGACGCC
ACTGCCGCATATACCATGCCGGCAAGCGATCCTGCCGTAGGACTATGCGCACTGGAATCC
AACAAAGACGCACCGGTGGATGAATTTCGCGATCTCAGCCTCAGTGCTTTACGTACCGCT
ACGGTCATGTCAAGCTCTGGCTCCGCCGTGATTACTATGCATGATCCTATGGTCATGAGC
ACCACTGGCGCATTGGAAGCACGTGCATACGTTGACGGCGAAGTCATCAACCAGCACGAT
CTTGACTCACTGCGTGACCAGCTAGGTATTACTACAGACAGCGCAGATACCACCCCTGCC
CTACCTGCTGATCCCTTGGCAGCATTGGGCTTGAGCACACCAACTACATCAGCTCTTGTC
CCAGGTCTTGCCGAGCTGGACTGCCTCAACACTGATCAAGCTCGCACCTGGCATGACCGT
GACAACAGCATTGGCACTGGTAAACCAGCTATTCTTGCCGTGATTAACGCCGAGCTCGCT
GATGATTACACCCTGCAGATCCTCAAAAATAGCACTGCGACCCCCACCGACTCCACCGAC
TCCAGCGATACTGCTGAACGCTTCGTAGCGCAGCTACCTGCGGAAACAGCCTTTGTGCTT
ATTGATCCGGACATCGGCGCTGTGACCGATCTGTTCTTTATCAACAGCATAAATCAGGAT
CTCCCCGCACCGACAACCCAGATCAACTCAGTAGCGGTAGATCAACGTGACCCCAACATC
ATCTACGCGACCTTTGCCAATGATGACCGCGTGTACCAGCTCATGCTGGGT

>RXA00746-downstream
TAACCGCGACCCGTTTTTATCTG

>RXA00747-upstream
TGTGCTGATCCGCGCCGTGCCAACTCGCACTGGGTCGCACTGGGTCGCACAACCGCATAC
ACATACACACAATTAATCACCCTCAACACGAAGATTTATC

>RXA00747
ATGACATTTTTGCACCGTTCCGCCAGTTTCCACCCTCGTACCCACGATCACCTCAGCGAG
CTCGGTCTTGATCCTTATAAGCTCTCTCAAGACATCCCCACTGTTATTTATGAAGTCCAG
CCGCACAGTGTGTTCATTTTAAAATTCAACACTGCCGATGTTCGGGTCTATCAGGAACAC
TCCGATCTCTTTGTGCGACATGCTGTGCTTGTTGATCCAGAACAGCGTAAACATGAGCAT
GACCAGCTCCTTAAAGAGATTCTCGACCTCGATGCCCCTCGTGTCAACGATGATATTAGT
GGTCGCACGACAGTGTTTCTCCACGATAAAACAGTTGTTACGCACAGTGGTGGCCCCATT
GCGATTATTCCGCACAATCCCGATGTCGCCAGCGCCGCTGCGTCAGCTAATAAACACAAA
CAATCTGTGATGACAACATCCAGGCATCCTTATGCGCAGATGTCTCTCAGCGACATGCTG
AAACAAGGCTTCACGCTCACACCTCTAGAGTTCCCCTACTGCGCTGTTGATGACCCCGAC
AGCTCACGCCACACAATGCACGTCATCAACGTTCGAGATCATACAGTG

>RXA00747-downstream
TGAACTACCGCGCCGCTAGAGAT

>RXA00748-upstream
AAGCCTTATTCTCCTCTTAACTACCATGAGGTAACCATCTAAAGTAGATGGTTGCAACAA
CTTTTCATTACATCAACATGTTTAAAAAAGGACACTGATT

>RXA00748
ATGACTTACTTCGCACTCGTTGCTCGCAATTACGCTGAGACAGGTGTCTCTGTTGAATTC
CATGAGGTCGATGATGACGCAGATAACTCAAATGGCCCCAACAACACAAGCAATTTACCT
CTAAAACTTCTTCGAGATCACTCTTTTGATGCCACTGTTGTCTATGGTGACCTGGTGCTT
CACACCTCAGCACATCTCAGAGATACGGCTATCGCCAACTCAGACAACCGTCCGCGAGTA
GTGACCACAGCTCAAAAATTCTTTGATTACATCCGCTTAGCCACCAGACACGGTGCTATC

CACGACATGATCAATAACGCGCCAGATACCGGCACTGACATCGTTGTTATTACGGCCACT
AATGATGCTCTTATTAGTGATGAATCAGAATACTATGACGAGCTTTTTCATATTCTCGAA
TCCGCACAGGGTGTGATTCTTAAA

>RXA00748-downstream
TGATTGATTAATTGATATGATTA

>RXA00749-upstream
CGTTTCGATCATTTGTAACATTCTTATTACAAGACTGGAAATAAAGGTGAGTCAATCATA
CAGTCAGATGTGGTCATCGGCAAAACAGAAAGGAATCCCG

>RXA00749
ATGTTACGAAAAACAGTTACCGGTGGAATTGTTGCTCTTATTGCGACTGCCACTCTCATG
AATTCTGTCTCTTCTGCTGAAGAGGTATCCGGAGATGTCTCAGCAGTAGATCTCGCATTT
GCAGAATTCGAACGTACAACTGCAGAGGACGTGGCCAATGGAGTGCCAGAGGCTATAGCT
AATGCAGAAAAAATTTCCAATTTCACTCCGAGCGAACTAGAGGGCTTCAAGAGTCTTTTA
GCTAGTGATGCAGTGCTGAGGTCGGTCTCTGGAGAAGAAATTCTCCCAGATAATGTTGAA
GTGGTTCAGACGGACAACGTAGGCGACGAAGATCCAAATGTCATTTCTCCAGCAGCCTGG
CAGGGTTCTGATTATATTGAGGGGTGTTTAACGAATACTCTCTACGGAATTGAAGTCCTA
AAGGTTTGTACTGGTGGAACCTACTACTCCAATGTAGGAATCGCTACTTCTGTCAGCAAT
CCTCGCAGTTACGTAAAGTATAACAGTGCTCCAGGATTGGCAGTGACGACAAGCAATCCA
CGTGGAGGTATAGAGGGTGGTCTTGCGGCCTTCTATGGTGATGTTAACCTTGTTGCTTTT
CCAAATATTCCATGGGTGGGACCAATTAGTTCTTCTGCAGGAACTCACCGCGTTGTCGCT
AGATCATTTCCGAATTCAGTGGTGCTTAACGTCTACTAC

>RXA00749-downstream
TAATCGTTTTTTAGTTTGAAACA

>RXA00750-upstream
TTTAAACAAAAGCGATAACAATGAACCGATGGTGTCTACGACAGAACCGACTCCCCCACC
CACTAACACCCCACCAGAAAATAACACCTCGACCGAACCT

>RXA00750
ATGGACTGGTCGATCATTATTAATGTGCTTGCCGTTGCTACTGTCGTGATACTCACCCTT
ATCATCGCAGCTGCATTATATAGGGGTTTCACACGCAACAAAATAAAAAAACTTGAAGCT
ATACGAGAAGCCCAGCAACACGAACGCGACAATCCCACTATCCGCATTGCTGATCTTCGC
GGCATCATGGATACTCACCACTACATCTACACCGACGTCATGGTTACACGTGCACATGAA
CTCATGATTACTGCACCCGCATTCTTTGATGTCACTCTCCCCGAAGCAGTGCTCTACGAA
GATACTAAACGTGCTGCTCATGATGCCCTTAACGGCTATAAAGACACCACTGTCGCTAGT
GCAGAGAAGATCATGCTTGTAGATGCAGTCACCGCAGCATGGACTCTCTATTCCACAAAA
GCAAACACCGGATCCACG

>RXA00750-downstream
TGATCCGAGAGCCGAGTACCGCT

>RXA00751-upstream
CGCAGCAACCCCGTCCATGAGGGCAGGGAACGCCACACATCCTGTACCTATACTGTGAGG
TGGCATAGAGTATCTCTAATTTAGAAAGTGGTGTAGAAGT

>RXA00751
ATGTTGGTACGTTCACGCACGTTGGTTACCGCTGCACTGTCATGTTCACTGTTGTTCGGA
GCAACGGTAAATGGCACGGGTGTTGCGATTGCATATGAAAATGTGTCTATGGCTGCTCAG
TATGAACCACGGTATGAATCCTTAGAAACGCGTCTCGGTTCTAGTGGAGTCTTTCCCAAG
TCGGTTGAACAGTCTGTTGAAAACCTTGCTGAATTACCAGAGGAGACTCGATTTTTACTT
GAGGGTGATTCGTTTTCAATTATTATTGATGATGGTCTGCTCGCTTCTCGATTGGACCCA
AATACAGGGGAGATTCGACATACTCTTGGGGCTTCGGGGATCAGCTACACCCCTGGTGAA
ATGAAACGATCTTATACAGATCGAGTGACTGTCAAGGTGGTCTACCCTGATGGGTCATTT
GATAGAGTGACACCCCATTCAGTGGTTTATGTGGCTGACAGTATTTACTACGGCATTGAA

AGCACGGGTTATCCTAAAGTCCGCAATGGTCAGACTGTCAAGATCCCATTGAGGGTGACG
GATGGTGGTACAGGAGCGGTTGGTGGGGTCCCACAGGGATCGAAGGTGGTCCGAGATCGT
TACGGCTCAATTGAGAATGCGGAGTTGATGGGTGCAATCATTCTCATAGATGAGAAGACT
GGCGATCTCACCTTCACGGCGCCTGATGATCGAACCGGTCAACTGTGGTTTCGTACAGAA
GTGACTTTCCCGGATGGTTCGGACTCAGAGGTTCAATATGTGATCGAGGTGACGGATCAG
CCTGAACCTGTGGATGTCATTCGTCCTGCCGGATCGTCTCTGAGTTCT

>RXA00751-downstream
TGATTTATGCCTGAGACTTAAGC

>RXA00752-upstream
AAGGTCAGCCGTATTTCGGTCAGTCAGCAACTAACTACGCTTATCTTCCGTGTACGATAG
ACCGTAGTTAACATAAGGAATGGAATAGGAGAATTGCGGC

>RXA00752
ATGTATTCCGACAAGCTGATTCTCTTGTTCCTTTCTGAGCAGGATTCAAGCTATGAATGC
TGCGTAGGTTTATTAGATGGCTCAGATGGACTTGATTATATTGAAAAGCTTCTGAAGGGT
AGGAAGCTGAAGAACCATTTTCTTGAATGGGAAGATATTAACAAGGCTGATGTTGCTCGT
GAAGAAATATATAAAGGGCAATTGGTGCATCTGGTGTTTGTGACGGCTCTTTCCACGCCT
GGTGAAATTTCTTTTGTTTTTCCAGGTCAATCTCTTATGAGTGCAACACTCGAAGAAGAC
TTTGCTGCGCTTGTGCTCGAAGAGGAGCGCACATCATTTAGACCTGAACTGTCTCACCTG
TGGTCACTCCCCGTAGGGTGGGTAGCTCCGGGGCTTGAGGGTTTCGTGGAGCGTAATTCC
GAGGCAGCT

>RXA00752-downstream
TGAACCACCGCTTTCTGAGCCGG

>RXA00757-upstream
CAGGTTTAGCGAATTCAATTTCTACCACTGCTCGAGGGGAATGTGCTAATTCAAGGGTTG
TGACCTCGAGCAACTTTTTATTCCGCTCGATCAAAACAAC

>RXA00757
GTGAGTTTCGGCGTCGTTAAGCGCCCCGATGCGTGCTACGCGCTTTTTGCCATCCTGATC
AAGCGCAACCAGGCGACCGCGGTTTCTGCGCCAATGGCGCGGCAGCGTCAGTGGGTTGTC
CACGCCCGGCGTGGACACTTCGAGCGTGTAACCCGCTCCGAAGTTGAGCTCTCCGCGCTG
CTCGGCGGCGTCGAAAAGCTCTCCGATTTCTTGGCTGAATACTTCCAGCTGGTCGAGATC
GGGGCGGGAATCCGAATCTACCTTGATGGCGACGGCGGATTTTGGACCTGCTTTGGTCAC
TTTCAGGCCCTCGAGGTCGAATTTGTGGGATGCGGCGAGCGGCTCGATGAGCGCAGACAG
AATTTCAGTGGTTGGAAAAGCCATAAAGACAAGGATAACCTGCCGGCAAAAATCATCGGG
CTATTACACTGTGAAGCCATGCGTAGGCGTATCCCCTCTGTCCTTGGTGTTTCTCTTCTG
GCTGCCTTTTTGGTGGCGTGCACCCCCTCCCCCAATCCGAATGCGGCGTTGGCCCAGATG
TATCAGGATGCGCTTTTTGATTCCCAGGCGATGTCAGAGGCCGAGCCTGAGCTTGCCACT
TTGCGCAGTCAGCACGCAGATGAATTATTGGCCGAGATTCGGCGTATTTGTGGCTTTGAT
GAAGGCCAGGTTCCGGAATCGTGCCAGGTAACGGTTCCTGCGATCGCTATTCTGCCCACC
GATGATCCAGAGAAGTATGTCAACGACAGTCAGGCGTTGATCCTTGATAATTTGGATGAC
ATTCCGGAAGATTCCGTGGCTTTAGTGGTTGAGCAATACATCGCGCAGGCGGAATTTGCT
GAAGGATCTGAGGTGTCCGTTCCTGTTGATTTGGAGCTCACCGAGGCAGAATTAGCTGCT
GCGAAGGACTTGGCGGACCGCGAGTTTTCCGCCGCGTGGTCTTTGGGCGTGGCTTTGGCT
CAGCTTCCGGAAACCGACCGCGAGGAGGTGGAAACGGCGATCAGCAACCACCATGACCGC
GCGTCGCAGCTGCAAATTATTACCTCCGGCACTACCCCAGCGCCAGGTTACGTGAGCGAG
CTGCCCGACCCCACCGACGAGACTTCAGCGCGAAGCAACATTGAAACCGTCGAAAACAAC
GTCACCCAGGCCTGGCATGCAGCTGCAAGCGCCGCAACCACCGACGCCTGGCGTGTCTTC
TGCGCGCACATCGCCGGCGATACCGCACGCGAATTAACGCTTATCGACGTCTCC

>RXA00757-downstream
TAGCAGTTTCACTGCCAATTTTT

>RXA00763-upstream
AGCGCGATTTGAGTGCTTTTAATACGATCGGAAGTATTCATGTCCCCAGGTTAGCCCCAA

GTTTGAATCTCTTGCAGGAACGTGGGGTAAAGATATAGAT

>RXA00763
GTGGAAAAATCCAGAAAACGACTTGTGACCATCGCAGCATCGACAATTGGGGCCGTTGCG
GTGGCTGGCGGCGCTTTTTGGATCGTTGATGCTTCCATCGCTGCGCACGCGGAACGCAAC
TTGTCTAAAGCAGTTGCGGAATCCGCAGATCTTGAAAACGACCCGCGAGTATTCCTCGGC
AGCTCCATTTACTCCACGGCGTTTTTTACCGGCAAACTCGACTCCGTAAGCATCGACATG
CTGGACGTGGAAATCCCCGGCGTCGGCATGGTGAATGCACGCACAGAGGTAGAAAGCGTG
GAAGTCTCACGGGATCAAATCCTCTCCGGTGACCTCGACGGCACCACTGCGGAAACCTTC
ACGCGCACATTACGCATGGACGGCGTCGCAATCGGCGCGCAGCTCGGAATCACCGACCTC
GACATCTCCCACCCCATCGACATCTCCCCCTCCGGCGGCATCACCTCAGAAGCGCTCCTG
ACAGGAACCCCACCAGACATGGAAGACCCGGTCAGTGTGCTGGTCACCCTTCGCCTAGTC
GGCTCAGAATTCCAGATGCTGCCGTACGAGCTTATCGACGCACCCTCCGGACTCACCCTC
GACGATGTCGCCCCCGACTTCACGTGGAAAATCGACACCCTGCAACTACCCCTCGCAGAT
CGGGCAATGGCGGTTTACCTATCTGGTGGCTCCGTCCATTTCCAATCTGAAGCCCGCAAC
GTCCAGCTCACCACCCGCGAACTATCACCACTAGCTGCACCGGAAGAAAACTCCGATGAA
TCC

>RXA00763-downstream
TAGATGCCAAACGTGCGCACCCG

>RXA00765-upstream
ACGGAAAAGTTTCTGCGTCTGCGTGGTCGACTCAGGATTCGCAATCAGAAGAACATGCAC
GTTATCTAAGAGTAGTGCCAAAACGCTAGTCTTGAGTGTC

>RXA00765
ATGAGCGAAAATTCCACCCCTAATAATCCAGTCGTCCCAGGTGCAGGCGCAGACGGCCCA
TCACTGTCCGATTCTGCAAGCATCAGCGGATCCGACGCAGTAAACCTCGCTGCCGAACAA
TCCAAGAGCACCGCTCACCGCAACATCCCAGGCCTAGGTGACCTTCCTATCCCTGACGAC
ACCGCTAACCTCCGCGAAGGCCCCAACCTCCACGACGGACTCCTCGCGCTCCTCCCTCTC
GTCGGCGTCTGGCGCGGCGAAGGCCAAGCCGACACCGCAGAAGACGGACAATACGCATTC
GGCCAGCAAATCACCTTCGCCCACGACGGTGAAAACTACCTCTCCTTCGAATCCCGCATG
TGGAAACTCGACGAAGAAGGAAACCCCACCGGCGTCGACCAGCGCGAATCCGGCTTCTGG
CGCATCAATCTCAAAGATGAAATCGAATTCGTCTGCACCCACGCCGGCGGAGTTGTAGAA
ATCTACTACGGCCAGCCACTCAATGAGCGCGCCTGGCAGCTTGAATCCGCATCTACCATG
GTCACCGCCACCGGCCCATCCACCCTTGGACCAGGAAAGCGTCTCTACGGACTGCTTCCA
ACCAACGAACTCGGCTGGGTTGATGAGCGTCTCGTTGGCGACGCCCTCAAGCCACGCATG
TCCGCACAGCTCACCCGCGTGATCGGC

>RXA00765-downstream
TAGTTTTTTCTAGTTCACCGTCA

>RXA00767-upstream
TCAAGCGCCATAACGCCTGATTATGCACGGTTAAGGCGCATCTCGCTCACTGGTGCTAAC
CACTTGCGCTTTTGGAAGGAATAACCCTTCCTGTCAGATT

>RXA00767
GTGGGTACTATCGAAGACGTGGCTAACGAACAAATCGAGGTCGCGAACAACACTGATCAG
ATTCCTGCAGGATACAAGTCCCCTCTTCTTTCTAGAAGTGGTGCGGCAGAAGCGCAGGGC
GCTGCTGCTCAAGCAGGTACTGAAGGTGTCGCGTGGCATTACGGTTCCCCTCTCGTCGAG
CAACGCATCTTCGAAACTGGCACGGGCTTAGTTGACCGTTCTAATCGCAAGGTGATCAAA
GTCGAAGGGCCTGATGCCCCCACGTTCCTCAATAATATTTTGTCCCAAAAGGTTGATTCC
GTTGAAAACGGCTTTACTGCCGGTGCCCTGGATTTGGATGCGCAGGGTCGTATTCAACAC
ACAATGCAGGTAACTGTCGTCGATGGGGTTTTCTACCTCGACACGTCCGCGGCGGAGTTT
GATACCCTCATCGGTTTCTTGACCAAGATGATTTTCTGGTCGGAAGTCACCGTCCAGGAA
GCCGATCTGGCGATCATCACTCTGCTCGGCCAGGAAATTGCCCTTCCGGACGCGGTCTTT
GCCCGTAGGGTCGATTGGAATGGGCCATCGCGTATCGACGTCGCCATCCGGCGTGAAAAC
CTGGAGGAGGGCGTCGACAAGCTCTTAGAAGCTGGCGCAAAGCTCACCGGTCTCATGGCT
TACACGGCCCGAGCGCGTGAAGGCGTTGGAGCCCGCTGCGGGCGTGGATTTGGA

>RXA00767-downstream
TGATAAGACCATTCCCCATGAAA

>RXA00768-upstream
GACGTCGCCATCCGGCGTGAAAACCTGGAGGAGGGCGTCGACAAGCTCTTAGAAGCTGGC
GCAAAGCTCACCGGTCTCATGGCTTACACGGCCCGAGCGC

>RXA00768
GTGAAGGCGTTGGAGCCCGCTGCGGGCGTGGATTTGGATGATAAGACCATTCCCCATGAA
ATCCCCCATTGGATTGGCCGTGGCGAACATTTAGGCGCTGTGCATTTGACCAAGGGTTGC
TACCGCGGGCAGGAAACTGTCGCGCGCGTTGATAATCTTGGGCGTTCCCCGCGCGTGCTG
GTTCTGCTTCATCTTGACGGTTCCGCACCGCTGGATCCTGTGACTGGCGCTGAAATCAAG
GCCGGTGCGCGCACCGTTGGTCGTCTGGGCACCGTTGTCCATGACGCCGATTACGGGCCG
ATCGCTCTCGGGCTGGTTAAGCGCAGCGCTTTGGATAAAGAACTTCACATCGATGATGTC
TCTGTAAACGTCGACCGCGATCTGCTTCCTGCGGAGGAAAGTGAACAACGCGGACGCGCA
GCGATCAATAAGCTCAAGGGTCTT

>RXA00768-downstream
TAACTAAAACGATTTATAGCGAA

>RXA00769-upstream
GGCTATTGTGTCTATCAGGAATACAGTTAATACATCTTGAAAAGCCCATGGGCCATCCGA
ATTCCCAGGATCGGCCCGCTCACTCCAAGGGGGTCAGGCA

>RXA00769
ATGGGTCGCGGTCGCGCGAAGGCAAAACAGACCAAAGTTGCTCGCCAGTTGAAGTACAGC
TCTCCAGACATGGATCTCGATTCGCTGCAGCGGGAGCTGGCTAACCAGTCTCCTAGGCGT
TCCTACTCCGATACCCCTGATGATGAGGACCAGTACGCAGAGTATGCGGACTGGGATGAG
GACGACACCGACAATCGTGCCTACGGCACAAAC

>RXA00769-downstream
TGATTTCGTGTGTCCTTAACTCT

>RXA00771-upstream
TACCCCTGTTTTGGAGAATGCTCCGAGCCAGGGGTACTTTTCTTTTCCTCACACACAGTA
GCTGCTGAGAAAAATGAAGACCTTTTGTTAGGTTGGGAGT

>RXA00771
ATGACCAACCCATACGAGGCCTTCATACCGCTCAAGCATCGTACGGGGATTGAACCCGAG
CACACCTTTTGGGAATGGGAAAACAAAAGGGTTCACATTGCAAGGAGACGTCGAGAAGCG
CCCGTCCGCGTTATCGTGGTGCATGGGCTAGGCACCCATAGTGGCGCCCTCTGGCCCCTC
GTCGCGGCCATTGAGGGCGCGGACCTCGCCGCGATCGACCTGCCTAAAACTCCGCTTTAC
GACGATTGGCTGCGCCTTTTAGAATCTTTCATCTCGTCCGAAGACGACGGTCGGCCACTC
ATCCTGATCGGTGCAGGCACCGGAGGCTTGCTTTGCGCAGAAGCTGCACACCGCACAGGA
CTGGTCGCACACGTCATTGCCACCTGCCTGCTCAACCCCTCCGACCAGCCGACGCGCCGG
GCACTGTTCAGGTTTTCACCGCTGACTCGGTTGATCCAAGGCCGCTTGCGCAACCGCGAA
ATTCCCGTGACCAGAGTGTTGAACTTCAGCAAAATCAGCCGCAGCCCAGCCCTGAGCAAA
TTGTGCGCGGCCGATGAATTTAACGGAGCATTCAAAATAACCTGGGGTTTCCTCGCGTCA
TATGTGCAACACAAGGCCAAACTGGGTGCAGTTCCCCTCACTCTGATGCACCCTGACCAC
GACCTTTTTGACTCCCGT

>RXA00771-downstream
TGAGCTCAAATCTGCGTACGCTT

>RXA00781-upstream
TTTCTTAGGAAATAAAACAGGGTGTCTTTGTGTTCAAAAGGTATAAAGGAAGAGTAGTTC

CGGTTAATTCCACCGGGATGAGATACCGAGGAGAACGCAC

>RXA00781
ATGAGCGAGAACAAAAACATTGAGATTGTCCACAATGAAGGACAGAAGCGCTTTGTTATC
AGCGTTGATGGAACGCCAGCTGGATTTGCCAGCTATTTAGACGGCCCGGATATCCGCAAC
TTCAACCACACTGTTATTAAGCCTGAATTCCGTGGACAGGGACTGTCTGCGCCATTGATC
AAGTTTGCTTTGGATGATGCACGTGAGTCCGGTATCCGTATTCATGATGCTTGCTCTGCA
GTCGCTGGCTTCATTCAGAAGAACCCTGAGTATAAGGATCTAAAGAAC

>RXA00781-downstream
TAGCTGGCACAGGGGGGTGGTTC

>RXA00785
ATCATCGCTACTCTCGGTGTGACCTTGCTGGTTGAGGCCCGCGGATTATTCTTGACGGTT
GCGTCCATTCCCATTCTGTTTGGTATTTTCACACCACTGACTTCGTGGTTTGTGTCCCAA
CAAGGCGTGGCTGCGAATGTGTCCCCTGGTGTTTCCGTCACGGAAATCCTCACGGCTGTT
TATCCTTTGGCGCAGTTGTTCCCCACCCTGATCATGGTCACTTTGGTGGCGGCATTGATC
GCTGTGGTGCGGATTATTCTGCTGCGCAGGAACCAGGAATCTCGTCAGGTTTCTGGGGAA
CTTACCCGGCGCGCGCAGCGTGAGGCTGAGGAAGCTAATCAGAATGCTGCTCGTCGTGCT
CGCGCACAGAGCACGAGGGTACAAAGTTCTAAAACACGTAACCGTCGCGCGCAACCAACC
GGCGATACCGGTTCACAAGTCACGGTTGATGAGTTGATCAGGCGTAGCCAGGAGCGCCGG
CAAACTGTTGCGCAGCGCCAAACTGAGCGCGGTGTGCCGTTTACTCCAACTCCGGGTCCT
GTGGTGGCCCCCAAGCCGCGCCCGAGCGCCCCTGAGGCGCCGGCTCCTACGGATGTGGGT
GAGCGTCGACAAGCAGCCCCT

>RXA00788-upstream
CGCATCCCTCTAGTTTTCCATCACCTCAATGAACGGCGCTAACTCCGGTTCATTGCGCAA
TTGATCCAGCACTGCTTGCAGTGAGGCCTCATTAGTTGGC

>RXA00788
ATGGCCTCCTCCATCAACATCGGAGTGTTCAACCTTGGAAATGCTGTTGCTGCCTGGCTT
GCTGGTGCAACCATCACCACTTCCCTTGGACTCACATCAGCCGGATTAGTTGGCGGTTTG
ATGACGTCCCTCGGACTAGTGTTGGCCATCGTGGCTGTGGTTTTGCGTCGAAAAGCGCAA
GGCACCCAAGCGACCATCAGCGTTGTGGAGCACCAGCCCGCCCAA

>RXA00788-downstream
TAAATAATTTCTCTCTTCTAATT

>RXA00795-upstream
TTTGGATTCTGGACACCCAAAAGGGGGTTTCGTACCAAACTCGTGACATACTAGGCGGGT
GGCTGAGAAACGACCGAAAATTTTTGATGGCAGTCGAGAC

>RXA00795
ATGATTATCTCGTTGGTAGTCTCCGCGATCATCATGTTGGTAGCGGTGGGATTCACGGGA
ATGTGTTCTTTCAATACAGGATCCCCTGAAAATGGGCAGGTACCTGAAGTTGATGCTTCC
ACTTTTATGTCAATGGAAGCGCGCGCAATGACTGATCATGCAACTAGGTTGCCGGAAACT
CCTGAAGGCTGGACCACAAATTCAGCTCGACGCACCATGGTGGATGACACCCCGGCATCT
GTAGTTGGATATGTCACCGCAGATGAGGGCTATATTCAGCTCACTCAAACTGGTGAAACC
GTTGAGGATGCTGTGGCTGGTTATGATACTCGCTGGCGTGATCTTTCTGAGTCTTATGAT
CTTGATGGCCACGACGTGGGAATTTACACCTCACAGGAATCTGATGTGCGTGATCTGCGT
GTGATGGATCTGGGCGATGCCCGCGTCATGGTCTCGGGTGCTGCTACCGATGAAGAATTC
AATGATCTGCTTCGCGCAGTTGCGAATTCGGAGCCACTGCCTACCAAT

>RXA00795-downstream
TAAGAATTGGTCGAACCACCAAA

>RXA00804-upstream

AATCTAGTGCAAGTTCCAGCGAAAACCTTCCAAAACTGACCAAGTTTAAGAAGATTCGCT
ACCCTATGAATCAGTTGTAGGAGTAAGAGGGGAGTTAGAG

>RXA00804
ATGAAGATCAGAAGTGCACGTGAAATCGCGGAGTGGTTCGTTGCCTGGGGAGATGAACTC
GATGCTGAAGTCTCCCCTTTGAAATTGCAGAAGCTCCTTTATTACTCCCAGGGTGAGCAT
ATAGCTGCAACAGGGCGAAAACTTTTCTCGGATAAGATTCTGGCGTGGCAGCACGGACCT
GTCACTCCGGGCGTTTATTCAGATACAAAATCATACGGCCGAAACCCAATTGATCCTGAT
GAGTTTGTGTCAGATGAATTTAACTGGGATGACTACTCAGATGTGTCAGATGAGCTTGTA
ACCGTATGGCGAAAATACGGCATCTATTCGGCGTGGGCACTGAGGGAAAAAACTCACAGT
GAATCGCCGTGGCTCGATGCCTGGGCACAAGGGCAAAATATTGAAATTACAGATGCTGCG
CTGAAAGATTTCTTCTTGGTGCAT

>RXA00804-downstream
TAGAAATTTGAAAAAGAAACGAA

>RXA00805-upstream
TGCTCCGCTGACAGTGGTGCGCCTGAGCAGCCCAAAAGAGACAAAGCGCTGGTTGAGGGC
ATATGGGGAAAGCGTGAAACTCTGATAGGGTGCCATATCC

>RXA00805
ATGGCAGAAAGTTTTATAGAGGTCTCGGCGGGGCATGCGGATCGGCGGATAGATAAGTTT
TTGCGGGCACAGCTAAAGGGCGTGCCCGCGTCGTTGATTTTCCGTCAAATGCGTAAAGGC
GACATTCGGGTGAATGGTCGTAAAGTGGATCCGAATTACCGGTTGCAAGAAGGCGACCGA
ATTCGAATGTGGCAGATGGATTTGCTGGCAGATTTGCCGCCACCGGTCGTCGATAAGCAT
ATTTTTAAGGCTGTCGCAGACAGCGTGCTTTTTGAGGACGCCGAATTACTGGTGATCAAT
AAGCCAGCTGGAATTCCTGTGCACGGTGGCACGGGGCACGGCGGTGGCGTGATTGAGGCG
CTGCGGCAGAAGTTTCCGCAGGAACGCGACCTGGAATTGGTGCATCGTTTGGATCGGGAC
ACCTCAGGTTTGTTGCTGGTTTCTAAAACGACATCTGTGTTGCGCGAGTTGCAGGAAATT
TTGCGAGACCGCGAAGAGGAGATTTTTCGGGGGTATTTACTCAAGGTCGAGGGGGCTTGG
CCTGGCGATTTGCGACAAATTGATGTGCCGTTGAAGCGGACGGAGACAACTGTTGTGCCA
CATTCGGATGGTTTGCGGGCGCGGACGTATTTTGAGGTTGTAAAGCGTTTGCCGGGTGCG
ACCTTGGTGAAGGCGCAGTTGGCGACCGGGCGGAAACATCAGATTCGGGTCCATGCGCAG
TATGCGGGTCACCCTATTGTTGGCGATCCACGATACGGGTCGCGTGGGGGCAGAGCTGCG
ACGATGCATTTGCATGCGGCGGAATTGGTGGCGCCTCGTGGGGCGGGGAAGCGTCAGAAA
TTCACTGCACCGTTGCCGAAGGAGTGGGGTATGGGACGGGTC

>RXA00805-downstream
TGAGTCGGGCCTTCGTGGAATCG

>RXA00808
GCTGGCTTCAATGAGATGATGCGTGGCCTGCGTGAACGTCAGCGCGTCCGTGACCTTTTC
GGTCGCTACGTGGGCGCTGAAGTGGCCAAGCGTGCGCTGGAGGAACGCCCCACTCTGGGT
GGCGAGGACCGTAAGGTTGCCGTGTTGTTTGTCGATGTCATCGGCTCCACTACCTTTGCC
GTCAACCACACTCCTGAAGAGGTTGTGGAGGCGCTCAATGAGTTCTTCGAGCACGTCGTG
GAGGTTGTGCACCGCAACAAGGGTGTTATCAACAAGTTCCAGGGTGACGCGGCGTTGGCG
ATTTTCGGCGCTCCCCTGCCCCTGTCTGATGCCACCGGTCATGCGCTTGCGGCTGCCCGT
GAGCTCCGCGCAGAGCTGAAAGATCTCCAGCTCAAGGCCGGAATTGGTGTGGCTGCTGGC
CATGTCGTTGCTGGTCATATCGGCGGTCACGCGAGGTTTGAGTACACTGTGATCGGCGAC
GCGGTGAACCAGGCTGCGCGCCTGACGGAGATCGCGAAAACGACCCCAGGCCGCACCGTC
ACCAACGCTTCCACGCTGCGTGAGGCCAACGAGGCGGAGCAGGCTCGCTGGACGCTCATG
AAGTCCGTGGAGCTGCGCGGACGTAGCCAGATGACGCAGATTGCGCGGCCTATTCGGCCG
ACGTTGGCGGATAGGTCC

>RXA00808-downstream
TAATACGCTTTTCGACGCAAAAA

>RXA00812-upstream
TTCACAGGTGAGCGTATCGCGGGCGGTTGAGAGGTGAGTTATCCACAGGCCGCAGAGGGG
GTCGTTGAAAGCACGTAAGCCTCAGGCCACAGTAGGTGCC

>RXA00812
ATGAACACCATCACACACCAAGCAATTCTCATCGCAGTGGAAGATCCGGTCCTGCACCCA
GAGGCCATGCACGTAGCTGCAGCCACTGGTCGGCCGGTTATTGAAACAACAAATTTGATG
GACATCTCCAGGCATTTTCACCGCACATCGGCAGTGCTCATTGATGCGTCGATGGCCTCT
CAATTATCACCTGGGAAACGCCGCGACAGGGTGTTTCTTCTCGATTCTGATCCAGGGCCC
TCTGATTGGAAAACGGCGATGAAAATCCACGCTGAGCAAGCCATGTTGCTTCCCGCTCAG
GCAGGGGAGTTGCTCAGCGCTTTAGGCAGAGATGACAAACAACTGCCGGTGGCTTCGGGC
CATGTCATCGGTGTTGCCGGGGTGGTGGGAGGAACAGGCGCGAGCACGTTTGCTGCGGCG
CTCGCAAAGCGGCGTGCGGAGTCAGTCACCACTGTGCTTATCGACGCCGACCCTTCCTCT
GGCGGCATCGACCTGTTGCTAGGAATCGAAGATGTGCCCGGCGCGCGGTGGCCTGATGTG
GGGTTGCGTCGCGGAACTGTCCAGGCTGCTGATGTGTTGAAAGCGCTGCCGAGCACTCCT
GATGAGGTCGTGGTGTTGTCTACGGCGCGGTCTAATATTCTGGATCCTTTTGCATTATCC
GAGTCTGATGTTTCAGCGGCGATTGATTGTTTCTTAAGCGCCGATAGGTCGGTGGATGTG
GTGGTGGATCTGCCTCATGCGAGAGTGCATCCAGATATTGCGGAGCGCTTATCCCACCTG
GTGTTAGTCATCCCTGCAGAGGTCCGAGCGGTGGCTGCTGCCAGGGCTCGGTGTCTGGAA
TTACAACAATTGCATGTATCCATCACGTGCGTGTTGAGGCATCGCGGGTGGTCAGGTTTG
GATGTTGCAGAAGTGGAAGAGATTTTAGGTGCGGATATTACCGCGGAGGTTGGCTCGATC
CAGCGGCTGGCTAAGTCCGTGGAGATGCATGGGCTGACCGGTTCTTTGCCGAGGGTTTTA
AGCTCAGCATGCGACGCGGTCCTCGGGGAGGTGGCGGCA

>RXA00812-downstream
TGACTGACATTGATCTGGTGGTG

>RXA00814-upstream
GCCGCAGGCTAGCTCAACTCGGGGTGCTCCGCGGAAATCCTGTGACCACGCAGGTGGTGT
GGGATTTGGACCACGGCATGCACGAAGGGAGCGAAGAGGC

>RXA00814
ATGGTTTATGCCCTAGGCCTTCTTAGCGTGGCGGTGTTGATCTCTGGTTCAAGGGGCCCC
GGCGCGCGTACCAGGCCACCAACACCTGGGAATGGCGTCCATCTATTCGCCCTAATTGCA
CTATTTTGCCTGGCCACAGTGCTATTTATCGTCGTTGACGCCTACACGATGATCGCCGGC
ATCATCATCGCCACAACTCTATTCTGGTATCTCCGCCAGACACACGCCGCAGCCCAACGC
ACCAAACAATCCCTCCAATTAGCCAGCTTCTTAAGCCTCTGCGCAGGCAATTTACGCGCC
GGGGTCACCATGGTCGACGCCATGGACTACGCGCTCGACAACACCACGCCGGACAAATTC
TTAAGCCCCACGTTGCAGACCGCAGCCAGGCAGGCGCGCTCGGGCGGCAGCGGGCCGCGA
GTGCTTATCGACGCCTCCCTCCCCGATCTTCAACGCCTCGGCCATTTGTGGGAAACATCA
GAACGACACGGCATCCCGCTGGTCGCCCTCATTGATCAAATGAGGTCCCGGATTTCATCG
AAGCAACGCCACGGCGAATCCACCCGAGCTGCACTCCAAGGACCGCAAGCAACCGCAGTG
ATCCTTACCGTGTTGCCACTAGCAGGAATGCTCATGGGCACAGCCATGGGAGCAAACCCC
CTTGGGCTACTCACCGGTGGTGGGATCGGTGGGTTCCTGCTTGTCATCGGTGTGGGCCTC
GATGCTGCAGGGTTTGTGCTCACCCACAAAATTCTCCAGAGCGCGAGCCCCTCA

>RXA00814-downstream
TGATTACAGCACTAGTTCTTGCA

>RXA00815-upstream
CCGGTGGTGGGATCGGTGGGTTCCTGCTTGTCATCGGTGTGGGCCTCGATGCTGCAGGGT
TTGTGCTCACCCACAAAATTCTCCAGAGCGCGAGCCCCTC

>RXA00815
ATGATTACAGCACTAGTTCTTGCAGCAGTGGCCATGTTCCTCGGTTCACCCAACCCTGGA
GTTCGCGGTGGATTGATAAGCCCCAAATCCGGTAAAAGCCTGCGTATCCGAGCTGGCCCA
AAAAAGCTGGGCAACGCTGACCCAGTGGATGTCTCTGCAGATATCGAACTGTTTTCAGCG
TGTTTGGATGCGGGTTTAAACACACGTGATGCAGCGCAGGTGGTGGCTCATGTTGCAGCC
ATTACGCACCGCGAACTGTGGACACATGTGGTGGCATTGCTATCGATTGGAGTGAGTGCC
CCTCAAGCATTCGCCCTGATGGCAGGAGTTGATGGGCTGGATGAACTAGCCAATTTAGCC
ACCGTGTCGCACAGGTCGGGCAGTGCATTAAGTGATGGGTGCAGGAACATTTCCACCTCG
TTGTTGGCCTCTGCTGGTGACAAGCGCACCGCCGCAGCAGAACGCGCAGGAGTGTTCATC

GCCCTGCCACTTGCTCTGTGTTTCCTCCCCGCATTCATGATTGTCGGGCTTGCACCAGTG
GTGCTCAGCTTGGGTACGCAACTTATCAATTTC

>RXA00815-downstream
TAGAAAACACACACAGGAGAAAA

>RXA00816-upstream
ATGCTCACCGCAACAGCCACTATCCCGGCACCGATTGGGCAGGTGAGCGCGAGTGCGGTG
TTCCCGGTGGAAAACTAGCTGTGCAAATGACGAAGGCTAC

>RXA00816
ATGACCATCGCCAGCGCTGGTGTCGCCTCCATCCTCATTAGCCTGCTGGTGGTGCTGGCC
TGGCAGGCGGGAAACCTCGTGGCCAGGGAACAAGCACAGGTAGCGGCCGATGTTTCAGCT
GTTGCCGGAGCCTACGCCTTTGCCCGCGGGGAACTACCCGACGCTGCCTGCGCCACCGCG
AAACACACAGCCGAAGCAAACAACGCACAACTAGAAAACTGCGCAACAGAAGGGGAGGAT
CTCACGCTCACCGTCACCGTTCGTGGACAAGAAGCCCACGCAAAAGCAGGACCTTTA

>RXA00816-downstream
TGAGGTTCCCAACAAGGTCACCA

>RXA00826-upstream
TCGGCGCGCGCGATCTGGTGCTCATCTTGGTGTGTGCTGCCATTTCCGCGATCGCTCTAA
CCGTGTCCATTCAGACTGGTTTCTTTAAGTTCTTGGGCAC

>RXA00826
ATGATCACAGTTTTAATTGATGGACAATCCGGTGCGGGCAAAACCACCTTGGCGGGTGAG
TTAGCTGCCCGCACCGGGTTTCAGTTGGTTCATTTGGATGACTTTTATCCTGGTTGGACT
GGCCTTGAAGCGGCATCGGAGATTGTTGCACGCCATGTTTTGGACGCGGACAACCCCGGT
TTCTTCACGTGGGATTGGCACAACAATTGCCAAGGCGATTGGATCAAGTTGGAGCCTGGT
CGAAGTCTCATTATCGAAGGCTCTGGATCAATCACTGCTGCAACAAAACGCAAGGCATCG
CTGTTGGGCGAGCTGGTGACCGTTCGTATCACTGGTCCTGAGGCTTTAAGAAAACAGCGC
GCCCTCAACCGCGATCCTGATTACGCACCATTTTGGAAAGTGTGGGCGCAGCAGGAGCAA
CGCCATTTCTCTTTAGGCGTTGAGGTGGATCATGAGATTGTGCTAGGTTCTGATGAGGCT
TCGGGACGACCCGAAGAAATCTATGACAGCCTGGGAACGGCCCAGAGTTCT

>RXA00826-downstream
TAAGAAAGTTTGACTAGAGAACA

>RXA00830-upstream
TGATGGTGGCTCGATTGTATTCGAGGGCAGCCCCGCGGAACTCATCAAAACTGATACTCC
AACAGGACGCCACCTTAAAGCTTATGTAGATTAGTTTCTT

>RXA00830
ATGGAAAACCCTGGTGATCTCGGCGCTATGCCACAGTACGGTTTTGAGCATATTTCGATG
CTCATCACCGCTGTGGTTTTAGCGATTCTTGTCGTCCCCATTGCTCGTCGATTCAACTTC
GCACCGGCATTTGGCTGGGTGCTACTCATCGCAACACTTCTGTCGAACCTGTGGAATTTT
ATGCCCGGCTATTACACGCTGGACCAATCTTGGCCATTCCACTTCTCAGATGCATTGCGC
ATTATTGCTGCCATCGCATTGATTAATCGCGCGCGGTGGGCAGTTTCAGTGACTATTTTG
TGGGGCACCACGATCAACCTGATGTCACTGCTCACTCCAGATGTTCAGTATTTACAGGTT
CCCTGGCTGGAGTTTTTAATGTACTGGTTTATGCACATTTCTGTGTTCCTAGCAGCTATA
ATTCTCATTTTCGCTTTTGGAGAAAAGCCAGGGCTGTCCGGAGTGGTTATGTCCGTTGCA
GTGGCGATTAGCTGGGGCATCATGTGCCTCATGGTCAACGCATTTTTGGGAACCAACTAC
GGGTACCTCTCCACAGAACCAGAATCAGCGTCAATTCTGGATTTGTTGGGAGGATGGCCG
TTCTACATCGTCGCGGAAGTATTACTCCTGTGTGCAGTGTGGGCTTTGTGGTCTTATCTG
ATTGATAAGCTGCCTATCACGTATCGCCCTGCTTACCGTCCGAAAACTCGGAAGGCCGCT
GCG

>RXA00830-downstream

TAACCGCCCTCTACCTCGAGAAA

>RXA00831-upstream
AGCTCCAAGAAAGTCAGTGCTGTGCATGGCTCGGTGCTGCTCATGCTTTTCGGTGTTTAC
ATGATGAGCATGTTCGCCTGATTTAGGTAGCCTGGTGGGA

>RXA00831
ATGAGTGCACTTGAGACATTGCAATGGCAGGACTGGTCAAGCGTCTTAATTGTGGTAGCT
CACCCAGATGATCCGGAGTATGGGCTTTCCGCGGCTGTTAAAGAATGGACAGACGCCGGG
GTGGAGGTGTCTTACCTGCTGCTCACCCACGGGGAGGCAGGTATCCAAGGTTTAGACCCT
AAAGAAACCGGGTCATTGCGCGCAGCGGAACAGCGGGCTGCATGTGATGTGGTAGGAGTT
AGAAATCTCACCATTTTGAATCACCCAGATTCCATGTTGGTGTACAATCTGGTACTGCGC
AAAGATATTGCTCGGGAAATCCGGATCCGTAAACCAAATGCTGTGGTGGTATCCAATTTT
GATGTAGAGGCCTACGGTGGTTTGAACCAGGCGGATCACCGCGTGGCGGGATTAGCCGCA
ATTGATGCGACCCGCGATGCCGCTAATCCGTGGGCGCAGCCAGAGCTGTTGCAGGAGGAT
CTGCAGCCGTGGGGAGCTGAAGTCATCATCATTGCCGGACACCCAGAGCCCACCCACACC
ATGGATCTGGCTAAAGATTCTGTTGATGCCGGAGTTGCATCCCTTCAAGCTCACAAGGAA
TACTTGGCCGCTCTTCCAGATCCCCCGAAGCCGGAGGAGTTCATTCCGGCGTTTCTCGAG
GTAGAGGGCGGTTACGCAGCGGCCTTCCGAGTTTTCGGACGG

>RXA00831-downstream
TAAGCAGGGCGATACGTGATAGG

>RXA00835
TTTGCTCCGTGGGCTCTCACACCAATTTTGATGCTGGGCGGCTCCTACCTGTGCTTCGAA
GGTGCAGAAAAGATCTGGCACTCCCTCCACAGGCGCATCAAAGGTGAACAGCACAGCACC
GAACCCAAGTCGCAGGAAAGCCCAAAGTCAGAGGATCAGCTGGTCAAAAGTGCCATCACA
ACTGACCTCATCCTTTCCGCAGAGATCATGGTTATTTCACTCAATCAGATTGCAGATCAA
ACTATCTGGATGCAGGCTGCGGTTCTTTTCGTCGTAGGTATTGGCATCACCGCGCTCGTG
TACGGCGTAGTCGGTGTTCTTGTGAAAATGGATGACGTCGGACTTACACTTTCAAAGCGT
GACTCCGCAGGTATCCAGAAATTTGGCCGCGGCTTGGTCAAAGCGATGCCCATCGTTCTT
CAAGTTATTTCTGTTGTCGGCGTTTTTGCCATGCTGTGGGTTGGTGGCCACATCATGGTC
GTTGGAACTGAAGAGTTAGGATGGGAACTTCCCTACCACCTTGTTCACGGACTAGAGTCC
TGGGCTAACGGTATCGGAGGCAGTGCTCTGGGATGGGTTGGCAATACTTTCGGGTCACTT
GTGTTCGGCCTCATTTGGGGCGCGATTATCACCGTTGTGGTCAGTGTGATCAAGAAGTTC
ATTCCACAGCGTGCGCAAAACTCGTCTCAT

>RXA00835-downstream
TAGTGGAGAGTTGTTCGCTGTAA

>RXA00836-upstream
GGAGAGTTGTTCGCTGTAATTTCGCTGTACAGTTAATATGACTTTTTACTGTCTCAATCA
ATTCACAAGTTTGCACGAAATTTAAGGAAAGGAGTGCCCA

>RXA00836
ATGTATACCCATTCAACAGGCACTCCTCAGCTTGATTTCGACGGTGACATCTATCCCCTT
CACCTCTTCTTCTCTGCACAGACTGCCCAACATTTCGCTCTCGAGCGCGTCAATTGGCAT
GTCTTACGCGCTATTGTGAAACCTGAGCAAGGCGAACTCATCGTCGAAGCGCTTCTCGCA
CCAATAGAATCCGCAACAAAAATCGGTGTTTGGGTTCAAGATGAATTTCTCGGGGTGATT
GCAGAGTCCCAGTTCCTGTTGAATTCTCAATTGTCTCGAATTTTTGCCTCTGGCCACCTG
ATTTCCAGCCAACTACTTCTCACACCGAGTAAAGGATCTCTCGCTTCAGTTCTTCTTCCA
AACCTAAAATTCGGGCTCATCAGCAATGATCCTCCACGAGCTGATTCCCACCTCTTACCG
CTAGGCAGAATGTGGCGCGTTGAGCCCACCGTTCATGCTCTGTTTGAGGATTTCTCACTT
GGCTCCACGATTCTTTTTGGGCTGAGGCTTGATTTAGAAGCCCTAATTGTCTCCTATAAC
GGAATAGAATGTGGCATCTTAAACTTTGATGACGCCTCAGCACTAAGCTCTGCTGTGAAA
TTCTCAAATGCAAATGGTCTCACCCCCACGGTGCTCGGCCACGTAGTCCGGGAGAACGGT
GAAACATCCTTCGAGATTGACGTTCTCCCACTGGAGTTGTGGTCGAAGAAGCAGCATCGC
CTTGAGGTTTTAAAAATCCCTCGGTTGATACCTAAAGAGGCAGATTCCCAAAATTATGTG

AAGGCGACAGCGCTCCTTTCAGACGAGATTCTGCGACCACAAACGCTGTCCAAAAAGGCA
CTGTCTTTGTCGGACACCGCAGTTAAGTACAGCCCTCATGTTGCTTGTGGCGTGGGGATG
TTTAGTCTTTTCGCCGTTATTCCCTTTGACAAGTTGAGTGATCATAGTGCGATGCTGCTC
GCAGTCATTAGCTTGATGCTTTTTGTGCTGGCATTAGTAATTCTTTTCAAGAGAATTCAG
TCAACTAATACTCAGCGTTGGAACTTGGCCTCGTCAGTCGGATTACTCGCGACACTTCCG
ATTATCATATTCCTGGTTGCTGATACATTGATTCCTCAGGGCAGCCTGGAAAACCATGCT
CAACCCGACGTACAGGTAACAACGTTAGCTAACAGGCGGCCAAGTTCACCTACCTCACTG
GACTCACTAGGCGCACTGAATTCACCAAGTTCGCCGAATTCCCCGAGCTCATCAATGCTG
CAAAACTCTGAAATGTTCGCCTCACCACCGATCGCCTCTGGGCAGTCACCGGTTTCGACG
TTCCGCTCATGGCTAGATCGATCCATTCTGCCACTCACACGAGAAAATTCCGCTTCAGAA
AGCGCAGTGACAGCTCTTGGACCGTCGATAGTGCAGCCTGCATCTGAATCGATTACAACT
CCAGCTCAAACGTCGCAAAGTCGCCACGCAATTGACGATGGTGACGACAGTAAAACCTCA
ACGGGAAGACCAGCTCCCACTACTAACTCGCCGATCATTGCTCTTCCCCCAACGTGGATT
ATCGGGCCGGAAGATCCAGAATCCACCGACCCTACAGCACCAACCGAGCCCACCGAGCCA
AGCGAACCTGTCGCAACCGACGAACCCTCAGAGACCTCTGAACAAACTTCA

>RXA00840-upstream
GCGATTAATGTGACAGGAGGAAAAGAAGTTAACTGAAGTTACTAATGTGACTAAAGTTGT
TCCCTCCGCATTGTCTCGTTGAAAGGTAAGTAAAACTCAA

>RXA00840
GTGACAAAGACACTCCCCCGACTGCTTACAGTCGCTGCCGCTCTAGCCATTGCACTCCCG
GCAACCCCGGTAGCATCGGCTGTCACACCAGTTGAACAAGCTTTCAACGCCTCATCGAAT
CTCTCCAGCGGTCTCCCCGTAGACCAATGGGGACGCCCCAACGAGCAGTTCCGCCAACAA
ATCGAACAGGCAGTAAACCAACCGTGGGTCCCGCAGGAAATCAAGAACATCGTTTCTCAG
GCCATGGGTTTTATCACCGGTGACGGCAGCGAAGGTGGGGACATTGAAATCCCCGACAAC
GCACCACGCATCGCGCAGTTCTTCTGGCCCACCCGATCAGAAAACTGCATCAACGGAAAT
TCTGCAGCCGTAGGATCTGCCTTCGCAGTTCCAGGACCAGCAGATCTCCCCCTCCCCGGC
GCAGGTGTCGGCCAAACCTCCTTCGTGTTCACCGCACTGGGAACTGGCCCCCTCGCAGAA
CAGCAAAGCACCGCAATGACTGTTCAATGGGCAAACTTAAGCAACTTCACCCATGGCACC
ACGACGTTGAGCAACACCGGAATCAACCCCGATGGCCCCTCAACGATTTCCGGTGTGGCA
GACACAGGACGCGGCATCATCGTCGCCTCCATGTCAGGCGGCCTCACCACATCCACCGAA
AACGGTTCAGCGAACTGTAATTTCATCCCGACTGCCGTCGTATTCGATGTGAGG

>RXA00840-downstream
TAAGAAAACAATGACTGATCTTC

>RXA00841-upstream
GCCTCCATGTCAGGCGGCCTCACCACATCCACCGAAAACGGTTCAGCGAACTGTAATTTC
ATCCCGACTGCCGTCGTATTCGATGTGAGGTAAGAAAACA

>RXA00841
ATGACTGATCTTCATCCCGTAAAGCAGGAAATTTTCAACACTGCTGAATCCATAAACACA
GATCCCAAGGGGTTTCTCCGCGAGGTAGACACCTTCAAAGTAACCGACTTCGGCCTGTAC
ATGGCTCGTGGTGCAAACCACCCCAAGTTCGGATACTTGGAAAGCTGGCTCCTCCCAGAA
CTTGGATTGCGTGCCAACATTTTCCACTTCCGCAAAGGCGTGGATGAACGTCAGGATTAC
TACATCGATGTCGCTGAAATTCGCGTCGAAGACAACATCTGGACCACCCGCGACCTCTAC
GTGGATCTCATCTCTGTCTGCGGAGAACCAGTAACAGTCATGGACATCGACGAACTAGCT
GCAGCAACCTCAGCAGGGCTTATCACTGCAGATGACGCTGAGCGCGCAATTGATGCCACC
TTGAATGCTGTTGAAGGAATCACCCGCCACGGCGACGATCCTATGCAGTGGCTGCGCTCC
AAGGGAATCGAACTCACCTGGGCTGACGCCAGCCAGGTAGAGCTCGTCCCTGCAGAG

>RXA00841-downstream
TAACTACTTCCTAACCGCTGCTT

>RXA00846-upstream
CTGCGGGAGACTCGGGTAGAAGCGAAAAATAACGGTATCCTCGGGGCTGCGGATGGCTGG

CCTGGGGGAATTTCAAGTGCTGCAAGTTGGAGGAAAAACG

>RXA00846
ATGTTGAAGAATGATCTGTCTGGTGCTCGAGTTGTAGCTGTGCATGCGCACCCTGACGAT
GAGGCGATTACCACCGGTGGTGTGCTTGCGGATCTTGCTGCTCGTGGCGCCGATGTCACG
GTAATTACCTGCACGTTGGGCGAGCAGGGTGAGGTTATCGGTGAGACATTCGCGCAGCTA
GTCAACGGTGATGCGGATCAGCTTGGCGGGTTTAGGATCCATGAGCTTTACGCCTCGCTG
GAGATTCTGGGCGTGCGTGGCATTCATCTGGGTGGCGCTGGCTGCTGGAGGGATTCCGGT
ATGGTTGGTGATCCTGCAAATGAGCATCCGCGTGCGTTTATTCACTCTGGTGACCGTGCA
GTGGAGCAATTGAAAGAACTTCTTGCG

>RXA00853-upstream
TTGGATCCAGTTGAGAAATTTCAGCCCCCATCCCCCACATGAACGCTGTTCAAAACATCC
AGCTTGCTTGTTGAACACTGTTCAGGTGTATGATTTTTTC

>RXA00853
ATGCCTACATCCTCTTCTCCTGCAACTGTGACTCCGCTAAAGAAGCAGTCTTCACGTAAA
CAGCTCCAAGACATCGCGCTTATTGCAGTTTTTGCAGCACTGATCATTGTGCTTGCTTTT
GTTTCCATCCCAGTTGGCACAGCGGGAGTGCCTATTGTTTTGCAGAATGCCTCCATCGTT
TTGGCTGGCCTGATTCTTGGTGGTCGACGTGGTTTTCTCACTGCTTTGCTGTTCCTGGCA
CTCGGCCTGATTGGCCTGCCTGTCCTTGCAGGTGGTCGTACCACTTTGGCCGCACTTGCT
GGCCCAACAGCTGGCTACATCGTGGGTTACCTCATTTCCCCACTTGTTGCAGGCATCATC
GCTTACCTCGCACCTAAAAAGCGTGGCGCTGGAATGTTCATCGTTTTAGGCCTGGCGGGT
CTCGCGGGTCTGATCACCCAATACGCTTGCGGCATCGTGGGTCTCGTCCTTCGTGCGGGT
CTAAGCTTGAGTGAAGCAACAATTGCTCAAGGTGCCTTTGTGCTGCCAGATTTGGCCAAG
ATCACCGTCATGGTCATAATCGCCGCTGGAGTTCATGCAGCATTCCCTGACATCCGTAAG
AAA

>RXA00853-downstream
TAGTTCCAACCCACTTTTCCTCA

>RXA00854-upstream
TTCATCCGCCCTGGAAGACGGTCATGACGGGGACCCTTCTTAGGGTCGCTGTCGGAGATT
GGACACGTAACTTCTGTGCTTGCGCTGTATTATCGTCCCC

>RXA00854
ATGCGTTTATCGGAGTTTCGGCAACTCATTGAAGATGAATTCGGAGAAGCCAAAGGGGAG
TGGATTGCACACTCGCATGTGATTGGTGCCCTCGGCGTCACTGCAGATGTTGCAGTAGAT
ACCGGGGTTGATCTGCGCGATGTATGGGAACAACTGTGCATTGATTTCAGTGTTCCCGAA
GAGCGACGACTTGGTAAAGATGAACCAGGGTTC

>RXA00854-downstream
TAGCTTGTTCGAGGGGGTTCGCA

>RXA00855-upstream
TAAAAACCTCTCGACGGACGAAGCGCCACAAAAGCAAGAGAAGAATATAAGTGAACCAAA
TTCCGTTTAGTGTACGTCTAGACGCCTAAACTTACCTGTT

>RXA00855
ATGACTTATTTTGCCGTGCTTTACACATACAACCCAGACAGCGAGAAAGTCGCTGAAGTT
CGTACCGTCCACCGCGAGTTCATTGCCAACCTTCATGCGGAGGGCAAAATCGTTGGCTCC
GGTCCTTTCGTGGACGGCGACGGTGGCGCGCTGATTGTCATCAAGTTGGAAGAAGGCTCC
AACCTTGTTGATGCTGAAACCCTGATGAACAATGATCCATTCCACGTAGAAAACGTGCTG
GACAACCGCGTCATCCGTAGCTGGAACCCTGTGACCAAAGATTTC

>RXA00855-downstream
TAGGCAACTTTTTCTTTAACAAT

>RXA00861
ATGGCTCCTCACAAGGTCATGCTGATTACCACTGGTACTCAGGGTGAGCCTATGGCTGCG
CTGTCTCGCATGGCGCGTCGTGAGCACCGACAGATCACTGTCCGTGATGGAGACTTGATT
ATCCTTTCTTCCTCCCTGGTTCCAGGTAACGAAGAAGCAGTGTTCGGTGTCATCAACATG
CTGGCTCAGATCGGTGCAACTGTTGTTACCGGTCGCGACGCCAAGGTGCACACCTCGGGC
CACGGCTACTCCGGAGAGCTGTTGTTCTTGTACAACGCCGCTCGTCCGAAGAACGCTATG
CCTGTCCACGGCGAGTGGCGCCACCTGCGCGCCAACAAGGAACTGGCTATCTCCACTGGT
GTTAACCGCGACAACGTTGTGCTTGCACAAAACGGTGTTGTGGTTGATATGGTCAACGGT
CGCGCA

>RXA00862-upstream
AGGTAGTTCCTTGGCGCTTGTGGTTTCCGCCTCTTTACTTTTAAGTGCTTGTGATGGAAG
CGGCTCAACGCCTACAACCTCTGCTAGTCCTGCTCCAGTT

>RXA00862
GTGACAGAAACTGAAACCGCTAACCCGGTCACCACAACTCGCACGCCTTCAGATGCTGCC
CCGTCGCCTACCACTTCAGAGCCCACTGGTTCAGAGTCCACCAACTCCCCTTCCCCCACT
GCTTTGCCGCCGTTGGGTTCCCCGTCGATGGATCAGAAGCAGCAGGCTCAAGTTGGTGAC
TCCGATATGTCGATCGCTGGCATCCGCGTTGCCGAGCACGAAACGTTCACACGAGTTGTT
TTTGATATCGCCGGTAATGGCCAACCTGGTTGGTGGGTCGATTGGGCCACTGATCCAATT
CAGCAGGCGTCAGGTCTTCCAGTTGAGATGGCTGGTGATTCCTTCCTCAACGTCAATATT
CAAGGCACTGGATATCCTGATCAGGTTGTCGTTCCAGGTATCGATACCGGATCATATCCT
GGTGCAGGCATTGTTGAAGACATCAACTTCACCAGTATTTTTGAAGCCCGTTCCCAAGTT
CTCATTGGTGTATCTGGTCAACCCCGAAATTACTCGGTCTCATTGCTGCAGGAACCAACC
AGGCTTGTGGTGGACATCGTTCAC

>RXA00862-downstream
TAGCGCTGGAACGCCG

>RXA00869
CTGTTTATCGTGGCTGCCGACCACCCAGCGCGCGGCGCACTTGCTGTTGGCGACAATGAA
CCCGCCATGGCTAACCGCTATGAACTGCTCGAACGCATGGCTATCGCACTGTCTCGCCCG
GGTGTGGATGGTGTGCTGGGAACTCCAGACATCATTGATGATCTGGCGGCGCTCGGACTG
CTCGATGACAAGATCGTGGTTGGCTCCATGAACCGTGGTGGCCTGCGTGGCGCTTCCTTT
GAAATGGATGATCGCTACACCGGCTACAACGTGTCCTCCATGGTTGATCGTGGCGTGGAT
TTCGCGAAAACCCTAGTGCGCATCAACTTGAGCGACGCCGGAACCGCCCCGACCTTGGAA
GCCACCGCGCATGCAGTCAATGAGGCTGCAGCAGCACAGCTGCCCATCATGCTCGAGCCG
TTCATGAGTAACTGGGTAAACGGCAAGGTGGTCAATGATCTTTCCACCGATGCAGTTATC
CAATCTGTCGCCATTGCTGCTGGTCTGGGCAATGATTCTTCCTATACCTGGATGAAGCTT
CCAGTGGTGGAGGAGATGGAGCGCGTCATGGAATCCACCACCATGCCAACCCTGTTGTTG
GGCGGCGAAGGCGGCAACGATCCAGATGCCACCTTCGCATCCTGGGAGCATGCACTCACC
CTGCCGGGTGTGCGTGGCCTGACCGTGGGACGCACTCTGCTGTATCCGCAAGACGGCGAT
GTCGCCGCCGCTGTTGATACCGCAGCGCGACTTGTTCACACAGATATTCAACAATTCACT
TCGCAGAGCATT

>RXA00869-downstream
TAAGGAATTTACACACATGTCTG

>RXA00874-upstream
AGCTGTTCCCTACCATTGCTGAACGGGAGTGGATTGTCACTTTAGCCCCTCACGGATTCT
TCTGGTTTGATCTCACCGCCGATGAAAAGGACGATATGGA

>RXA00874
ATGAGCATTGGCCAACACATCATCACCGAGCGTTTCTACGGCGCCAAGTCCCACACCATC
GACAACGTAGATATTGTGTTGTCCCGCGAATGTGGCGAGAACACTTTGGCTGTAGTGCGC
ATCAACAATGCGCTGTATCAGTTGTTGGTCAATGATGATGGCAAAGATGTTCTCAACGAC

CACGTAGAAGAGGTCGGTGCGAGTTTCGGAGCATGGACTGGCAGCTCTGCTTTTCCCATT
GGCCCTTTCACTCCACTCGGCACAGAACAATCCAATAGCTCTTTCATCACCGCCGACAAT
AAAGCGATCGTGAAATACTTCCGCAAATTAGAATCCGGGCAAAACCCCGATGTGGAGCTA
ATTTCTAAAATTTCCTCCTGCCCCAACATCGCGCCCATCCTGGGTTTTTCCTCCGCTGAG
ATCTCCGGGGCTAACTACACCCTGGTCATGGCGCAGCAGTACGTTCCAGGTTTGGATGGC
TGGTCACACGCGCTGACTACTACCTCTGGCAGCTTTGCAGAGGATGCAGAAAAGATCGGC
GAAGCCACCCGCAATGTTCACACTGCTCTTGCATCGGCCTTCCCTACTCGGGTAGTTCCC
GTAGAAGCACTCGCCGATGCGCTCACTACCCGCCTTAATGAACTAATCTCCCAAGCACCC
GAAATCGCCCGCTTCAAAGAAGCAGCCATCGACCTCTACCAATCGTTGGAAGGCGAAGCC
CACATCCAACGCATCCACGGTGACCTCCACTTGGGGCAGCTCATCAAAACCCCCGAACGC
TACATCCTCATCGATTTCGAAGGCGAACCTGCCCGCCCACTTAATCAACGACGCCTCCCC
GACTCTCCCCTGAAAGATCTCGCCGGCATCATCAGATCCATCGACTACGCAGCCTACTTC
GACGGCGAACACACCCAATGGGCCAACGAAGCCACCGCGCTATTCCTCGACGGCTACGGA
TCAATTGAAGACCAAGAACTCCTCAATGCCTACATTCTGGACAAGGCGTTGTACGAGGTT
GCCTATGAAATAAACAACCGCCCCGACTGGGTGAAAATCCCACTCGAGGCGGTCGAAAGG
CTTCTAGAC

>RXA00874-downstream
TAGTTAGTTACTCTGCGTCAAAC

>RXA00876-upstream
TTGACTATCTCGAATTAGGTGAGGGCTGGGAGCCAGAAATTTTGTGCTCTGATGCTGTTG
AAATTTTAGAAAATCTCATCAAGGAACTAAGGGGAATTCC

>RXA00876
ATGACATTGAAAATTGATCCCTCGTCCATCAGTAGTGCTGTGTCTCGCTTGAATGAGCTT
CAGCATCAAGCTATTACTGCATCTCAAGTGGGAATGAAATCAACAATTCTATCCGCGTTT
TCGCCCGTCTCTGGACTCGATCAATTGGGTTCCGGTCACGGGAATGTGATTAATGGTGGG
GCAGGCGCAGCAAACTCTGTGCTGAATTCCTATGCCGAACAAATCGAGTGGTTGTCTGCG
GCTTTGCAGGCTTCTGGTGCGGCTTTGACTGGCCAGGATGAATTATTCGCTAGGGGTATG
GATGTAGCGGATACCGGTGGCAGGGTTGTAGAAGAGTCAGTAATGTTCCCGGCGCGGCCG
GCACCTCGGTTTGAGTCTTTCGTTTTTAATCCACCAGCTGTTAGTCCTTCGTTGTCGTTG
GATGCGTTGTGTAGTCAGTTTTCCGGAACCAACTCGGGGGCGGTTTTGGAGGCGCAGGGG
TCTTGGGGCTCTATGGCGTCGGCTATTAGCAATGTGTCGGCTTCGTTGTCGTCGATTGCT
GGTGAGATTTTGGCGGAGAACTCAGGCGAAACGTTTGAGCAGGCTGCTGCTCGGATTAAT
GAGGTGGCGGCTGCGGGGGCGACGTTTGCTGCGAATGCGAAAATGATGGGGGCGTCGGTG
GGGACGCTGAATCGGATTTATATGGGGCATCGCATGCAGGTGTTTATGGCTGCGACGTCG
ATTAAGGCGATTTTGGATCCGGTGCAGAGGCTTGCTGCGGAGAGGGCGTTTTTGGCGTCG
TTTCAGGCTACTTTTCAGGCGGATGTGTTGACGGGTATGCCTCCTGTGAGCAATTTGATG
CAGATGAAGGGGGCGAATGGTTCTGCGGGGGAAATTGCTCTGGGGATGGATGAGATTGCT
GGCAGTGGGCAGGCATGGTCTGCGGCGGGGTTGACTCCGTCGGGGGCTGCGCAGGGTGGT
GTCGCCAATGCGGGCAGTATCGCGCCGGATGCAGCGGTTCAAGGTGCTGCGGGGCAGAGT
GGGGTTGGAAGTTTTGGCACTGTCACTGATCAGTTGGATGGCATCAATATTGGGGATATG
TTGACCTCTGCTGCCTCAGCTGGGCAGAGCCTTGCGAATGGTTTGGCGATGCCTACTTCT
ACGCCTAATTCGGCGTCCGGTGCGATTCCTTCCTCGATGTCTGCGGCATCGCCGCTTGGT
GCGTTTGGCAGCGGTGCAGGGTTGGGCGCACAGGGTGGCTCGATTGGATCTTCGGCACCT
GGAGCGATCAGTAGTCGAGCGGCCGGATCCGCAGGTGGTTCGGTACCGGGAATGACTGGT
GGTCCTGGCGCGCCGGGGATTACCTCGGATTCGTTGATGGGAGCTCGAACTCATGGTGCT
TCTTCCGCGGGAGCTGTCGCTCCGATGATGGGTGGTGCTGGCGGAATGTCTGGTGGCGTC
GTTGGTGCAGGTGGTACTGGTTCTCAGAGCAAGTATGCGCGCCAGACTGGATCGTCGGTT
GGATCTAGTTCGCAGTCGGGTTCTGGCCTGGGGATGGTGGGATCAGGGAGTGGGAAGCCG
TCGATAAGCAATTTTGGGCGCGGCATGATGCCGATGATGCCCATGATGCCCATGGGAGGC
GCCGGCGGTGGGCAGAAGAATACCGGCAAGGTGAAAACGGTGACGTCTGCGGTGGAGGAA
GACCGCAATTTGGCGGCGCTGCTGGGTGATCGGGGGCCGGTTGTTCCGGGTGTGATTGGT
GACTGGGTGAGGGGC

>RXA00876-downstream
TAACGCAACAATGTGTCTAAGCT

>RXA00881-upstream
ACCTGACCGAGGAAGCCGACGAGCTGACCCCAACGCTGAAGGTCAAGCGCAACGTTGTTG
TTCGCCGTTACGCAGACGCCATCGACCACATCTACAACCG

>RXA00881
ATGAGTAACACAGAGACCCAATTTGATTGGGATGGATCGACATGGACCCGCACCGAAGTC
GGCGAAGCACCAACACGCTTCGCTGTGGGCGTGATGGAGGATTTCGCCTACATTGCAGCC
ACTGGCACGGACGGGGATGAAGAGTTCTTTACTTTGGGCTCAAATCCGGGTCTGACGTTT
GGTGATCCCGAGTGGCTTTTCGCTCAGGATAATCCGCAGTATGTGGTGGAGTGCATTGGC
CAGCAGGGAACCGAGCCGGCAGCCCTGAAGGTTGTAGATAAATATTTGTCGCGACTATCT
GATGAGGAGTCACGTGGCGAACCCACGCGGATTCTCAATGAATTGGTCTCGGCGATGGAG
TTGCCGGCATTGCCGTGG

>RXA00881-downstream
TGATTTTTCTCGGGCTTTAGTGA

>RXA00882-upstream
AAATAGCTGAGAAATTGGCTAGAGGACGGCTAGCAAACCGGATCAAGACCGGCTAGAACT
TTAGCTACGAGGCAAGAAAAGGAAGGTGTGTTGGAACGCG

>RXA00882
ATGAGCAGTACAACCGCACAGCTACGCCACCGAGAGCTGACCCAGGAGATCTACAACATC
GGCGACGAGGTCGCTGAATACATTGAGCACATCATGGAAGCAGTCTCCGACTGGGATCTG
GAGCTCGTGGAAGATTGCCTCGCTGAATTCGATGAGATCATCACTGAAGCCCGCGATGAC
TCCCGCACTGTTGTGGCTGAACTTTCAGGCCTGCGTCACGCACTAACCACTGGTATCCGT
CAGGGCACCGTGAGCGCTAGAGCCACGGTGGAGGTGGACGTCGATAAGCCGGAACGCCTG
ACCGCCTCCGAGCTGGAGCGCGACTTCGATATTGATGCCGGCCTCGTTGATGTACGCGAT
CTGTCGACCGCGCTCAATGCGCGCACAGACGCTGTGGTTAAGCGCCTGGAGGCCACTGTG
GAGTGGGTGCTGGCGGAAACTGACAAGGTGGCCAACGATCTGGATTCCCTGTCTCTGCCA
CTGCTTTATGGCCGCGTTGCAGCGGTGATCGAAAGCGCCACCAGCGCATGGATCAACGCA
GTGGGCACCGCCAATCCGGCGTATGTGCGCACCATGCGAGGCAGCAACCCGCCACGTTTC
CTGCTTGAGCGTGCGCGTATCGACGCTGTCGTGGCCCGGGTTGCAGACAAGCTTGCGCAA
AAGCGCAACGCTGTTTCC

>RXA00882-downstream
TAGAAATCTCGGTGCAGCAAAAA

>RXA00883-upstream
AATATACACACCAAAAACTGACATGCCCCAAGCCTAGTGCCTGCCCCCTATACATGATTA
ATTGATGTTAAACATAGCGAATTCCTAAGAACAGGGTAGA

>RXA00883
GTGCAGGGTATGAAACGGAAGATGGTCGCAGCGGCGCTGGCAACAGCGCTTCTTTTTGGG
GCTGCACCTGCGCACGCTTCCGAATTGGTAGAGCCCACCACAGTTGCAGAGTCAGTGGCA
CTCGATCCCAACAAAGCAATCAATATTCTCACCCCAGATCTCTGGGAAGACATTGAGGCA
AAACCAGGCGATATCGTCCACATCCCCTACCAGGGCACCCGAAACTACGAGGACCTCACC
GTAGAAGTCGCGAAACCTTTCGAAGATTTCCAAATCCTCGTCGGACTCGACAACAGCATC
GTCATCGCAGTGCCAAAGAACTTAAGTGGCGCAGCATCAGTCGCCCCAGTTTTCACTGTC
TCTGACAAAAACGGTGAGATCGACTCTTTCACCATCAAAGTAAGCGTCGAGCCACGCCGC
CAAAGCGACGAAGAAAAGCGCTCCGCACTATTTGATGTCATCTCTGAGCTTGCCTACCGC
ATGCCTCATCTGCCATTCGTGTCAGAGTTGCTGAAGTAC

>RXA00883-downstream
TAGAACAGTAACGAGAAAACCCC

>RXA00887-upstream
AAGAAATCCGCAACCATCGCAGCGACAACGCTTCCGTGCATCGCGAAGGCGGAGAAGAAT
CCGGTTTCTTTGACAAGCTCCGAAACAAGTTCCGCAAATA

>RXA00887
ATGTCACTGCCAGTATTTATCTCTGATTCCGCAGCCGGACCAGGCGAAACCATTGAGCTC
GCCGGTCCGGAAGGCCGGCACGCCGTCACCGTCAAACGGATCCAGGTAGGCGAAAAGATT
TCGCTTATCGACGGCCGGGGTACAGCGCGCACCTGCACGGTCACCGCCTTGCAGGGCAAA
GACCGCCTGAACGCTGTGGTGGATTTGGTCGAGGAAATCCCCGCACCGAACCCACAGGTC
ACCATCGTGCAGGCTATCCCCAAATCAGAGCGTTCCGAGCTGACCATCGACCTGCTCACC
CAAGCTGGCGCCGATCGGATTGTTGCGTGGCAAGCATCGCGCTGCGTAGCAAAATGGGGC
GGCAAGGAAGCAAAATCACTGGCTAAATGGCAGGTGGCTGCGGAAGCAGCCGCCAAGCAA
TCGCGGCGCGCAACGATCCCTGAAATTCTTGGCGTAGTGGGGGAGGAGGGCGTCGAAAAG
CTTATCGACGAATCCGACCTGGCCATCATCCTGCACGAAGAAGCAACCGCCGCGATCCGT
GAACTGGAATTTTCCGGCAACGTCGTGGTGATCATCGGACCCGAAGGTGGCGTCGCGCCA
TCGGAAATTTCACGCTTCGTCGACGCTGGCGCACACACCGTGAAACTAGGCCCTGAGGTG
TTGCGCACTGCCTCCGCAGGCATGGTGGCGCTCGCAGCTATCGGCGTGCTGTCTGACCGC
TGG

>RXA00887-downstream
TAACATTTCTCTGACATAACCTT

>RXA00889-upstream
TGGTCCGCCACCAACTGGTTGGACACATTGTGGATGCATACGAAGACTATGAAGAACGCG
AGGCCCGCGAATTGAAACGCAAACGCCAGGAGACACGGCC

>RXA00889
ATGAGCATTGAGGTATTCAACGAATCAGGATACGACGGCGTCAATGAAGAAATGCTCATT
GATGTCCTCTCCTTCGCACTCGGGGAAATGGACATCCACCCCGACGCCGAAGCATCCATC
CACATCGTCGACGTCGACACCATCGCCGATCTCCACGTGAAATGGCTTGATCTTGAAGGC
CCAACCGACGTGATGAGCTTCCCGATGGATGAGCTCACCCCCGGCTACTCCCGCCCCGAC
GGCGCCACCCCCGGCCCCGCCATGCTGGGCGACATTGTGCTGTGCCCAGAGTTCGCGGCA
AAGCAAGCGACCAAAGCAGGCCACGACTTAGCCCACGAGCTAGCTTTGCTGACCGTGCAC
GGCAGCCTGCACCTGCTTGGCTACGACCACGTCGATCCAGCCGAAGAGCGTGAAATGTTC
GCCCTTCAAAACGAGCTGCTTGCCGATTGGTACGACAACGTCGAAGCCCGTGGCGTCACC
TACCAGCCAAAACCATCCGGCGCCGGTGCATTCCCCACCGCTGCTGATCGTCTGGAATTG
GACGAAAAGATGGAAGCGGATGACTCTGGCTTTGGAGGCGTTGAGTCC

>RXA00889-downstream
TAGGTGGAATCCTCAGTTATATG

>RXA00893-upstream
ACGCCAACGCAGAGTGTTTAAAGAAACTGGCAGTTGGAAAGCTGCAGTTGATTTAGCCTG
CGACGAACTCAACGACCTCAAAGCACTGGACTAAATAGCT

>RXA00893
ATGGTGGAATCCCAACACATCATTTTCATCCCGGAATCCCAACAAACACCCGACGAGTTT
ACCGAGGTAGTCAACGAGATTCCCGCCGGAATCAAACCACGGATCGTACCGTGGAGCGGT
AGTGTTTCCGCAGGTGTGCAGGCTGTGGAATCCATCCTCGACCGTGAAGAAATCCGGCGC
GTCATCCTGGTCGGCGCTGGAACCGGAGCTGGAGTGGCGTTGGAAATTGCCAAGAACCAA
CCCCGCCGCGTGGAACGCCTCGTGCTGGATTCACCGTTGGTGACCTTTGATGAGAAACAA
CTCAAAGGCATGAGCACCGCACTGAAAATGATGCCAGGATTCTTCTTCCGAAAGAAGAAC
AAGAAAGACCTCCTGCAGCAGGTAGAAGAAGCCCGTACTGCAGTTCCGATGGGATTTTCC
GAGATTACCATGCCGACGTTAATCATCCGAGGCTCCGCTGCGAAGGCTGGAATTGATTCT
GACTTGGAAAAACAAATCCCGAGCGCTCGGGCTACCACCATTATTGGTGCCAATTGGCTG
ACTTACACAACGCATGGACGCCAAACTGGTGCTGCGATTGCGGAATTCCTCGCCCAA

>RXA00893-downstream
TAGAAGGGCACGCCTAAACGCCA

>RXA00895-upstream

GTCGCGCCGGAAAGATAGACTAAGCCACATGACTTCGGACATGCAGAATTCTCCACAGCA
CTCGGCCACGCCTTCAGAAGAAAAACAAGGCGGACTGCCC

>RXA00895
ATGCGCGGTTTGGCCATGATTTTGATCGCCGTGGCCGTATTGCTCGCAGCGTGGGCACTG
TGGTCAATGCAGGGCAAAGACGACACCTCCACCACCAGCGCCGGACAAACCCAGTCCACG
GAAACCAACGCGGGAACTATTGCTGAATCTTCTGGCTCTTCGGATTCCGAGCAGGCATCA
GCAGAACCTGGAACCTCCGAAGAAACCTCTGCTGAGCAGCCAGCTGCAGATGGCGAAGCC
GCTAATGCTGCTGGGGCCGCTGCTGCTGGTGGCGCTAGTTCGGCTAACGGCAACTCCACC
CCAGTGAACACTCTGTACGTGCTCAACAACTCCACCGTCCCACAACTTGCAGCACGAGTG
GCAGACAGCCTAAGCGGTGACTACCAAAAGGTAGAGTCCGGAAACCTTCCAGACACCATC
ATTCCGCAGAACACTGTGTACTTCACCGCTGGAAACACCGAAGCTGAAAAGGCTGCACGT
GAACTCGCTGACCGCGTCAGTGGCGTAGCAATGGAACGCAGCGATGCACTGCCAACCGAA
ACAGAAGGCAAAGATGCCCTCGTTTTGGTGCTGGTCCAAGACGTAGCGCTG

>RXA00895-downstream
TAGTTTTCTCGGATTTGTTGGAA

>RXA00904-upstream
AAGCAGTGCAGTACCAGGCTGGAAGTGTGGACAACA

>RXA00904
ATGATTAATACCATCCGCTCCGAATGGACCAAACTTGTCACCACCAAATCCTTCTGGTGG
ACAACCGCACTAATTCTGGTCTTCAGCCTGGGATACGCAGCGCTCACCGGATCACTCGCC
ACCGGCGAAAGCTTTGCATCACTGTTCCTTCTCGCAGGCAGCACAGTCACCGGCCTTTAC
CTCCTTGGCTTCGTGGTGATCATGATCCAATCCATCATGATGTTCACCACCGAATTTCGA
TTCGGCTACCAAACCCAAACCTTCCTCGCCACACCAAAACGCTGGGTTGTCGCCGTTTCC
AAATGGTTGCTGTACCTCGTGTTCGCCGTAGTGTTGACCTTCATCACCGTGATTCTGTGC
TTCTATCTAGCCAAAGCCCTGGCATCAGACACTGCAAGCTCCACCCTGGTGGTGTGGGAA
GATACGCAAGCACGACGAATCATGTGGCAATACCCACTGGCAGCAGCACTATTGGTAACT
TTCTGTTCCGGAATTGCGCTCCTGCTGCGTCAAACTGCAGGAGCAGTGGCACTGGTGCTT
ATGTGGCACTTCGCTATCGAAAACCTCCTGTCTTTCTTGCCACGCATCGGCGAATACGTC
GGCAAGTATGGTCCCTTCACCAACCTCTACGCATTCATCACCGACTATCAATCAATTGAT
CCAGGATGGTCCACCACCATGGGAGCGGTGTACTTCGGAGCGTGGGCATTCGTGCTGTTC
GCACTCGGAATCGTCGTCCTAGAAAAGAAAGACGCC

>RXA00904-downstream
TAAAATGCCCTCTAAAATATCGC

>RXA00908-upstream
TCGGTCCTCCACCTAACAGGATCCTTCACACCCTTCTTTTCAATATCTAGAAAAGACCGA
TCCGCCCAACATCTTTTTCATGACGCAAAGGACCGTGTCA

>RXA00908
ATGTCTCTCTACACCCGTACTCAAAATACCCGTCACTCCACCATCATCGAGTTCCGCCGC
GAGCAGACTCGTAATCACACGATGGAGCCAATCCAGTCCGAGCCACGGATCTACGCTGAC
GATCCTTTCCGTGCACGCTTCGGACACCAACTCCCCCGCGGACTTCGCGAAGAAGCACGC
GGCATGGAATGGCGCACCTTCACCAACACCTACGCACCAACCGGCAACCTGCGCATCAGC
AACCTCGAGTCCGAGGCACGCCGCGGAGGAATGTTCCACTTCAACGCAACCCTGATCAAC
AACTGCCAGGGCGAGCGCACCACCACCGACGCTCACATCATGGCAACCGGCCCAGTTTCC
GCATGCACCAACTTGCTTGCCGACGCCGGCCGTCGCGTTGAAATCCTCGAATTCCACCAA
TTCGACATCTTTGAAGCAACCGTCACCTTCATCTACACCTGCAACAACGTTTCCCGCACC
TGGGCAATGGGCTTCGGCGGTACCCCTGAGCAGTCCGCTGCTTCCGCAATGAGCTCCGCA
GCTCACTTGCTCTACGGA

>RXA00908-downstream
TAGGTTGCAATAACATTCATTCC

>RXA00915-upstream
CTTGGCTGCAGGTCCACCATCAGCACAGGTCTTTGACATGAACGTAGCTCGCCGCGACGT
TTCTTCAGGACCTTCTCTACCTGGTGAGGGTGAGTTCTAA

>RXA00915
ATGTCCGCCGCCTATTCGCAGGACACCATTTTGACGGTGTTTCTGGGGAGGGGTCTGACC
GCTGAAGGGATCCGACAGACCCTAGAAGACTTCGCAGAAACCGGCCTAGTCCGCAACCTG
GTGTGGATTGATGCCGATAGTTTCCACGAGTCTTCATCTGAAGTCACCCACTTGGCAACC
AACCAAGACGGTCTTCCGGAGCTTCAGCGACGACCTTTCAATGAGTTGGTGTCCCGGTCA
CGAACCACCAAGCTTCACATCGGTGTCATCAACGTCATTGATGGCAGCGAAGGCATGCTT
CATGCAGAAGAACTCAACCCATTGGTTGGGATCATCGACAGTGTCTGTTCACACCACCAA
ATTCACCGATCCAACGTGATGATCGGTGCGGTGGCTGCCACACTTGATGAGGAACTTCCA
ATTCTTCGTGGTTATGTGAACCTGATGCTGGCACCTGAAGATAGCCACAGCCCAGGCACC
GCAACAGTGACCTACCGTCATGGTTTCAGC

>RXA00916-upstream
AGCGGATCCAACGACACAAATGGTGGATTTGGTTCCAGCGGCGGCTTCGGCGCGCGATAA
CCTGTAACTTGCGATTAAAAACTAACTTAAGGATTTACAC

>RXA00916
ATGAAGAAAGTTCTCGTTGTCGGCTGTGGTGGTTCAGGTGCCAAAACGCTCGCTTATATG
ATGGACCAGCTCAAGACCACCCTGGCGGATAGTCTTCCCGAGCGTTACCCAAATCCAAAG
GAAGCAAAACTTCCTGGTGCGTGGCAGTTCGTGTCGGTGGATGTTCCGACCTCCCCAGAA
AGCCCCGGCCCGAACCTTCCGAATGTTCCAGAAGCCGGTGGACGTTATATTTCCTGTGGT
TCCTCGGATCGCTATGCCACCGTTGATACTGCGGTGTCCAACCAGCTCTCCTCCAGGGGC
GCGTTGGGTGGCGTTTCTTCATGGGCGCTTCGAAACCCTGATTCTGAAACCACCCCAATT
AGTAAAGGTGCGGGCCAGTACCGCTCCATTGGCCGTATGTTGATCCTGAGCCGACTTCAG
GAAATTCAGGCTGAATTACGTAAATCATGGGATGTGTTGTTCAGCGGTGAGACTGAACGT
GAGCTCGCTGACCTTCGTTCTGCACTGTATGGCACGTCTGTTTCCAGTGGTGAAACCTCT
AAAGAGCAGCCAATTATCTTCGGTGTCTCCTCCATGGCTGGTGGCGCCGGTGCTTCGATG
GCTCTAGATATCTGCCGCCTGCTCACCGGTCTTGAAGGCAACGCAGTGGGTCTGAGCTCA
CTGTTTATGGTGACCCCGGATATCTTCTCCCAGCTTTCCCCAGACCAGGTTGCCGGAACT
AACCCAAACGCGCTGGCCATGTTTGCCGAGCTCGCAGCAGCACAGATGGGTGCAGCTTCC
GAAGAAGATGCCCGACTGTTTAACGCTTTGGGTGTTTCTGTTGGCGATGACTCCATCCCA
GTTGGACGTATCTTCCCAGTGGGTATTCGCTCCGGTGAAAACGGCGCTCTGCTTGGTGAT
GGCAAGCCAGATACCGTCTACCGCGCACTCGGCCGTGGCCTTGCAGCTCTGATGGCTGAT
GAAGTGTCCATGGACAACTTCGAGCAATTCACCCTCGGCAACCGTGGTGGCGGAAGTGCC
GATCAGAGCAAGTACGCATGGGGTGCACAGGAAGCTAAGAACATTCCGTGGGGCAGCTAC
GGCTACTCACAACTATCCATGGGTCGTGATCGCTACGCAGAATACGCCGCCCAGCGACTG
GCACGCTCTGCCGTGGATCGTCTGCTCAAGGGACACTTTGATCCAAGCAATGATGCGGCC
TCTGACCAGCAGCTTCAAAAGCGACTCGAGAACAACCGTCCATCGCTGATGGGCAACCTC
AGCGACGTTTTGCCCGTCAACGCGCCGGCAGGGGACTGGATTTTCCATAGTTTCAACCAG
ATGATTGAAAACTGGACCCAGCGTATGAAAGCAATCATCAAGAGCCAAATTCCTGCAGCT
AATGGCCAGCGCGGAAGTGAATGGCTCGGGGATGTCCAGCGTGCTTTCCAATCATCCAGC
CAGATGATTGATAATGACTCCCGCCATGAGCTCTACATGGGTGTCGCCGACTGGGCCAGT
GCTGATGTGTTGCAGCGCCGAGTAGTCGAGTTGCTTCGTGATGAGATCGCAAAACTGGGC
GTTCCTTACGGCGTCAGCGTGATCGAATCTCTCAGCGCCACAATCCAAAACCAACTCATC
GGACAGCTTTCTGATCTGGCAAACAACCGTGCACCTGAGGCTGTTCAACTAGACGATGTC
AGCCGCAGTGAACTGGACAACAGCAAGGGCAGGATCGACGATTCTGACAGCTACATCCAG
GAAATCGTGTCACGATCCACTGGTCAACTACACACCCGCGCAGTGCAATACATTGCGGAC
CACATGGCTTCGGTTCTGGACGATTTCCTCAAAAATTTCATCTACCCACTTCAGCGCACC
ATCCAACGTGAGCACCACTCCCTAGAAAAGGACTACCAGCTCACCAACGATGTGAACCTG
GGAATCTCCCAGCTGAAAACCAACGTTCCAGCACTGTGGCCAGATGAATCTCAAACTACC
GTCCCGTCACGTTTCAGTCAGGCAGCCAACGAAGTCTTCCTGACCGATGTCGCCTCCTTC
CCGGAGCAGTTCCAAGCACACGTCCGCTCGTCCACCGATGACATCAACGAACAAAACGAT
TACTCGAGCGCCCTGCAAGAGGCCTCAACTCGAGTAGTCAGCGGTGTGTGGGAATCCAAG
TCCGGCTCTGAAAAAGCACCACGCGATCTCATCCGCCTCATCGACGTATGGGTTGCCCGT
GACCTGACCAGGGATCCGTCCGGTTCGGGAAGCCTCCGCGACCCTAAGCAAGCACGCTTT
GAGCTGAAGATTGATACCGGCGAAGTACTCGAGCGCTCCCGCCAGTACATCCGCCGCCCT
GGTTTCTCCTTCCAGCAGTTCATCGCCAGCTCACTGCGTGAATTCATCACCGCGCCGGGC

TTGGCAGACCACGAGCGTCGCGCGCGCCGTCAGCAGGTGCTGAGCAAGTTCAGTGAGGCA
ATGACCTACGCGCTTCCATTGGCTCAGATCAACCCTCAACTGGTTCGTGCGCTTTACGGC
GATGAAGTCCGCTACAACTTCAACTTCTCTCGCATCCCATTTGCCGGCGATGAGCTTGGA
TCCAGCCTGGAACAGGCAGTTCGTGATTACCCGAACCACCGACCAGCAGATATTTCCAAG
CCACTGGGCAAGGCTTTGGTCTCCCAAGGTGAAGAGCGTTCCATTGATATCTTCGGCTCT
TACCCCAACTACGCGCCGATCGTGTTTGACTCCCTGCTGCCTCCAATCGAGAAGCAGTGG
CGTCAGATCACCGGCGATCGCACGGAATTCTGGCATGGCCGCCGTACTCGTCCTTTGACT
GCTGCACTTCCAATGACAGACCTAGAGCGCAACGCCATGGTCAAGGGTTGGTACATCGGT
CGTCTGGTCGGACGAGTATTCTTCCCCGCAACTCTAGACACTGCGGATACCACTCCAGTG
CAGATCTACGATGAGAAGTCTGATTCGTGGATCAACTTCTCCACCCCAATGCTCACCCCA
GTGTCCCGTTTCCGTGGAAGCCTCGATTGGCTGCCAAACCTTCTGGAATCAGCATCATTG
GCATGGGCACGGGCAGGCGAGCGTCCTGTCTTTGAATCCGTCGAGCCTTACATCCAGCTC
CGCCAACTGTGGGATGATGCTGCGAGCCCATCCTTGCCAGGACGCACCACCCGCGGTGAG
AAGCTGCTGCACGATTGGCTTTTCGACGGCAACCGCATGGCTGGAAACGTCCTCCAGATC
CCAGGAACCGAAGCTGGTGTCACCCCAGCTGCACGTTTTGAGGCTGCGAAGAACTTCCTG
CAGCGCCAGAACGAGATCTCGCAAAATTACGTCCCAAGCGACAAGCTTCGCCAAGGCCGT
CTGTTCACCACCGCTGATCGTCCATTTGGCGACGTCAAGGATCGTGAACTAGCAGCACAG
ATTCCAGTGTTTGCTGACCTTGCAGCCGATGTTTTTGATGGCACCCAAGAAATCATCGAC
ATCCTGGAAAAGTGCTTGGCTGCAGGTCCACCATCAGCACAGGTCTTTGACATGAACGTA
GCTCGCCGCGACGTTTCTTCAGGACCTTCTCTACCTGGTGAGGGTGAGTTC

>RXA00916-downstream
TAAATGTCCGCCGCCTATTCGCA

>RXA00917
CAGCTGAATATGCAGCTGGTGGGCCGTGATGGTCAGCCACGCATCCTTGAGGGGTCCGCG
CTGGTCGATCTTGGTTTCACCCGCGCAGATACCGGCGAGTTCGCCCCTTTGGCTCAAGGA
ATTGATATTTCTGGCGGCGAATTAAGCTTCCCGCTGGATACGATTTCGCAGCTCCCAGCC
ATCGGCACGGTGGAAGCGCGTACCACGATCACCACCGCAGGCGTCGATGATCTCCCCGGC
ACCACGTTGAGCCCAATTCTCAACACCACGCGCATCACCATCACTCAGCGCGATATGCCT
CAGCTGCCAGCGTCGGTTCGCTTCACAGCGGATGAGGACGTTGTTACCGTAGACATCCCC
ATCACCGGCCCCGGCAAGGTATGGATTGCACCGGGAACCCAGCTCAGCGGAGTGCTTCCA
GACGGCGTGGACGGCATTGCAGCATCAAGTACTTTCGACAGCCCAGATAATGCTTTGGTG
CTCGGACTGGATGAGCAGGGCACGATTCCTGTTGAACTAACCGTGAGCGATCTTCGTGAC
GGACTGGTCAACGGCTCGATTCCACTCCAGATCTCCAACGCTGAGGGCGCCAATGAAACC
AGCGTGGATCTGCCGACAGAAGGCACGTTGAGCGTTCCCATTAACGCCTCCACTTTCGCA
TTGGCATTCATTTTGGCCCTTGTGCTTTCCCTCCTGATTCCGCTGCTCATTTTGTATATT
GTGCGTTTCCTCTCCGCAAAGGTTCCGTCCTCTGCGATGAGTGGCGTGCGCATTCCAGTG
GAATTCTCCGGTGAAGCTCTGCGCTATGCGGGCAGCACTATGCCTGATCTCGCATCGCAA
ACCACCGCCACCAAGCAGGTCGTTGTTCATGGAGACACCTTCAATGTGGAAGGCCACAAA
CTTAAAGTCCAGCGCTTCCAGCTGAACCCGATTGCGTCTCCTGCAGTGATCGTGCAGACC
GACCCGTCGATCAGCTTCGACGGCAAACAAAAGGGCACACAAGCTAAACTCCCGCTGGCG
GTCCAAGGCAGTTGGTTCCTCACTGCAAGCGGCGCTGACCCTTCCAAGATGGAACTCATC
GCCCTGACAAACCTGCCGCTCGAGCAGGGCCAAATCGACCGCATGATCGCAGGTATCACC
AGCAAAGCCCCTGATAGGGCACGCGAACTACAAAAATTGCTTGACGACGCCGCGACCTCC
CAGCCCGCAAAGGTTCCACCGCGCGCCCCAGCCGCGCAGGGCCACGTCGAAAAGCAAGCT
CCTAGTTTTGGCACTGGTTCCGGTGGTGGTTTCGGCTCCAGCAATGGTGGAGGCTTTGGC
TCCGGTAGCGGATCCAACGACACAAATGGTGGATTTGGTTCCAGCGGCGGCTTCGGCGCG
CGA

>RXA00917-downstream
TAACCTGTAACTTGCGATTAAAA

>RXA00921-upstream
TCTGGGAACGTGGATTGGTGGAAGCAGGTGAGTTGCCCGTGGCCTTGAGATGGACTCATG
TCACCTACGCGTCCTTTAGAGGAACTGCAGGTAGGGGTGG

>RXA00921
GTGGAAGGTGGAACTTGGTCTGCTCAGGCCACTAAAGAAGACCTCCAATTTATCGCGGAG
GTTGCGCCCACTCATATTGAAACGGTGACCCCTTTTGATGATTTCATCTCATCAGAAGAT

ATCGATGCGTTGCCGAGGAGGTTTGAGTACCGTCCTTTGGCAGGCCGATCGTTGATCATG
CAGTCTGTTCCTGCAGGTAAAGATGCCACTGGACGTCCAGGGAATGTGTTCACCCATGCA
GTATTTGATGGGGATCTAGAAAGCCCACTGGAGTCTGTTTATCCCATTTCCCTGTACCGT
TCACCTGATTTGCTGACCCCTTTTCGTGCAGCCGCGGTCAACGCTGCCGAGCTCCCTTTG
GATGCAGGCGAGCCGAGAATTGGCCCCATCACTGATCTGTCCTTGTCGTGGATGATGATC
GACAGCATGTTTGGCGATCGCAGACAGCAGTTCTACCAGCTTCAAGATGCTCTCCAAGCT
GGAGATAAAGCTACTGTTTTGGTTCTGAACAGCACTAACGAGGCAGCATATTGGCTTCAA
GCGTTGTCTTCTACATTGACTCCGAATGAAGCCCGGCGTCTGTTGCACTTCTCAACCTTT
GAGCGTGCTGCTACCTTGCCAGCTCCAGATAAATCAATGGAGGCTCGTTCTCTGTTTGTG
GTCCCAGGAATTGATCGTGAATTGTTGGCGGAGCATTCAGGGATTGTGATTATCGATCCG
GAGATTCCACAGAGCCAACCTTTCGGCCCGCAGGGATCCTGGTCCCGAATGACAGAAGGG
CTCTTCTCCGACGGTTTTGATGCTGATGAACTTGTCGCAGGGCTGATTCGTGCCAACGAG
AACCTGGATAATAGCCAAAAGGAACTCGCTCAATTTGGAGACGGTTTAGCGCGATTTATC
CGGAATGGCCGTTTTTCCGGCACGCACCCGCTTCGCGTACTTGCTGATCAGCATATGTTT
GGAAAGGTGCCAGACAAGCCAGCACCTAAGGTGGAGCCTGTCGCTCCGGCACCAAACCCC
AATGCAATTTGGGCGCGTGCATCTGAGGTAGTTCACAATCCTCGGAGAGCATCAGAATCA
CAAGATTGGCCAAGTCTGAGGCGATTGCCGGATAGTCGGCGCAGGATCATCAATATGTCA
GAGCAGGCGATCAACAGCATTGAGAAGCTTCATGATTCGCCGGCACAGGATCTTGTTGCC
TATTTGGATTTCCTTTTGAAAACTGAGCTTGCGACAAGCATTAATGCTTCGGATCCCTTT
TTTCGGAGTAGTTTTTCAGACTTTCCAGCGATGGACAACTGGCGACACATTAAGTTCACC
GAGGATGCGCACCCTCGCTTGAGGGAACTACTCGTGGACGCAGAACGCGATGCTAGGAAC
AGAGCACCTGCGGCAATCGTCTTGGACCATATCGTTCCGAACTTCAGCAGAGATCGGTCT
TTGCCAGACATCGAAGACTGGACGAGAAGCGATGAAGCTCAGCAGATCTTTGCAGGAATC
ATTGCGGGTGCGTCTGTTCAAACTGGTAGAAGCCACTTCATGTGGGATCTTTTGCGGGCG
TATTTTGGAGTCGCTTTGATCGGCGACGAAGATACCTACAGGGCTTTTACTACTCTCACG
GTCGATTCTGTTCTTAGTTTCGTGCAGTTAACTCTTCAAGAGGGCAGAACGGAAGACATT
AGACGATTCGAGAAATATGGTGAGCAGATTGCCCGAGAGGATTTGCCGTCGATTCTCACC
AATGCTCGAGCAGTACAGCAATATCTCGGCTATATCGACCAAGATATCATCAATAAGAAA
GTGTCCCGGTCTAGGGATGTTAACCAGATTTTTACTGAGATGGCGCGCGCTATCATCAGA
GCAATTAGCCGGAATAATATTGGAAAGGACATGCGGTCA

>RXA00921-downstream
TGAACGTGATTCGACTGGATTCC

>RXA00926-upstream
ATGGAGACACCTGGGGCTGGAACCACCAGAAGGCACCATCGGCGATTATTAGCCACCTTA
GGTGGCCAGGATGTTCCATGGTCTGGCAAACTAACTAACC

>RXA00926
ATGGACATCGTTTTCCTCATAATTCTTCTAGCCATTTTTATCGTTCCCACTTTCCTCATG
AGCCGCCGCCAGCGCGCACGGATGACTGAAATCCAAAAGCTGCAGGACTCTGTCGTCCCA
GGCGACCGCATCGTCACCACCGCGGGACAGCACGCAACGGTCATTTCCACCACTGCAGAA
ACCGTTGATCTAGAGATCGCGCCGGGTATGATCAGCACTTTTGAAAAGCTTGCTATCGTG
CGTGTGCTGTCCAAGGCCAATGAACCTCAGATGTTGGATGAGCCGACGCTGTTTGATCAG
CCAGAAGACGATCAGCCGAACGATGGTTTCGATGGACGCACTGACGGACATCCTGAGAAT
CGT

>RXA00926-downstream
TAGAAATTAATAATAATTCAGCA

>RXA00930-upstream
ACGGCGCACCACACATTTGGTGGTGTATTGAGCTATCTCTGGGCTGCGTGAGAAACCATT
TTCCGGTGGATGATGGAAGCTAGACGACGAAAGGGAGCAT

>RXA00930
ATGTCTGGCCACTCAAAATGGGCGACTACCAAGCACAAGAAGGCTGCTAACGACGCCAAG
CGAGGCAAGGAATTTGCCAAGCTGATCAAGAACATCGAAGTTGCGGCACGTACAGGCGGT
GGAGATCCGTCTGCGAACCCAACGCTTGATGACATGATCAAGAAAGCCAAGAAGGCTTCT
GTGCCGAACGATAACATCGAACGTGCACGCAAGCGTGGCTCCGGCGAAGAAGCTGGTGGC

GCTGACTGGATGAACATCATGTACGAGGGATACGGCCCCAACGGCGTTGCCATGCTTATC
GAGTGTCTGACCGACAACCGTAACCGCGCAGCTACCGAAGTTCGCACCGCAATGACCAAA
AACGGTGGCAACTTGGGCGAGTCCGGTTCCGTGTCCTACATGTTCACCCGCACCGGTGTC
GTCACCGTACAAAAGGGCGATCTTAGTGAAGATGACGTGCTCATGGCTGTTCTTGAAGCT
GGTGCTGAAGAAGTCAACGACAACGGCGATCTGTTCGAGGTTACCTGCGCACCAACTGAC
ATTCAGGCTGTTCGCGACGCACTCGTGGAAGCTGGCATTGAAGTAGAAGATTCTGAATCA
GACTTCCGGGCATCTGTTCAGGTCCCCCTGGACGCTGACGGTGCACGCAAGATCTTCAAG
CTTGTGGACGCGTTGGAAGATTCCGACGATGTGCAAAACGTCTACACCAACATCGACTTG
AGCGATGAGGTTTTGACAGAGCTGGAAAACGAC

>RXA00930-downstream
TAGTTCGTATTTTCCGCACTCCG

>RXA00932-upstream
CCCAATTAATTTATGCACTTCGGTGAGGTTACTCACAAAGAGTAGCGTGCAAAGCCCAGC
AATAAGGTGATGTTTCAACGATTAGGTTACGGTAGGGGCC

>RXA00932
ATGACGCCACAGAAACTTCACCGTTTTGCAGCCCTTTTAGAAATGGGTACCTGGACCCTG
CTGATCATCGGCATGATCTTAAAATACAGTGGAGTGACAGACGCCGTAACCCCTATTGCC
GGCGGTATCCACGGCTTTGGCTTCCTCTGTTTTGCAGCCATCACCATCACCGTGTGGATC
AATAATAAGTGGACATTCCCGCAGGGTATCGCAGGTTTGATCGTCTCTGTTATCCCGTGG
GCTGCATTGCCATTTGCATTGTGGGCAGACAAGAAGGGCCTCGTTGCCGGCGGATGGCGC
TTTTCAGATCCGTCCGAAAAGCCACACACTTTCTTTGACAAGATCTTGGCTCAATTGGTC
AGGCACCCAATCCGATCCATTTTAATTCTGCTGGTGATTATCGCCGTCGTCTTCTCTATC
TTGCTGGCGATGGGACCACCTTATGATCCAGATGCCATCGCAAACACTGTGGAT

>RXA00932-downstream
TAAACAACAGCCTCCTTCACATG

>RXA00933-upstream
CCGCGGGGCTAAAGCGCGCAAACGCCTACGACTGGTCGACAGTATCCACCCAGGTCATGG
CAGTCTATGAAACCATTGCGATCGACAAAGTGAGGCTTGG

>RXA00933
ATGACCCTTGTTTACCTCCTCATCGCTGTCGTTGTCACCGCAACTGTTCTGTGGGCGTAT
TTCACAGCACAACGCCTCAACCGGCTCCACATCCGCACCGACTCAGCAAGACAAGCCCTG
CAAGCAGCACTGGATCGCCGAGCAGCACTAGTAGGTGCGTTGTTGCCCGATGCAGCAGAA
GCCTCAAAACGCGCTGAGGCAATTCCCCTGGAATACTCCCGCTTCTCCCAACGCGCCCGC
GCCGAACGAGAAATCTCTGAACTCATCTTGAAACAGGGGAAGACCCTTCCAGATTCCATC
GTGGACGCTGCCACCCGCGTGGAATTAGCCCACCGCTTCTACAACGAAGCCGTCAGTGAC
ACCCGCGATCTTCGAACCCGATTGATGGTCAGATCCTTCCGACTCGGCGGCACCGCACCC
TTGCCGGAGTACTTCGAACTACTCGATACAGATCTGCTGACT

>RXA00933-downstream
TAAATGTAAAAAAGCCTCCTTCA

>RXA00940-upstream
TGCTCAACGGCACGCTGAAGGGCACGGACATGGACATCATCACGGCAGGCGACCCGGACG
TGGTCGCGGTGGACGTGCTGGCAGAGGCGATCTGCGCAAT

>RXA00940
GTGATTTTGGTGCTGCTGGAAGCTGAGTCAATGCGCGGCTACCAGATCATCACCACCATC
AGTGAGCAAACAGAAGGTAACTGGACTCCAAGCCCAGGAACCATCTATCCAACCTTGTCC
ATGCTTGAAGATGAAGGCCTGATTTCCATCTCCCATGAAATGGGCAGAAAAATGGCGCGC
CTTACAGAAGAAGGCGCGCAGGAAGTGGCAAAGAACAAGGATGCGTGGGGATCAATTCTG
GAGGCTTATCGCAATCCAGAATCCCGAGAGGTGCGGGTGTTTAACATTCGCTCTGAGTTT
CACAAGGTCAGGGAAGCAGCGAAAGCTGCTCCCGACGATAAAGCAGAGCAAATAATCGAG

ATTTTAAGGAGAGCAGCAGATGACATCAAGAGACTA

>RXA00940-downstream
TAACCCCAGTACCATGCAGCTGC

>RXA00943
AAGCCTGGCGTGAAGTGGCGTGCAACCAATGCTACAAAGCGTGGCAAGAAGCAGCTGCAG
CAGGCACTTTCAACCAAATCTGAGACTGAAAAGTTCGGTGAGAAGGCCTCTGATTGGTTC
AACGATACTTCTGACAAGGTCACCGAGTACGCGTACACCGCTCAGGATTTTGTCGGTGAG
AACAAGGATGACTGGATCAAGTCCGCAACCGAGACTGCTCACAAGGTCGCTGATACTGTG
AGCGATTACGCTCACAAGGCTACCTCTTACCTTGAGGAGAACAGCGGTGACTGGCTTGAG
GCTGCGCAGGCTAACGCCAAGACTGCTCGTAAGTCTGCAGTGAAGGCTGCCGGCAAGGCT
CACGAAAAGGCTAACTTTGCTCTTCAGGTCGCAGAGGAAACCTCTGGTCGCGCCAACAAG
AAGGCAACTAAGAGCTACGACAAGCTTCAGAAGCAGGCTGATAAGGCCATCGATCGTGCA
CAGAAGAAGCTGAAGGGCATCGAACTT

>RXA00943-downstream
TAAGTAACTTCTTCCTGATTGAG

>RXA00946-upstream
GGGCCGGTGTGAATAAAACACCTTCCCCAAATAGACAGCATGGTCTAGATTAGCTTGAAA
CGAAAGCGTACATTCGCAGCAACTAACGGAAAGCACACTC

>RXA00946
ATGACTCACACTCTGCAGGCAACTAATCCCCTTGATCAAACCGCTTGGCACGCTTGGCAT
TTCTCCCGAAACAAAGAGGCCATCAGCCGCACCGGCGCCACCAGCCTGAGTGCCACAGAG
TGGATTAGCGCCACCACACTCAAGGACGCGCACACTTTTCCTTCACTTCCCGGGCGATGG
TATAAACGAGGCGGCGGGGTAGTGGGAGCACATTTACCACCAGCTTTCGCAACAACTGGA
ACGGTGCAACTGCGCCCCGGTGAGCTCTTGATAGCGGAAGATTTCACCCTCACCGTCATT
GAACGGCTTGGACAGTTTGCACTTCAGGTTTTTGATGCACGCAATCCGAAGCGTTTTGAA
TTCCACTCCATCGCAGCTTTCCCACCGTCCGAGGAATGGCGGATTGAGGCTCGCTTCTTC
CCGGAACCTGACACTGTTAACACCGCTGCAGCTGATGGAGTTATCGTTGCCACGCCTACT
GCGGGTTGGGTGCACTTTTTGAAGGGCCGTCTGGATTACCGTCTTCGTGTAACCGTTCAG
AAAAATAATCTACGGGCACTATTTAGCGACAATTCCTCGACGTTGGGCGTTTATCAGCAT
CGTTTTGTCGACATCCCACGCCCTGATGCCGAGGGAAACACCATCATTGATTTCAACCGC
GCTTATCTTCCCCCAAAGGCATTGAACCGAAAGTTCCTGTGCCCATCGCCCAGCCTGAAC
AACCACCTCAATCTCACCGTGGAGGCAGGGGAGAAGTGGGTGGTTGCTGGAGGA

>RXA00946-downstream
TAATACTTGCTAACCGTCCTAAA

>RXA00949-upstream
GCTCAAGGATCCTTCCTGGGCAAACCAAGCAGCCCTCGCACTAGGTGCGGAACCCAGGTA
TGTTCACCAATACGACTACGTACTTTAAAGGAGAGTTGAC

>RXA00949
ATGAAGGTTTTCATCATCGGCGCTGCGGGTGGCATCGGCAATCGACTTTCCAGCCTGCTT
CACGCCAGGGGAGATGCAGTTAGCGGCATGCACCGCAATCTTGAGCAGGCCTCAAAAATC
ACAGACACTGGGGCAACTGCCGTACTCGGGGATCTCATCCACAACAGCACGGAGGAGCTT
GCGGAGCTTTTCCGCGGTCACGATGCCATCGTATTTTCTGCAGGCGCCCACGGAACAGGG
CAAGAAAATACCACGCTTATCGACGGCGCCGGCCTCCGTAAAGCCGCCGACGCTGCCAGC
GCGGCCAACGTTTCACGCTTCATCTTGGTCTCTGCGTTTCCGGAATCCTCCCGCGGGGAG
AACACCACCGAGAACTTTGAGCACTATATGAAGGTGAAGAAGTCCGCCGATGTCTACCTC
AGTCACACTGACCTAGACTGGGTTATTGTCCGACCAGGCGTGCTTCAAGATGAGGCAGGG
GATGGTTTAGTCACTGCTGGCTTAGCGATTAATTACGGCAATGTTGCTCGCGATAATGTC
GCAGCGTTCATTGATGAAGCTCTGCATCAACCGCAGTTGTCAAAGATCATTGTTGAACTC
ACCGACGGTTCAACTCCGGTGGCGGAAGCCGTAGAACGCCTCATCAAG

>RXA00949-downstream
TAAAGACGAAAAGAGGGAGAATG

>RXA00959-upstream
TTTGGAGGCGGAGCATCATACCTTTTAATGTCAGGATCGTGCAGTGAAGAATTCAGGATG
AATTACTCGCTGGAATATTGGTGGGGATAGAGTTGTTGTT

>RXA00959
ATGACGGTGATCGGAATTATTCTTGGCAGCCTTTTTGGCGTTCTTGCAGTCCTTCTCATC
GTGGTTGGTGCTTTGGGGTGGGCGGCTAAGCTCCCTGGCAACCCGGTTGTGGGCATTCGT
GTCCCTGAGGTGCGTAAATCCCAAGAATTGTGGGATATGGCGCACCGTGTCGCTGGCCCG
TTGTGGGTGCTGTCGGGAGTTTCCTTTGTTATTGCATCGCTAGTTGCGTTTGTTGCTTCT
GGTTGGATGTGGCTTGTTGTGGCGTTGGGTGTTGAGGCTGCCATCGCGTTCATTGGTATG
GGTGCGGGTATGGCTGCGCATACTGGT

>RXA00963-upstream
CTGGCTCTGACGGCGTCGACTTGTTCTGCTTCTCTGATACACCAATTTTCGAGGCCCTTA
ACCTCGCACGTACTTTTACTCCGGAAGGAATCTAGAACTT

>RXA00963
ATGCGTCTTGCAACAATCCGCACCAACGGCACCACCATTGCTGCTCGTGTTGAATCTGAA
AACACCGCTACCACCATCGAGGGCTTTGCCAACGTCGGTGAATTACTCCAGGAATCCAAC
TGGCGCGAGCTGGCAGAAAACGCTGCTGGTGAGGCTGTGACCTTTGAAAACAAGGAGCTA
GATGCAGTAGTTCCAGCACCTAAGAAGATTGTGTGCGTCGGCCTTAACTACGCCAACCAC
ATTAAAGAAATGGGCCGCGACCTCCCTGATACCCCAACCCTTTTTGTTAAGTTCCCTGAC
GCGCTCATCGGACCTTTCGATGATGTTGTCGTTCCAGAGTGGGCTAACAAGGCTCTCGAC
TGGGAAGGCGAGATGGCAGTTATCATTGGCAAGCGCGCACGCCGTGTCAAGCAGGCCGAT
GCTGCTGAGTACATCGCT

>RXA00969
ATCCGACAGGAAGAGCGCGATGATGATGCACGTCTGATCGTGGTCACCCACTCTGCGCTG
GAATCTGATCTTTCCCGCACCGTTGAACTGCTGAAGGCTAAGCCTGTTGTTAAGGCAATC
AACAGTGTGATCCGCCTCGAAAGGGAC

>RXA00969-downstream
TAATTTTACTGACATGGCAATTG

>RXA00971
AACCACGCCGAAGCCGAAGAACTCGACGAAGCCCTCTCCCCGCTCATTAACCGCCTCCGC
GAAATGGGCTTTGACCCCACCGAAACCGAAGAAGCAAACTCCCTCGCTCTACACAGCTGC
CCATTTGTGGTCAACGACAAACGCCCATCAGCCTTCGTCTGCGCCATCCACGCCGGATTC
ATCCAAGAAAGCCTCGGTGAAAACAACCGCATCCAGCTGGAACTCAAACCACTCAACGCG
CCGGGCACCTGTAAGGTTCACGTGTTCAGCGAA

>RXA00971-downstream
TAATTGCTGCACTAATAAGGCCC

>RXA00973-upstream
TTGTTGGTGCAGGCCTTACAGCCATTGCACTGAGTTCCATGCTGTCGCAGCCAGTACAGG
CCTTCACCATGACCATTGAGATGGTGAGTGTATTTTTCAC

>RXA00973
ATGAACCACTCTGACGACGATCGCATGCAAAAGTGGTTCCAGATCCGCCGCGAACTGGGC
AAAGAAATTGTGAAACAGCTTCAAAAGGATCTGCCCGCAGTCGCCTCTGACATCGGCTCC
ATGGTGTATTCCTCTGATCAAGTTCCCCTCGGAAACGCCACGCTCACTGCATACGGAGAC
ATCGGCAACCGAGTCGCTTCCGCTGCAACAAGTGCGAGATACAACGTAGAGGAACTCCTG

GACGCAATCGAAAACGCACGATTTGCCATCTGGGTTCCAAATTACGACAACTCCTACTAC
CTCTCCGGCGAGGAAGGTGCCGACGAATTCCAAACATACCTCATCAAAGATGCGTCAAGA
TTTCTTGAATCCTCCGGGAATACTCCACCCGAGAACCCGCAGTACAGCGACTCCAAATTA
ACCTTTGCTAGCGAACTACTCCCCTTCTACACCGCATTTAACAACTCGACCTACCCACTA
CTTCATGCTTGTGTGCAAGGTGAACCAACTGAAGTAGACCTCTACTTCTACGAGCTCGAG
CAGGCAGAATTGAAGGAAAAAGAGACTGCACAGCTCTCGAGTGGATCAAGTTTTGGCTCC
AGT

>RXA00973-downstream
TAGTCAGAATTCTCCTAAAGGGC

>RXA00978-upstream
TCCTGGGTAGCATGGGCTTATGAGCACTGATAGCCAAAACCCTGTAAGAAAATCCTGCGC
ACAGCCACATTCTTGTTCCCAAGAGGTGCGATTGAAAGCG

>RXA00978
ATGTCCAGGTCACCGCTTACTAAAGGTCTAAATCAACTTGAACACCTCGAGTTAGATAAG
TCACTAACTGCGTGGTCGTGGGCAGAAGATGATCCTTTGTACCTCGCAGGTGAGAACTTA
AACGGCAGTTACCTCATTGTCGCAGGACGAGTGCGGGTCTCTCGCGACACCATCGACGGG
AAAGAACTCACCGTTGATATTGCAACGCCCGGCGATGTTATTGGTGCGATAGATACAGAA
CCTCAGCCGGCAGTAGATTCCGCTTGGGCAATAGAAACCACCTGTGCGCTGTTTCTTCCA
GCAACCGCGTTGGCAACTGTGATTGAACAGCATCCAAGTTTTGCTTTGGCGATGATTCGG
ATGCAGCAGCAACGTTTGGCTACAGCCAGAGATCATGAAATTAACCTGACTACGACCACA
GTTGAGCAACGAGTAGCTATTGCAGTGAGAACTCTGGGACGAAAAATCGGGCAACGACGA
CCCGATGGAATCTTGCTCATTCAAGTTCGAATCCGGCGGGAAGATGTTGCGGGTTTAGCA
GGCACCACCGTGGAATCTACTTCTAGAGTTTTGGCGCGATTACGTAAAGAAGGGGTCATT
GATAGCGGTAGGGAA

>RXA00978-downstream
TGATTGCCGTGGTCGATGAACGG

>RXA00986-upstream
CTACTTTGATAACACCGCCACCCAAGCCAAGCCGGAGTGATCTCCGTATCCTTTAAGGC

>RXA00986
ATGACTTTAAAAGATAAGTACGACACTGAAGTAGCTGTTTCTAATAATCAGGACAAGCAC
CAATTTGAGGTCAGTTACCCTGAAGATGCCGTGACTGCTGGCTTTGCTGCATACCTTGAT
AAAGGTGATTCGCGGATCTTCTATCACACCGTTGTTGGCGATGAATTCGGTGGCAAGGGA
CTTGCGTCAATTCTTGTTTCAGAGGCGTTAAAAGCCACAAAAGAAGCTGGTCTTACCGTG
GTTCCGGTATGTCCCTTTGTTAAAGGATTCGTGGAAAAGAACGCATTCGAGGGTTACCGC
AAACCAAACCATGAGGATATGGAGCTGGTGAAGAGCCAGATG

>RXA00986-downstream
TAGAAACTACTCAACTTCCAGAA

>RXA00987-upstream
CGCGGGCTGCTTACCACGCAGCACAGCTAAGCTTTAAGGCCCTCCGGGGCCTTTTTTGCT
TTTCGACGCCTACCTCCTTCGGAGGCGTATTCTGTCGTTC

>RXA00987
ATGCCTAAATCTCTGACCTTTGAAGACAGCATTAACATCGCAGCGCCCATCAATCAGGTC
TACGCACTAGTTTCTGACATCACTCGAACTGGAGAATGGTCGCCCGTGTGTGAGAAATGC
TGGTGGGATGAAGACGAAGGCCCCGTCGTGGGTGCGCACTTTACTGGCCGAAACGTCACA
CCTGAGCGCACCTGGGAGACACGGAGCGAGGTTATCGTCGCAGAGCCAAATCGTTGCTTT
GGTTGGAGCGTGACTGATGGAAACGTCAAGTGGATTTATTCCATGGAACCGTTAGAAGAA
GGCACAGTATTGACTGAATCATGGGAATTTACCCCCAAAGGTCAACGATTCTTCCACGAC
AAATTCGGCGACAAATCAATTGAAGAAATTGAAAAGCGACGCTTGGCAGCTATAACCGGA
ATTCCAGAAACACTGGTTGCCATTCAGCGCATTCTGGAAGTTGAG

>RXA00987-downstream
TAGTTTCTACATCTGGCTCTTCA

RXA00988-upstream
TAGCAGAAGACACCGATGTACAGTCCGGATCAGGTGTTGTGATCACCGGTTCAATCGTGA
CCGCCGGCGATGCGCGCACGCTGTTTGGAAAGGAACCTGC

>RXA00988
ATGAGCAAGCGTGAAGAATCAATTGAGTACGGACCATTAGGCAAAGGCCACGATCCATTA
AAGGATCCCATGAAGGGTATCCGAGGTGTCATGGCCGGCACCTTAGTGATGGAAGCAATC
ACCTTAGGTCTTGTTCTCACCGTGATTCTGCGCGTGGACGACGGCATCTACTGGACCACC
TTCAACTGGGTCTATGTATCAGCAGTCGCGATCGCACACTTTGTTGCTGCATTTCTGCAA
AGGTTTAGTTGGTCCATCCCGATGAACATCGTGCTGCAGGTTCTTGCACTTGCCGGTTTC
TTTGTTCACCCCGCGATGGGCTTCGCCGCCATCATCTTCATCATCGCGTGGGCGTACCTG
TTCTACCTGCGCTCTAATCTGATTGATCGCATGAAACGCGGGCTGCTTACCACGCAGCAC
AGC

>RXA00988-downstream
TAAGCTTTAAGGCCCTCCGGGGC

>RXA01005-upstream
TGGGCACCGTCAACGATTGGACTCACGAAAGCTCCGACGACTAGAAATAGTAACTGTGTT
GGACACTTTTCACCTCCGCGTATTGAGCGAGGATGAGTGG

>RXA01005
ATGGAACTAGCCCGCGCCCACCACGCGCGGGCTGATTCATTCACCAAAGACCACTTGAAG
CGTCGACAAGCGCATATCAAGCACCCCGTCTTCGACTTCCTCTTCGAGTACTACCCCGTG
CGCGTCGCGCACCTAAAAACCTGGCACCCCGGCATCGGCGTGTTTCTAGAAGGCACACCG
CCGCATGCCACCATGCGCGATTTTTTGCTTGTCGACGCCTCCCTCCATCACGCAGCCGGC
GTCCAGCTTGACCTGGCCTCCTATATGCAACGCCGTGGGTCCTCTGTGCGCTACATCCAC
GAACTGTTGTCCGCCACCCGCGACAACCACGCCCAATTTGATTGTTTTGGTCTGCACGAA
TGGGCAATGGTGTACAAATCAAACGATCTCCGCCATGACCTTCCCCTGCGCCTTACCCCA
TCGGAAACCGACCGTGTGGTGGAAAGCCACAACATCAAATGCACCCACTTTGATGCCTAC
CGATTCTTCACCACACCAGCCATCCCGTTGAACCTCACGGTGTTAACCCGCGAAGATCAG
CCACGCAACGATCAATGTGGTTGTCTGCATGCCACGATGGATCTATACAAATGGTCCGCA
AAGCTTGGCCCTCTTGTGCCAGGTGATCTTTTCTTGGACGCGTTTGAACTAGCCCGCGAC
ACCCGCATCTTGGACATGGAGGCTTCGCCTTACGACGTCCGCGGATACGGCTTTGGCTAC
GTCCCCATTGAGACCGCCGAGGGCAAAGCCGAATATGTCAGTAGACAACGCGAGCTGTCT
GAACGAGCAAAACCCATCCGTGACCGGCTTGTCTCCATTACTAAACAAGCTCTACAGGCT
AGTATT

>RXA01005-downstream
TAGAAAATTAGACTTGTCAATGT

>RXA01007-upstream
TCTGAACCAATATACCGATCAGTCTAAAAGTGTGTTAAGTTCTGGAACATAAATTAGCTG
ACACGTAAAGTAACTTAAAGATTCACTGGAGGTAAGCCTA

>RXA01007
GTGTTTAAAAAGCACAGACACGGTCTCGGCTCCCCCGAAACCAAACCACGCTCAATAACC
CGCCGGTTTTTCACCGCGGCCGCCGCTACGCTGGCAGGATTGGCAGTCCTGTCCGGCTGC
ACAGCACAACCCTCACAAGCAGAAGACAACACGCTCACTTACTTAGAGCCACAGTTCTTC
CGCACCCTGTACCCACCATCAGCGGGCTTTTACCCCAACGGCAGTGTGGTGAACAACATT
GCAGACCGCTTGCTCTACCAGGATCCTGAAACCTTGGAACTCAAGCCGTGGATCGCCACC
GAACTCCCAGAAGTAAACGAAGACGCCACGGAATTTACCTTCAACATCCGCACCGATGTC
ACCTACTCCGATGGCACCCCGCTGACGGCTGAAAACGTGGTGAAAAACTTCGATCTCTAT
GGCCTCGGCGATCAAGATCGACGCCTCACCATCTCTGAGCAGATCACCAACTACGACCAC

GGCGAAGTAGTAGATGAGGACACCGTCCGATTCCACTTCTCTGAGCCTGCACCTGGTTTT
GCTCAGGCCACCAGCTCCTTCAACGCTGGCCTTTATGCCGATTCCACCTTGGAGTTCGCC
AATGAGGATTTCGCGCCAGGCAACGCCCAAAACGTCATCGGCTCCGGTCCTTTCGTGATC
ACCGATGAAACCCTAGGCACCAACCTCACCTTGACTGCGCGTGAGGATTACGATTGGGCA
CCACCATCACGCGAACATCAAGGTCGCGCGAAGCTTGACGCCGTCAATTATGTCCTCGCG
GGTGAAGAATCCGTCCGCATCGGAGCCATCGTTGCTGGCCAAGGTGATATCGCCCGCCAG
ATCGAAGCGCCAGTGGAGGCACACCTGAAGGATGCAGGCATCCCGATCATCTCCGCAGCC
ACCAACGGTGTGAACAACAGCTTCAACTTCCGCTTCAAAAACGAGCTGCTCTCAGACATC
CGTGTTCGCCAAGCTCTGATCCACGCGATCGACCGCGAAAAGATCATGCGTGTGCTGTTT
AGTGATTCCTATCCGCTGGCAACTTCTGTGCTTGCGCAAAATGCACTGGGCTACAAAGAA
CAAGTAGATGCCTATGTCTACGACCTAGACAAAGCAACAGCTCTGCTTGACGAAGCCGGC
TGGACCCTTGATAGCGACGGCATGCGTCGCAAGGACGGTGAACTTCTAGAGCTCACCTTC
AACGAAGCCCTCCCACAGCCTCGTTCACGCGAAGTTGTCACCATGGTCCAAGAACAGCTC
GGTGATCTGGGCATCAAGGTCAACCTCAACCCAGGTGACCAAGCAGCCCAGGACGCTGAC
TCCAAGGATCTCAACAAGATCCAGGTTCGCCACACCATGGTGGGTCGCGCAGACTATGAC
GTGCTGAAATCCCAGCTGTACTCCACCAACCGCAACGAGCTGTTGAACATGACCGTGGAA
GGGGAGACCGCCGATATTGGCGATCCTCATTTGGAGGAACTCCTCATGGCTATTGCATCC
AGCCCACGCGAAGAGGACCGTGCAGCAGCATCTGCCGCAGCACAGGATTACATCACCGAG
CAGGCATATGTTCTTCCACTGTTTGAAGAGCCAGTTGTCTACGGCGTGCAGCCTTACGTG
AAGGGCTTTAGCCCCGAAGTGATCGGCCGCCCCAGCTTCTATGAGACCTACATTGACCAT
TCCAGCGACCATTCCAGTGAGGAGGAC

>RXA01007-downstream
TAAATGACTACCTCGCAGATTCT

>RXA01008-upstream
ATTTATGTTCCAGAACTTAACACACTTTTAGACTGATCGGTATATTGGTTCAGACCAACC
TGTCTAATTGGGGTATTTATTTTAATGATCAGGAGTTTTC

>RXA01008
GTGAGCACAACCGATAAGCAGGTAGCCATCGTTGGAGTTGGCCCCAGAGGTATTTCCATA
CTCGAAAGGATCGCAGCAGCTCTCAACACAGTTTCCCGCCCCAAACAAGGCTTGACCATC
CACCTGATTGAGGATGCCCAGATGGGTGCAGGCAACGTGTGGCGCACTGATCAAACCCGC
ACGCTGTGCATGAATACTCTGGCCGGTGCGGTGACATTATTCACAGAGCCAGGCTCTACG
GTGAGCGCTCCAGTGGTGGAAGGACCACTGCAATTTGATTGGATTCGCCTGCTGCGCGGC
GATGAGGATTTGAGCGGCATTCCTACAAAAGCCATCGAGCTGTTCCGCACCTACCCCCCA
GCTGCATCCGTGGCGGAGGATTTCAAGGAAGAGCTAGCAGCCACTGTTATCCAGTCCAAT
CCTTCCCGTGCTCTTTATGGCGCATATCTGCGGTGGGCTTTCGATGTCGCTTTGCAGCTG
TTGCCACAGTGGGTCAAGGTCGAGCAGCACCATGCGCGCGCGATTGGCATCCGCGAAGAT
GGTGACCGCGATGTGATCACCTTAGATAATTCTGAGATGATTTCCGCCGATTCCACTGTG
TTGGCTGTCGGCTGGCAAACCCCCGCCCCCAATGCGGAGGAGCTGTCCATCGCGGCTGCT
TTGGAGGAGAACCCTGATCTGGTGTGGGTCAAGCCCGGCAACCCTGTCGAGCAGGATGCC
AGCCTCATTCCCGCTGGCGAACAGGTGCTTGTCCGCGGGCTGGGCATGGGATTTTTCGAT
ATCATGGCGCTGACCACCATCGATCGTGGCGGCATCTTCCACGAGGATCCCAGCACCCGT
TCCGGTTTGCGCTACGAGGCATCTGGTGAGGAACCACACTTTGTTATTTCCTCCGGGCGC
GGCTACCCCTACCTGCCTAAATCCGATTACAAATCGCTGCCACCAGGGGCAAAGCTAGCG
CGACTCAAGGCTGTTATCGCGGCGATCAACGCGCAAAATCGTGGTGTCGCATCCATCAAC
TATGATGCGGAAGTGTGGCCAGCTGTTGCTCGCGACGCCTACGAAGCCTATTACGAAACC
CTTGATCGCGTAAGCCCAGAATCTATCCGGACCGGTCTGGATAAAATTGTGGAAATTATT
GATGAGGTGGACGTCGATAAGCTTCCTAAAGCACTCGCCGCGCACACCGATGACGTCTTT
GACCTGCATGCTTGGGAATTTCCGCTCGCGGGAATTAATGAAAGCGTCGAGGCGCTGACC
GCACGCATCGCGGACGGCATGGCCCGCGATATTCGCCATGCAGTAACGGCCTGGGACAGC
CCGCTGAAATCCGCGCTGTGGTCCATTTCCGCCGCGCGCAAACCCAGCTCCATCCTGGGC
GCGGAAGGCCGCCTGACCTTCGAATCGCGCCGCAACCGCTTCGCCGCCGTCATGGCGATC
GGCCAGATGGTCGGCTCCGGCCCACCGCTTTTCCGCACCCGCGAACTTCTTGCGCTTGTC
GACGCCGGCCTCGCTCACTTCGCCGGCGCCCGCCCCCGCCTCAGCGTGAGCGACGGTCAA
TGGCAGATCTCCTCGCCCACCACCGGCGATACGCCGCTGAGATCGAAAGTGCTTGTCGAC
GCGTGGATGCACAACCCAGATGTGCGTCGCAACGCCGACCCGCTAGCACTGTCTTTGGAA
GATGCCGACCGGGTACGCCCCTTCAACGACTATTCCGTCGACGGAACCGCTGCCCCCACA
GGCTCCCCCGAAGTTGATCCGGCAACCCGACTTTTGGTTCACCCCAACGGCAACCTCGAT

CCGCGCGTGCACCTGATTGGCATCCCAACCTATGGGCAGCTGGCCGACACCACCATCTCG
CCGATGCCTGGAACCAACCCGCTCATGCTGCAAGAAACCGACAAAACAGCCGTTCACGTG
CTAAAGCAGCTCGGCTTGATC

>RXA01008-downstream
TAGGGTGAGGTGAGTTATTTAAA

>RXA01011-upstream
CCCGCAAACCGATTTCACTCGCCGACTCATCGACGCGATCCCAGGATCGCGCTATCGTGG
TGGCGAACTCAATCTTGGACTATAGGAGCAGATCTTAAAA

>RXA01011
ATGTCAGATCTCATCGACATGCTGGTTGGAGAAGACCTCCCACAGCTGCGTGACAACCGT
CCCCAAGCTCGCGACAATGCACAAAAGAGCTTCGAAGCTCTGCTCGAACCGGTCAACCCA
GGAACCTTCAGCTTCGGCGAGCGTTACGCCGTGGCCACCTATGTTGCAGGTTTGCACCAA
TTCGCGCCAGCTGTAGATCTCTACCAAGATTTGCTTCTCGACGACGCCCCAACCACCCTG
GCAAACGCCGTCTCCGATGCCATCGACGAGGGCCTATCCGCAGGCCCATACGGCACCTAC
CGTGAACCTGGACTTGAGTCCGAATCAGAGCCAGGCGGATCTGTGCGCAACGATGCCGCC
AAGCTTGGCGAGCGACTTGCAGCAGCATTTGATTACGCACACCTACTAGTTTTCCACCCC
CGTGATTCCCGCCCCGAGGTCCTTGGTCGACTCTCCGGCGCTGGCTGGAGCGCGGATGAC
ACCGTGACATTGGCTCAGCTGGTGTCGTTCCTGGCATTCCAGCTGCGTGTTGCCTACGGC
CTGCGCACCCTCAAAGGTGAAGACATTCAGGTGAAAGCTCCTCGCCTGAGTATTCCTGAA
GCGAAGTGGGAACTGTCCAACAACGGCTTTGAGATCTCCACCTATGAAGAACTCAACCGC
CCTGAAGCGTTTGTGAACCACTCTTTGGGCTGGAAGCCATGGGTACCACCAGTAGCAAAG
GCAGATCTCACCGAAGAACAGCTGGATTCTTTGATCCAGCCTGAGCGCGCTGATATGCCA
TACTTCCGTCTCTTGGCACGCGATCCTGCAGCATTGAAGGCGCGTACCCTGACCGATCTG
GATATCTTCTTCAACACTGACGGCGAAGGCCTAGGACGTGCAGAGCGTGAACTCGGCGCC
ACCGTTACTTCCCGCTACAACGGCTGCGTGTACTGCGCATCCGTGCACGCAGGACGTGCT
CAGGAAGAATCCGGTCGAGCTGATGATGTCAACGCACTGTTGGCAAGCATCGACTCCGAT
CTGGGTTCTGACCAGTGGAATGTCATCCGTGACGCTGCTCGCGCACTGAGCTCCACCCCT
GCTGCTTTCAACCAGGGATGCATCACCAAGCTGCGTGGCGTTGGATTCAGCGACCTGCAG
ATCGTGGACTTGATCAACTCTGTGGCGTTCTTCAACTGGGCGAACCGCCTGATGTTGTCA
CTGGGTGAACCCGAAGTGCCAAAGCGTTTCCTG

>RXA01011-downstream
TAAAACGCATAACCCCGAATACC

>RXA01016-upstream
TGCCCGTCGAGGTGAACGCCCAAGAATAGTTCTCTTTCGTCGACTTCTCACGTTGATACC
GCTCGGCATCATCCACCAAATTCTCCAGCCGGGTGAAGCA

>RXA01016
TTGTTGCCGTATGCAATAGTCGGCCTGGTCATTTTGCTGCCATCCTCCTGGTTGCCTCGT
TGGGCTGTCGCAGTCCTTGGCGAAGTGTCGCTTGTGCCAGCGGTGGTTTTCGGTGGCGGG
TTCCTGCTTATCCCCTCAATGTTCCTGATCGGTTCAGCGCTCGTTAGGTATGGAGTAGTC
GATCGGGCAGAGAACGCACCGCGGGCTATGGGAGTCTTTTTCGCCGTAAGCGCAGCAATC
GCTATACCTACGCTGATCATCCAGGCACGTGACATCACTTCTTCAGGCTTCTCGATCGTT
TCCACAGTGGCGGGACTCGCGCTTGGCGGCGTCTACATTTCTTTAGTGTTGCTGGCCTTG
CATACACCGATTCGCGGTGCACTCGCTGCAGTTTTCGCACCTTTAGGGCGTATGGCGCTA
ACCAACTACATTGGTGCAACGATCCTCATGCTCATTGGCGGGCTAATCGTGGATCTTCCA
CACAGCACATCATGGACAGCTACGGTGCTCCTAGCTGCGGGTATTCTCATTATTCAAGAG
CTACTTTCTGCTTTATGGTTGCGCCACTACACACAGGGGCCACTTGGGTATCTATGGCGT
TGGGTGACTTGGGGAAGCCGTTCCCCCTTCCTTACCCGTTCCGCATCA

>RXA01016-downstream
TGACAGGTACGGAAGTGTCCTAC

>RXA01017-upstream

GAAATTTGAGGGGGCGCTACCCTTAGAAGGTGCGCAATGACACCACGATAGTTCGCGCCT
AGTGTGGATTGCTAGAAAACTTTAAGAAAGAGGAAATAAT

>RXA01017
ATGGCTCAAAAAGTAACCTTCTGGTTCGATACCACCTGCCCATTCTGCTGGGTCACCTCC
CGCTGGATTAAGGAAGTCGAACAAGTCCGCGATATTGAAATCCAGTGGGTTCCAATGAGC
CTCGCTGTCCTAAACGAAGGCCGTGATCTCCCAGAGGATTACAAGGAGCGCATGAAGGCT
GCATGGGGACCAGCACGCGTTTTCGCAGCTGTCGCCACCGACCATGCTGACAAGCTCGGC
GACCTGTACACCGCAATGGGTACCCGCATCCACAACGACGGTCGCGGACCAATCGAAGGT
TCCTTCAATGATGTCATCGCAGAGGCACTTGAAGAGGTCGGCCTAGACGCTGCACTTGGT
GAAGTTGCAGACACCACCGAATGGGACGACGCACTTCGCGCATTCCACCAGACCGCAATG
GACGAGGTCGGCAACGATGTCGGAACCCCAGTGGTCAAGCTCGGCGACACCGCTTTCTTC
GGCCCAGTGCTCACCCGCATCCCACGCGGCGAGGAAGCAGGAGAGATCTTCGACGCTTCC
TTCAAGCTCGCAAGCTATCCCCACTTCTTTGAAATCAAGCGCAGCCGCACTGAGAACCCA
CAGTTCGAC

>RXA01017-downstream
TAATTAACGCTGTCTCTGCTTAT

>RXA01021-upstream
CGAGAGGCTTTTTTGGCTCTAAGCCTTTTAGTCGTGCGAACGAAATCTTAAGCAGCCTCG
GTGCCACCGAGATCGATTGGTCGCTGTAAGGTATCTGATT

>RXA01021
ATGTCCAGTTCCGAAAGCTCGCGTTCCGAAGGCTCGCAGCCAGCACCGTCTGTACAGCCT
GAACGCCGTGCTGATTCAACGGGGGCTCCTGCGGCAGCTTCCAAGGAAGCTTCCCAACAA
ATGGACGCTGCCGGAGTTCTTGAGTGGGCCAGGACCGCTGTCGAGCAGCTTTCTGAACGT
CGTGCAGAGATCAATGCACTGAATGTCTTTCCTGTTCCAGATGCAGACACTGGATCAAAC
ATGACCTACACCATGACAGCTGCGTTGGATGAAGCGCTGAAACTGGGGGAGTTGGGTGAT
GTCGCAAGGATTACTGAGGCTTTGGCTGTTGGTTCTGTGCGTGGAGCCCGAGGAAATTCT
GGAGTAGTCCTTAGTCAGGTCCTTCGCGCTATTGCTCAGGCAGCTGCTGACGGGGTTATT
GATGGCCACACAATCCAAGAAGCGCTATCCATTGCTCGCTCCCTAGTTGATCGCGCAATT
ACAGATCCTGTGGAGGGCACTGTTGTCACTGTGTTGCGTTCT

>RXA01023
CCAGCCAACGGGGGAATTAACAAAACCCCCATGATTATTGCCCTAGTGTTATCTATTGTG
TTGGTTTTGGCGGTGCTGTTCGGCGCCCGAGTCCTCCTTGGCCCCGCCGGCCAGCAACAG
ATAGCCATGAGTGGGCTTCCCGCCCCAGACGCAGAATCTGCTGAGTGCGCCGCATTACTC
GAGGATCTCCCCGGCGAGGCCTTCGGGCACACCCGTGCAGAAATCATGGATCCTGTTCCA
CCGGGCGCTGCCGCCTGGTCCACCTCAGACCTCGAGCGTGTGACGCTGCGTTGTGGCGTC
GATATGCCATTCCAGTACACCGCGCTCGCCAACACCGTCGACGTCGACGGCACCACCTGG
CTACCTGTCTCCGACATGACCCCCGGCTCCTCCCTGGAGACCTGGTACTCCGTCAACCGC
TTCCCCGTCGTCGCCATCACCGCCGATGACATCAGCACCGACAGCGCCGACAACCCCGTC
GACCCCTTCAGCAGCGCCGTCGACAAGCTAGAAAAGCGCGACGGCCAGCCCTTCGACGCC
CCACTTACCGGCTTGAGCTCAGCCGGCACCACATGCACTTCGCTTTTCGACGCCCTCCCC
CGCCAACTCGAAGTCGGCGGCGACGACGGCACAACGTACGAACGCATCGAGGAGGACCGC
ATGCAGGCCGCCGGATACTCCGACGACGCAGTCGCGTGGGACACGCCGGGATTAGAACCC
ATTGTGATCCGTTGCGGCGTGGAGCCTTCTGAGAACTACGCAGCCGGTGCCATGTTGCAG
CAGATCGATGACATCCCGTGGTTCGAGGACACCATTTTGGCCTCCGGTACCACCTCGTCT
ACCTGGTATGCCCTTGGACGCGAGATCGACATCGCCGTGTCTCTGCCTCAGGCTGCTTCC
TCTTCCCTGATTACTATCTCCGGTTTCATTGAAGACACGGTTCCTGCGGAA

>RXA01023-downstream
TAAGACATAAAAAATCGCCCCAC

>RXA01028
TTTTACCAAAACATTTTGGCCTCTTCACGCGGTTCTAATACCTTCCTATTCTCTGTCCCC
TATATCCCTGCAACAGAAGGAGAAGAAACCCACCCTGCAACAGATACCAGCACTATTGCG

ACACCAACCTTGAGCTTTGATGCTTATGGTAATAAGGCCGAGGTCATGCCGACTCAATCC
ACTGTGGATAAGCGCGTGCCCTCTTTGCTGCAGTATTACACGCGTACATTCCATGTGCGA
CAAGATACGCAGCAGGCTGTCTTTGATGTTATTGGCGCCAACCCCGTGCTCATCGCCGCA
GCAAAAGCTGCATCCATATCACCGGCTTCTGCTGATTCACGTAGAAAGAAGGGCCTGGCC
TCCACCAACGCTGACCCAGTAGCCAAGCATGTACTAGAAATTGCAGGAGCTGATGTGGAA
TCGCTGCGCCATGAAAAGGATCTCAAGGTCACCAAGCACACTGGCCAAGACCCAGCACTG
CCTGTCGTGGTCTTTAACCAAACCATTTGGCATAACCCCAACGACGATGTGATTAATGCA
TTACTGGGCGCTATTGACCAGGATGCCTACATTGACATGGCGATCTCGTCCTACAACAAG
TCCTGGCACAACATTATCCCGGCT

>RXA01028-downstream
TAACTACCGCTGGGTAGACCCCT

RXA01029-upstream
ATGGGTGGTTGTCTTAATTAAGGGTGTTGCGTGAAACACGCAACCGGAGAGGAGGGTGAA
GTGTGGGGTTCCTTGCGGGCGTATGTCCGGGGTGCTTGCT

>RXA01029
ATGCTTCAAACGATTTCATTCAAGAAACTTAATTTATTAACAACTCTTAAAAGAAAAGGA
GAGCTGGTCATCATGATCACTCGTCACGATGTTCCCTACATCATCGCTCCGCCTGTCTAC
GCGATCTTTGCGAGCCTGATGACCACGCCACCATGGTTTTATCGAACCACCTACACCATT
GACGGTTTCGATTTTAAGATCAGCTGGGTCTACACCATCACCATCTACATCAGCCTCATG
ATCCTCATTATCGGGTTCTACCAAGCCAATATGCGCAAAGCGTGCCCTTATGAGGAAGAT
CCTTTGGTCGATATTTGGCACAAGGTGTGGAGCACTGCACTCTTTATCCTACCTATCGTT
TTATCCATCGCGGTGTACTCACTGATCACACAGCGCGGGTTTGACTGGTATGTCATGGTG
TTTATTCTCCCTGTAGGCTTGATGATCGCTTATGGATTCTTCAAGCCCTGTGATTGCGAC
AAACACCGT

>RXA01029-downstream
TAAGGTATACTTGTCCAAGACTT

>RXA01031-upstream
CAGCTGAACTTGATCATTTTGATGATCTGCCAGTACAGCGCCAAGAAGATCTTGGCACCT
TAGTTGTTATCTCTGCTGTTCACGCAAGCGACTCTGCGGC

>RXA01031
ATGAAACTGCTGCAATACGCAGGTGGTGCTGTCTATGTCGATCCAGAAGATTCTGCGCAG
TCCCAAGACCTGGATGCCAGCACTGCACGTGATGTTATCGACGCTACCAACACCGCCATG
ACCACTATTACCTCTCGCCCCACCATGATTGTGCACCTGCACAAGGTGCGAAAAGTCATT
GAGATTTTATGCAACCCTGCACTCGGCGGTGAACCTGTCAATATCGACCAGGACGAGACC
GGAAAACAGGTGTACACACCCACCCCAACGCTTGTCGCCTATCGCTTTATCTCTGACAAA
GAAATCCTGCTTCATTACCTGGCGCAGGCGGGTGTGCAGGGTGTGGAGGTTTTTGACGGG
TCGCCTGACATGCTGAGCCGTTGGAATGCGGGACGCATTCCGGTCTTACTTTTGCAGCCT
GCGTCTGCTGGTCACGGCTTGAATTTCCAGCACGGCGGGCATCGCTTGGTGTGGTACAAC
CTGCCCGATAATAACGAGCATTATATGCAAGCGAATGCTCGTCTACATCGCATTGGTCAA
AAGAATCCCGTGACCATTCACCGCATTATTACCGCTGATACTTATGATGCGAATATGCCG
GCGATTCTGGCCGGTAAAGCAAATAGACAGCAACGTCTCATCGACGCCGTGCGCCGTGAT
CCAGTC

>RXA01031-downstream
TAAGACCGGCACGATCGCACCGT

>RXA01032-upstream
AGCTAATCAGCACCACCTACAACACCACAAACACACCCCAATCAGCATGATCGTGCCGGT
TGGGGTGTGTCTTATCCCCTAAGAAAGTGACACCTTTACC

>RXA01032
ATGTCAGACCACGACGCCCCACAAACACCGATCCCCAAGGGGTTTTGGCAGCAGATCGAC

CACCAACTCGATCGCCTCGGCACGCAGCGCCCAGAGACCTTCGCAGCACTGCGTGACATT
TTGCTTGATCCTGCCTACACCGCCATTGTTCATGACCGTAATCGCTACGGCGTTGTCACC
TTTGACACCAACTCAGCCTTCTTCTCAGGCTCTGGCGGAGACAACGGCTTAGCCGACGTA
CTCATTAACTGTGATTGGCGCATGACTGACTACCGCGCCGAGTACTACTACGTCATGACA
CATAAATACACCAAGGAATCGTTTACCTATATCGAGGGCGACGTGAAACGCGGCGACCTC
ATCCCGCCTAATAAT

>RXA01032-downstream
TAAGGACAACCGCCATGACTCAG

>RXA01033-upstream
ACGTCATGACACATAAATACACCAAGGAATCGTTTACCTATATCGAGGGCGACGTGAAAC
GCGGCGACCTCATCCCGCCTAATAATTAAGGACAACCGCC

>RXA01033
ATGACTCAGATCGCCATGTATCTCGCAGGACCCATGACAGGTATCCCTGAATACAACTAC
CCCACCTTCCATGCAGCGGCTAATAAGTTCCGTGCAGCTGGCTACACCGTACTCTCCCCC
GCTGAAGACGAATATGAATCCCAGCTCACTGCACCATTGCCTGAGAACGCTGAGCACAAA
TACGACCACTACTTGCGTCTCGGTATCGAAAAGCTGCTCAAGGCTGATGCTGTCCACATG
CTTCAGGGATGGCAGAGTAGCGCCGGTGCCACTCTTGAGCACGATATTGCACAGAAATTG
AGGCTTGCCATTACCTATGAAGAACCACCAGCATCC

>RXA01033-downstream
TAAGGCGCCTCCGGCATAGCGTA

>RXA01034-upstream
AGAAAGTATGTCAATAACTTTGACATAACCTAAACACAATAAATTATGTAGTATTATGTG
ACACTAAGTTATTACATTTATTACATGATTGGTTAGGACT

>RXA01034
ATGGACATGGCCATTATTCAGTCGGTCGAATACACATCTGATGTCTCACATGAGCGCATC
ACCAATGTCGTCTCTGTAGGCGTGGTCTACGAGGGTAAACAGTATGTAGTGGACCTTAAT
GGTGACGACATTGATACTGAGCTCGATATGATCACGCTCAAAGAAGTCATCAAGATTGGT
CGTGAGGAATCTGCACGCCAGATCCGTCGTGGATCTGTAGATGCAGAGCTGCACCGTAAG
GCGCGTTTGTGGGCTATTGACAATGACATGGCCGTTGGTCAACGTGGTATCGTGCCACAG
GAAATCATCGACGCGTACAAAGAGTACTGCGAAAAAGAAGGCATTCCTTTCGAA

>RXA01034-downstream
TAAGAGCCCTGTGGAGAATTGTT

>RXA01035-upstream
GGCAGTGATGCACCGCACTTGAGAAAAATAAATCATCTCAAGAAACAAACTAATACGTTA
TTATTGTAATTTAATTAGAGAAAAGAAAGTGACTTTTAAA

>RXA01035
GTGCTTATTCGCATCGCCGAGCATCAAGGCCGGCTCCATGTCCATAGCCCCTACTCAAAG
GCTTTTGCCGCCCGCGCTCGAAAGCTCAACGGTCTCTGGTCACCCGAAACGAAGACCTGG
CATTTCAGCCCCGATAAAGAACAACCGGTGAGACGCGCACTCAAGGATGTCTACGGCTGG
GATGAATTCACCACACCCGAGCTATGCACGGTGCAGCTCACTGTGACCCCAGAGGCAGTG
CTCAACAAACACACACTCACCATCGCTGGTGTTACACTTCTGAGCCGTTTACGCAGAAAT
TACTCGGTGTGGTTGGGTGATAATGTCCGCATCATCAGTGGCAATTTCCCAGAAGCAGCA
GGATCACCCCAGTACCCCCTCATCATGGGTGTGAAGGCTCAACCCGTTGTTATCCATGTG
CAGGAATTCCCTGTAGATGCTGTTTCGACTATTCCCCCGCGATTTAATCCTATTGTTATC
ACTGCACCGCCGAGCATTGATATTGCTGCTCTTCGAGCTGAACGCGAACAGCTCACCCGA
CGCATCAGCGAAATTGACAAGAAAATCGCACGTGCTGTGCATCCAACCATTCAGACTGAG
GCTGCC

>RXA01035-downstream

TAATAATGATGCAGACTCTCAAG

>RXA01036-upstream
CTGAGGCTGCCTAATAATGATGCAGACTCTCAAGCGGAAAATTCCGCTCATCTCATGCAA
TGACCTCAAAGAAGTGCAGTTACTTTTTCTTAAAGGTCAG

>RXA01036
ATGCACACAGTCGGCTACAAGCTAGATACCGATCTTCGCAAGCTCACTAATACCGATGTG
CTTGATCTTATTAACGCGCTCTTCGGCACCACTGTGACCAGCGCAGATGACGAAGCAGCA
GATTTCATTGACTCTGATCCTCAGTTTGCAGTGCTCGTTGAGCTGGCCTACCACGACTGT
GCACGCCGCGCTGCCATGGGTCTATCCAGGGTACAGCAGCTCATCTATGACAATGCGGCT
AAATCAACCTACTACCGCAGCGTCGCAGCTAGACATCGCAAACACATCCGTGAACTCCAC
GAGCAAACACAGCGAGATGGTATTCACTTCGACAACCCGTTGTCTCGTGCAGTCATCAAC
GATCTCAGCATGTCCATGAACCGTGCTCGACTAAACCGCATCGCTTCATGGAAATCAGCC
GGCGTACAGCGCTATCTCAACCCCACTATCTCT

>RXA01036-downstream
TAGAACCACACACAACCAAGAAA

>RXA01037-upstream
CGACTAAACCGCATCGCTTCATGGAAATCAGCCGGCGTACAGCGCTATCTCAACCCCACT
ATCTCTTAGAACCACACACAACCAAGAAAGCAGTCACTAC

>RXA01037
ATGACCACCTCATCACCCCTTAAGTCCAAAAATTCCCTTAACGGCGCGCAGACCACATTT
GTCCGCAATTGTGTTGCAGACGGCCCAACCGAGGTAAAAGCCACCATTGATGCACGTGGC
GGTATCGAACAGCTCCGTGACAATGAGATTTCACAGCTCCCCGACAAGCTGTGGTTCAAT
AGCGCAACCTCCGCATCCAATGACGAGTTCACCACCGATAACATCCGACTTGGGTTGCTC
TACAACATGGCACTGAATAAGGCATCGGCTCATCGCTATGAGCTTGCTGCCCGCTGGTAC
GCCATTGTTAGCCCTCAGCCATCGCAAGAAGCTAGCCACAAGCGCATCGCGTCCTGGCAC
CTTACCCAGCTGCACGCACTGGTGACCCTATCTCGCACCCTAGGGGTCATCATTCCTGGT
GATGAGATCGACGCTCTAGCGCAGTCTATGGAGAATGCTCGTCAAGTTGGCACCGAGAAT
TGGTCCACTGTCACCATGCGCACCTACGTGACCAACCGCAAGGCATCC

>RXA01037-downstream
TAATGACTCGCGATATTTTCCAC

>RXA01038-upstream
ACGCTCTAGCGCAGTCTATGGAGAATGCTCGTCAAGTTGGCACCGAGAATTGGTCCACTG
TCACCATGCGCACCTACGTGACCAACCGCAAGGCATCCTA

>RXA01038
ATGACTCGCGATATTTTCCACGAGGCTGCAAAACTCATCGCACACCTGGGGTGGAGGGAC
GCTTTTCCAGCACTACAGCGCACTGACCCAGCGCCAACACATGCTGTGCCGATCAGGGCC
TTTGATCTCAAGGCGGGCGCCGTCATCACCGATGAAAATCGAAGCAATGCTTATATCTAT
GACACCCTTGTCATCACGCAGCCATATAAGCACGAGTTACCTCATCAAAACACCCACCCT
TTTGAGTGGGCCCTGGAACAAATTGCCACGCTTGATCCGGCGTTCTCGATCAAGCTCGAT
CGCTCAGTGACCGTCCCTGAAATTGGACTCTACGCCCGCACACTGCATGACCTTAATACT
CGGCATCAAGACTTCTTGGCACAGCGCAACGCCATGTTGCTTGTTGTTGCCCGTCGTGGT
GTTGATCCAAAAAATATCGCAGACGTACTTGGTTTAACCACCAATCAGATACATCGGATT
CTCAGTGCTACTCCGGCTGATTCCCCTACTGATTTAGGCGTTAACCCCGCCACAACAATG
GGTGATGTAGTGAGGTTTATCAAGAAACGTCGCACCACTATGCAACTACGCGGCACCGCT
GTCCGTGCACTGCTCTATCACGGCCTTACGCCGGCAGTCATCTCCCGACTAAGCGGCATG
TCGCGTGCGGGTGTCATCAACGCAGCCAAGGCATTCCCCACCACCATCAACCACAAGGTC
AAGAAAAGAAAGCAGCACTTCCATGTC

>RXA01038-downstream
TAATCTCGGCACATACTATGCAG

>RXA01039-upstream
AAACCTATATGTTAATAGTAACAGAAATTAATAAGATACTAGAGTTTAATTTGTAGTATC
CAGGGAACATTAAACGGGTAAAGGTAAAGGACAAACGAAC

>RXA01039
ATGGCGATTAAAGGCGCAATGCCGAAAAATCGAGTACCAGGTGTGGCAGCAGGTGCGTTT
ATTGCTGCTGCCGTTATTGCAGGTGGATCAGGCGTGACCTTTCTCGCCCAAGGCGGTGGT
GATGTCAATACAGTGGCCGTCGTCGAGCCACAGGACGAGGTAAAAAATCAGGTCGTGACA
GAAACCGAAATTGTCACGAAGGTTCACGATCCTTCTTCATCTGACGCCAGTGATGCTGAC
AGCAACACAGGCACCGCCGAAGGCGCAGACTCAGATCACAAAGAACCCCGTGAGCACGAC
AGTGCTCAAGAGCCAACGGCTCCGACCGACCCCACCTTGACCATTACCGGCAACGGTGAC
ACACCAGTATCAGCACTTGATGCTGTCGCAGGACCTGCCCGTCCAGGTACGGTGCACGTC
ATTGAGAATGGCGAAACCTTGTCCTCTATTTCTCAGGACAGTGGTGTGCCGGTTGGGTTG
ATCATTGATCGCAACAAGCTTGTTGATCCAGACCTGATCTATGCAGGCACGCCATTGGCG
ATTCCGACTGAGCAGGAACTTGCTGCTGCGATACAG

>RXA01039-downstream
TAATGTAGTGGTAGAGGGTTAAA

>RXA01040-upstream
TAATTTCTGTTACTATTAACATATAGGTTTTTTAAAGTTTCGTCTACATAAACCTGCAAC
AGAAATCACTACACCCAGTTCTCGAAAGGCTTTTTCTCTC

>RXA01040
ATGACCTACCCAGTTACCCCTCAACCTGTGCAGCCAGCACCAGTCGCCGAAAAGATCAAG
GCATCAAGCCTCAAAGAAGGCACTCAGGTATTTATCAAAGGTCGGGTTAATTACTCCCGC
ATCGCAAGCTTTATTACTGGTACCGAGCGCGAAAACCGTAATCGCGACAGGCTTCACCCA
ATCGAATTCGACTACACCTCCCTGACTTTGAGCCACCCTGAAATCATCTACGGCAACCCG
CAACAAAAGACCAATGAAGAACTCTTCCTTGAGCAGCGAATCTTTGTCGGCAAGAAGCGT
CCTGAAGAGGGTCCAAAATTCTCCATTGACAACAAGAGCAACCGTCTACCACAGGTTTGG
GTGCCATCCACCAATGCTGATGGTACTTATGAGCAGCTTGAAGGTCTCGAAGGTGAGCTC
GACGCAGGGCTCAACGTCATTATTCTCATCGAGTTCTATAAGCCACGTACACAGGTTAAT
CGCGGCTCCCGCCTCAACGCCGTGTTCCTGCAGGAGCCCATTCGTTACTACACCCCTGGT
TACAATGCAGATAAGCTCGCTGCCCTCGGAATCGTACTTAACGCACCGCCAAAGGACACT
ATTCAGCTCGTTCCTAATGAGGTCGCTGCAGGACAAGACCAGTCCACCACCGATGCATCC
GGTCTCCCGCTTCCAGGCCAGGGATATAGCGCACCTGATCAGCCATATCAGGCGCAGCCT
CAGTATCAGCAGGCAACCCCAGCGGCTGCACCTCAGCAGTACCAGGCCCCACAGCCCCAG
TACCAGCAGTCAGCTCCACAGGCACAACCTGCACCGGCACCAGTTGCGCAGTTCCAGCAG
GCAAGCGCCTCAGGCACCTGCTCAGCCAGCACAGCAGCAGTATCAGGCACCACTTCCTGC
CGG

>RXA01040-downstream
TAATCCTCTTGCAGCAGGTCAGC

>RXA01041-upstream
ACAGCAGGCAATGCCTACCCAAGCCCCACAAACACCGGCACAACCAGTTCAGCCACCAGC
ACCACAAGCCGGTTCTGCATTTACCGATGCTCCGGGTGCT

>RXA01041
GTGCCACAGGCACCAGCAGTTCAGGCTGCTCCCGCTGTAGCTCAGGCGCCTGTCGCGCCA
GTAGTTGATATGACCGAGCCAGCATCCCCATGGGATCTTCCAGCTGCACCTAGTCAGCCA
GCGCAGCCAGCTCAGGGCATCACCTACCCGGCA

>RXA01041-downstream
TAACAACCAGCACAACCCTTAGA

>RXA01042-upstream
TTTTTTCACCAGGGTCGAGGCGCGGTCTGTGTGCCCACCTCGACCCACTTTTCGCCCACC
ACTTTTCGTCAACCTACCAACAACAAAGCCCAGGTCACTT

>RXA01042
ATGGTCAACCCTTTTCACACGCTTGATAACTCACCGTTTGATCCGGTGGCACAGTTTCCT
GCGTTTTATCACAACCCGCTTATCAATCACTTGGGCCGCCGTCGCGCCTGGACAATCTCA
GACATCAACAAACGCCCCATCAATGTCCAACAGATGCTGACCACGGCCACCTACGGTAGC
CCCGTTATTCATGGTGCCCGCATTGAAGACGCAGCAACCTCCCTACTTACCCTGGATGAA
CTGCGTACACAGATTCCCACCGCTGCCAACAATGCGTTTTATCTCGATGCTGTCCAAGAT
GGCTGTCTTATTTTAGATATTGAAAAAACCTGTCCCCCCGAGGTCGCAGCCACACTACTC
ACGCTCTCCCCCACCGCCTTTTACACAGAGGTGTCCATGAGTGGTCGTGGCTATCACCTC
GTTATGCCGATACCAGAGAATTTTGCAGCGTTTCCTGCCGTACACAACAAACCCAGTATC
AAACACCCCAAGCGCTGGTTCGAAATTCTTACCTCACAGTGGATCACCTTCACCCGACAA
CCAATCCCAGAGCATGTTCTCCATCACAGTGAATCTGCTAACACAAGTGCTGTGCCATGG
TTGAATGATCAACCACTTACATGGGAAAACGTCTTTGCAGACTTAGCTAAAACTGTTGCA
CCCAACTTAAAAACCGGTGCCGGACTTACCATCACACCCAATGCACTGATGCCACCAGAT
CTCAGCGATGCTGAGCGCATTCGCGACGATGAAGTCATCGACTCGACCTGTCGATTATTT
GCCGAACATTACTCGAAAACACTTGCGGACTTCTATGATGATGCATCCCGGTTCGAGTTC
AGCCAAATTGGTGTCATTATCAATCTACTGCTCCCCACTATGAGGATGCATCCCACCACG
ATCAGTCTCGACAAACCCATCAACTCCGATCACATCATCAGACTTCTGTTCGCTGTCGCT
ACTCGCGTGATCACTCACCGCAGCAAACATGATGAGGAGCGATCTGGCGTTCCGTATCTG
ATGTATCAGGTTATTTCCTGCCTTGACATGCGAGAACACCCCGACAATGGCGACTACCGT
GTCGTACCCTCCCGGCATAATAGAGACCAACACAGCAACAACCCCTCAGCTCATGTGGTC
CACCAACAACCACAACCCCAGCCCAGCGCAGCAGATTCGCCACATCACTACCGTGCACTA
CCCCAAGAAAACACGGTGTCCGAACACAGTTTTAAAATCTATAACCCACCAGCCACACCC
CCTCTAGGAGGTGAAAAT

>RXA01042-downstream
TAGATTTATTATTAAAACACTTG

>RXA01043-upstream
TACTAGGTATAGCAACGGATTAAATAATCACTATAATTAATTCTTTCCGTACTCATTTTA
ATCACTACCTATTCACCACTTGAACGGAGCGTTTTTCGCC

>RXA01043
ATGTTGAAATTCCGCATCATCTCCACAGTCACTACTGGATCTCAGCCAACTCCACGAAAA
AGCTGGAGCCACCCCGACACCACTCTCCTGGTCACCATGGTCACTGCACCATCGCTGTGC
TCAGCCATCAACGTGTGGAACGCAACTGAGCGTATTCCCGCTCAAAAAATCCTTAATGTC
GAAGAAGTACACGTTCTTGGTGAGTGCAGCGACGCCATCATCTCTACGTCACTAACCAAA
AAGGACAATCCGCACGCACTTGTGCCCGATGATTTCGACCAAATCGGCGATGTGTTTGGC
TATGCGCAAGACAATGTAGCTGTTTTTGATGTCATTGTCGCAGCACTGGGCGGTGCTGGT
TATGGCCTGCTACCCGGACTGGTCATGCACCACATTGATGAGCACACCGTTGCACTTGTC
TTTGATACTGATTCCCCTACTGGGACGCATATCCTCGGTGAGCGCTGCGTGTACTCCGAC
ATCATTCACATGACTGACGATAAGTCTGCCCGTGGCTGGGGTGCAGTCATTGCCATAGCA
CGAGCCATCATCCTCAAAGTCGAACAGATCATG

>RXA01043-downstream
TAGTACCCCACCATGACTCACTT

>RXA01044-upstream
CAGATAGCCACTACCTACACGCATCTGTTGTGCTGAAACAACAGCGCGACACTCACTCTT
CTCATTACTCAACAACTTACTTTTAAGGACTACATAACTT

>RXA01044
ATGTCTCTCTACCTTGACGACACTTTGTCTCGCATCGTTGAACTTGATCTCAAAGACACC
CGCATTGTGCCGTTTCTTGCTGGTGAACCAGGTATCGGTAAAACCTCATTCATCTACGGC
ATCGGCGAACGTGCAGGCTACAAAGTCTTCAGTATCTCGGTTAACACCCTTGCCGATAAG
GGTGACCTCACGGGCGCTCGCACCCTGCAGGACCCTGCCGATGGCAAGTGGAAGCAGATG

TTTTTCCCGCACGCGACCTTCGTCGAAGCAAATGACTATGCACTAGCAAACCCAAACGAA
ACGGTCGTCATTCTTCTCGATGAGATTAACCGAACTGATTCGGATGTCACCTCTGCCTCG
ATGACTATCTCTACTGAGCGTCGCGTTGGTACCACCGATCTAGCACCCAATGTCCGCCTT
GCTGTCACCGGAAACCTCACCGGTAATGTCACCCACCTTGATTCAGCATCTCTGACCAGG
TTCTCCCTCTATGAGGTCAAGCCATCCGCAGAGACCTTCATGAACATCATGGGCGGCCGC
CTCAACAAGTACATCCGTACCGTGCTGACCAAATACCCGGAATACATCTTCATGAAGCCA
ACTACTGCTACTGCTCTTATTACCACTGGCGATGATGATGACGACCATACAACCAATGCG
AAGCAAATGATGGACTTCAACGCTGTGCTCGGTTCAGACCAAGACATGGTTCAATTTACC
GCACCTAGAACTATCGAAGGTTTGTCCGTCTGGCTCAACAACGCCGATGATGACTTTCTT
CGTCTACTTCTACAAGAAAAGGTGGATGGTCTTGCTCGATCCATGAGCTTGCTGCAGGCT
ACGCTCGAATCTCACACCGGCGATACCGCTTTTACCGCAGAAGTCCTCAGCGAAATGACC
AATGATCTGCTGAGCTCCGCATCGCAAGCTCCTAGTGGTCCAATCAAACCATTTGTCTAC
GACCGACTCGCTGCTGCACCAAGCAATACTGTACTGGAACAAGAGGTTCACACACTCAGT
CTCAATGACCGCGCCGATGTCTTGTTGTTTGCCCTCCATGACACTGTAAACAACGCTGCA
CCAAGCATCATCGCTCACCTTGCATCTGAAGGCGTACTTGATGAACTGCCCAAAGACAGA
ATCAGCAAAATTGTTTCACTCGGTCCTGTACCAACGGCAAACTATCACGCCTTGACCAGA
CAGGATACAACGTTGACTCGAAATCTCGGTCCCGCTGTCTTGGGCTTCTTGGAAAGT

>RXA01044-downstream
TAAAGCAATTTCCTAAGTACCTT

>RXA01045-upstream
CAGCTGAGGTAGTCATCTGTCTACCTGCGTGGAGTAGACACTAAATCCTGTCCACGCACC
CTTACCCTTCTTGACACTAGTAATTGAAAGCGATCCCCTC

>RXA01045
ATGGTTACCTTCAGCGTCGCAAATCACGCGCCTCATACTTTTAGCCCATTCGATATTGAA
CCACCACTCACCGGTAACGCCACCACCGACGAACATGGTTACGAACACACCTCAGTGCTA
GAAAAACTAGCCTCCAACCACCTGTTCAATCCAATCAATCCGCAACACCCAGTCACTATC
ACAGCCACCGAAAACGGATCAACCGTTGATCTTGATGCAGCAGCACTAGCACAACATCTT
GCTCTAGCGATTACCCCAGACTCAATGCTGGCAAATCATCAAGGCTACAACCGTGACATG
ATGGGTCTACTTTCGCAGCTTACTAACCATGTTGGCTTTGATCGCCGATTCATTGTTGAC
CAACTCTTTATCTCCCAAGTGCTCAAAGCGAATCGTCTACCAGCACCGGCAAACAACGTT
ATTTACACCGTGCCCAATGACGTTATCCCATCTGCTAAAGACATCTTGTCCACCACTGCA
AAAATGAACAATCCACTGACAGTTACTGCAAGTGCCCCAATTACTGTTGACGACATTCAC
ACAGCCTATGAGGTATTTTTCGCTTCTCTTGCCTCAGTGTTTTTCCCTTATACCTACGGT
GCGGTATTCCTTAACAACGCAGAATTCGTTGAGTTTGTTGATTACCTTATTAACGAAGCA
ACAACACTGCACTCGGCATCACTCATCTCCAACAACACCTTTAATAGGTTCCAATCAATG
CGTAACATCTCCATTGATAATCTCACCGCCGAGTTTCTCTTACGCAAAAATGAAGCAGAG
ACAACTGATGATTATTCATTCCCCCGCGTACTTGTTTCCCTGCTGCATTCTTGGGTGAAA
CTCAATCACGATGATGCTCGTGCTAACAATGATGCACCCACCTGTGCACTAGCACCGTTT
AGTGTGGCTCAATGGATCATGCCGGAGACCATTGTGTTTATTAATGCTGAAGCTCATGCT
CATGCATCCTCCCAGGACATTGAGAAGAAATGGAAGGAAATTAATGCGGCGTTAACAGGG
TCTATTCGTATTATGTCGCCAAATGCAATTTCCAAGCTGCAATCTGCTCAGCATCTCGGG
ATGCAAGCACAAATGCAGGCCATGCGTGCTCGAAAAGATCACCACAACATGCAGAAGCGT
TCCTCACAAGAAAACGACTTTTCCAAGGCACTCCCCTCACCACAGACTATCGTGCTTTCT
GTCGCAGAGGTTCTGCGCAAACTCACTCACGTACGCCAATCGCACAACCCTCAGAAATAC
CAGAAGAAGTCTCTGACCAGAGCTTCTCGCCGACACCCGGATAACCCTAATGTCCCTGGC
ACCATTAAGAGCAAGCTCTTCTACCCTGACCTGCATGTTTATGTAGATACTTCTGGTTCG
ATTAGTGAAGAAAGCTACCGCAACTCTGTGGTTCTGCTCATGCAGCTTGCCACCAAACTG
GACATCAACCTCTATTTCTCCACCTTCTCTCACGTGCTCTCCGAAGAAGTACTATTGCCG
ACCAAGGGTAAAACACCACAGCAATTGGCAGCTCTTATTTCGGCCATCCCAAAGGTCTCT
GGCGGTACTGACTATCACCAGATTTGGGATTACATCCAGATCAATCCGCAGCGCCAAGAA
CGCATGAATCTTGTGTTAACTGACTTCGGATTCATGCCGAATCGCGGCTTAAACATCGAC
CACCCAAGTTCTATTTTCTACGTCCCAATCCTGCCTGACTACGGCAGCTGGTCAATGGTT
CGAAGAGATATGTCTCATTTCGCAAATGAAATGGTTGACTTCGACCCCTATATCCACAGC
CGACTACTCGGCGTACACGGAAAA

>RXA01045-downstream
TAGCAGCTGATCCATCTAGGGTC

>RXA01046-upstream
TAGCGATCCTAGGCAAAATGCACCAGCTAACCCCACCGCTCAACCGCCATCTGCCCCCAC
CTCACACTCATCACAGCAGGGTCTCCCTCCGGGCGCCATT

>RXA01046
ATGATCCCTTTTCCAGGGCAACCGCAGCAGCAAAGCGCACCCAATGACGAGACCCGTTTC
ATCGACCTTAACGAACGTCATAAAGATGATGAACCAGCCCTGTTTCGCGATGATGTTATT
GATCAAACTCTCGCTATTTTGATCAGTAAAAATAAGCCCAATGCGCTACTCGTTGGGCCT
GCCGGTACAGGTAAATCCCGTATCGCAGAAGATATTGCGCGCCGCCTTGCCAATGATGAC
GTATCTATTCCCGATCAGCTTGTCGGCCACCGTATTCTTGATGTCTCCATTGCAGAGCTT
GTTGCTGGTGCTGGCGTTGTTGGTCAGCTCAAGAAACGCATTCTGGATCTCATCAAGTAT
GCGACCGACCCGAGTAACAAAGTCATTATCTTTATTGACGAGATTCACCAAATTGCTGGT
GATCAGTCCAGTCACAGTGGATCGCAAGCCAAAGTTGCTCAGATTCTCAAACCCTATCTT
GCCCGTGGTGACCTTCGTGTTATTGGTGCCACCACCACCCAGGAAGCTCGTGACTTCGAT
CATGATCCAGCCCTCAAACGCCGTTTTAGCAGAGTAAATGTCGATGAATTTGATCGAGAT
CAAACGCTCACTATTCTTCATGCTGCACGTGATGGTTACCTCAAACATTTCAACAACGCT
GTCACGGTATCTGACGACGTACTGGGCTATGTCTACACCTACTCGCAGCAATTCAACCCA
GGCAATACAGCACAACCTGATGCAGCACTGACGCTGTTTGATAAGGCGTTGGCTTCCCTA
ACTATGGAGAAACAGCGTCTGATCAACAACCATGTCATTGCGCCGTCGCTCAAGTTCCCT
GTGTCAGAAAGGCACATCCATAACACCGCTCGCAAACTTGCCTTTGGCTCTCAAGTGCCA
GCCTCCATCAATACTGATGATGCTCGTGACAAACTCGAAACGTTGTTTGGTCAAGATCAT
ATTATTGAGCCAGTACTCACCGCTATCAAGCGTGAACAGCTTGGTATTTTCCCTCGCACC
AAACCATTGAGCTGGGTGTTTGCTGGTTCATCTGGTGTGGGTAAAACAGAAATGGCGCGT
ATTCTCTCTCGCGCCATTAATGGCGGCGATCCCATCATTATCAATGGTCCCGAATACATT
AGTCCTGAGTCCATTACTGGCCTTATCGGATCATCCGATGGCTATATCGGCTCTAATTCT
AAGCGTGCTAAACCACTCGACCCGCTGATTTCTAATCCGCGTCAGGTGATTGTGCTCGAT
GAATTTGAGAAGTCTCACCCTCATTTCCAGCAATTGTTCATGGCAGCTCTTGATACAGGC
ACTATGGCGATGGCTAATGGCACGACATTGAATTTCTCTCAGGCCATTATCATTGCCACC
ACCAATGCAGCCCGCGACAAAATCGGTCGTGACAGCTTTGGATTCGATTCAGATAATTCA
GGTGTCCTCGGTTCTGCTCAAGCAGCAACTGATCCGCGTGCACAGGAACGCCTCAAGTCA
CTGATGTCCAAGGATTTCCTGTTGAACTGCTCAACCGTTTCCAGAATATCTTTGCCTTCA
ACCGCATTGATGCAGGCACCTACCGTGAGATTCTGGACAATCTCTACCAGCGTCGCCGTG
ACGCCGTGCTGCTTAGCCACCCCGCATTACGCAGCACAGATCCCTGCAGATATTGATTCA
GACACTCTTGATCAGCTGGTGGAAACCACCTTTATCTCAGATTTTGGTGCACGTCCTGCT
GCACGCACCATCGAAGACCACATCGCATCCTTGCTGATG

>RXA01046-downstream
TGACCAACCTTTTAGGAGTACAT

>RXA01047-upstream
AACCACCTTTATCTCAGATTTTGGTGCACGTCCTGCTGCACGCACCATCGAAGACCACAT
CGCATCCTTGCTGATGTGACCAACCTTTTAGGAGTACATC

>RXA01047
ATGATTGATACCACTGCTAACAGCACCTCAGGCACCCTACCTACACTCACTGCTGACCAA
GCTGCGTTTATCACCGGTTTTTGCGAGGCTGCTATCTTCACAGCCACCGTCACAATAGAT
AACGAACCTATATTTCTTGATGAAGCGTTCTTCTTAGGTCAAGAAACCTATACCGACATT
CTCATGAATCAACTCCGCACCAATGAAGCCATTGTTAAAGACTGTCTCGACTTCTTCCTT
GACAACTACACCACAATGAACAAGCTCATTGTTGATGGTCTATGCCCAGATTGGGAGCAC
CACGGCCATGATTTCCTACTCACCCGTGACCATCATGGTGCCGGATTCTGGGATCGTGGC
TACGACGAATACGGTGCCCAACTCACCGACAATGCCGAAAAATATTCAGAAAACTGTCTC
AATTTCTGGATTGAGCCTGATAGTGACCCTCTCATTATCAACTTCGAGTACCAC

>RXA01047-downstream
TAACACCCCTTGACCTTATTTTT

>RXA01058-upstream

CTCCCGTAATAGGGGTAATTTTGCAATTAACTGCGCTTAAAGTAAGAAACATTGCTAATC
TTTATCTGGGTAATTAACAATCGATTTTAAGGATATTCTC

>RXA01058
ATGCGTAAACTTCGTACTGCTTCCGTTGCACTGCTGACCGCAGGTGCACTTGCACTGACC
GCTACTCCTGCAATGGCTCAGTCCACCACCGGTTCTTCTGCATCTTCTCAGGTTGGCGAC
GCACTCGGTGCTAGCGACTACGAGCGCGACATCTGGGGTTCCTCTAAGGACTTCGACGAT
GTAACCCCATTCGGTTCCGCTTGGTACGGCTACACCCTGGCCGCAACCGCAGTTGCTATC
TCCGGTCTTGTGTACGCAAACCTTCCTGCAATCGAGCAGGCTGCTGCACAGGCCGGCATC
AAGCTGGAGATCCCACGCTAC

>RXA01058-downstream
TAATTGCCACTGCAATCTTAAAT

>RXA01062-upstream
ACAACACGACAGTTGTAACTAGTGGTTTCAACACCATTATCGGTATGACTCGTGGCGACT
CGTATCTCTCTGATGATCTCGATGACCTGGGTTAAACCCG

>RXA01062
ATGAACGAGCAGGAACGAGAAGCCTTAGAGGATGCTGCCCTTGAGGAAGCTGCCTTAGCC
GATGAATTAGCTGCATTAGAGGCTGAAGCTGGCGTACAAGGGTCAGTCGAGCCTTATGAC
TATGCAGCAGACCTTGATGATGAGGACGAGTTTGATGAGGACCCTTTTGCTCAGGATGAA
CCCCGTGACGCTGGTCCGCTAGGTGAGTTGAGCAGTGATAACCATGTCTCTGAGGCTGTT
GCTGAAGACACTGGGACAAGTACAGAAGAGTCTGCACAAGAGGGCAGTCACGAAGAGTCG
GTAGACAATCCCCGTGATTTCACCGGCACTGCGACAGCGGTGCGATCTTTTCGACCCAGA
CTTCCCGTACCCAATGCACTGCGACCAGGACCACCCATCCGAACACAACCGGCAGTGAAC
ACCGACATATATGATGGCGGGCAAGAGAATACAGCTGGCGCGACTGCCGCAGATGTGGGG
GCGGGA

>RXA01063-upstream
ACTTTCTTGTAGAGGTCTGGGTAGTGGATAAGTTAATCAACTATGAAATAGACTAACTTA
ATCATTAACATTAATGGATTTTCGGAGAATAGGGATAGAC

>RXA01063
ATGGCAGACGAGAAAAAGGTTCATGTACGTGCCACACTGCGCTTTGATTCAGACACCCAC
CAGCGGGCAATTTATTGGGCAGATCGAAAAGGTATCTCGCTGAGCGCGTATGCAGAAGAG
GCGATCAGAGAGAAGATTGATCGTGATAACGGTGTGCACGTTATTCCGAATTCACTGTTG
GATAACCGCATGAACCAAATCATTGATCAGCTCAGCTCGTTTGGTCGTGAGTTGGCGAAC
AACACGACAGTTGTAACTAGTGGTTTCAACACCATTATCGGTATGACTCGTGGCGACTCG
TATCTCTCTGATGATCTCGATGACCTGGGT

>RXA01063-downstream
TAAACCCGATGAACGAGCAGGAA

>RXA01066-upstream
AAACGTATTCCTTGACCTGCGCATCAAGGTGCTGAAGAACTGGCAATCCGATCCAAAGGC
TTTGAACCGCCTGGGCTTCTAGCTTTAAGGGGGTGAGTTC

>RXA01066
ATGCGTAGGGACAGTTTTCGGGACCGCGCGCTAGTAGTCAAAACTTATGATTTTGGCGAA
GCCGACCGCATTATTGTGCTGCTCACCCGAGACCACGGCATCGTGCGCGGAGTTGCCAAA
GGAGTACGCCGATCCAAATCCCGGTTTGGGTCAAGGCTGCAGCTTTTTGTGGAACTCGAC
GTGCAGCTCTACCCAGGTAGAAAACTGTCCACCATCTCTGGCGCGGACACCGTCGGCTAC
TACGCATCAGGCATCATCGAGGACTTCACTCGGTATTCCTGTGCGTCCGCCATCCTGGAA
ATCGCCACCCACATCGCAGGACTGGAAAACGATCCGCACCTGTTTGAAGAAACCACCCGG
GCGTTGAAAAACATTCAGGACTCCCCAGAACCCATCCTCAACCTAGACGAGTTCATGCTC
CGCGCCATGAACCACGCCGGCTGGGCACCAAGCCTTTTCGACTGCGCAGCCTGCGGCCGA
CCAGGACCTCACAACGCATTCCACCCAGGCGTCGGCGGGGCAGTGTGCCTGTACTGCCGA

CCGCCGGGAAGCGCCGAAGTCCCACCAGAAGCACTACACATGATGTGGTTGGTCGCCAAC
GGCCAAGCAGCCCGCATTCCCCGGGAACACCCAGAGCAGCAAACCACCATTCACCAACTG
ACAACCGCGCATCTGCAGTGGCATATTGAAAGAAAGCTGCCCACGCTGGCGGTGCTGGAT
CAGGCC

>RXA01066-downstream
TAGTGCTTAGGCTTAGGCGTCCG

>RXA01068-upstream
TGGTCTACCAAGACAAGCTGTTCCCTGATTTCACGCAGCAAGATCTGTACGACGCGGTCC
TGGAATACGCCAAGCGGGATCGCAGATTCGGAAGCGCATA

>RXA01068
ATGCCCACCAACCAGCCGACGCCAGCCCAAATCAAACGCTGGCGCGGATACCTGGCCAAT
GAGCAAGCAGAGGCCGCAGCCTACCGCGACCTGGCCAAACGACGCGAAGGCGAAGAGCGA
GACATCCTCCTAGCGCTCGCCGACGCTGAACACCGACACGCCGCTTACTGGGTGGAAAAG
CTCGGCCCTGATGCCGAAAACCCACCAAAAGCCGACGTCAAAACCCGCCTGCTCGGTTTT
CTAGCACGCCGATTCGGCTCCGTGTTCACCCTGGCACTCATGCAGTCCGCCGAAACGCGC
AGCCCCTACGACGACGATGCCGACGCCTCCCGCCAAATCAGCGCCGACGAACGCATCCAC
GCCGAAGTCGTTCGAGGCCTAGCCAGCCGCGGCAGAGAACGCATGAGCGGCAACTTCCGT
GCCGCCGTATTCGGAATCAACGACGGCCTGGTCTCCAACGTCGCCCTCGTCATGGGTGTC
ATGGCCACCGGCGTGCCCGCCCAAATTGTTCTCATCACCGGCATTTCCGGTCTGCTCTCC
GGCGCGCTATCCATGGCCGCCGGCGAATACATCTCAGTGCGCTCCCAAACAGAGCTTCTC
GACGCCTCCCTCCCAGACCCCAAAGCCCGCGAAGCCCTCCACGCCCTCGACGTCGAATCC
AACGAACTGGAACTCGTCTACCGAGCCCGCGGAATGAGCGAAGACGAAGCGCGGGCAAAA
GCGTCACAAGTTTTCCAAAGAATCAGCGACCAAAAACGCATCAGCGACAACGTCCTCGGC
AGCACCGAAATCCAAAGCGCCGGCTCCGCTCGTTCGGCCGCCACATTCAGCTTCCTGTCC
TTTGCCATCGGCGCATTCCTCCCGATCGTCCCATACGTCTTCGGCATGGAAGGCCTCGCC
GGGGCAGTGGTGTCCCTAGTCCTCGTCGGACTATCACTGATGGCAACGGGCGCGACCACC
GGCCTGCTATCGGGAAAGCCACCGGGAATCCGCGCGGTGCGTCAGCTGTCGATCGGCTAC
GGCGCGGCGCTGGTCACCTACGTGCTCGGCCTCCTGTTCGGCATGATCCTT

>RXA01068-downstream
TAAAAGCTCTTGCTTCTCGACGT

>RXA01069-upstream
TCCTAAGCTCTCTTGAGTACCTGAGACCTTCTCAGCAAAACACAAAGTGCCTTCACCCAA
CCTGGGGTGGAGGCACTTTCTCATTGCTAAGGTGTGCATC

>RXA01069
GTGAACGATTTACCGAACCTACCAAAGCTGCCCTTCAACTGGACATGGGTGCTGGCAACT
GTTGCCACGACAGTGGTGTTGGCGGGTATTGGTTTGTATGTGTATTACCCGTCGTTGCCA
GATCCTATGCCGGTGCATTGGAATGGATCCGGGGAGGCGGATAATTGGACGCCTAAATCG
GTGGGTTCGTTTCTTTCACTGATTTTGATAGGGCCAGGCATTATTTTGCTGACCCTGTCG
GGTATGCAGGCGTTGCTGACCATGCAGTCTGGAGTGATCACGCAACGCGGTGGGGCGAAA
TCGGCGAATGAAGCGCACCGGCAGTGGGAAACCTACAAGGCAACAAGCATGCACATGGGT
TGGTACATGTTTGTGCTCAACGCTTTGATTTTGGTGATGATCCTCAATGAGTTCCGCCCA
AACCCTCTGCCTGGTGGATTTATCATCGGGCTTATTGGAATTATTGCTGCCACGATTGTC
CTGTTGGTTCTGATTGGAAAAACAACCACGAGTTTGGCAAAGAAATACCCCATGCCTGAC
CAAGATGGAAAGACGTGGGGGATTTTCTACAACGATCCGGACGATAATCGGATCTTAGTG
GAC

>RXA01071
AACATTCTGTACGCGCTGCTTGCTCTGTCTGTCATTGTTGCCATCATCGGCATCATCAAC
ACCCTGGCACTGAATGTGATCGAGCGTCGCCAGGAGATCGGTATGCTCCGCGCAGTTGGC
GTGAAGCGCGGACAGGTCCGCACCATGATCACCTTAGAATCTGTTCAGATCGCCATCTAC
GGTGCTGTGATTGGTATCGCGATTGGTCTTGGTCTGGGCTGGGCCTTTGTGACAGTGATG
TCAGGCGAAGGACTAGACGCTGCGGTTAGTATCCCGTGGGGTCAGGTCGGACTGATGCTT
GTTGGTTCCGCTGTAGTCGGTGTTATCGCCGCGCTGTGGCCGGCAGTCAAGGCATCTAGG

ACACCACCTTTGGATGCGATTACCGAC

>RXA01071-downstream
TAGTTTTAGCGGCAGTTGAATCA

>RXA01074-upstream
CGAATGAAATCACTGGGCGGGAGTTCACCCTCGGCGAGGAGCCTGAGCGCTACTAGCTTT
GCCACATTTCACTAAACGCCCCGCACAACCCCAAGCAGCC

>RXA01074
TTGGCGGAAGCCGCAGGTCTACGCTGGCTCGCCGAAGCATCTTCAGCTGTGGCACAGGTT
GTTAGCGCCGACGCAGAGCAGATCACGACTGTTGGCGTCGAAACGCAATTGCCCACACCC
GATGCGGCCTTCAAGGCCGGCGAAGAGCTCGCCCGCATCCACCTTGCCGGCGCCCCAGCG
TTCGGCTGTCCACCAGCGGGCTGGGCGGGGTTAAACTACATCGGCACCCAGGGACAAGCA
TGCTTATCGACGCCCACCTGGGGGTGTTTTTTACTCCCAGCAACGCGTACTCCCGTTTGCG
CGCCGGGCACGCAGGCGAAATCACCTCACCGAGCACGCACTCTGGGTCGTGGAAGCCGCT
TGTGATTTGATTAGCGAACTTCCCGATGACGTTCCCCCCGCCAGAATCCACGGCGACTTG
TGGTTTGGCAACCTACTTTTTGGCACAGACGGGCCTGTGTTTATTGACCCCGCAGCTCAC
GGCGGTCATCCCGAAACTGATCTCGCGATGCTTGATGTATTTGGCGCACCCTATCTCGAT
GAAATCCGGGAAGGTTATCTGTCTATCAACCCGCTGCCAGACGGGTGGCGTGAACGCACC
CCCATGCACCAACTCCACCCTTTGGCCGTACATGCGGCGTCTCATGGGCCAAGCTACGGC
GTGGAACTACTCCACGCCGCCAAAGCGACACTCAAACTGTTGGAT

>RXA01074-downstream
TAACGCCACCAATTTTCCTGCGG

>RXA01075-upstream
GCGGTGCGTGTTCATTAGCAGGTCAAGCGCGTAATTGAGGGCTAGACTGGTTAGTACCGG
ATATTCTTTTTTTCTTTAGTTTGTGGGAGTGGAGATAACT

>RXA01075
ATGGACAATCCAGTCAACATCCTCAATGAGCAGGAAGCTTTGGAGCGCCTGCAGTCGGTG
TCTCTTGGTCGCGTGGTGGTTCGTCGCAGCGATGAGATGGACATTTTCCCGGTGAACTTC
ATTGTGGATAAGGGCGCAATTTACATTCGTACAGCTGAGGGCAACAAGTTGTTCAGCATG
AATCTCAACCACGATGTGCTCTTTGAAGCCGATGAGGTCAAGGACGGAAAGGCCTGGTCC
GTGGTGGTTCGTGCGACCGCAGAGATTGTGCGCAAGCTGGATGAGATCGCTACTGCCGAC
ACTTTGGAGTTGAAGCCTTGGATTCCAACCCTGAAGTCCAACTTTGCCCGTATTGTTCCG
AATGAAATCACTGGGCGGGAGTTCACCCTCGGCGAGGAGCCTGAGCGCTAC

>RXA01075-downstream
TAGCTTTGCCACATTTCACTAAA

>RXA01076-upstream
TCCTCCCATTAAGCACCTTGTCTTCCGGAAGCTTCCACCCCAAATTCCAAACCCCAAATT
CCATGCCCCGGATGGACATTTTTCATTACACTCGGGGGCT

>RXA01076
ATGACTCCAGCTCACATATTTTCTGAAGGTCCAATCAATAGTGTTGTTCTCAGCCAGGAT
GAGGATGGAAATTTCACCACCTCCTACCAGGACACGTTCTCTGATCCATCATTTTTGGGG
GAAGGTGACGTTCTAATTGAGGTTGGTTGGTCCAGCTTGAATTACAAGGACGCAATGGCT
CTGAAGGGTGATAAGGGAGTGGTGCGTACTGTGCCACTGATTCCAGGTATCGATGTGGTG
GGCACTGTGATCGAGAGCGCTGATCCTCGCTTTGGTCGTGGTGATGAAGTGGTGCTGAAT
GGCGCTGGTTTGGGGGAGAACCGGCATGGAGGTTTCACGCAGCGGCTGAAAGTGCCGTCT
GAACCGTTGCTGCATATTCCATTTAACTTCTCCGCGCAGCAGGTGGGTGCGTTGGGTACT
GCAGGTTTCACGGCTGCGCTATCGGTGAATGCTCTGGTCGATCAAGGTATCAAACCGGAG
GATGGGGAGATTCTGGTAACTGGTTCGACTGGTGGTGTGGGTTCGATTGCACTTCACCTG
CTGAATAAGTTGGGATATACGACGGTCGCGGTGACGGGGCGTCGAGAAGCGCATGCCGAA
TACCTGACCAGCCTGGGCGCAAGCGACATCATTGATCGCGCGGAGCTTTCTGAAAAGGGC

CGGCCGCTGCAGAAGGGGCGTTGGGCGGGTGTAGTGGATTCAGTGGGATCCCACACACTT
GTCAATGCGATTGCTCAGACAAAATGGGGCGGAATTGTCACGGCGTGTGGCATGGCTCAG
GGGCCGGATCTGCCGGGAACGGTGTTGCCGTTTATTCTTCGTGGCGTGCATTTGGTTGGC
ATTAACTCTGTCGATGCACCCCGTGAGCTGCGTCGACGTGCGTGGGCGTTGCTGTCCGAG
CATCTTGATACCGCGGTGCTAGATGATATGACCACTGTGATTGATGTCAAGGATGTTGCT
CAAGCTGGCGAAGATTTGATGGCTGGCAAGCTTCACGGACGTACCGCGGTGCGTGTTCAT

>RXA01076-downstream
TAGCAGGTCAAGCGCGTAATTGA

>RXA01078-upstream
ATCATTCACGAGCTCGATAGCCGACAGGTTTCTGAACTCACAGAAGCCCTGGCCAAAGTC
TCCACCACCCGCAGCTAAAACTTTTTGAAAGGAGCTCATC

>RXA01078
ATGAGCAACGCAGTACCCCACAACGTTTCCTTCAACTTTGTTCCCCGCGCTTACCGTCCA
GAAAAGCCCCGCACATTCGGCATGACAGAAATTCGTGCACCGTACTACTCCACTTTCGGC
ACCCGACACCTCCAGGATGTCTTCGATGTTGCAGGCCAGTGGGTGGACGGCATCAAATGG
GCAGGCGGTTCCTTCTCCCTGGTGCCGACCGAACAGGTGCGTGCTTTTAGCGACATCGCC
CATGAAAACAATGCCTATGTGTCTTCCGGTGGCTGGATTGAAACTGTGCTTCGCTACGGC
GACGACGCAGTTGATCATTACTTAAAGGAAGCCAAGGAAGTCGGCTTCGATGTTATTGAG
ATTTCCACCGGATTCATCATGCTCAACACTTCAGGTCTTCAGCGCCTGGTAGAAAAAGTG
GTCAAGGCAGGCCTCAAAGCAAAACCTGAACTAGGACTACAGATTGGTTCCGGAGGCGAC
TCTGGTGAGGCTGAACTTGCAGCCGAAGGAAAGAAAGACATTGGCGATCTGGTTGACCGC
GGTAAAAAAGCTCTCGACGCCGGCGCATCCATCATCATGATCGAATCCGAAGGCATCACC
GAAAACGTCACCGAATGGGATACAGGCGCTGCCGCGTCCATCATCAATGGACTGGGATTA
GAAAACGTCATGTTCGAAGCCGCCGACGGCCCCGTCTTTGAGTGGTATGTCAAAAACTAC
GGCAACGAATGCAACCTGTTCGTCGACCACAGTCAAATTCTGCAACTTGAAGGGCTGCGC
CAAAACATCTGGGGCAACAAGAGCACCTGGGGACGAGTAATCAACCCTGCGCCT

>RXA01078-downstream
TAAATACCAGGTCAGGGAGGGCA

>RXA01083-upstream
GTCGACATACTGGCACGCAAGATCTGTGTACCCGGCCCACGTGCCTAAAACTAGGTGAGC
GAGACCTTCGAGCAGTTCCTCGAAGGAGAGTGATCCACCT

>RXA01083
ATGTTTCCGCGAATTCCGCTGGCAATGTGTGCTGTCGCAGCAATCCCTGCTGTTGTGCTC
AGGTTTTCTGAGCTGTCGGCGTCACCTGTGGCGACCATGCTGATTTTTGGTACCGCAGTG
GTTGCTGCCTCTTTTGTGTTGGCGTGGGCAGCTGAAGCTGTGCGCAAAGATATTTCTGGT
GCGTTGGCAGTGGCCTTGCTTGCGTTAGTTGCAGTGCTTCCTGAATATGCTTCTGAAACG
GTTGTCGAGCACACTTATCAAACATCGGCGGCGAAT

>RXA01083-downstream
TAAGAAGGTGAACAGTTGACGCA

>RXA01085-upstream
GAAGGGTCGTAATGAGCGTTGCCGCAAAAACTTCAAAGGTGGTGGCACCAAAGATCTTAA
GCAGACTGATCGGACCTTTGATCAGCTGCGAAAACAGCGG

>RXA01085
GTGACGGATAAAGCCCGCAACCGTGACGTACACAATGAGCAGCAACTGGCACGCGGTGAA
ATCGGAGAAATGCGCTCACCGATGTGGGTTGAGGTGGGTGCTGCGATTCTGGGCGTGTTT
GTCCTGGTTGTGATGTGGCTGGCCTGGGGCGGTATCGGGCTGCTGATCCAGACCATGATG
AATACTGGCTCACCTAATGACAAAGAGCTTTTTGATGAGCTTGGTGTGAGACCCTATTAT
GTTGCTGTCGAACAGCAAATCGGCACCAGTAGTGCTCACACCACGTGCTACCAACCGCTT
GATGAATTTGGCAATAATTTTGGCGACTGTACGCGTAGCGTGCCTAAAGAGCCAGTGTGG

TACGCCGATTATGTAGCTAGTGTGTTCGCAGAACATGGCTTTGATGCACCAGAACCTATT
GATAATTCGGTGGGTAGCTGGCTGTTATTTGGTCATGTGGGCATTATTCGGGTGACGTTT
GTGATTGCGGTTGCAGCGGGTGTGTATGCGATGTCACGCGCAGCAATGATGCGTCAGCTA
GAAACACAAAACGTCGCTGTGGACACCACCGATATTAACCAGCACACCAATGACGCACGT
TTGGCGATTCCGCAGGAGATTGTGCGCGATTTGAGTCTGTTCCCCGATGTCGGTGCACAC
TCACCAGTCCAGCCCTCAAGCATGATTTCCCATGTGATGCTGTCGAATAAGGGCTTGAAA
AAGGTGGATGTAACGCAGTTTGCACAGGAGACAATTATCGACAATGACACTGGTGAAATT
GTCTCTGAAAAGGGTGAAGTGCTCTATGACGGTGCAGGACAACCGATCACAAAGAGCTTG
CCGATGATTGACAACGAATTTAGCCATGCGATTTTTGACAAATCAGATGTCCCGAATCTT
CCCGAGCTGCGACGGTTCTTTAATCCAGCAAAGATTGAGTGGAATCCTGGTGGTAGT

>RXA01088-upstream
TGCCTTGAGTCTAATTCTCCCGCCCGTGCGATGGGTTTAAGCTGGACTGATAAACCTTTT
GTGAACCGAATTTTTTAACTGATTTGAAGAAGCGAGAATA

>RXA01088
ATGGGACTGTGGATCGATGCAACCGCTGGCGTTGCAGGGGATATGTTGCTGGGAGCACTC
ATTGATGCAGGTGCAGAACTAGAAAAAATCCAACAGGTTGTGGAAGCAGTCATCCCCGGT
GACGTGCTCTTGCGCACCGAAGAGGTAGTGCGCCAAGGCCAACGAGGCATCAAGCTGCAT
GTGGACGCACAACATGAACACCATCATCACCGCCACTTAAGCACCATTAAAGAACTGCTT
GTCAATGCTGACATCCCTGAACAAACCAAGCAGGATGCCTTAGGCGTTTTTGAACTCATC
GCTATCGCTGAAGGAAAAGTCCACGGCATCGAGCCGGAGAAAATCCACTTCCATGAGGTA
GGAGCTTGGGATTCCATCGCAGACATTGTGGGTGTGTGCGAAGCGATCAGGCAGCTTAAC
CCAGGTTTGATTGCTGCATCTCCGATTGCTTTAGGATTCGGACGCATCAAGGCAGCTCAC
GGAGATATTCCAGTGCCAGTTCCAGCCGTGGCAGAGCTGGTGAAAGGCTGGCCCACCCAA
ACCGGAGCTCTTATGGAGAGCACCGAACCTGTTGGTGAATTAGCCACCCCAACTGGTGTT
GCGTTGATCCGTCACTTTGCCACCCAAGATGGCCCTTTCCCAGGTGGCATCATCAATGAA
GTTGGCATTGGTGCAGGAACAAAAGATACAGAAGGCCGTCCAAATATAGTGCGCGCAATT
TTGTTCAACACCTCTAGGAGTAACCCAGATACCCGCACACTGGTGCAATTAGAAGCCAAT
GTTGATGATCAAGACCCACGGCTGTGGCCAGGAGTAATAGAGATCCTCTTTGCCGCTGGC
GCAGTAGATGCATGGCTGACTCCAATTTTGATGAAGAAGGGCCGTCCTGCACATAGGGTG
TCAGCATTGGTGGATAGCTCCGAGGTGGAAGCAGTGAAAACCGCATTATTTGCAGCCACC
ACGACTTTTGGGATCAGATCATGGGAAGTCGAACGAGAAGGCTTGGACCGTCGTTTCGAA
CAAGTCGAGGTGGACGGACACACCATCAACATCAAAATCGGTTCCCGTGATGATCAAGTA
ATCAGTGCACAGTCCGAGTTTGAAGATATTCGGTCTGCAGCGGTGGCCTTGGGAATTTCA
GAGCGGGAAGTTGTGGCAAGAATTCCGCAAGGCACCACCGAG

>RXA01088-downstream
TAACAACCAAAAGGTCGACTGCT

>RXA01091-upstream
TCGTCGGAAAAACTGGCGATACTATTGATAACGGGCATGGGTTCACCTTCGATAAAGCAC
GGTCTATGCTGGACTATCGCCTTTTGACACGAGTATCGCA

>RXA01091
ATGGTCCCGAACACAGTCCTTATCCATGACGAAACCGCCGATCTGGCGACGCAGATCCAG
CGGCTGGAACATATCATGGCGTGCCTGCGCGATCCGGTCAGCGGATGCCCGTGGGATATT
GAACAGACCTTTGCCAGCATCGCGCCCCACACGATTGAGGAAGGCTACGAGGTTGCCGAC
GCCATCGCGCAGGAAGACTGGCCCGAGCTACGCGGCGAGTTGGGCGATTTGCTGTTTCAG
ACCGTGTTTCACGCCCAAATGGCGCGCGAGGCAGGCCATTTCGCTTTGGTTGACGTGGTG
AAGGCAATTTCGGACAAGATGGTTTTGCGCCATCCGCACGTGTTCGGCGCGCAGTCGAAC
GCGAAATCCGCCGACCAGCAGGTGAAGATTGGGAAGTCATCAAGGCGCCCGAGCGCGCGG
GCAAAGCGCAAAAGGGCGTTTTGGATGGCGTCGCGCTGGGACTGCCTGCCC

>RXA01091-downstream
TGATGCGCGCGACGAAGCTGCAA

>RXA01092-upstream
TGAACCCATGCCCGTTATCAATAGTATCGCCAGTTTTTCCGACGAGATGACCCGCTGGCG

GCGTCACCTGCATCAAAACCCCGAAATCAGCTTTGATTGT

>RXA01092
GTGGAAACTGCGGCCTTCGTGGCCGAGCAGCTGCGCAGCTTCGGGGTGGATGAAATTCAC
ACCGGCATCGCGAAAACCGGTATCATCGCCCTGATTCACGGGCGCGAGGCTGGCCCCGTC
GTCGGCCTGCGCGCCGATATGGACGCGCTGCCGCTGACCGAGATTACCGGCGTCTACTAT

>RXA01096-upstream
ACCGTGAAACAAACCGGCGGTGCGTGCCACACTGGTGCCCACACATGTTTCGACAATGAC
GTTTTGCTGTAAAAGCAACAACGATTAAGGAAGAAATCTT

>RXA01096
ATGAAGCCACGCGTGCTGTCAGCATTAGGCATTGGAGCTGGCGCCCTGGTTGTCTGGATC
AGCTCACGCATGAACTGGGTAACCATCGAGGCTTTCGACGATAAATCAGGTAGTGTCACC
CAATCTATTGTGGGTGCAACCTGGTCTACAGAAATCATGGCGCTTGCACTTGCTTTGCTC
GCTGCCTTCGCCGCCGCGTTGGTGCTCAAGCGCATGGGTCGGCGCATCATTGGTGGTATT
TCGGCGCTGATCGCGGTGGGTGCCAGCCTGTCTCCACTCGCGCTTCTCACCCAAGACCCA
GACGCAGAACGGGCCCGAACCCTGCTGACCTCCGGTGTGGCCTCACAGAAGGCTAATTCC
GGAACCCTGCTGTCTGATTGGGCGGAGATCATCAATACCACCACCCATCCACTGGCGGCA
GTGGTAGCCATGATTGGCTGCGCGCTAGCCCTAGTCGGCGGCGTTGTCCTTGCCATGCGC
CCTGCCGAGGACACCGCGAAAAGCAATCAGTATGAGCGTAAACAGGCTCGCGCTGAGAAA
ATCCACACCGATTTGGCCCAAGATCCAGACTCCGGTCGTGTGATGTGGACGCACTCGATG
AAGACATTGACTTCACCGAGAAGACTCAGAAATCCAAAGAAACCCCAGGTCAAAGCTAGG
GTGTGGCACCCTGATTTCTTTCGCCATGTGTGTTCGGGA

>RXA01096-downstream
TAACCTTAAACACAGCATTGGTT

>RXA01102-upstream
ATTCTATGGTTGTTGGGAGAGATGACTTAATTTGGAATCACGGGCTTTAACACGCGCTGA
CATTGAGCAACTTCCCAGCATGTGGAAAAGCCCAGGTTTC

>RXA01102
GTGGCTGTCCTCGTGGCGGTTGCAGCAGCGTTCGGCAGTTGGTCACTCCTTCTTCCCGTC
GTACCGCTAGCGGTCCTCAACAACGGCGGATCAAGCGCTGTCGCCGGTGCCACCACTGGC
ATCTTCATGGCAGCTACAGTGATCACTCAGATTTTCACTCCCGCTGCGCTGCGGAAAATT
GGCTACACCCCAGTGATGGCTTTCGCCGCATTCATGCTGGGTGTGCCAGCCATCGGGTAC
ATCTTCAGCGTCGAGCCAATTCCAGTGCTGGTAGTGTCCGCACTTCGAGGAATTGGGTTC
GGTGCGCTCACCGTCGCAGAATCTGCGTTGGTGGCTGAACTCGTTCCCGTACGCTTCTTG
GGCAAAGCTTCTGGAATGTTGGGCGTATTTATTGGCCTTTCCCAAATGCTTTTCCTGCCT
GCCGGGTTGGCGTTAGGTGACCAATTTGGCTACAACGTGGTCTATGTTTTAGGTGCCGTT
ATCGCACTAGTTGCAGCGGTGATGTGTCTGCGTATTCCGCAGGTTAAGGCAGCGGCAAAG
CAGCAACCACAGGTGAGCGAACAGGAGCGTTCTGTTTCCACCTGGAAGTTGGTGCTGGTT
CCCTCCTTGGCTGTTACCAGTTTGTCAATGACTTTTGGCGCAGTGTCTTCATTCCTTCCA
GCTGCAGTCATTGAGTTAGATCCAGGATTAGGTGCTGCATTAGCGGGTATTATTTTATCC
ATTACCGGTGGTTCTTCAATGGTGTTCCGCTACCTGTCCGGCGTTATCGCTGACCGCCGC
GGTGTGCCTGGTACCACGATGATTCCTGCTCAGATCATTGGGTTCTTAGGTGTCGTTTTA
ATCACCGTCACAATCTTCCAAGGCTGGTCCGTGTGGCTTTTGATTATAGGTGCAGTGATG
TTTGGTGGTGCTTTTGGCATGGTGCAAAACGAAGCGTTGCTTTCAATGTTTTTCCGGCTT
CCTCGCACTAGAGTCTCCGAAGCCTCCGCCATCTGGAATATCGCCTTTGATTCGGGAACA
GGAATCGGAAGCTTCCTCCTTGGCATAGTTGCCGCATCGCTTGCTTACAGTGGTGCTTTT
GGTTCCGGAGCCGTGGTGATTTTGTTTGGAATCGTTTTGACCACCGCCGATCGAATCATT
GGGCGGCACCGCATTACTGAATACAACAACACCCGCGCGCGTTTGCGCCAGGTGCCAGTC
GCTCGGCGTGCAGTGCAAGGGCTGCGCAACAGGCGCAAAGATCGC

>RXA01102-downstream
TAAAACGCTTTTCGACGCCACCC

>RXA01103-upstream
CCGAAGCAGAGTACAAGGCTGTTGCCCGTGCGCTGCGCGGTGCCGTAGAGATGGATCCTC
GTCAAACAGGAATCCCATCCACTAAGGGAGCGCTCTAGAC

>RXA01103
ATGAACTCTTCTCCCATCTCTGATATGGTCACTGCGGCTGTGCAGAACGAACCAGATGCG
GGCGACCGATGGTTTATTTATGGTTTGTTCCTCATCGCCGGGCTTTTCTTTGGCGGTGCC
TGGTCTGCATATAAATCAGAAAACAAAATCCTCATGGTTGCAGCCGGCCTCATCGCAGTG
CTGGCAGTGGCTGGAGGAATTCTATGGTTGTTGGGAGAGATGACT

>RXA01103-downstream
TAATTTGGAATCACGGGCTTTAA

>RXA01107-upstream
GGGTACATCAGAGTTCATTTGAATTAGACTTAAAACTTAAAATGACCACCCCAGATTTAC
CTGAATTAAACCCGCTTTCACCTTTGAGATACTGGAAGGA

>RXA01107
ATGGATTTCACCTCTGTGAATGATCGAAACGTCCCTGCACCCAACACCTCCATTCCTTTC
CCAGTTGACCTGAATCGAGTGACGGAGGCTGTTGATTCCTTGGGCTACCACTATTTGAGC
TCAGAAGATCGCATCATCGTGCCGTGGCAAGATCACCGCATTTCGATGTACTTCAGCCAC
GAATCAGGGCAAATGCTCACCATCCTTGGTCGCACGCGCCTTAATTTGGACATGTTTGCC
ATCAACGATGCGGCGCGAGCTGTCACCGAATGGAATGCCGAACGCATCGGGCCAACAGCC
CTCGTCCATCTGGGCAACGACGGCGAAGTGGAATTGAAATTCCGCACGACCATCTGCATC
GATGAAGGGTTAAGCACCCAACAGCTACGCCAATTCATCAACCTGTCCTTGGACACCACC
GCCATGGCTGTGACCTATATTCTGGAGCGTTTTTCAGAACTTAACTTCAGCGACACCGGA
AGCCCTGACGACACGAACAATGCCGATGAACTCAGCGACGAACAAGACCAAGCAGATCTC
GTAGAGAAAATCCGGGGGGCTGTACGTTCCCACTCCAGTTGAAGAGCTCATCGAATCCCTA
GAAGACGCAGAGTGGGAAGAATCAGACATGGCAGACGAGGATGCAGAAGACGACTACCTA
GACGATGACTCAGAAATCGAATGGGAAACAGACGATGACTACTTCGAACCTGAAGAAGTC
GACATGGACGAACTCCTCAACGGTTTCCTCGAAGATTCTGACATCCCCCAGGAAGTCACC
TTGGAACGCATTCGGGCACAACTGCATGCCATCGGCGTGGTAAAAACCAGCGGCGAAGAC
GATTTCATCATCGCGTGGATCAACGAAGTGTTTTTAGGCTTCTTCGTTGATAATGGCCCC
ACTTTCCTGGTGAAAGGTCACTGGGATCCCAGCATGGACCCCACACGCGACTTCATGAAA
CTGTTCATGATGTGCAATCAGTGGAACGAAAACTCTCTGACTACCAAAGCTTTTTGCCAT
ACTGATGACAAGGGTCTCCAGGTCCGGGTAGAGTTCGCGGTCTCTGTCGCTGAAGGCCTC
AACGACGATCAACTACAGCACAACATCGCACTGTCAATTCATCATATTTTGCAAGCGATT
GATTCCATCAGCACAGAAGCCACTGGATCATCAACGGTGGAATGGCCGGAGAAAAACCGC

>RXA01107-downstream
TGATCATTAAGGTCTTCCAAGAA

>RXA01108-upstream
GTGGCCAGTGGAAGTTCTGCGACTAATCCACAGAGCTTAAAACTCCGGTTGTCAGTTCAG
GTTGCAAAGTTAACAGTCAACGGCTGTATTCTTTAGAGCC

>RXA01108
ATGACATACCCCGGCATCACCTCTGACCACAATCCTTATGATGGATACACAGGCGATGAC
GGGGCCGGAAACAAGCGCAACCTCCCAAACCGAAAGAAAATAAACAAATCGGTGGGAGTT
TACGCTGGTGTGTTTGCCCTAACATTGGCTTTATACGCCATTGGGGGAGCCGCATGGGGA
CTGCTCCGACCCACTTATACCGCTTATGTTGAAGACGCTGAAACAGCCTCCATAGCGGTG
GAAACCAACACTTCTTTTGCCGGCTATGCCTGGTTTGCGATCGCCACCGGTGTGCTTGCA
GCAGCAATCGCATTATTCGTTTTCCTGCGCACCCCTCAACATCGAGGCCCAGTTATGCTC
CTATGGCTGGGAATTGTATCTATCGCAGGTTCCGTGGCATTCCTGGTGTTTGGAAACGTG
GCCTCGACGATGCTTCATGGTTCACCATCTGATTACGCCTCAGCGATCGGTGCGTCTTTC
CAGGTAGCACCCACTATTACCCCTGGTGTTGCGTTTGGGGTCGCTCCATTTTTGAGTGTG
TGCATGTATTGGTGCGCGGCATTTGTGACACCTGAAGAAGAGATAGACCAGGACGACGCA
GGCCAGGGGACTTCGAAAGCATCGGGGTCTGAGATGACTGGGGCTAGTGGC

>RXA01108-downstream
TAGGGGCTAGATGTGCGCAAACA

>RXA01109-upstream
GGGTCGTCAGCTAGATTGCTTTGCTAGGGTAATCTGCGTGAACCGTCCGGGAATTTTTAA
GTTTTCCGGAGCATGTCGATGATTTATCAGGAGCAGAACT

>RXA01109
TTGTCTATTAGCCTTTCCTCAAAGAAGGTTGCTTTCGCAGCACTCATGGTCACCCCACTT
CTCTTGACCGCATGTGGCAGTGATTCATCTGATACTGAAGCAGCCTCATCCAGCGCAGCG
ACGACGACAAATTCTTCCTCATCCAGCGCAGCGACCTCGGCGGAAGCAGCAGAAACCACC
TCGTCCGAATCTGAATCTTCCGAAGCAACAACCATTAACGAAGAGCAGCAAGCACAGCTT
GATGTACTGTCTCAAGAGCTGTCTGAGAACCCAATTACCTTCGCTGAAGCTGCGCCAGTT
GAAAACGGCGAGACCGCTTCCCCAGAAGACACAGCTGCCATCGAGGCTCTGGTTCGCGGA
TACACTGACACCAACACCTTGCGTAGCTCCCTTGCGTACACCATCAACAACACCTGCACC
CGCGTTCTTGAAGCCAGCGGCGCTGACGCTACCCAGCTTGATCTCAACACCATCCCTGAT
ATCCCACTGGGTGGCGAAGGCACCGGAACTGTTGATTCCATCACCGATGTTGTGGTCAAC
GGCCAGGAAGCATCCGCATGGGTCGTAGCAACCGCCGGTGGAACCACCGACTCTGCAACC
CAGCGCTTCTTCAACGAAGGTGGCCAGTGGAAGTTCTGCGAC

>RXA01109-downstream
TAATCCACAGAGCTTAAAACTCC

>RXA01119-upstream
CCGTAAAGACGTTGGCGAAGTCATCATCAACGGTGCCGTTGCCCGTGGCGAAGCCGAACC
AGAGATGTTGGAAGCTGTCGCAGAAGAAAAGACCGCGTAG

>RXA01119
TTGGCAGGAGTTATCACCGGCTTTGCCATCATCCTGTCGGTTATCGGCGTTGGATTTCTT
CTGGCAAAGCTGGGGGTCATCAATGATGACAAACAGCGCTTGGTGTTAAACCGCATTGCT
TTTTATGCGGCAACTCCAGCGCTGCTTTTCAATGTCGTTGCCCGATCAGATCCCAGCGCG
TTGATCTCACCGGTCATTGTGGTGACATTTGTGGCCACGATCGTCACAGCAGCTGTGTAC
TGCGTGATTTCGGCGATTTTCTTTAAGAAGGATATCGCCACTACGGCGACAGGAGCTGCG
GCTTCTGCCTACGTGAACTCCAACAACATTGGCCTGCCGGTGTCTATTTATGTGCTGGGA
ACAGGCGCATATGTGGCACCGATTCTGGTCATGCAGATGGTGATTTTCGCGCCCATGATC
CTGGCCGCGCTGACCTCTGGTGATGTGAAAGGCTCGCGCGGGCAAAAAATATGGGCTGCG
GTGAAAGGTTCACTGCTCAGCCCAATTGTGTTGGCCTCTATCGCGGGCCTGATCGTGTGT
CTGTTAGAAATTCAGCTGCCAGCCGCAGTCATGGAACCCACCATCATTTTGGGCGGCGCA
TCCATTCCGTTGATTCTGATGAGCTTCGGCGCATCATTGCCCTCAACCAACGTGCTGGCT
TCCAAGGCGGATCGCCCCAGCGTTCTTACTGCTACTGCGATAAAAATTGTGGGTATGCCC
GCCATCACTTGGCTGATCGCCAAGGCGTTTGGTCTGGAGGGCGATTACCTCTACGCCGCT
GTTATTTTGGCGGCGCTGCCCGCCGCGCAGAATGTGTACAACTACGCGGCGACGTACCGC
AAGGGCGAGATCGTCGCCCGCGATACGGTCTTCCTCACCACGTTCCTAGCGCTGCTGGGC
ATGCTAGGAATCGCGGCCCTATTTGGTCGC

>RXA01119-downstream
TAGGGCTTCAGGCTGCTTTTCGA

>RXA01121-upstream
AAAGATTTACTGCGTACAACTCTAACCAACAATATTGGCAATGGGTTGTTCCATCTTAGC
GCTTTACCTGTGAACTCTGCAGAGCGGTACGCTTAAGCTA

>RXA01121
ATGAATCCCGAATTTATTCACGGCGCAACCGAAATTGAAACCACAAACAGGGGCCTTCGC
CCGCATCGACTCAGCAAAGAAATAGTAGAACGCTACTGTGATCCCCAGTTTAGCGCGATG
GAACGCCAACCATCGGGCGTGCGCGTTGTGTGTCGCACCACCGCCACCTCCGTCACGCTG
ACCACGTATTCCACGCGGGTGGTGTACCTCGATTCCGGCCGGCCGGGCGGCAAGATTGAT
GTGCTTATCGACGGCGCCCCCACATCTTCCACGCCAACTTCCGGGGGCGAGACCACGGAA

GTCAATTTCATCACCGGCGCCACGGAACGGCGCCTGAAAGATCCGCAGGTGCTCACAGTG
GATGGACTTTCAGAGCAGGAAAAGGTGGTGGAGTTCTGGCTGCCTCACAATGAAGAAATT
GAAGTGATCTCCCTTAAAGCCAACGCAGCTTTAAACACTGTCGAAGACACCCGTCCCGTG
TGGATCAATTACGGCAGCTCCATTAGCCACGGTTCGGTTGCCACTGCCCCAACCAAAATT
TGGCCAGCCATTGTTGCCCAGTCCAAAAACTACAACCTGCGTAACTTCGGTTTTGGTGGC
AGCGCCATGTTGGATCCTTTTATGGCGAGGCTAATCAGGGATACTCCAGCTGATCTGATC
ACCTTGGAAATTGGCATC

>RXA01122-upstream
TATTCGACCAAGGCTGAGCAAAAAGGCGCTAAGCTGTGGGGAGATCGCAAGCCCCTATCC
GGCCTCTACTAAGCCCCGAAGTTGAAGGGAAACTCCCCCA

>RXA01122
ATGCCGTTTCCAGCACTGTTGTTGCCGCTGATTTTCTGGACAGGAATTGCAGCTTTGTCC
TCTTGGGCGGTCAGCCGTGCACTTCCGCTGCGCGCCGATAATTCCATTGAGATTGATGCG
CCGGTGGAAAAGGTCTGGGATTTCATCGAGGAGACCAACCGCGTGCCGGAGTGGAATGAG
CACATTCTGTACGTGCAGGCGCCTGGTGAGATCGAGCAGGGCATGAAGCTCAAGATGAAA
ACAAGGCACCCAGAGACCAATCGCCTCACTTTGAAGTTTCGCCCCACCATCGACGTGCTG
CGTCCACACCGTGAATTGACGTGGTCCACCAAAATTGTTGCGCGTTGGCTGCTCACCGTC
ACCGACACGATCGAGCTGAAGCCTTTGGAAGATGGTCGCACTGAGGTGGATCAATCAATG
TCCTTTAGTGGCGTACTATCCCCCGGAGTGCCCTTTTTGGCCAGCATCAGCAGGATCAAA
GAGAACTCAAACCGCCAGTTGAAAGCACTGATCGAAGCCGAG

>RXA01122-downstream
TAAACCTCCAACCCCTACATAAC

>RXA01123-upstream
AAAGAGCAGTGATTTTTCCCGATCCCCCCCTGGCCGCCTAGCGGAAATTATTGATACCGC
GTGGCGGTTGGTGGAAACACGTGGCTGGGCGAATGTGAGC

>RXA01123
ATGCGAACCCTGGCCGCGGAGCTAAATATCAAGGCGCCGTCGCTGTACAAGCATGTAAAA
ACGCGCGAGGATATCGCCGCACACATCGCCACGAAGGCATTTATTCAGCTGGGGCAAAGC
CTGCATGAACATTGTGAAAGTGTGGAGGATTTGCTTGCGGAATACCGCTCCATGGCTCGG
GAAAATCCAAATATTTACCGGCTTCTCACCAGTTCAGAGTTCCCCCGCGAGCTACTTCCA
GAAGGCCTAGAAACTTGGGCAGGAACGCCATTCTACCTGGTCACCGGCCACGATCCGATC
AAGGGTCAAGCACTGTGGGCATTCGCGCACGGCATGGCCATCCTGGAAATCGACGCCCGA
TTCGCCGGCCCCAACAATGGATCCCCCGCGGATGGCGTGTGGGAGATCGGCGCGCGGGCA
TTTGACACACAAGTATTCGACCAAGGC

>RXA01123-downstream
TGAGCAAAAAGGCGCTAAGCTGT

>RXA01127
GGAATTGGCCTCGCAGCATCCGGCAACATCGATGCCACGGGCACCAACCCTTCCATGTTC
GAGCCAGTCCACGGCTCTGCACCAGATATCGCAGGCCAGGGAATCGCAGACCCAACGGCA
GCAATCCTATCCGCTGCGATGCTGCTGCGTCACTTAGGTGATGAAGACAACGCAGTACGT
ATTGAAACAGCCATCGCAGCTGATGTGGCTGGCCGAGATAACTCTCAGCCGATTTCTACC
ACTGAGGTGGGAGACCGCATCGTCAAGGCGCTGCAAAGC

>RXA01127-downstream
TAAATTTCAACGCCGACCCCCTT

>RXA01128-upstream
ATTCGAGTACAAATAAATTTGAGAACAAAAAGATGGGGGGAAATATGTTAAAGTGCGTTA
TATTGCTTTAGCGAAAGTAACTTCCATGCATCAACGTTCG

>RXA01128
ATGAGCTTCACTTTCATTCGTACTTTTTTCGTACTTTTTGGCATCACGTTGTTAGTGTCA
TGCGTTCCAGAGCCTCCTGACTCCTACACTAAAGAATCCACTGTGCTGCGGTATCAGGTC
TCTGATTTCAATCTAAACTTCGTGGAATTAGCAGTTGCGCTTGGGTATTTGAACAACATT
GAGCTCCAAGTAGTCGGATCTGTACAAGGCGGCGTTGAGTCCATTGAATCGCTCAAAAAG
GATGACATTGACTTCGCGGCAGTCCCCTTCATTGGCCTTGTTGCAGGAGAGATAGCCACC
GGTGCGCCCATCAAAGCAGTGGCCGCAAGTTACGGAATTTCCCACGATTCTTCTTCTGCA
CTTCTAGTCCTTAAAGACAGTGAGATACACGAAGTGCACGATCTCATTGGCAAAACAGTT
GGCATAAACACCCTCGGTGCTCTGGGATCTGCGATGGTTGAGCGTCATCTATTCGACGCC
GGTCTCACCGAACCTGAGATCGTGAGCGTCACTCAACGTGCATTACCCGGTGAGTACTTA
GAACAACGCCTCTACCAGGGGCAAGTTGATGCAATTTGGGTCACCGATAGCGCTAAACAC
CAAGCGCTTGAAACTGGAGATTTTCGGATCTTGGCAGAGGATTCAGACCTTGTGCAGGAA
CTCAACACTGGCTGCATGGTGGTGTCGCAAAAACTCATCGACGAGCACCCCGCAGTGGTT
GGAGAATTAGTGGATGGAGTAGCTCAGGCAATCGAGTTTGAACGATCCCACTCCCCTGAA
GAAGTGCGCGAAGTTTATTTCAACTACCTCGAAGCCCATGGTCAGAGTGATAGAATATCC
AGCTTTAGATATTGGGAGCATTCGGGCATCGCAACCCGAGGTGGAGTGCTCAGTGATAGG
GAGTTCAGCATGTGGTCCCACTGGATTGACCGCCAATACGACGTCCCCGATATCAATCCA
GCAAGTATTTACACCAACCAATTCAACCCATACCGAAAAGTAAACCCCTCGCCA

>RXA01128-downstream
TAAAAGGCAAGGGGGTCGGCGTT

>RXA01129-upstream
CAATATAACGCACTTTAACATATTTCCCCCCATCTTTTTGTTCTCAAATTTATTTGTACT
CGAATGCAGGATTTCGAGACAATGAGGCAGTTTTTCTTTT

>RXA01129
ATGGTTAATCTCATGTCGGTCGAACTCGAAGAAATCCGCGATTTCTTAGCAGGATTTGAA
CCTTTCGCGCAGCTACCAGCCGAGGAACTAGATCAGTTACCTGGAAAAATGAGCTTGCGC
TATTTTCGGCGTGGGGAAGAGATCATCCCAATTGGTGTGCCCAATCATTACATGGGGGTA
ATCAGATCGGGTGCCATTGATGTTCTTGATCAGGAGGGCGTACTGCTGGATCGCCGTGAC
GCGGGGCGCTCGTTTGGCTATTCCACGATGGGGCCAGAACGAAATTCTCGGTACCGTATG
GTTGCCGTGGAAGATTCCTTGGTGTTGCGTCTGGGGCGTGATGATTTTGATGAGTTAGCC
AAGCGCAACCCTGATCTGAACCGTTACTACTCCAGCTGGTCGAAGCGTATCCGCGCCGCT
GCTGATCAATTGCGCCAAGAATCTAGTTCGAAGGTGCTGCGCACGAAGTTGGGGGAGTTC
AAGATCGCCAACCCGATTTCCTGCAGCCCGGACACCACGATCATGGATGCTGCCATCAAG
ATGCATGAGTTCGGGGTGTCTTCGTTGCTGGTGCAGATCGATGGGGAACTCAAAGGCATC
ATCACCGATCACTATATGCGCAGCAGGGTGGTGGCGAAGCATTTGGATATTCAGCTGCCG
GTCTCTGAGGTCATGACGGTGGATCCGCGTTGCGCGACCTCGCAGGGGTTGGCTTTTGAG
GCCATGTTGTTGATGTCGGAGCTGCGCATTCACCACTTGCCGATTGTGGATGATGGCCAA
ATCTCCGGCATCGTCACTGCAGCTGACATCATGCGCTTGCTGCGCCACGATCCGATTTAC
CTCACTGCGGATCTGTCGCGAAAAAATACCGTGGAGGAATTGGCCAACACCTTCCAGTCG
GCAGCGGAGGTGGCTTCGAGATTTATTGATCGGGGAGCTTCTGCGGAAGAAGTCAGTAGC
TTGCTCACCGTGGCTGCGGATTCTTTGGCAAGAAGGCTCCTTGTGCTGGCGGAGCGGAAA
TTTGGTGCACCGCCAGTTCCGTATTGCTTTGTGGTGGTGGGCTCGCAGGGCAGGAAAGAA
ATGGGACTGGCCTCTGATCAAGACAATGCCCTTGTTCTGGACAATTCCTACAATGACCGC
GAGCATGGACAGTATTTTGCAGCGCTGAGTGAATTCGTGTGCCAGGGCCTCGACCGCGCA
GGACAGGTGCTGTGTCCGGGTGACATGATGGCATCCAATCCGGAGTGGCGGAAAACTGCT
GACCAGTGGATCTCCACCTTCCATTCCTGGATTACTGCGCCGGAGCCGGATGCGTTGCTG
CATGCCCAGACATTCTTTGATTTCAGGGGAATTTACGGCGACACCGAGATGGCTAAGGAT
GTCCACCAAAATGCGGTGAATATGGCCAGGGGTGCGCGTCGCATGCATGCACACTTGGCT
AGTCTTGCGGCCCGGCGCGATCCTCCGCTGGGGTTTTTCCGTGGTCTTGTGGTGGAGCGT
TCTGGTGAATACGGCGCGACGATGGATATTAAGAAGGGTGGCACCGCGGGCATCGTGCAG
ATGGCGAGGCTGTATGCGCTGGCCACGGGTAGTGATGCGATTGGGACTCGGGAGCGGTTG
ATTGCTGCGTCGGGCCATGGTCAGGTGTCGCGTAAGGGTGCGCAGGATTTGTTGGATGCC
TTTGATTTCTTAGCGGCGATGGCGTTCCAGCACCAGGCGCGGTTGATCAAGGTGGGGGAG
AAGCCGAACTATCACATTGATCCCAAGACGTTGGGCAAGATGGATCGGGAGCATTTGCGC
GATGCATTTTCCATTATTAAAGATATGCAGTCGGCGTTAGCTACTAAATATCCGGTGAGG
AACATC

>RXA01129-downstream
TAGTGTTGGGGCGTCGAAAAGCG

>RXA01131-upstream
GAATTCATTCAAGGTGGTAAGGCGGTTTTCGCTCTTTTAATACAGTTTTAAAGGTAGATT
TGGGAGAGAAGATTTCCCTTAAGAAAGGTTCTTAACAACC

>RXA01131
ATGCCGCCTGCGACGCTGTTCAATGTTTTGACTTCAGCTGGACTTGACCCTCACCAGTCA
GGTGATGCCATTGTTGTCGAGTCTGCCCATTTCACATTGACGTTCACGTGGGATGAGTGG
CTGCGAGCTCAAGCGACGTGGGTGGGGGAGTTGAGTGCGTCGGATTATGTGCGTTCTATT
GTGGCGATTAACTCTGCCCATGATGCACGGGCAACGCCGAAGATGATGTTGGATGCCCCG
ACTGGTCTGACAACGGTGCTTAAGGCGGATAAGGGTCAGTTGCAGGCGTTTGCCGTGGAG
GCGCTGCCGATTGGCGATGGCCTCAGCGAGGCTCAGTTGGCGGGGTTTGTGGCTGCCGCG
TTTGATGGCGCCATCGACCTCACTCGTGAGTTTCATGCACTTTACCCGGAGCGCTCGCCG
CAGGAGCGCGGCGCAATGCTCAACATTAAGCTTGTCGACGCCTCCCCCTCTCAAACAGTT
ACGCCCGTGCGAGTAGCTAACTGGTTCATGGATCAGGGGGTGGAGGAAGTTCCTTATGAT
GCAGCTTCTGGGCGCATCAGCTTTGAGCTGGGTGACACCCCAGTGGATGTGATTTTGGAT
GATCCCGAGTTGTTGAAGATCCAAGCCGTGGTGGTTGCTGACCGCGATGTGGAAGCCACT
GAAGTTTTACATTTGTGTAATCGAGCGAACCTGGATTCTGATCACTCCACCATTTTTATG
CGTTCGGATGGGGATGATGTGGATTTCGTCGCCACGGTTGCGGTGCCGATTCGTGCTGGT
CTGAACGATTTCCAGTTGAGTCAAGCCCTGCATGATGGGGTAGTGGGGGTTGTTGGGCAG
GTACGAGCTGTGATCAATCAGCTACAC

>RXA01131-downstream
TAGTGAAGTCCATATAGTGAGAA

>RXA01134
AGTGCAACCCAAGACACCGGAGTGTGGAAGGGTATCTTCGCACTGCTCATGGGCAGGGGA
GCACGCGACTGGCGCACCGGACAGCAGTTTGATCGCTGGACTTTTGATGAGCTGGGTTGC
AATTTCCACCAGATTTTCCCCACCAAATGGTGCAAGGAACGCGGCATCGATCCTGTCCTT
ACGGAATCAGTACTGAACCGCACCCCGATGGGTCGCCGTACCGAAGTAGTCATCGGCGAT
ACCCCTCCATCCCGCTACCTGTCTCGTGTTCAATCCAAGTCGCTCATGGGTGATGAGGAA
TTCGATCAGATGCTGGATACCCACCTGCTCAGCGCGGAAGACCTGCACAGTTCCAACACC
ACGCACTTCTTTGCTTCTCGACGCACCAACTTCATCGACATGGTCGAGGATGCCATCGGT
AAAGCGGTGATCAGGGACGTCAACGAGTCAGATCTCACC

>RXA01137-upstream
TCGGTTTGAACGCAACTGCTTGCGCTTGGGTGAGCTTTGAGGATGTCTTCATTCCTGGGG
CTCAGATTCTAAGCCACGATTTCCTTACCTTGTGGCATCG

>RXA01137
GTGCGCCCAACCTTCGTGATCCTACGGATCTCCGAATACTTCGGTGTCGCTGAAGCTGCG
ATTAATGCAGCCACTGGACGTCTGACCAGCCTCAGCGAAGTGTTTATCGACAACGCTGCC
GAGATCCAAGACAACCTTTCTTCGCTGGTCGCGCTTCAGAAAGATTTGGCAGAGCGAGTC
AACGTTGAAGGAGTCAATCCTGTTACTCCAGTTGATCTACTGGAACTTCGCCTCGGTTCC
GCGCAGCTGGCCGTTGCTGCAACTGCCATTGAGGTTCGTGTTGCTGGAGGAGCAGGTTAT
GTAAAGTCTTCATCAACGTCTCGTCGTTTCCGTGTTGAAATGGGAGCTTGCACGGGTCCG

>RXA01137-downstream
TGATCTACAGGCCACGCAAAACT

>RXA01140-upstream
TATCCAACTTCCCGATTTTCAACGGGATTACGCTTGGGATGTTGATCGCATCCGAAGCCT
TATAACCACTGTTCTTCGTGGTTTTCCAGTAGGTGTGCTG

>RXA01140

ATGGCACTAGACACCCGCGGCGAGGAAATGCGTTTCCGGCCACGCGCGCTGTCCGGCGCC
CCAGATACGGGCAAGGATCCAGGTCTTTTGCTTCTCGACGGACAACAGCGCCTCACCACC
CTTTATCATTGCTTCAGTGGCGATGGCTATGTAAATACGGTGGACTTCCGATCAAAGAAA
GTGACCCGGAAGTTTTATATTGATGTTGCTAAGGCTGTTGAATCTCCGGTCATGTCCGAT
GAGGCTATTTTTTCAGTCGACGAAACCGGCAAAATCATCTCCCACTTCGGTCCAGTGATC
GACGGCGGCATCACCGATTTAGAAACAGCACTTGCTCATGGTTGCCTTCCAGTTTCTGTG
CTGCTGGATGATAACGGCACTGATTTCCTCTTTGACCTCGCCGATATGGCAGGAGAAGGC
GCTCGCGAACACGCGAAGCGCTTCCAATCACAAATCGTTAAGACCTTAGTTAGTTACGAC
ATCCCAATGATCCGACTGGATCGTGAAACCGCCAAGGGTGGAATTGGTTCCATCTTTGCT
CAGGCCAATAGCTCTGGCTTGCAGATGGATGTCTTTGATTTGCTCACCGCGGTGTTCGCA
GCCGATGAATCGGTGGAGACCGAATTCTCACTGCGTGATGACTGGGTGCGGGTTGAACGA
AACCTTCGCCAACACTCCGCACTTGATGGCATCGGCAGCACGGAGTTCCTCACCGCAGTA
GCCCTGTTGGTCAGTGCCCGCAAGGGACATGCGTCTGGTTACCGTGAAGATATCTTGAAC
TTGACG

>RXA01148-upstream
ATAGAACAAGGGTAGCCAAATTCTTGGAAACAGCGCGGGCCCCCGAATCCACAATGCGAA
TCCACAATGTCACCTGAAGCCGTTAAAGTAGGTGATCATT

>RXA01148
ATGACCAGCCCAGTTGAAAACGTTAAGAAAAAGCCACGCCCATTGGCGCTGTCACCGTCG
CGCGCCGGGGATTACCAGCAGTGTCCCCTGTTGTATCGCTTCCGCGCGATTGATCGCCTG
CCAGAGCCTAAGACCGTCGCCCAGGTCAAAGGCACGTTGGTGCACGCTGTGTTGGAATAT
ATGCACAAGTTGCCGCGTGAAGAACGCGAATATCCAGCCATGGTGAAGCAACTCAAGCCC
ACCTGGGCGCAGATGTGTGAAGAAGACGCAGAGCTCAAAGAGCTTGTTCCAGAAGATGAG
CTTTATGATTTCCTCGTGGATTCCCGCACCCTGCTGCGTGGCTACTTTGAAATGGAAAAT
CCTCAAGGTTTCGACGCCACCGAATGCGAAATGTACGTGGACACTGTGCTGCCCAACGGC
GTTCCTGTTCGTGGTTTTATCGACCGTGTGGATACCGCCCCACCGGCCAAGTCCGAGTTA
TCGACTACAAGACTGGCAAGAAACCAAAGCCGCAGTGGAGCCAGCAAGCGCAGTTCCAGA
TGCTGTTCTATGCACTGGTCTACTGGCGCATGTTCAATGAAATCCCAGCTCAGCTTCGTT

>RXA01148-downstream
TAATGTACCTCAAAGTCAACGAT

>RXA01153
CCGTTTTTAAGCCCGATCGTTACTTCCACGCACGCGGTGGTGGCGTATTCCACCGCGCGT
GGATTTGGTGAGCACCGGGTGCGTTGGGACTATGCGCAAGAGTCCCCACTGCGCGATACT
CGTGGCTTTGATCTGCGCCGATACCACCAGGCCCCTGTGGTGGATCCGCACGCCATTGGT
GTGGCCAACGTGTTTGTGCCCAATGGTGCCAGGTTTTATGTCGATCACGCGCACCCGGAA
TACTCCTCCCCAGAGGTCACCAATGCGTGGGATGCCATGGTTTACGACGCCGCTGGTGAC
CACATCCTTATGCAGGCCGTCTCTGATGTTGCGAGTTTCACCAGCCAGAATAGGTCTGTG
TTGGACGGCCATGATCCGTGTCCAGCTTTGAAAATCTACAAAAACAATGTCGACGGTAAG
GGTGCTAGCTACGGGTTCCACGAGAATTACCTCTACTCACGTGAGACGGATTTTGATGTG
CTGGCTCAGGCATTGATCCCATTTTTTGTGTGCCGGCAGGTCATCATCGGTGCCGGACGT
GTG

>RXA01154
GAGGGCATTATCAACACCCGCGATGAACCACACACCGACGCTGATCACTGGGGTCGCCTG
CACGTGATCATCGGCGATGCCAACATGTCGCAGACTGCGAATTTCCTCAAATTCGGCATG
ACCTCCCTAGTGCTGGATGCCATTGAGGCTGGGGTGGATTTCTCTGAACTCAAGCTGAAG
AACGCAGTGAGTGAAGTAGCAAAGGTCTCCCATGATCTTTCCCTTACCCACCAGCTGCGA
TTGGCGGATGGTTCAGAGCTCACCGCTATTGATATTCTGCGCCGCTATTTGGACAAGGTG
CAGCCGTTTGCAGAAACCCCAGTGGAACAGCGTGTCACTGCGCTGTGGGGTGAAGTGCTG
GGGCTCCTGGAGAATGATCTGCTCTCCACCAGCCATCTCCTTGATTGGACTGCAAAACTT
GCCCTGATCAAGTCTTTTGAGGCGCGTGGGCTGTCCATTAACGATCCCAAGATGTACCTC
ATTGACCTGCAGTACAGCGATATTGATCCACAGAAGAGTCTGTATCACGCACTGGTATCC
AAGGGGCGGATGAAAACACTGTGCAGTGCGCAGGACATTGCAGATGCAGCGGCCACTTCA
CCG

>RXA01155-upstream
ACAGCTTGCTGGATGAAATCGACGGACTGTTGGAAAACAACGCCGAGGAATTCGTTCGTT
CCTATGTACAAAAGGGTGGCGAATAGTCACTGTGAGTACC

>RXA01155
GTGGAATCCGCATTGACCCGCAGGATCATGGGCATTGAAACGGAGTATGGCCTCACCTTT
GTTGATGGTGATTCCAAAAAGCTTCGCCCAGATGAGATAGCTCGAAGGATGTTTCGTCCC
ATCGTGGAGAAATATTCCAGCTCTAATATCTTCATACCCAATGGTTCCCGGTTGTATCTT
GATGTGGGTTCCCACCCGGAGTACGCCACCGCCGAGTGTGATAATTTGACCCAGCTGATC
AATTTTGAAAAAGCTGGCGATGTTATTGCAGATCGCATGGCTGTAGATGCCGAAGAGTCG
CTGGCGAAAGAAGACATTGCTGGGCAGGTGTACCTGTTTAAAAACAATGTCGATTCCGTG
GGCAATTCTTATGGCTGCCACGAAAACTACCTTGTGGGTCGCTCCATGCCGTTGAAGGCG
TTGGGTAAAAGGCTGATGCCGTTTCTGATTACCCGCCAGCTCATCTGCGGCGCCGGCAGG
ATCCATCACCCCAATCCTTTGGATAAAGGCGAATCCTTCCCCTTGGGCTACTGCATATCC
CAGCGCTCTGACCACGTGTGGGAGGGCGTATCAAGTGCCACCACTAGATCACGCCCCATT
ATCAACACCCGTGATGAGCCACATGCGGATTCCCATTCTTACCGCAGGCTGCACGTGATT
GTGGGTGATGCCAACATGGCAGAGCCCAGCATCGCGTTGAAGGTCGGCTCCACGTTGCTG
GTTCTGGAAATGATTGAGGCAGATTTCGGTTTGCCCAGCTTAGAGCTTGCCAATGATATT
GCCTCAATTAGGGAAATCTCCCGCGATGCAACAGGATCCACACTGTTGTCCCTGAAAGAT
GGCACCACCATGACTGCCTTGCAGATCCAGCAGGTGGTCTTTGAGCATGCCTCGAAGTGG
TTGGAGCAGCGCCCCGAACCAGAATTTTCTGGCACCTCCAACACAGAGATGGCCCGCGTG
CTGGATCTGTGGGGTCGCATGTTGAAAGCGATTGAGTCCGGTGATTTCAGCGAAGTGGAT
ACAGAAATTGACTGGGTGATCAAAAAGAAGCTCATTGATCGTTTCATTCAGCGCGGCAAC
CTTGGGTTGGATGATCCAAAACTTGCCCAAGTGGACTTGACTTATCACGATATTAGGCCA
GGTAGAGGCCTATTTAGCGTGCTGCAAAGCCGCGGCATGATCAAACGGTGGACTACTGAT
GAGGCGATTTTAGCTGCGGTGGATACCGCTCCTGATACAACACGTGCTCATTTGCGCGGG
CGAATCCTTAAAGCGGCGGATACTCTGGGAGTACCTGTGACTGTCGATTGGATGCGTCAC
AAGGTCAACCGACCGGAGCCACAATCGGTGGAATTGGGGGATCCT

>RXA01156-upstream
AAGAACTAAGAAATACCGATTTACGGCAGGAGA

>RXA01156
GTGAGTGTAGTGAACGCAAAGCAAACCCAAATTATGGGTGGCGGCGGACGTGACGAGGAC
AACGCCGAGGATTCCGCACAGGCATCTGGACAGGTTCAGATCAACACCGAAGGTGTGGAC
AGCTTGCTGGATGAAATCGACGGACTGTTGGAAAACAACGCCGAGGAATTCGTTCGTTCC
TATGTACAAAAGGGTGGCGAA

>RXA01156-downstream
TAGTCACTGTGAGTACCGTGGAA

>RXA01158-upstream
TAGGACGTTCAAGGAATTGGCTGAATCAACAAGCGCCAAGGTGGTTAAGCGCCCTCGGCG
AGTTATCTCAAAAAAGAAGAAGAAGTCTCCTACGGGAGAG

>RXA01158
ATGTCCATTGTTGAGCACATCAAAGAGTTTCGACGCCGACTTCTTATCGCTCTGGCGGGC
ATCCTCGTGGGCACCATTATCGGCTTTATTTGGTACGATTTCTCATTTTGGCAGATCCCC
ACTTTGGGCGAGCTGCTGAGGGATCCGTACTGTTCTCTGCCTGCTGAATCCCGCTGGGCC
ATGAGCGACTCAGAGGAATGTCGACTGCTCGCAACCGGCCCGTTTGATCCATTCATGCTT
CGCCTTAAAGTAGCGGCGTTGGTGGGTATGGTTCTTGGCTCACCCGTGTGGCTGAGCCAG
CTGTGGGGCTTTATCACCCCAGGTTTGATGAAGAATGAGCGCCGTTACACCGCAATCTTC
GTCACGATTGCTGTTGTGCTGTTTGTCGGCGGTGCTGTTCTTGCGTACTTCGTCGTTGCA
TATGGTTTGGAGTTCCTCCTTACCATTGGTGGAGACACCCAGGCAGCGGCCCTGACTGGT
GATAAGTACTTCGGATTCTTGCTCGCGTTGTTGGCGATTTTCGGCGTGAGCTTCGAAGTT
CCACTGGTGATCGGCATGCTCAACATTGTGGGTATCTTGCCTTACGATGCCATTAAAGAT
AAGCGACGCATGATCATCATGATTTTGTTCGTGTTCGCTGCTTTCATGACACCCGGCCAG
GATCCTTTCACCATGTTGGTGTTGGCGCTTTCACTCACCGTTCTGGTAGAGCTTGCCCTG

CAGTTCTGTCGCTTCAACGACAAACGCCGGGACAAGAAGCGCCCAGAATGGCTTGATGGC
GATGACCTCTCTGCATCACCACTGGATACTTCTGCTGGTGGAGAAGATGCTCCAAGCCCA
GTCGAAACCCCAGAGGCGGTGGAGCCTTCGCGGATGCTGAACCCAAGTGGGGAGGCGTCG
ATAAGCTATAAACCCGGGCGCGCCGACTTCGGTGACGTGCTC

>RXA01158-downstream
TAGGGCCTAGCCAGGTACCCTTA

>RXA01159-upstream
CATCAATCAATGTGCAAGGGTTTCATTTCTGGAAATCGTGGTCACCCCACATTCACCAGT
CATGAACAAGCTTGTTTAATGTGAATTTGGAGTAGACCAC

>RXA01159
ATGTCCCTCGGACCATGGGAAATTGGAATCATTGTCCTGCTGATCATCGTGCTGTTCGGC
GCGAAGAAGCTGCCTGATGCAGCTCGTTCCATCGGCCGTTCCATGCGCATCTTCAAGTCT
GAAGTCAAAGAAATGAACAAGGACGGCGATACCCCAGAACAACAGCAGCAGCCTCAGCAG
CAGATTGCGCCCAACCAGATCGAGGCTCCTCAGCCAAACTTTGAGCAGCACTACCAGGGA
CAGCAGGTTCAGCAGCCTCAGAACCCTCAGACCCCTGACTACCGTCAGAACTACGAGGAT
CCAAACCGCACCTCT

>RXA01159-downstream
TAAAGTTGGGCAGTTTGCATCTA

>RXA01160
AAATCATCCAACAAAATCAGCGACCTTGCCCGCCAGCTTAATCTGTTGCCGTATTTCACC
AGGTATAAAGGCCGTACCGTCATGGAAGCAGCGCGCGATCTTGGCCAACCCTCCTCCCAA
ATCATGGAAGACCTCAACAGATTATGGATGTGTGGTCTGCCAGGACTTCTTCCAGGTGAC
TTGGTGGAGCTTGATCATTCCTTTAAGGAAGTAAAAATCCACAATGCTCAAGGCATGGAT
AAACCCTTGCGCCTCACACCAACTGAAGCCGGTGTTTTGCTGCTGACACTTGAATCCCTG
GAATCCCTCCCCGGTATTGCGAAACAGGAAGCGGTCGTATCTGCTGCGAACAAGCTACGC
GCCATCATGGGGGAGTATTCCTCGACTGTTTTCGACTCCACTGGAGAAGACCTCGATGCT
GAAGTTCTAGAGATCATCCGCGACGCCATGGATTTACACCAGCAGGTCAGTTTTGAATAC
CACTCGCACAGATCAGACAACACCAGCCTGAGGCAAGTCAGCCCTGCTCATATCTTCACC
CATGAAGGCGAAACCTACATCAAAGCCTGGGAAGAAGCTGTGAACCAATGGCGGACGTTT
AGGCTTGATCGCATCCGAAGCATTGTGCTTCTTGACAGCAAAGCAGTGCACCCGGCGCGA
GGGGTTTCAGTATCCACGGACGATCCTTTTGAGTTCGCAAAATCTTCCGATATTGCCACG
TTATTGCTGCGTGAGGACGCAATGTGGTTAGGCAATTACATGGCCATGGAGGTGGATGAA
ACGGTGGAACCGATTCGCGATAGCGACGGATTCAGCTGGCACACAGTCCACTTTCCGCTG
CTTTCTAGGGATTGGTTCGTCCGATTCGCGATTGGCCATGCTGAGCATTTGAAAGTAACT
AGTCCCGAAGATCTTCGGAAATGCATAAAGCAAAAGGCTTTTAGTGGTTTGTCAGCGTAT
GATCATCACGTAGAG

>RXA01160-downstream
TAACACCCAAGAGTAAGACGCAA

RXA01163-upstream
ACCGTACCCACAGACACACCAGAATTAACAGAAACAGACTGAAAAACAACATCGCTCGAC
ATGCGCGTAATCCTAACCCGCGCACACTAATGTGGCCGAT

>RXA01163
ATGGGCTACACCAACCTCAACGACACACGGGTCTTGCGCGCCGGGTCATGTGATGCCTGG
TGGCGCACGATGTCTCCGCTAGTGCAGCAGGGAAGTGAGGCAGTCTTTCGGCGCATCATG
GGTCTCTCGCGGCGTCCTGATCGGAAACCTGGCTTTGACGATGTCCCACATTTCGGCGCA
GCTGTTCGAGTTCCCGGTCTAAAACACGGCACGTTGGTCAATGCTGCACCCTTGAAAGTT
TTGGGCGCACGGGGCGAGCCCAACCCCGCGAGTTCGTACCGTTTTGAATACATCACCGGT
GATTCCGCAGGTCGAGCCATCACTGCGACCGGCGCTGTCCTCTTTTCCACACGCCCCTGG
ACAACCGGCCCGCGTCCCGCGATCGCCATGGCTCCATCCACCCAAGGCGTCGCACAGCAC
TGCGATCCCTCCCACACCTGCGCCATCGGACTCAACGCATTCTATGACAAACCCTTCGAC

GCAATCATTGCTTACGAACTCCCCGTCATCCTCTGGTTTCTAGCTCACGGACTTGACGTT
GTGTTCATCGATTACCCCCGCGACCCCGCAACCGGCGTCCAATACTATTGCGATTCCATC
GCTGCAGCTAAATCGCTTCTCGACGCCGTCCTCGCCTCCAGACAACTCGGCCTTTCACCG
GAAGCACCGCTTGGCCTGTGGGGATTCTCCCAAGGAGGCGGCGCC

>RXA01165-upstream
AGACCACTCACATTGCACATCTGCAGCTGCCAGGAAGTCTCCACCCAACAGTTTTCTAGG
TCACAGGGATCCATTAGCCATTTGGTCCTTGTCGAAAGGT

>RXA01165
ATGGTGGGGCATGTGCCTGCAGCAATAGCAATCCCATATTTCATTATTGAGATCCTCGCC
TTCATTGGTGTCGTCATGTGGCTCGGTTTCGGCTGGGCTTTGGGTCTCCTCGTATTGTTC
TTCGTCGGTGGACTTCTTCTAGCCGGCGTGGAGCTTCGTCGCATTAGTAAGAGTGCCGCC
ATTCATCAGGCTTCGGGCCAGGGAAGTGCGGGAGCGATCGCCGGAAACATTGGGCTGACC
GCAGCTGGTGCCATTTTGGTGGCCATGCCGGGGTTTGTGTCTTCGATTATCGGTTTGTTG
TTCATTTTTGCACCAACCAGGGCGCTGTTCCGCAAGGTTTTGGCCAAGCGCATGCGCAGT
GCCATCGAGAACCTAGGTGTGCGTGGTTTTGAAGCCGTTAATGGTTACCGCACCCAGGCA
TCCTACGGAAACTTCGGAGCGGCATTCAATGGTGGTGCGCAACAACCATCAAATGAGCCG
ATCGTGATTGATGAAGACGAGATCCAAGCCTGGACTTCTGATCTCAAACCTGAAGATTTC
ACCAAAGGTAAAGATGAATCCGACGGTGAGAAA

>RXA01165-downstream
TAAGTGACACTGTTTGTTCGGCT

>RXA01166
CTCACCGGAGTGATTGCCTACGCCATCGCGGGACTTGCAGTGAACTCTTCAGAGATGTTT
GAGGAAATCATGTCGGTGTTAAATGAACGCGGAGTCAGTGATGTGCTGAAAAATATCACC
AGCTGCGCGGGAGGTTCCTTGTTGGCCAGTGGCTACTCGTCTTCCCGCGGGTGGACACAT
CAGGGCACGCCGCTGGCAGACATTCTGGACGATCTGCCACTTGTTGTCGCTGAGTTTGGG
AAGCAAAAGCTGGGTCGTGTGGCGCCAGAAATCCCAGTGCTGTTGTGGGGCTCTAAAAAT
GATGATGTCATTCCCATTGATCCCATTAGGGAATTGCGTGATAGCTGGGCGGACAAGGGT
ACGCCATTGACCTGGCATGAATCCCAAGCGCCGCGTGTGCCAGGACGCACAGGTCTCAAC
CATTTCGGGCCCTATTTTAGAAACCTGGAAAAGTACTCGGGATGGCTCATAGATCATCTT
GTC

>RXA01166-downstream
TGAGTGCCGTTTTAAAGGCTCGG

>RXA01167
CCTCGCCAGCTCGTGAAGTACAAGACCGCAGACGGGGAAATCTATGAGGTTCCCTTCGCT
GATGATGCGGAAATCCCCGAGGAGTGGATGTGCAAGAACGGTAAGCTAGGCATCCTCATG
GAAGGTGAGGGAGTCGAGTCCAAGCCGGTCAAGCCTCCACGTACTCACTGGGATATGTTG
CGTGAGCGTCGCTCAATTGAAGAGCTGGATGTGCTGCTGGAAGAGCGCATCGAGGCACTT
CGTAAGCGTCGTCGCAATGCAGCGAAACTGCTGAAGGCTCAGCAAGAGGCTGAAGAAGCA
GAAAAGGCAGCTGAAGAGGTT

>RXA01167-downstream
TAATCTTCCTGCCTAAGTTAGAA

>RXA01169
ATCCCCGTCTTCCTGGCTGTTTTTGTGGGTTCAGATGCCCTTGGCTCAATCTCTTTCGGC
CCATTTGTAGAAGCATTTTTCCTCCTGATTCTCATTCCACTTGTTGCTGCTGCGGGAACT
CAGCAAGTGGCAAGAAAGTGGCAGGTAGGACGTACAATTATGGCTGCTGCAGAAGCAATC
ATGGTGCCTTTAATGATGCTGACGTTGTTCGCTGTCATCGCATCGCAAGTGGAAGCTGTG
AGTGGTCAATTCACCGATATCGCCACAGTAGTGCCACTATATGTCGCCTTTTTGATGGTG
ATGATTCCAATTGGTGGCGGGATATCCAAACTCGGTGGCTTAGGTTTCAAAGAGCAACGA
GCCATCGTTTTTAGCGGAGCAACCCGTAACTCTTTGGTCGTTTTACCTTTAGCGTTAGCA

CTTCCCGCAGGCCTGGAAATAGCGGCCGTCGTAGTTGTCACTCAAACCCTCGTGGAACTG
ATTGGCATGGTTGTCTACGTGCGCATCATCCCTTTAATTTTCCATGAAAAGCAGACATAC
AGGAAACTTTCAGGCATAGGGGAGTCA

>RXA01169-downstream
TGAAACAGAACGGCAAGCTAAGG

>RXA01170-upstream
TACAGGAAACTTTCAGGCATAGGGGAGTCATGAAACAGAACGGCAAGCTAAGGTGACATA
GTCACTTAAACTAAACAAGAAGGGTGGAGGACCCAAGCAC

>RXA01170
GTGAGTCTTTCAAACAAAGCTAAAGGAATCGTTGCAGTAATCATCGTCGCCTGGATCGTC
GCGATGGCTGGCATGGTCGCATACGCGTCAAGCAATAATGCTGATAAGACATTTCCAACT
GCAGGTGCGCTAGAACAAACCGTCGCAGCATTTGATAGGCAAGGCCTTCAGGTCTCTGCA
GTCGCACTGGCAGACATCTACGGCGATGAATACGTCTCCGCGGCGATTCTGTGCGAAGGA
ACTCCAACCGCAACACTCGAGCAGTCACTGGGCGTAGACCTGTCTGAGCTGAACCTGGAC
GAGTCTGGTGTTCCTTCGGGCGTGTCCTACTTGGCTCTGTCCAATCAGGATGGGGAAGTT
GTCTACGACAAGATTGATCGTGCCAACGTTGATCTCTGCGCAACGCCACTCAATGGTGCT
TTCAGCGCTTATTCATTGATGCCAGTTGCCAAGGTTGGCGAGAACTCCTGGGCGATCGCC
GCT

>RXA01170-downstream
TAGGGTTTTAAGGGTCAATCCGC

>RXA01171-upstream
GTAGAAATTTTCCATGCAGAGGAAAGCCGATAATGGGGCAGAACCCCTTCCCGCCAAAAT
GACATAATGTACATTATCGGACAATTATCCATATCTGGCC

>RXA01171
ATGTCGCAGGCCGCTGGTAAGTTTAAGCCCATGACTTCAACGCTCGCCGAATCAACACTT
ACATCCCTTAAAGAACTTGAGGATCCAAAGATCCTTTCCGTCAATGAACGCCACGGCGAT
GATCACGCAGTGAACCTCACCAAGCTTCGCGCCGTTGCCAAAGAGCTGAAAAAGAACCAG
CCGCTGGCTCGTGAGCTTTGGGCAACCGACGATACAGCCGCACGTTTGGTGGCGTTGCTT
ATTTGCCGACCCAAGGAATTTGATCAGTCTGAACTCGACTCGATGATCCATGAGGCTCGC
ACGCCGAAGGTTCTTGATTGGTTGATCAATTATGTGGTCAAGAAGAATCCTCATTGGAAC
GATCTCCGTGTGCTCTGGCTTGAAGATCCCGCCGAGAATGTTGCGGCCGCCGGCTGGGCT
CTCAACACTCATGCCGTTATCACAAAGCCGGACGCATTGGACGATTCCGAAATCCTTGAC
ACCATTGAAGCTCAGATGAAAACTGCCGAGCCTCGCGTACAGTGGTCAATGAATGAATGT
TTGGCGCAAATCGGCATCCATCGTCCAGAGCTTCGTGATCGTGCCATTGCCATTGGTGAG
CGCCTGGAAGTTCTCAAAGATTATCCGACCCCTCCAAATTGCACCTCGCCTTTTGCTCCG
ATTTGGATCGAAGAGATGGTTCGCAGGAAAAAA

>RXA01171-downstream
TAACCGACCTGTTCCCTATCTTT

>RXA01173-upstream
AGATCTGTTTCTATGTATTAAAGATCACACCGAGTGGTGGAATTTCCTCAAGTGATTTAC
CCACAATGGACTTTGTTGATACCCAATTCGAGAAAGGCCA

>RXA01173
ATGCACGTGAGCACTCTTCCAAACAAGAAACTGCGTACTCGCATTTTCGCAGGCACCGCT
GCCGTCGCACTGTCACTTGGTGTTGCGTCTTGCTCAAACGCAGAAGATGCTGTGGATAGC
GCAACAGATGCTGCCAACTCTGCAACCTCCGCCGCGGGATCTGCAATTAACGATGCCACC
GGCACTTCCAGCGCATCCACCACAGAGCCTTCCGGAACCTCTGGATCCGACTCCGGGTCT
GACTCTGCTGGAGGAGACACCACTGAAGTAGAAAGCGCCGATGGGTCCACCATCAGCATC
CCAACTGCCGTCGTCACCGCTGCAAATGCTGCAGGATTCAGTACCCCGGAATCCGTGGAA
GAAGGCCCGAATGGTGAGTCATTGGTGACGTTCCCTGAAGGCTACATTGTTAACTCTGCA

GAAGGTGGTGCACAAGCACTGGTCGGCATGATCGGTGAAACCTGGATCGGCGAAGGCGGA
CTATCCGCGGCAGTGGGTCTCCCAACTGGGCCTGAAGAAGCAACAACAAATGGTTGGACT
CAACAGTTCACATCTGGAGTAATTAGCTGGCTTGATGATGGATCAGGACAGTTCGCAGCT
TCTGTTGAACCTGCT

>RXA01173-downstream
TAAGGGAATCTCACCTGGCCTCC

>RXA01174-upstream
ATATCGCAACCGCTGTTAATGAAGAGGAAGAGGCTCGCGATATCGCGAAGCTGTGCCAGG
AGATGGTGGAATTAGCTCGGAATATTGAGAAGTTGAGGTA

>RXA01174
ATGAGCAACATGCAGGGAAACGATTCCAAGAAATCTAGCGGCGCGAGTCGTGCGGAGAGC
CCACTGATCAAGTTCCGGACATTGATTATCGTCATCTTTGTCATCTTGATCGTTGGTTTG
GCATCTATTGCAGTGGGACCTGTCGTGTACCAGCTCATCATGGGACCTGGTGTGAAAACC
GAAGGAATCCAGGCTGATGGCGCAGCACCTGCGTCCACCGACATGAACGGCACCTGGGAT
GTTGCCCCAGGGAGTATTCCAAACACCACCTCAGCTGGATTCACCTTCGCTGAGATCCTG
CCAGGCGAAGAAAAGATCACCTCCGGCTCAACCACTGGTGTCACTGGCGAAGTGGTCATC
GAGGATAACTCCCTGATCTCTGGTCTGATTACCGTCAACATGACTCACATCACCACCGAT
CAGGAAAAGCGCGACATCAACGTGCGCACTAAGCTCTTCCACACCGATCAGTACCCAGAA
GCAACCTTTGAGGTTACCGATTCCGTTGATCTTTCTGCGCTCCCAGACACCGGATCCATT
GCTCAGGTTGTCATCCCAGGCGAGTTGACCATCCACGGTGAAACCAAGGCTGTGGAGCCT
ACCTTTGATGTACTTCGTACTGGTGACCAAGTTATCGTGGCTTCCGATATCGAAATCAAC
CGCCTCGACTTCGGTGTAGAAACCCCAGAGTTCATCGCCGCAAAGATCAATGAGACCGGC
GAGATCAACGTCCGAATCGTATTGGAGAAA

>RXA01174-downstream
TAAACCATGATGGCATCACGGAT

>RXA01176-upstream
GAGCTGTGCACCTTGTGACCTTTTGTGACACTGCTCAATGCTTTACGGCTACGATGAACA
ACAAACCGACGTTTTCGACGCTGTGAAGGACTAATTGCTA

>RXA01176
GTGCGTTATTTTTACGATACTGAGTTCATTGAAGATGGGCGCACGATCGAATTGGTCTCT
ATTGGAATCGTCGCAGAAGACGGTCGCGAGTATTACGCAGTTAGCACACAGTTTGATTCC
TCCAAGGCGAACGCTTGGGTGCGCGCCAACGTGTTGGACAAATTGCCTAATCCTTCCTCC
AAAGTGTGGAAATCTGCAGACACTATAAAGCGCGAAGTTTATGAGTTTCTCACCTCCACC
GGACCAACCCCTGAACTGTGGGCCTGGGTGGGCGCATATGACCACGTGTTGTTGGCACAA
ATGTGGGGCGATATGGCGGGGCTTCCTCGGGAGATCCCTCGTTTTACCCGCGAGCTTCGC
CAGTATTGGGACATGGCTGGCCGCCCAACGCTGCCAGAGCTGCCGAACGGCAACCACGAT
GCGTTGATTGATGCGCGTCATAATTTAGCCAAGTTCAAAGTGTGCATGGCAGCGCTGCCT
TTGGGTAAAAGGGATCGCGTCTCT

>RXA01176-downstream
TAGTCGATCTGCTCCCATTCCAT

>RXA01177-upstream
TGTTCATCGTAGCCGTAAAGCATTGAGCAGTGTCACAAAAGGTCACAAGGTGCACAGCTC
AGTTCCTTAAAAACCGCTGGATACGGATACACTATTTTTC

>RXA01177
ATGCACGGTGAAAAACTTGTGGATGGCACTGAGGGAAATCTCAGTCAATTCCAATGGCGC
GATATGGCTACAAATCAGACGCTGAGAAAAGCACTGTTAGTGCTTTCTACCATCGCTCTA
CTCTTGACTTTATGGCCTTCAATTTTCAATGTTCGGGCCATCGAGTCTTTTGTTTTCTTC
TTCCATATTGATACTGACGTGTACCGCGCCGGTGCTAATGCATTCTTGCATGGCGAGAAT
CTGTATACCCAGGACTACCAAGTTGGTAGCATTCAACTTCCCTTCACGTACCCACCGATT

TCTGCTGCGCTGTTTGTTCCACTTGCAATCCTTGCAAGCAGTGTAGCCGGAATAGCATTA
ACGCTTATTTCCACGGTGTTGCTGTGGTGGAGCGTAGCTATCGTCTTGCGCCGAGTGCTC
AAGGGTCTCACGGATGCTGATTCCAGGTTTGTGTCCTATTTGATTCTGCCTATGGCATTG
TCCACGGAACCTGTATTCCAGACCCTGCAGTTTGGCCAGGTCAACATCATTTTGATGGCG
CTGGTTCTCATGGATACCTTCACCAAAAAGCCCTGGTTGCCACGTGGTTTTTGGATTGGT
TTGGCGGCATCCATCAAGCTGACCCCCGCAGTCTTTGGCCTTTACTTCCTAGTGAAGAAG
GACTGGAAGGGCGCTGGAGTAGCAATTGCTTCTGGCGTAGGTTTTTCCGCCTTGGCGTTT
ATCCTCTCACCTTCAAGTTCCAAGATTTACTGGACTGAAACACTCAACGACCCTTCTCGC
ATCGGCAACCTATCTTATATTGCTAACCAATCTGTGCGTGGAACGCTCAGCCGAATGATG
CATGAACAGCAGGATCTCGTCGAAAAGCTTTGGCTTGTGGCAGTTGTCTTGTGCCTTGCC
GCTGTCGCCGTCGCCATGTGGCGCGTGGTACGCGCCGGCAACCCGTACGGCGCCGTCATG
CTCAACTCGTTGATTGCTCTGCTGTGCTCCCCTGTTTCATGGTCTCACCACTGGGTATGG
CTGATTCCAATCGCTATTGGTTTGGGGGCAAGTGCGTGGAACCAGCGGCGGACTGCTCCA
GGAATTGCCGCGACGGCTGGAGTCTTGGCGCTTCTGACCACGATTCCGATGTTCATCACA
ACATTTTGGAACATGCCATACGATTCAGAGTCTTACCCATTTTGGCCATTGATTCTGCAG
CCGTCGGGCAACGCGTATGTAGTAGTGGTCATCGCTATTTTGATCGTCGCGATTGTGAAT
CCAACAGTTTTGGGCAGTGGCAATAAAGCTGTTTCAGGCCAGGCAGAGAAGAAGTCCTCC
CCTGCGTTGCTTGTTGTTTTAGCGATTGCCATTTTCTACCTCTTTGCCAATATTTGGTTT
AAGGGAAACAATCAAAACAAAGCGCTCATTCAGTACCCACTGCAGACTATGGAAGGTCGC
GGTCTCACTGACTTCGGCGAGCTTATTTTTGAATTCGCGGCTTCCTCCAACCAGCTTGTT
TCCCTCTGGATAATCGGCGCCCTCAACGCCATCGCATTGGCTATTACCCTGTGGTTCCTC
CTTCAGCGTTTTGCTGGGAAGAAGAGCTCCTGGCTGATTTATCTCAGCACCGTGGCTGTT
GCGCTGATGATGTTCTCAGTGCAGGATGCCTTGCAGTTTGGTTCGCTGACTCTCGTTGCA
CTCGCATTGATCACTGTTGATGTGTTGAGTGTCAGAGAGATTGGCCGCCGCGGGCTGCTC
ACAGGACTTGCAGCAGCCCTGTTTGGATGGCCAATTCTGATTGTTATCGGATTCCTCATT
CACCGACGTTATGCAGCAACAATCACAACCACTGTCACCGCAGCTGTGCTGTGGATCTTA
GGAATTCTGCTCAATCCAGACGCCTTCAACCTCAACCTGCTGCGTCAATGGTTCAACGGG
CGCGATGGTCGGGACAATTTGTCCTTCTATGCTTTCCTTGCCAGGTGGGTCAGCGAATCC
CCAGCA

>RXA01177-downstream
TGATGTTCGTATGGTTCATCGTC

>RXA01178-upstream
TCAACCTCAACCTGCTGCGTCAATGGTTCAACGGGCGCGATGGTCGGGACAATTTGTCCT
TCTATGCTTTCCTTGCCAGGTGGGTCAGCGAATCCCCAGC

>RXA01178
ATGATGTTCGTATGGTTCATCGTCGCCCTAGGACTTGGTGCCTGGGCAATCCACCGCACC
TGGTCACATGGATTCAAGGACCTCTCCGTTGCACTGAGCATCGCACTACCAACCTTGGTG
CTCCCCATAGTGGAACTCCACCACCTCGTGCTACTTCTTCCACTGATCGCAGTGTTGCTT
CGTCAAGGACGCGTGGCAATTTCCTACCTCATCGGATTTATCTACCTAGTCTCATGGACT
CCGCAACACCTGTCCTACTCCACGGTATTCCCACTTAATGATCCAGCACCAGAAGGGTAC
GTCGCCCACTTTGGATGGTATTTACTCGTTGAACCAATGGCGGTAGCACCGGCAGCTATA
ATCCTCGGAGCATTTATTGCCTGTGCTGCAACCACACCTAAAACAAGTCAGCTCGTGCAG
GTCGACAAGTCAAGCGCGGAAAACACCAAG

>RXA01178-downstream
TAAGCCTTACAGTCCGACAGCCT

>RXA01184-upstream
TAAAACACTTCTGAAACTACAGCTGACGTTGTGGGGAAGAACTATTAAAGGAAATAAAGC
GGCAATAGTGATGATGTCGCTGATATCTTTTTACGCCTTG

>RXA01184
ATGGGTTTGTTTGGTTTCGGCATCTTTTTGGCTCTTGGGCTTGGGCAAGACCACATGGGC
ATCCTTGCTGGTGTTGTCTCGGTCGGCATGGTGGCTTATTGCATTGCTGCGTTTATGTGG
CCGTCAGGTGAGGGGCAGCTGGATCCGACTGCATTTTCCACCATGCCGCTATCGGCGAAG
CAATTATTGCCTGGATTCGCTATCGGTACGCTCCTGCAGTCACGGGGGATTATTGCGGTG

ATTTGTACGGTGGCGACATCCATTATTGCTGCGGTGTTTTTACCTGTTGGTTCGTGGCCG
ATGATCGTGTTCATGATGGCGGTATCGCTGGTTACTACGTTGCTTTTGGGTGAGTTGCTT
GGGGCGTTGACCTCGGGTTCTTCTTCTAGGGTGAGTAATGATCGCCGTACAGTTCTTACT
TCCGTTGTCTTCATGGTGTTTGTTGTTGGCTATAACATGCTGATTGGCGCGGATGGAATG
AGTCGAATCGATGCCATTGGGGCTTATACAAAGTGGACACCATTTGGGGCGGGTGCAGGT
GCTATTGAGGCTTTTGCTGTTGGTTTGTGGGGTGAGGCAGGCCTGTTAACATTGCTGGCT
TTTGTTTATGTTGCTGCTGGTTTCTGGTTATGGTCACAGCTGATTAATCGCGCGCTCACT
GCGCCGCTGGACCAAGGTGGGCAAGGGCAAAGCGCTAAAGACAGCGCCGGTGAAGGCAAG
AAGGTTCTCTTTCTGCCAGGTATTCCTTGGTCAGTTGGAGGTGCCATTTTCTCGAGGTCG
CTGCGTTATATGTTCAGGGACTCCAGGTTGTTGGGATCAATGATTGTGTTCCCGCTTCTT
GGCGTGCTGTTTATTTTCCAGAGCTTCACCGTTGAGTTTTTCATGATCTATGTTGGGTTG
ATCATGATGGCAGTGTTCGCAGGATCCGTTGCTACCAATGATTTTGGCTATGACGGCCCT
TCGTTGTGGCTAAATATCGTTGCTGGTGTCAAAGCCCGAACGTTGTTGATGCCCAGGCAC
TGGGCATCAATGCTGCCGGGAAGTGTGTCAATTGTGGTGTTTATGATCATCACCATTGTG
CTCGCGGAGAATAAGACCACCGCTGTGCTGATCTGTTTTATTGGCCTGGGGATCTTTATC
TCCAGTGCGGCTGTAGCGTTGTTGGTCACCACATTTAATCCGTATCCGACTTCTAAGCCA
GGCACGAGTCCTTGGGGCGATCGAAGTGGCTATTCCGGTGCTGCGTTCGTGGGAGCATTT
GCCGCACTGTTACTGGGATGGATCCCGACGATTCCTACTATCGCATTGGGTATCTTTGGT
CTGGTTACCGATCAGATGTGGATGATCATCCTCGCGGAGGTGCTGGCCATTATTCTCCCA
GTAGCTGTGTACATCGGCGTTGCTAAGGTGTGTATTCGCAAGGTGGAGAAGGATCTTCCG
GAGATCTTCGACAAGGTGAAAACTCACGTGAAA

>RXA01184-downstream
TAGAAAAATGCGGGGT

>RXA01186-upstream
TTGCTCATACAGCCATTGAACTCGTAGAATCACCGTTCCGCCACCCAAATCAGCCCAATA
AGTTCAACAATTACATAACATCTGAAAGAATAGGGACATT

>RXA01186
ATGGCTACACCTGTACCACTGGTTTTTAACGCACCTAAGCGTGGCATGCCCCCAACCCAC
TTTGCGGATCTTAATGATGAGGCTCGCATTGAGGCTCTTAAAGAGCTCGGCTTGCCCAAA
TTCCGACTCAATCAGATCGCTCGACACTACTATGGTCGCCTCGAGGCTGACCCACTCACT
ATGACGGACCTGCCTGAAGGTGCTCGTCAAGAAGTCAAGGATGCTCTTTTTCCAACGTTG
ATGTCTCCTCTGCGCGTCGTCGAAACCGATGACGATACAACTCAGAAGACGTTATGGAAG
CTCCATGATGGCACTTTGCTTGAGTCTGTTCTCATGCGCTATTCAGATCGCTCCACGCTG
TGTATTTCTTCGCAGGCTGGTTGCGGCATGGCGTGCCCATTCTGTGCAACTGGTCAGGGC
GGTTTGGACCGTAACCTTTCAATCGGTGAGATCGTGGATCAGGTTCGTAATGCTGCTGCA
ACGATGCAGTCAGAGGGCGGTCGTCTGTCCAACATTGTGTTCATGGGAATGGGCGAGCCT
CTCGCTAACTACAAGCGCGTGGTGTCGGCTGTTCGTCAGATCACGCAGCCAAGCCCTGCG
GGCTTCGGCATTTCCCAGCGCAGTGTGACTGTCTCCACCGTGGGCCTCGCTCCAGCTATC
AGGAAGCTTGCCGACGAAGAGATGTCCGTAACTTTGGCAGTTTCCTTGCACACTCCAGAC
GATGAGTTGCGTGACACTCTCGTGCCAGTCAACAATCGTTGGCCTGTCGCTGAGGTACTG
GACGCTGCTCGTTACTACGCAGATAAGTCTGGCCGTCGCGTCTCCATCGAGTATGCGCTC
ATTCGCGATGTGAATGACCAGGATTGGCGCGCAGATATGCTGGGCGAGAAGCTGCATAAG
GCTTTGGGCTCCCGTGTGCACGTCAACTTGATTCCATTGAACCCAACTCCTGGTTCTAAG
TGGGATGCTGCACCAAAGGCTCGTCAGGATGAGTTTGTGCGTCGTGTGATCGCCAAGGGT
GTTCCATGCACTGTGCGTGATACCAAGGGACAAGAAATCGCTGCGGCTTGTGGACAGCTT
GCTGCGGAGGAATCTGCT

>RXA01186-downstream
TAAGCCCTCAAAGCTCAAAAGCC

>RXA01187-upstream
CTATTCTTTCAGATGTTATGTAATTGTTGAACTTATTGGGCTGATTTGGGTGGCGGAACG
GTGATTCTACGAGTTCAATGGCTGTATGAGCAACAGACCT

>RXA01187
GTGGATCCATTTGAGACCAACCCAAACGACCTTCCCACCGGTTTAGACCCAGCATACGAA

GGTAACAGTGAGTTAAACCCGCTTGGAGGAAAAAATATTCCCGACGAGCCTGAGGTGACT
GCAAACACACCTGCAGTTCAAGAAGAACCTGCTTACTCGGAGCCAGAAACTGCCGTTGAG
TCGAAGCGTCAGGCGAAGCAGAACACAAAGAAGTCCGAACCTGTTGTGGCTCCAAAACAA
ACACTTGCCGGTGGCACGTGGGTAGCTCTCATCGTAGGCGCACTTTTGCTAATCCTACTG
TTGGTCTTCATCATGCAGAACCAAACCACCGTAGAGCTTAACCTTTTTGCGTGGACCTTC
CAATTCCCAGCCGGAATCGGTTTCCTACTAGCAGCCATTACCGGTGCATTGATTATGGCG
CTTGGTGGTGGCGTGCGCATGTTTGAGTACCGTCGCAGT

>RXA01187-downstream
TAAGAAAAATCCGT

>RXA01195-upstream
GGTTTCGCGCCAGGCGACATTGTGAGTAGGATCGTCTAAAATCGTTTTCTTATCGCAGGA
AGGACTCAAAAAGGCCGTGGAATATTTGACCTGGGGTTTG

>RXA01195
GTGATTGTTGCAGTGTCGGCAGTTCTTCTTGCTGCCTGGCGGTTTTTCACCTTACGTTCT
CGGGGAACCACTGTGATTCTGCGTGAGTTGCCACAAAGCGGTGTGCATGGCTGGCGCCAT
GGATCATTTCGCTACAACGGCAACGACTTGGAGTACTTCAAGCTGCGCTCTTTGTCTCCC
ATGGCTGACCTTATTTTGAACCGCCTTTCAGTAACTTTGCTTGATCGTAGAGATCCAGCT
GCTGATGAGGCGGTTTTTATGTCTCAAGGCTTAAAAATTCTGCACATTAAATCCAAAAAT
GATCAGATTGAATTAGCTTTGGACGCCCACGGGGAGATGGCGTTTACTGCCTGGTTGGAA
GCAGCACCAGATGCGCGGGCGGAGCATTCATTGAATCCACGTGATTTCAACCGCTTTCGA
GCCAGCAAAGACACCCGCAAAAACCGC

>RXA01195-downstream
TAAGTAGACGTCATTGTTATGGT

>RXA01196-upstream
GGGCGGAGCATTCATTGAATCCACGTGATTTCAACCGCTTTCGAGCCAGCAAAGACACCC
GCAAAAACCGCTAAGTAGACGTCATTGTTATGGTGGGTGC

>RXA01196
ATGCGTTTAGTCATCGCCCGTTGCTCAGTTGATTATGTTGGCCGTTTGGAAGCTCATCTT
CCGTCCGCCGATCGCCTTTTGATGGTTAAGGCGGATGGTTCTGTATCCATCCATGCCGAT
GACCGTGCCTATAAGCCACTGAACTGGATGACACCTCCATGTTCTTTAGTTGAAACTCCC
ATCACTGATGAAGATGGTGAAGCAACAGGGGAAAGCCTGTGGGTGGTGGAAAACAAAAAG
GGCGAGCAGCTTCGAATTACTGTGGAAGAAATTCATTCGGAACAAAACTTCGATCTAGGC
CAAGACCCAGGTTTGGTGAAAGACGGAGTGGAAGATCATCTCCAAGAGCTTCTTGCAGAG
CACATCACTACGTTGGGTGATGGGTACACATTGATTCGTCGGGAGTATCCAACAGCTATT
GGGCCTGTCGATATTTTGTGTCGCAACTCTGACGGCGAGACTGTCGCTGTGGAGATCAAG
CGTCGTGGTGGCATCGACGGCGTTGAGCAGTTGACCAGGTATTTGGAATTGCTCAACCGT
GATGAATTGCTCAAGCCTGTTCATGGAGTGTTTGCAGCCCAGGAGATTAAGCCTCAGGCA
AAGACTCTCGCGGAGGATCGTGGCATCAAGTGCGTGACGTTGGATTATCAAGCGCTTCGT
GGCATTGAGTCCAATGAGCTGACATTGTTC

>RXA01196-downstream
TAAGAACATGGGCCGAAAAAATA

>RXA01197-upstream
AGCAACAATCATATCTGCCACCCTACCTTGGGGTTGGCATGTGATGACTAGCTTGCCCAA
TCCTCAATATTCCCCCACCTGCTATGCCTAAAATTAAGCC

>RXA01197
ATGTCTACCGAACAGTCTTTGAATATCCCCCACGAATACGTCATCTGCCTCGATCATGTT
GGCATCGCCGTCCCTGACCTCGAGGAAGCCATCGAATTTTACCGTTCCGCATTCGGCTGG
GTAAACCACCACCAAGAAATCAATGAGGAACAAGGCATTTCAGAGGCCATGATCGGCCCC
AAAGACATTAAAAGCACAGAAGGCATGATTCAGCTCATCGCGCCGCTCAACGAGGACTCC

ACAATCGCCAAATTCCTCGAAAAGAAAGGTCCCGGCATCCAGCAAATGTGCCTGCGCACC
AACAACATCGATGCGCTCTCCGAGCACCTGCGCCGCCAAGGCGTGCGCCTGCTCTACCCC
GAACCCAAAAACGGCACCGGCGGTGCCCGCATCAACTTCCTGCACCCCAAAGACGCGGGC
GGCGTGCTGCTCGAGATCACGCAGCCTCAAAGC

>RXA01197-downstream
TAATTGCTTATCGACGCTCCCAG

>RXA01198-upstream
TTCGGTAGACATGGCTTAATTTTAGGCATAGCAGGTGGGGGAATATTGAGGATTGGGCAA
GCTAGTCATCACATGCCAACCCCAAGGTAGGGTGGCAGAT

>RXA01198
ATGATTGTTGCTTTTTCTGTAGCCCCGACTGTTACTGATAATCCAGATGCTGAGATGGCC
GATGCGGTCACGGAGGCGATTCGAATCGTCCGCGCATCGGGTCTGCCTAATGAAACTAAC
GCGATGTTCACGCTCATTGAGGGGGAGTGGGATGAGGTGATGGCGGTGATTAAGGAGGCC
ACTGAGGCGATCTCTAGGGTATCTCCGCGTACATCGTTGGTAATTAAGGCTGATATTCGT
CCGGGACACACTGGCCAATTGACGAGGAAGGTGGAGGCGGTGGAGGAACGCCTAGCTAGG
GAT

>RXA01198-downstream
TAGCTTTGTACTTAAACTTGTTG

>RXA01206-upstream
CCGTGCCAGTGATGAAAAGCCGGCGAGCCGCCAAACTTGATTAAGTGATTGTCACTTTGG
ATTGTCATATTGGGCGAATAAACCGGTAGGATTCCCCTTC

>RXA01206
GTGAGCGCCGAAAATACCGAGAACACAGATTCCCCATTTGAAATCTCCGAGTTTGATGAT
CACCGACGCCCCCTCCAGCGGGCCCTCAAATTCGGTTCCATCGCCCTAATTGTCTTCACC
CTGATCTCCCTAGCGATCTGGGGTGCAACTCGTGGCGTACCCGGCGTATCAGCAGTTGTT
ATCGGCGCAGCAGTTGGCGCAGGCTTTGTCCTCTTAACGGCTCTCAGCGTCCTGTTTACA
ACTAATTCCAACGTCACCACC

>RXA01207-upstream
CTTCATGATCTCACCGGCAGAGCGCGTTTTGTTACAGCGCGTAAACTGTGACTTTGAAAA
ATTTTTGAACAATCCGTACACCAACTTCAGGAGAAAAACA

>RXA01207
GTGAGCAGAATCTATGACTGTGCCGACCAAGACTCCCGTGCAGCAGGCCTAAAGGCGGCT
GTCGATGCAGTCAAAGCCGGTCAGCTCGTTGTCCTTCCCACGGATACCCTTTATGGACTC
GGCTGCGACGCTTTCAACAACGAGGCAGTAGCCAACCTTCTGGCCACCAAACACCGTGGC
CCCGATATGCCCGTTCCAGTGCTCGTCGGCAGCTGGGACACCATTCAAGGACTTGTGCAC
TCCTATTCTGCGCAGGCAAAAGCGCTTGTGGAGGCGTTCTGGCCTGGTGGACTGTCCATC
ATCGTTCCGCAGGCACCAAGCCTTCCGTGGAACCTTGGCGATACCCGTGGCACCGTAATG
CTGCGCATGCCACTGCACCCAGTTGCCATTGAATTGCTGCGCCAAACCGGACCAATGGCT
GTCTCCTCCGCCAACATCTCCGGACATACTCCTCCAACCACCGTGCTGGAGGCTCGTCAG
CAGCTCAACCAAAATGTCGCTGTCTACCTCGATGGTGGCGAATGCGCGCTGGCCACCCCT
TCAACCATCGTGGATATTTCAGGCCCCGCACCAAAGATTTTGCGTGAGGGTGCCATCAGC
GCAGAACGCGTTGGCGAAGTACTTGGAGTGTCGGCAGAAAGCCTGCGC

>RXA01207-downstream
TAAATGGGAGTCGGTTTCGCGGG

>RXA01210
GTATTCCCAGTCGGAATCCCTTTGTTGCTCTTTCTCATCGGAAATGGTGGGGCAGCAGAG
TCCGCGAACTCCTTCGACTACTTCGTCATGTACACCCTGCTATTTGTGCAGTTCTACACG

GTGCTGTCCATGGCAACCACCCGCCGTGATGAACGTGTGCTGAAAAGGCTGCGCACGGGA
GAAGCCCGCGACATCGATATCATCGGTGCCATCTGTTTCCCCGGCGCGCTCCTCACACTG
ATCTTCACCGTGGTGATCATTCCATTGCTCATGGTTTTGGGAGCTCCCGCGCCCATCAAC
CTTGTGCCCATTGTGTTTGCCGTACTGATCGGACTACTTCTTTGTAGTGCTCTTGCCTTG
ATGACCAGCGGTTTCACCCGAAACGCCGAAGCCGCACAGATGACCTCCATGCCCGTGTTC
ATGCTTGCGATGGGTGGACTTGGATCAATCCGCTTCGTATTCGGCGACAGCATTGTGGCT
GATATCTTGGCCTACACCCCATTCGCCGCGATCAGTGACCTTGTCCAAATCGGCTGGGCT
GGCGCCACCTTCGCCGACAGCGTTGGTGGAGTAGAGGCAGCAAACTTCGCTGGAATTTTC
CAAGACATGCTCATACCACTTGGAATTCTGGCAGCGTGGACAGCTGCAGCGGTGTGGGCG
GCGAACCGCTACATGCGCTGGGACTCGTACCGC

>RXA01210-downstream
TAAGCCTGCAGCCGACGGGATTA

>RXA01213-upstream
AACTCTGGCAACAACATGCGCCTTCACTCCCTCAAACAAATTTTCATAAACACCCCACAT
CATATCAACCAAACGGTGTAGTTCTTCTAAGCTTTCACCC

>RXA01213
ATGACAAATCCCACAGAGGAGCGCAACGCACGCCGCCTCATTTGGGCCAACGGCCTGCAA
AACATCGGCGATCAAATCGTTGCCGCCAAAACAGTCCTGCCCTGGTTGCTGCAAGCCGCT
GGCGCGCCGGGCTTTTTGCTGGCGCTTCTGGTTCCAATCCGCGAAGCCGGATCGATGCTG
CCGCAAGCTGCCATTACTGGCTGGGTGCTGAGGCAGACGTCGAGAAGCAAAGTCTGGGTG
ATTGGCTCGAACGGCCAGTTCGTCTCGGCGCTGGGTATCGGCGTGGCTGCGCTGTTTTTG
CGTGGGTGGGCGCTGGGCATCACGGTGATCGTGCTGCTTGCGGCGCTGTCGCTGTTTCGA
TCGATGTGTTCGATTGCATCGAAGGATGTTCAGGGCAAGGTGATTTCCAAGGGCAAGCGT
GGGCTGGTAACGGGCCGCGCGACGGTGATTGGCGGTGTGATGGGCCTGGTTGCAGGCCTG
GCGATCGCTATTTTCTTGGGCTCGCATTCCCCGACGAGGGTGCTGGCCGCAGTGGTGATC
GCGAGCTCGTTTAGCTGGCTGTTTGCCTCCATTGTTTTCGCGCGCATCGAATACGCGAAG
CCAGCGACTCCAAAAAACGCGCCTTCCGCAAACCCGTGGGTGCGTCGCTGCATCGCCGCA
TTAAAAGATGATAAAGCTTTTCGACGTTTCGTTCTGGTTCGCTCAATGATGCTGGTGACA
GCACTCTCCACGGCTTTCATCGTCGCACTCGCCGCTGAATCCGGAAACAGCATCGACTCC
TTGGGATTCTTCCTCATCGCCTCCGGCTTGGCGTCCATGGTTGGTGGCCGAATCTCTGGA
ATCTGGTCGGATCATTCCTCCAAAAACGTCATGGCGGGCGGTGCCCTATTCGGTTCCATC
GTGTTAATCCTCGTGGTGCTCAGCTCCGCGTTTGCACCCGCGCAGATCAACACGCTGGTG
TTCCCGTTGAGTTTCTTCCTCATCACCTTGGCCCACACCGCCATCCGCGTGGCCCGCAAA
ACTTATGTAATGGACATGGCTGAAGGTGATCAGCGCACCCGCTATGTTGCCGACGCCAAC
ACACTAATGGGTGTAGTTTTGCTCATTGTTGGCGCATTATCTGGCTTCATTGCAATTTTC
GGAAACGAAGCCGCACTGCTCTTCTTGGCGGCAATTGGCCTGCTTGGAACCATTAGCGCC
CGTGGCCTCAAGGAAGTATCCGCCGGA

>RXA01213-downstream
TAGTTTTACAACTTTTCCACCCA

>RXA01218-upstream
CTAAATATGCTAGCACGATGGCCAAACCTAATCCAAAAACCGGCAGTATACTGATTGGGG
TCACATTAGCCAAAAGGCACTTTGAGGAAGTGGAACTCCT

>RXA01218
ATGGCACGACTTCAGCACGACATGATTTTCATCAACCTACCAGTATCTGACCTTGCAGCA
TCTAAGCGTTTTTATGCAGGTCTTGGCTTCAAAGAAAACACCGTCTTCAGTGATGAGCAC
ACTGCATCTTTTGAGGTCAGTGACGCCATCGTGGTGATGCTTCTGGAAACCGCGCGCTTC
AGTGATTTCACTAAGCGCCCCATCGTGGAGAAGAACGGCTCCCGCGAAGTGCTCAACTGC
CTGTCTGTATGTTCCACCGAGGATGCGGATGAGTTCGTGCGTCGCGCCCAGGAATTCGGA
GGCACGATCACCCGTGAGCTTGCAGCGGAAGGCCCCATGTACGGCGGAGCTTTTGATGAT
CCAGATGGACACGGTTGGGAGCTGATGTACTTCGATCCAGAGGCACTCGCTCAGATGATG
CCTGAGGGC

>RXA01218-downstream

TAAATATTCTTCAGGGCTTCTCG

>RXA01229-upstream
TAGCCCCGAAAGACGGCGAGGGTTGGCTCTGCTTCGTTGTGGGAAAACTAGGCCCTTAAT
AAGCTGTGCTTATAGGGTCTCCTGCACCGATAAAGGACTG

>RXA01229
ATGATCATCTCCACTAACACCGCTCACCCCCTGCACGAACCGCACGTACCCAGCCACCAC
AATCGTATGAATACTCTGCGTGCCGGTGTGCTGGGTGCTAATGACGGTATCGTCTCCATT
GCTGCGCTACTGCTCGGTGTGATCGCCACCGGCGCCAGTGACACCGTCGTGTTCGGCGCT
GGTTTGGCCTCAACGATCGCGGGGGCGGTATCTATGGCTCTCGGTGAGTACGTCTCTGTC
TCCTCACAGCGTGATACCGAACGGGTGCTCATCGCAAAAGAAGCGAAGGAGCTGGCCGAA
GACCCGACGGCCGAGCACGTCGAGCTGTCGGAGATCCTACACTCCTACGGCATCTCCCCT
GAGACTGCGAACCAGGCGGCCACCGAGATCGGGCAGGGCGACGCCTTGGGCGCCCACCTT
CAGCTCGAGCTCGGTATTGATAATGAGCAACTGACCAGCCCCTTGGCCGCCGCCTTCTCC
TCGGCCGTGGCTTTCCTGCTCGGAGCACTGCTGCCGATGGTGTCGGTATTCATCGCCCCT
GCAGGCTGGGACGCCGGCGTGGTCTTCGTAGTCACGCTGCTGGTCCTGGCGGTGACCGGG
TTCATCTCAGCCCAGATCTCGGGTACCTCCCCAATGCGCGCGTGCGGGCGCTTGGTGATC
GGTGGTGCCCTCGGCCTGGCCCTAACCTACGGT

>RXA01231-upstream
CCTGGGACGTCTTCCCCGAGGCGTGGGAnGACATTGAAGGTTTACCTGGGCTTTCGTGCC
CCAGGCATCGAGCACTTCACCCCCCTATGACGCCTTGCAA

>RXA01231
ATGCTGGGCTACACCTTCGTCATCTTTATCCTGGCGCCGTTTCTCATCCTCACCGGAATA
GCGATGGCCCCGGCCATCCGGTCCCGCTTCCCGTGGTACGTCAAACTCTTCGGCGGCCAC
CAGGGTGCACGTTCCCTGCACTTCATCGCCATGGTGTTGATGACGGGCTTTGTCATCATG
CACnGTCGGCCTGGTTTTTTGGTCCATGGCGACTACAACATGGTCCACATGGTCTTCGGC
GATATGAACACTGACCGTGCGGCGCAGGCCTACATCATCGTGATCACCACCATCGTCAnT
GGTGGTGTTKTTCTGRATCGKGCTCAGTATATTKGTMRCTGGCTKACCGRGMCCGCGCCM
WGCGGTTYACCGCCAGCWTCATCKGAGWTMGGWCGCAAAATCTTTNCTCAWCCGGCTGCG
TCCCCGGATGAGCAGGCAGAnnAnCACCTACACGGACAAGGACATCTCGCAGTTCCACTG
GACCAATGGCCTGCCGCCGACCGA

>RXA01231-downstream
TGATGAATCCCCCGAGTGGATCG

>RXA01234-upstream
AGAAACAATAGCCAGACCCAGAAGAGCAGACTGGAGAGCTTCGAGGATTTAGTGCTCCTG
TGCATTTATTCGGGTCACTTCAACGTTGAAAAGCATAGGA

>RXA01234
ATGTGGAAGTTCATGAAGACTCAATACGTATGTACCACTTATTTCATCGCTGCACCCGAG
GATGAAGACGAGGCGTACCAAACTTATCGCAGCCGAATGAACTCTTTGGCAGCATTGAAC
GGCGCTGACGTAGTTTCAGTGGCAGATGGCCTACGGATGGAAGTAGACCAGGATATTTGG
GGAAGCCTTGCTGAGCAGTATCAGATTGAGCAAGAAGGCCTGTATCCCACTGGTCACAAC
TTGTACTTTGTTGTCACCGTGGTGAACCTAGATGATTCAGATGAGGTTTATGACCGAACA
ATGGAGCATCTGATTATGGATGACCCTTATGTGCGAGTGGATCGTTTCCCAAGCACTGTC
CATGCCAGCACCCAGATCATGTTG

>RXA01234-downstream
TAGAAAAAGAAAAAGCACCACCC

>RXA01237-upstream
AAACCAAAAATCACGACGCATTAAGTAACAGAGACTTAAATTAAGAACTCCGAACAACAA
CTTCGGATTGTTTCATTTTTGAGGATGAAAGAGCTTTTCA

>RXA01237
ATGAACGTACAGTTTGAATCAGACATGGCCGTCCAACCAGGAAACACCATGGAAGCTACC
GTCACCGACATTCGTGATGCCAAGCGTAAAACAACCCAGCTTGATTCAGTAACGCCGTTT
AAGAAGAATTGCCCGAGCCGCACCTTGCTCGACACCATCAGTGACAAGTGGGCGGTGCTG
ATCCTGCTCAGCATGGAAAATGGTCCACAGCGCAATGGTGAAATCAAAGATCAGGTCCAA
GGAATTACCCCAAAGATGCTCACCCAGCGTCTTGGAGTGTTGGTGGAAGACGGACTGGTC
ACTCGCACCTCCCACGCAGTTGTGCCGCCTCGTGTGGATTATCAGCTCACCGATCTGGGT
GCTTCTGTCATTGAGCCTTGCCGTGCGATGTATTCCTGGGCAGTGGAGAACATTAAGCAA
GTGGAGGCCTACCGCTCAGCA

>RXA01237-downstream
TAAGAACACTTGGCAAACCTCAC

>RXA01246-upstream
GGGAAGGAGGAGAAGGCTGCTGTGAGCTCTGCAGCCCCCGTCCGCTGACTTTCAATGCTT
CATGGACTCCCCGATACACAACCTCCGAAAGGGAACCCCC

>RXA01246
ATGAAGCGCACTATCACCATCGCCGCTCTCGCCTTGACCTCCACCCTGGTTTTGTCCGCC
TGCGCAGATAACACTGAGGGAGAAAACACCGACACCACGACCATCGCCACTACGTCCGCC
CCCGACACCACCGAAACGACCGGGGCCACCACGGATCCTGAGACAGAGACGGGGGCGGCC
GGAGAGGTCTCCGCCGAGCACAATGATGCGGACATCATGTTCGCGCAGATGATGATCCCG
CATCACCAACAGGCCGTGGAGATGAGTGAAATCCTCCTGGCCAAGGACGATATCCCGGCC
GAGGTCATCGAGTTCACCCAGGGTGTTATCGATGCCCAGGGCCCGGAGATCGACCGGATG
AATACCATGCTCGAGACCTGGGAAGAAGATCCGGTCACCGGTGATATGGGTGAGATGGAC
CATGGCGGGATGAGTGGAATGATGAGCGAGGAGGACATGACAGCCCTCGAGGACGCCCAG
GGCACCGAGGCTGCCCGGCTCTACCTTGAGCAGATGACCGCCCACCATGAGGGCGCGGTC
GATATGGCCCGCGATGAGGTCACTGATGGCCAGAACCCGCAGGCCATCGCTCTGGCTGAG
CAGGTCATTGAAGATCAGGAGGCCGAGATCGCCGAGATT

>RXA01249-upstream
GAATTGACGTGGAACCGAGCAGCGATCGCAGCCCGCCGCCCTTACCCTCGCCCTCACGGG
GTGTTCGGCCGCCGACCCGGAACCCACCGCCGACGGGACG

>RXA01249
GTGTCCCAGGATACATTCCTGACTACCCATGGCCTGGCCGCCATGGACGCGGTGGAGATC
ATTGATCACCTCGACCGGCAGAAGGTCACTGAGCGTCCCACGGATCTGATCGCCTCAGTG
CGTGCCGATGAACTGCTGCTCTCGAGCGATGACCAGGAAGTCGTGGTCGATCTTCCCGAC
AATCAGACGTATGTCTCGATCGCACCCTACCTCAACTCCACCCACGACTGCTTCTACCAC
AGCCTCACGACCTGCCTGGGGGATCTCGACAATGAGGATATCCATGTCATGATCACCGAT

>RXA01251-upstream
TGTAAGCCGAGAGCGAACCTGCCAAAAGTAAGGGGCGGGTTCGCGGTGACGTCGGTAGGA
TCGAGCGAAGAAACCAACAAACTTCTTAGGAGCCATTCTC

>RXA01251
ATGACCCAGCCAGATATGTCCCAGATCCTCGCCCAAGCTCAGCAGATGCAGGCTCAACTA
CAGGCCGCTCAGCAGGAAATCCTGGCAACCACCGTTGTCGGAAATGCAGGAAACGGGCTG
GTTACCGTCACTATGGCCGGCAACGGCGAGGTCTTCGCAGTGACCGTTGACCCAAAGGTC
GTTGACCCTGAAGATGTCGAAACCCTACAGGACCTTCTGCTCGGTGCATTCAAGGATGCC
CATAACAAGGTCGCAAACGTTGCTGAAGAGAAGATGGGCCCACTATCCCAGGGCATGGGT
GGCCTCTTC

>RXA01251-downstream
TAATTAGTTGCTAAACGCAGGGC

>RXA01263-upstream
AGTGGCCTTTGGAGTTATTTTGATGACGGTATCGGCGACTGCTGGGATCCTCCTCTTTTT
ATCTCCAAATAGAAGCCAAGCTGCGCCACCCCAATTTAGT

>RXA01263
TTGACCCCGTATGATCCAACCGCTGTAAATAAGGAGTCGGAAAAAGAAGCAGCAAAGAAT
CTGTTTGGCGCTGAGGCGTTGACAGTGGATCCGGATGCCGGTGAGGTTGTTGATCGAGTA
GATAATTTTTATCCGACGACTGCTAAGGCAAAACGAGATTACCCAAGTAACTATGCAGCG
GGTTGTCACCAAGAAGTCAATGAGACTAGTCCTGAGTCATGTGTTTATGGTGATAAAAAT
TCTGATTTTTCTGTAGCACTTGTCGGTGACTCCCACGCTGGTCATTGGCTTCCTGCCTTG
GAACCAATTGCTGAAGCACAGGGGTGGAGATTGGAAGTTTATACAAAGTCACAGTGTCCA
CTCATAAGCACTGCGATCAAACTTGGTGAAACTTTTTATGCAGAATGCTATGAGTGGAAT
GAAAAATTACTTGCTAAGCTAACTGGACCTTCTGCACCAAATCATGTGATTGTAAGTAGC
CAACGTTACGCTTCTGCAAATCCGTTAATCGATAGTGTCGCGACGGGAACCGTTTCCGAA
GGATATGAAATGGCATGGAATTCATTAAAAGATGCAGGTGTTTCTATTTCTGTACTTCTT
GATACTCCTCGGCCGCAAATTGATATCCCAGAATGTGTAGCATCAAACCGCGATAATCTC
TCAGAATGTTCAGTTCACCGGAGCGTTGCGCTTGGGACTGAAGCTCATCCTCAGCAAAAA
ACTGCAGCTCAAAATATAGACGTGCCTGTATTGGATTTGAGTAATTGGATTTGTCCGGAA
GAATATTGCTCCGCTGTTATCGGAAATGTTTTGGTATACAGGGATTCACATCATTTGACC
GCTACGTATGCTCGTAGTCTCTCTAGCGCATTATGGAATGAGTTGGTTGCCTCAAATGGT
GAGCCTTTTAAG

>RXA01263-downstream
TAAGAGGTAGTTGTTCAAGTAGC

>RXA01266-upstream
GATTGTGAAGTTTTATATCTGTCATATTCTGGTGATTTTCGCCCTGCTCATGAAGTGGCG
GACGAGCAATGGCCCGATATAGATTTAGTAAGGAACTAAA

>RXA01266
ATGCCAAAAGTAAGTGTGGTTACTGGTTTTTATAACCGCTGTGAGCATTTAGAACGAACC
ATTGAGTCTATTCTTAACCAAACTTATAGCGATTTTGAATTAATTGTTTTTGATGATGCA
TCGACAGATGGAACAGCTTCACGATTGTTAGAGTTAAAAGAAAAATATGATGATCCGCGT
TTCCGATTTATCATTCATGAAGAGAATAAAGGTTTCGTAAAAGGGTTATCAGAAGCAATT
TCTGGAGCTAAAGGGCAGTATATTGCAGTCCAGGGATCAGGCGATGTATCTCTTCCTCGC
CGTTTAGAGCTTCAGGTAGAGTTTCTAGACGCGAATCCTTCGGTAGGTGCTGTGGGTGGT
GCTATCTATAATATTCAAGAAGATACGGGAACACGCAACCCACAGAGATTTGAAAAGCCA
ATTGCTACATTCGATGATTTATTGACATCTAATCCGTTCACTCACGGAGAAGTGATGTAT
CGCTTAGACCTTTATAAGAGTATAGGTGGGTATCGAAGTGGCTTTACTTTTGCTCAAGAT
CGTGATTTATGGTTGAGGATGGCGAAAAAAGCAGATCTGGGTATCATTCCAGATTTTCTT
TATCACCGTTACACACTTTTAGATGGTGTCTCTTTCGTCCCGGATAAAACTATACGTCAG
CGATGCTTTTCAGAAGCTGCGGTGCGACTGGCATTAATGCCAGAAGAGGAAGGAGCTTTA
GCCTACTCTAGGCTGGAAGCTGAAGGGCCTACTGCCGTAGTTCCTATCGCTGATAGAGCT
GTTCAGAAATTTGTCCCTAAAGCGGCTATTCGCTTATGTCTATATGGTGCTCCGGAAACT
GGTTTACACATGGCTCGAGACTATATCCAGAACCCTCTGCGCCGTACCATAGTTGTAGTT
TTGATCAGCATCTATTCGTCTAGATTAATTAAGCCTCTTCAAGATATTCTATATAAGTCT
ATTTTTAAGGGGGTCTCGATTTCTAAACCTATTAAGAGTTCACTCGTGAAGTTTACAAGA
AGAATTCAAGGGAAG

>RXA01266-downstream
TAGCGAAAAACCGCATCTACCAA

>RXA01267-upstream
TGCTAGTTTTAAAGAGGCGTTGAGGGGTAGTATCGCGTAAGTTTATTAGTGGTTAGCGTA
GATTTTTCGAATTGAAGATGTTTCTGAAAGGTATTTAGAT

>RXA01267
ATGTATGCAGAAATTAATGGCGGTTTTATTCCAGAGGGCACCGTGCGGGTAAGCGGCGCA

AAAAACTCTGCTACTAGACTTCTCGCGGCGGCACTGCTAACCGATGAGGTGGTGCATCTT
GGTAATTTCCCAACCAAGCTTGTGGATGTTGAACATAAAATTCGCTTTATTGAAGAGCTT
GGCGGAAAAGTGCATGTCGACCATGATGAGCAAATTTTAGTAGTTGATGCTAAGGATCTT
GCAGCGCGAGAAATGACTACTGATGAACTGAATATTCCGATTCGAACTACTTATCTCCTA
GCAGCAGCGCAGATTGGGCGTGGGGAAATTGCTCGAGTTCCTTTTCCTGGGGGGTGTGCT
ATTGGAGGAGGTCCTGCTGGCGGACGAGGATATGATCTTCATCTTATGGTCTGGGAACAG
CTAGGTTGTAAAATTCTTGAAAAAGATGATCACATTGAAGTAACTGCACCCCAGGGCTTT
ATCGGGGGAGTTATTGACTTTCCTATTTCTACTGTGGGAGGCACTGAAAACGCGTTACTA
TGCGCAAGTATTGCTTCAGGGGATACTAAAATTGCCAATGCTTATATTACCCCTGAGATA
ACTGATCTTATTGAACTTCTGCGACGTATGGGTGCGGAGATCACTGTCTACGGTACCAGC
CGTATTCATGTAAAGGGTCGAGCAGGTCTTTTGCAGGGCGCATATATGGACGTAATGCCG
GATCGTATTGAGGCATTGACGTGGATCGTGTATGGAATTATTTCAGGCGGAAGGATTACC
GTCGAAGGTGTTCCATTTAGCTCGATGGAAGTTCCTTTTATCCACCTTGAGAAGGCTGGA
GTGGATCTTTTCCGTAATTCAAGTTCCGTATATATTACACCAGAATGCTTGCCTTCAGGC
TCAGTTCAGCCATTTGAGCTAGCGTGTGGAACTCACCCCGGAGTAATTTCGGACATGCAG
GCACTTTTTGTTCTTTTAGGATTAAAAGGTGCAGGAACTTCACGCGTCTATGACTATCGA
TACCCAGAAAGAATTGCATTTGTTGAGGAATTGACAAATCTAGTTTCGGGCGACAAATTA
AGTGCAGAGGCTGGCAAGATCACTATCCAGGGAGATGCTACTTTCCGGCCAGGATATGCG
AACTCAACTGATCTACGTGGTTCTATGGCTGTTGTTTTAGCGGCGCTTTGCGCTGATGGA
AAGTCCACGATTAATAACGTCCATATGGCGTTACGTGGGTACAACGAGTTGGATAAAAAA
CTTCGTTTACTTGGTGCGGATTTAACTATCAGAGAAGGCGAAGTTCCTTCACCT

>RXA01267-downstream
TAAGAACGAAAGTTTTACATTGA

>RXA01268-upstream
TACCGATGTTAAATCATTATTTAATTGGGTGCTATTGCTTAGGAAAATTCGTCCAAGAGT
GCTGATAGTTGGAACTCCGAAAGCTTCATTGCTGGGAGTC

>RXA01268
GTGGCAGCACGAATTGCTCGAGTGCCACGAATTGTCTATGTGGCACATGGGCTGCGCTCT
GAAACTGTTTTAGGCTTAAAAAAGAAGATTCTAGTGTTTTTGGAATATTTGACCCAGTTG
TTTGCACATCAAACTTTGGCTGTAAGTCATTCTCTGAAGAAAGCAATTGAAGATGCGCAC
CCTCGTTTTAAAGGAAGAGTGCAAGTCTTAGGTTATGGCAGTATGAATGGAGTTGAGCTT
GATCGCTTTAGAGTTCCATCCCTTGAAGAGAAATTATCTGCTCGTAATGCTTTAAACCTG
CCTAGTAAATCTGTCATTGTTGGTTTTGTCGGCAGAATAAATAAAGATAAGGGAGGAGAT
CTTCTCGCTGCTCTTACAAAACATGAGGCTTTTACCCGATTGCGACTGCATCTCTTAATT
ATTGGTGAATTGGAAGACGATGACTTGCGAGAAGCATTCATTAAATTAGTTAATGAAGGG
CAGGTTACGATTACAGGATGGATTGATTTCCCTGAAGAACCATTAGCTGCAGTTGATGTT
TTGCTTCACCCAACTCAGCGAGAAGGTTTAGGTATGTCTTTGCTGGAAGCTCAGGCTATG
GGAGTGCCTGTATTGACGAATGCTGTGACTGGAACAGTTGATGCAGTAACAAGTGGAGAA
GGTGGCTTTTTTGCCGATGACGATTCTGTTGAGTCCTGGGTTTCTAAGATTGATTTATTA
GTTTCCGATCCTAAGTTAAGAGACCGGATGGGACGTGCTGGTCGCCAGTTTGTGTCAGCT
CGTTTCAATCGTGATGATGTCGCAGCTCGTTTCAGTCATTTCGTGGAACAATTCAAAAAA

>RXA01268-downstream
TAGGGCTCATTCAATTTCAATAT

>RXA01271-upstream
GTGAATCCGATGCCGGACAGATCGCAGCAACTCAATTTGGAGATTCAGTTTTAGCCTGGG
TTGGCGAAACCCAATTTATTTCAAAAGATGGTGGACAAAC

>RXA01271
ATGGCAATAAGCATTGGTAAAGCAGGACAGAACTTAAAAGGGTCAGTGCCTATCGGAAAA
GTCCTTTTTCTCATTGATGCCCTTGCCTGGATTTCTGCACTATTTATCGGTGTGGTTTTG
CGGTATGAATTCAATCTGAGTTCTATCAACTGGAGTGCGTTTGCATGGTTCGGGCTTGCT
GCAGTTATTTTGCAGTTTGTTCTCGGACTTTCTCTCCATCTTTACCGCAAGGGATTACGT
CACCTTTTCGGTAGCTTCGAAGATACACTAAACGTTTCTATCTCGGTCATTGTTGTCGGT
GTTGTCCTTTGGATCGCCTCACTATTTGTTGGTCAGCGTTGGAAAATCTCACGCGGTGTC

ATGCTGCTAGTTATCCCGCTTGCTCTCGTATTCGTATTGGCAGTGCGTTATCTCGCGCGT
ATGCGAGTTGAGCGTTTTCGTCGTCCGGCTGCGGATTCCACACCAGCATTGATTCTTGGT
GGTGGATACATCGGTACCAACCTGATCCAGTGGATGATGTCCGATCCTAAGTCGCCTTTC
CGCCCAGTCGGCGTTATTGATGATAACCCTGAATTAGCATGCCAACGCGTACGTGGTGTG
CCGGTTCTTGGCAAGTTTGATGATATCGCCCAAGTTGCATCAGACACTGGCGCAGAACTT
CTTATCGTTGCTATTGGTGATGCCGACTCTGCACTTTTAAGGCGTGTCCAAGATACCGCT
AATAAAAATGGTCTTTCAGTAAAGGTAATGCCGGCTATTGACCGCGTCGTTTCTAAGGGC
GTTCGTGGAAACGATTTGCGTGATCTCTCTATTGAAGATTTGCTTGGACGTCAACCTGTT
GAAACCAATGTTTCAGAAATTACTGGCTATCTAACAGGTAAGCGTGTTCTTGTTACCGGT
GCAGGTGGGTCAATTGGTTCCCAGCTATGTACGGAAATTGCCAAATACGGACCTGCTGAG
CTTATGATGCTTGATCGCGATGAGACTGGTTTGCAGCAGGTTCTGATTAACGTTGCTGGT
AACGGTTTGTTGGATACGGATGCTGTGGTTCTTGCGGATATCCGCGAAGCAGACGCGATG
AAAGAGATTTTTCTCAAGCGTAAACCAGAAGTTGTCTTCCATGCAGCAGCATTAAAGCAC
TTGCCAATGCTGGAGCAGTATCCAGATGAGGGCTGGAAAACAAACGTTCTAGGAACTCTT
AACGTTCTTGCTGCCGCAGAAGCTGTTGGTGTTGAGACTTTCGTCAATATTTCCACCGAT
AAGGCAGCTAATCCAACCAGCGTCTTAGGGCACTCAAAGCGAGTCGCTGAAAAGCTGACT
GCCTGGTATGGACAGAATTCCACCAGCAAGTACCTATCGGTTCGATTTGGAAACGTCATT
GGTAGCCGTGGATCGATGCTCCCGACTTTCACCAGGCTAATCATGGAAGATAAACCGCTA
ACAGTGACGCACCCGGATGTCACTAGGTTCTTCATGACAATTCCTGAAGCTTGCCAATTG
GTCCTGCAAGCCGGTGGTATTGGACGTTCCGGCGAGGTTCTCATCCTTGACATGGGTGAG
CCTGTAAGCATCCTTGAAATTGCACAGCGCATGATCGCAATGTCCGGTAAAGATATTGAC
ATCGTGTTCACCGGCCTTCGCGAGGGCGAAAAGATGCACGAAGAGCTGGTTGGTGATGGT
GAAACCGAAGATCGTCCATTCCACTCAAAGATTTCGCATGCACATGCAGAAAGCCTCGCT
CCTAATAATCTCGATAGAGATCGATTTATGCAACGTGCTGGAAAACTAGCTTCAACAGAT
TCGGAGATCATC

>RXA01271-downstream
TAAATGACTAATGAACGAATTTT

>RXA01273-upstream
GACCTATTCAGCGCTGGATTTTTTCTGGCATTTTCTTGGCAGTCAGTGAGTTGCTAACGT
TCTATTGGTTAAAAATTGATCTGCAAGAGGACTGCAAAAT

>RXA01273
ATGGAATTAAGGGAATACGCGACAATCCTGATGAAGAATTGGGTGTTGATCGTTATCGCA
TCCATTCTTGGAATTGCAGCGGGCGCTGGTTTTTCCCTTCTAGCTACACCGGAGTATCAG
TCACGTACTCAGTTGTATGTATCGGTGCGGTCGGGGGCTGGGACAACCTCTGACATGGTT
CAGGGTGCTAACTTTTCGCGTCAGATTGTGAATAGTTATGTTGATGTCATTAAGACGGGT
GTTGTTCTAGAGCCGGTTGTTGATGAGCTTGGTCTGGAGTTGACGGCTAACCAGTTGAGT
TCTCATATCAGTGCGGCTTCTCCTGCTGATACTGCGTTGATCAACATCACTGCTTCTAGT
CCTTCTCCTCAGCAGGCGGCTGAGATCGCCAATGCAGTGGGGGAGAGTTTCAAGAATGTG
ATTCAGACTGAATTGGAACCAGACTCCGGCGATGGCATGAGCCCGATTAACCTGACTACT
ACTCAGGTGGCTCTGGAACCATCTTCTCCGGTCAGTCCTAATGTGATGATGAATATCCTC
CTCGGCCTACTTGTAGGTCTTGCAATAGGTGTTGGTATTGCAGTGCTTCGCGCGGCTTTG
GATACTCGTATTCATTCCTTGCGCGATATTGAAGAGGTTACTGATAAGCCACTTTTGGGC
GGAATCATTGCGGATTCTGAAGTTGAGAAGCACCCGTTGATCATTAAGCACAAGCCGCAT
AGTCCTATTGCGGAGTCCTTTCGTGCGTTACGTACTAACCTGCAGTTCCTTAACGTCGGC
GGCTCATCTTCAGTATTTGTTATCTCCTCTGCTAATCCTGGTGAGGGTAAGTCAACCACT
TCTGTAAACCTAGCTTTGGCGCTTGCAGAGGCCGGCTCCCGTGTAGCGCTGATCGAAGCT
GATCTTCGCTTGCCACGAGTGAGCAAGTACCTCGGAGTTGAGGGCAACGCAGGTCTGACT
GACATTCTCATTGGCAAGGCCGAGGTTAATGATGTGTTGCAGCGTTGGGGTAGGACTCAG
TTGTACTATCTCCCGGCAGGGCGCATTCCGCCGAACCCGAGTGAGTTGCTTGGTTCAGCT
GAGATGGACAAGGTCATTGCGGAGCTTGAGGAAAGCTTTGATTATGTGATCATCGATGCC
CCTCCGGCGTTGGCGGTTACCGATGCTGCAGTTATTGGTCATGGCAAGGCTGGCATCCTG
ATTGCGGTCTCCGCAGGTTCTACAAAGAAGCCTGAGTTGGAAGCTACGCTGTCCACGCTT
GAGAATGCGGATGCCAATGTTGTTGGCGTTGTCGCTACGATGCTCCCGCCTAAGTCTGTG
GCTGGTTATGGCTACGGAAATTACGGCTACGGCGACACCTCCAAAATCAATGCCCCTAAG
CCCGACAACACCGAACTAACCACCACCGATGCTTCCAAGGCCAACAATGAGCAA

>RXA01273-downstream

TAGCTTCACTATTCTCACTGTCT

>RXA01275-upstream
CGCCATACTAGGCTCGGCCTTTTCGACGGGAACTCGGATAGGCTTCTGTAAAACCATCCC
CGTTGAAGAGAGACTCGTGGCTGAAATAACCACCCCATTA

>RXA01275
ATGGAAAAAATTCGCTCACCCGCAGTCCAATCAGATGCACTGCAGGTTTTTAAATCAGCA
CTTGCTGCGACAGTCACGTGGTGGATTTCGGTTAACCTCCTTAACTCCCAACTACCCTTT
TTAGCTCCCTGGGTAGCGTTAATGACGATGCAATTCACCGTCTACCACACCTTTATCAGT
GGAATTCAGACTGCAATTGCTTCTGTCATCGGAGTTGGACTTTCCTTTGTCATAGGCACT
TACTTAGACGTAAGTGTGTGGACTTTTGGCCTTGCAATGGTCATAGGATTAATAGGTGCA
CGAGTACCAAAGCTCCGCGCGGAAGGAATAGGTATTGCTACTACATCCATTTTTCTTCTT
GCCTCCGGGTTTGATGATCAACAACCCCTTCTATACGACCGTATTTTAGAGATCCTGCTC
GGCGTGGCTGTTGCCATAGCCATCAACCTCATCATCTTTCCTCCCTTACGCGACCAGGAG
GCAAACATGGTGGTAGGAAACTTAGATCGGAGGATGGGTGAGGTTTTACAAAAAATGGCC
GATGAGCTTGCAGAAAAGTGGAATATCGACAATGCAGATGAGTGGCTGGAAGAAATTAAT
TCTATTAACAATGACCTAGAAAAAGCGTGGCACTCCGTGCGGTTCGTTCGCGAAAGCCGT
CGAGTTAATCCTCGTAAAATCCGCATCCAAGAGGGCCGCCCCCAGCCTACGGAAACAAGT
TATGAATCAAACCTCACCAGCATTGATGAAGGGATCGCTCATTTACGCCACCTTGCCCGT
ACTCTTCGTGATACCCCGATTATAGATTCCGACTGGGGATCCAGTATTCCAGCAACAGTG
GGTATCCCTTATGCACGATGCCGGAGCTTTGCTCGCAGATCCGAATCAGGAAATAGATCC
TATCCGCGACCGGCTCTC

>RXA01275-downstream
TAAACTTTCAAGTGAGATGAGTG

>RXA01276-upstream
CTAGATGCCCGGAAAATAGCATCTCCTATACACCCAAAAAAAAGGGGAGCGCTGACAGAA
AATAGTAATAATTTTGACAGCTCGTGCAAAGATGATTGGC

>RXA01276
ATGCGTAAAACCCTCATCACCATGCTCGCGACCACCGCGATCGCCTTTTCCGCCATCTCA
CCAGTGCAGGCGCAAACCGTGGACACAGACACTGACGCCTCCGTGTCATCTGAGCTGAGC
AGCGGCACAAGCTCAGGAAGTTCAGAGGATTCCGAAGATTCTGACATCTCCAACCGGGAC
ATCATCTTCGGCATCGCAGCTATCGCTGCAGTCGGCGGACTTATCGCAGGTGGTGTGCAC
TGGGCAGTACAACAGCGCATGATCCCAAATCCCCTCCCAGGAATCATTCCAAATCCCCCT
GCACTGGCACCTCAGGCGCCTGCCCCAGCACCTGCTCCCGCTCCTGCCCCTCAGGCAGTC
GCGCCCCAGGTTGTCGCTCCCCAGGTTGTCGCGCCTGCTCCAGCCCCAGTACAGACCAAC
CGCACCTACAAAAACTGCACCGAAGTATGGAACGTCCTGGGAAGGTCCATCCGCCAAAGC
GATCCAGGCTACGGCACACACCTCGACCGCGACCGCGACGGCATCGGCTGCGAATCACGC
CCTAGG

>RXA01276-downstream
TAGTTTGGGTTTTGGGGATCTTC

>RXA01281-upstream
GGACAACCTCATCAAATGCAAACATGCGCCACCGCGTCCCGGAAAACCAGGGGCGATACC
GCGCTTGAGTGCGAGGTGCCGTCAATTCCCAACTACAAGA

>RXA01281
GTGGGACTCAGCCGTTCACATTATCAGCTAGCCGCAGAAAACACCAAATCCCTTGTTAGA
ATGGTTCCCATGACTGTTCCTCAAGGAAACGAACCAGCAAAGAAGCTCGCCACTGACCTT
AACCGAAACCAAGTCGTGGATGAACTTTCTGCAGCTGTTTCCCGAGGTCAACTCACTTTG
GAGGAATTTGAAGATCGCTCCTCCAAAGCATGGAATGCCCGCCACTTAGACACTCTTGTA
GAGCTGATCTCTGATGTGAACGACAATCCCTACACTCTGCTTGGTCAGCAATTTCCCGGC
GCCTCCTATGCGCCGGCGGCCTACGAGACCACTCCCCCAGCGATGCCCAATGTGTCAGAT

CCTGTAAATATTGTCCGCAACAGGATTACCGGCAACCCGAATGGCTCCAAAATGTCGGTC
TCGTTTATGGGTGGCACCGTGCGCAAAGGTGGATGGCATGTGCCTAATGTTCACACATCC
TTCGCCATGATGGGCGGCAATCAGATCGATTTGCGCGACGCCTTCCTGGAAAGCGACCGC
ATTCAGATCAACGCCTACACATTCATGGGTGGCATCGAGATTATTGTTCCCGAGGGTGTT
TTTGTCATTTGTGATGGCATGGGCATTTTCGGCGGCTTCGAACAGTCTGTGGACAAGGCC
GGTGCACTCAATCCCGCGCGCCTGCCAAGCAACGCGCCCACGGTCCACATCAAAGGCCTG
GCGTTCATGGGCGGAGTCAGCGTAGTCACCAAGAAAAACATT

>RXA01281-downstream
TAAAAAGCTTGTCGACGCGCCCC

>RXA01282-upstream
CAGGATGGGTCGGAACGTTCGCGTCGTTTGCGGTGTGGTTCTGGGTCATTTGGTGGGCAG
CGGTAGGAAATACAAAAAGCCCACTCTAAGATGGCAGGGT

>RXA01282
ATGGATGAGCTGCTCAAACAGGAAGTCAAGGATTTCCTCACCACCAGGCGTGCACGGATT
ACGCCGGCCGCTGCGGGACTAGAAACGCAGCCGTGGAGTGATCGTCGGGTGCCGGGGCTT
CGGCGGGAAGAAGTCGCGGATCTGGCGGGCATTTCTTTGGAGTATTACATCCGGTTTGAG
CGCGGAAATCTCAAGGGTGCATCGCCTGAAATATTGCAATCGTTGGCTAAGGCTCTCCAA
CTGAGCCCAATTGAGCGCGAACACCTTCACAATTTGGCTTATCGCGCCGACCATCCGCGC
AACCTACCTAGTGCAGAGACCCCAACGGCACCCCTCCAGGACATCGTTGATGCGGTCACA
GATAAACCGGCGTGGATCCGCAACGAGCAGATGGATATTTTGGCTACAAATCGGCTCTGC
GCGGAACTTTACGCCCCGATTTTCAAGGATCTGCCCGATCGGCCCAACACTGCGCGGCAT
TGCTTTATCGGCGCAACAGCCTCCGAGTTCTGGGTGGACCGGGATCAGTTCAGTGCGGAG
TTCGCTGCCAAACTACGCCTCGAGTACGCCCGGCGCCCCAGCGTGCCAGGTTTAAAGGAG
CTTATCGACGAGCTCCATCAGAAAAGTTCTGTTTTCCGCGATAATTGGGCGTCTGCTGAT
GTTTTGTCATTCGGCTCTGGCATCAAACGTTTCAGGCACCCAACACTGGGGGAGCGGGTC
TATGAATACGAGACGTTTAATCTCAATAGTGCACCGGGGTATGTGTTGAGCATTTACTTT

>RXA01282-downstream
TAGGTGGTGGAGGGGCGCGTCGA

>RXA01294-upstream
ATGAAGGGATACCGCTCCTTTTCGGGGGTACAGCACTCCAGCAAGACTCATTCGGCTCAG
TTAGAGTTCACCACAACGACTCAAAAAAGAAAGTGGCAGC

>RXA01294
ATGTCTACGATTCCTGATGTTTTCACCAGTGAAGTGTTCCCTGAAATCAGTGGCACCAAA
GAATTCCGTGGCCTGACTTATATGTTCTTTGATCAATTCACTTTGCCCACCGCAGAACAG
CTTGAGCAAGCTAAAGCAGCTGGCTGGTCACTGATCACCTGGGGATGGTGGAATAGCGAC
ACCGATCTTGAGGATGTCGAATTGGAAGACATCACTAATGAAGGCGACAGCCTACCAAAA
CTCACGGATGAATTCGCTGTGTCTTCACTGAGCACCTTCGATCTAAATTCCCAAGGTCTG
CCCAATGATGATCGTGAGCCGCAACCAATTGAAGAAGCCGACTCACTAGATGACATCTTC
TCCGAGGAAGAGGGCTGGGGTCTAATGGCAATCAATTGCCCGAATTGGCAAGTCCCAGCA
GCGTGTGAATGGCTCGGCTGCATGAATGTTGGTGAACCATTTGAAATGTCACACGTACTT
AGGGTGTGGCAGAACAGTTGGGGCGTCGAGGCCCTGGCTTTTGGTGGTGAAGAAGACGAC
GCGGATCTGCTGCTTCGAGTCCCTGAAGAAAGCGAAGAGCTACTGAAGGCTCTCGCAGTC
GCTTCTGACCAAGTCACTACCTACAAGCATGAAGATCTGGGATTCTTAGCTAGTCTTTGG
TTTGAC

>RXA01294-downstream
TAACTACAATCAATGTCATGACC

>RXA01295-upstream
TTTCTGGTGTTACCCTCGGGTAATTGTAAAAAATTCATTGATTAAAAACGATCAGCCAAT
TGGCATGCTCAGACTCCTTGTGAAGAAAGTGACAGTTTCG

>RXA01295
ATGACCGAAAATCTTGATAATGCGTTGCTATCCATGCGGATGAAACCTGTACAAATGGCG
CTTATGACACTGGGCTACAACCATGACATGGCGGTGACCGATTCCGGTATGGAACTTATA
GTGCGCCGCCCAGGGCTGACCGTGAACTTCAACTTGGATTCGGTCACCTTGTGCATCGTC
GCTGATTTCATGTGGCATGGCTGTGTCCCTGCAAAGAAACAGGCAGAGTACCTGCGGGCC
GCTAATGAATTCAACAGGCCAACCCGTGATCTGCAGGTGGTTTTAGATGAAGCTGATTCA
AAGAACATGACTGTGCGAGGTCGTGAATTCTTCTTCTCAAGCGTCGGCGCAACGTGGGAA
CAGTCGGCAGAGTTCGTGCACTACTGCATGAATGATGTGGCAACGACTTTCGTGTCTTGG
TGCGAACAAATCTGGCCGAAGTTTTCCCCTGAACGCGTAGAGTTCAACGCAACTCCTCCA
GATGTGGATTTCGAGTTCTCTGAAGATCAACTCAAAGAAGGCAATCCCTTCGGGCTGATT
GACGAACCCACCCCGCTGGTTTCTTTGGATCGTATCTACCAACAATACGAATTAATGGGT
GCGGATCAACTCAAGATGGGGGAGGACTTCGTTGAGTATCTGCATATGGGTCAACGTGTC
AGTGCATGGTTGACCGATGGCAACAACGGCAGCGATCGAAAAACCCTAGCGGTGTCTTCC
GGTACAGGTGTGAAAATCAAAAACAAGAAGCAACTTCAGGAACTTCTTGGACTGTGCAAC
CTGTACTCGAAAGAACATGTACTGGTCACAGTATTTGCGGAAGAGATCGAAAACGGCGCA
AGGTGGGGTATTTTCGCCGAAGCACGCATCGATCTACCGGCAGGGTTAAACGATCATCAG
TTGTGGGTATTCCTCGCCAACTCCAGCAAATGGACTGCAGAGGTGTGCCTGACCGTGGCA
CACCGACTGCAGAAC

>RXA01295-downstream
TAAAGGCAGAACTTAAGCGTTCA

>RXA01296-upstream
TAAAACTCCTGTTCGAAATTGCCCAGACAGGTGTCCACCAACACTGCTACATTGCATTGG
AGATCCAGAATCGATCACTCTACGACCAGGAAAAACTTTC

>RXA01296
ATGTCCATCGAGCAAGCAATCACTTCACTCTCCGCAAGAGTGCGGGAACTAAAGCCCATC
ATCGAGACTGAAGAAGCCACCAAAACCGCACTGATCATCCCCTTTATCAGCAACGTTCTC
GGCTACGACGTCACTGATCCTCGTGAAGTCATTCCGGAATACACTGCTGATGTTGGCGTC
AAAAAGGGTGAGAAGGTCGACTTCGCTATCAAAACCGGCGATGATTTCCACTTCCTCATC
GAATGCAAAAAGGTCGGCTCCCCACTCAGCCTCGATCACGCTAACCAGCTCGTCCGCTAT
TTCAATGTCACAGACACCGAATTTGCCATTCTCACCAACGGCGAAATCTACCAATTCTAT
GGACAACTCGATGCAGCCAACCGCATGGATGCAAAACCATTCATGACCTTGGATTTGAAC
AATATTGATGCCCGTCAGTTCCCTCATTTGGAAATGTGTACCCGCAAGCATTTCAACCCA
CAAGCGCTAGCCGCCAACGCTGAAGAACTGAAGTACATTGCTGAATTGAAGAAAGTCATC
GCGAATCAATTCCAAGAACCTGACGTAGAAATCGTCAAGATGCTTGCGGCGACAGTCACC
ACAAAGCGTATGACTGCACAAAATCTGGAATTCTTCACCCGCTTGGTTAATACTGCGTCT
TCCCAGTTCCTCAAAGACGAGGTCAATCGTAGATTGCGCTCCGCCCAAGTCTTTGAGGAT
CCTGTCCAAACACAAGGTGCTGATGCAGAAACACCAGCAGAGGACGAAGCAGTAATCGAA
GAAGTGGTTTCAGAAATCGTGACGACAGAAGAGGAAATCCACGGTCATTCAATTGTCCGT
GCAATTTGCTGCTCAGAGGTATCGGCACAAGAAATCACCATGCGTGACGCAAAATCCTAC
TGCGCTATTCTCTTCCAAGACAACAACCGAAAGCCAATCGCCCGTTTCTACTTTGATCGC
AAGATTCCACGCATCGGCATCTTCAATGCTGAAGGCGAGCAGGAACACTTTGATTTGGAA
TCCATCGAAGATATCTACAACCACGCTGATCTTCTGCATTCCCGCGTCGTAGCATTGAAC
GCT

>RXA01296-downstream
TAAGTTCTGCCTTTAGTTCTGCA

>RXA01301
TTCCTCCGCCTAGAAGGCATCGAACCTAAAGGTCCTGCCCGCGCCTACTACTTTGGCGAT
GTCTCTGACACCGTAGACATCCTGATTGGTTTCCCCGTCAGCCCCGCGCAAGCAGAATCC
CTGCGCCGCGGCGCATTGAGCCAATCCGGTGGCGACATCGATGACGTTGTCCTCCACCAC
TTCCGCGACATGAAAACCATGCACAGCCGCCACTCCGGCCCCTTCGATGGAGTCGAGCGC
GTCTGGGACGAAATCCTCGATGAAGTCGAAGACCTCGGATGCACTCTGCCATCCAGCAGC
ATCGGTTGGGAAGAATACATCGAGGGCCCAGCCACCGCTGATACCTGCGACCAACTGGCC
TCTGAAGTTTATGTTCAGGTGTGCCAAGCACCGGTGAAGTCTGCA

>RXA01301-downstream
TAAAGATTCACCCGGAATTTCCC

>RXA01304-upstream
ATGCAGGTAAACGAATTTGTGCTTATATCAACATTCGTGATTCGGCAAAATTAATTAAAC
TGAAAAAGGGGATTAATTACCCCCACTTGAGGAGAAATTG

>RXA01304
ATGCCCGCACAGAACAAAAACCTCCCAGGATCCGTCATCGTTGTGTCTGATCGGATTAAA
TCGGGAGAAAGAATTGATAAAGCAGGACCCGTAGCAGTAGACCTTCTTCAGGAATCAGGC
GTGGAGATTTCCACATTCACCGTCGTGGAGGAGGGCTTTGAACCTGTCCATCAAGAATTG
GTTAAGGCGTTGGCGCGCCGGGATCGCGTCATCATCACCATCGGCGGAACGGGCGTGGGG
CCTAGAAATCGGACGCCGGAGGCCACAGAACCGCACATCGATACGCTACTGCCGGGTCTG
ATGACGCAGATTTTGTTCTCTGGACTGTCCAATACCGCGCAGGCGGGGTTATCTCGGGGG
CTGGTGGGCTTGAGTGCTCGCGATTCCACGGCCGCGCTCATCGTCAACGCGCCGAGTTCT
TCCGGGGGCGTGCGCGACGCGCTCGGGGTGGTCTGCCCGCTTTTCGGTTCCATTTTTGAG
CGTCTT

>RXA01304-downstream
TAAAAGATTTTTGCTTATCGACG

>RXA01306-upstream
CGTGCCTGTAAAATGCGCTCGCTCTGCTGAAGACCACCCAGACAATCACCCCGCTCCGAA
GGAGAATCGATAAGCC

>RXA01306
ATGACTGAATGGTATGTCGTTTTACCCGCCACTATTCTACTCATCGCGCTGTCTGCGTTT
TTCGTCATCATTGAGTTCGCTTTGCTTGCAGCTAGGCGGAACCGGTTAGAGGAGACTGTG
GAAACCTCGCGGTCTTCCCGCGCTGCGTTGCGAAGCCTCAATGAACTTACTCTCATGCTC
GCGGGCGCGCAGTTGGGAATCACCATGGTGACTTTCGCGTTGGGTGCTATCACGAAGCCG
TGGGTTCATTATGCTTTGATGCCGCTCTTCGAATGGGCGCGTATACCGCTGGTTATGGCA
GATGTCATTGCGTTTATTTTGTCGCTGTTTATCGTAACGTTTCTGCACTTGGTCATCGGC
GAAATGGCTCCGAAATCCTGGGCAATCGCGCATCCGGAGACGGCACTTCGAACTATCGCG
ATTCCCGCACGGGGCTTCATTAACCTGTTTCGTCCATTGCTGCAGTGGATCAACAAAATG
GCGAACGATTTGGTCCGCAAAGTTGGTGAAACTCCCGTTGATCGAGCTGCAGCTGGTGGC
TATGACACCGATACCCTCCATGCCCTCATTGAGCATTCCCGAGAAACTGGCGCTCTGGAT
CAGCAATCCGCCGCCCAAATCAGCGGAATTATCAAGCTGGATAAAATCACGGTCGGTCAA
ACCCTGACCGCATCTCCATTTACGCACAGCGCCAGCGCCACGGTTGCTGAGGTGCAAGCC
GCAGCTCAGCGCAGTGGCAGCTTGCGTGTGCTTATCGACGCCCCCTCCCACCTTTTCCCA
CACGTCATTCATGTGCGAGACACCCTTGGTGCCTCGCCAGACGAGAAGGCTTCGAAGTGG
TCTCGCCCAATCCTCACCGTTGCTGAGACCGACACGTTACACCAAGCGCTGGAATACATG
CGGGAGCATAACGAGCAGATCAGTGCGGTGCTTTCCGCTGATGGGAAAACGGTGCTTGGT
GTAATAACTTGGGATCACATCTTGAAATACCTGTGGCCTGCATCGGTG

>RXA01306-downstream
TAGCTAATTTGAGGTGCGCTGAA

>RXA01310-upstream
AAGGAACGTGCGCGTGCAGCTTTCCGAGGCAAAGACGACTAGTCTTTAATCCAAGTAAGT
ACCGGTTCAGACAGTTAAACCAGAAAGACGAGTGAACACC

>RXA01310
ATGTCCTCCGCGAAAAAGAAACCCGCACCGGAGCGTATGCACTACATCAAGGGCTATGTA
CCTGTGGCGTATAGCTCTCCACACTCATCCCTCGAGCGCAGCGCAACCTGGTTGGGCATG
GGATTCCTCCTCACTGCTCTGGCAGGCGTTGGCGCAGTCCTCTTCGCAGTCGGCGCAAAC
AGCGTTGGCCAGCAGCAGGAACACTGGGTCCTCTACAGCATCATCGGTGTTGTATTCGCC
GTTGTCTGCACAGTTTTGGGCACCGTCCTGATCATCAAGGGCCGAGCACCTTACAACCGT
TACGTCAAGGAAACCGGCCGTACGCAG

>RXA01310-downstream
TAGTTTCTGTATGCAGGTTCTTT

>RXA01313
GCCCTACGCCTCATTTCACAGCTGCTTGCACCATCTGCGGCGTTGAATTTTAAGTCCGAG
CGCAATGCCGTCGACGTGGCAAAACACATGCTCGCCAGCCAGGCCCAACAACGCGGTTCC
GCACTCGTTGCGCTAGACACCCGCTCGGAAAACGCCGACGCCGCCACGGCATTAAGAAAG
TCACTGCTCATCCGCAGCTGGACGCAGCGCGGCACCCACCAAATACTTGCCGCCGAAGAC
GTCCGCTGGATGACGCTACTATGCTCCCCACGCATCCTGGCTGCTTCAGCCAAGCGCCGC
TCCAGCCTTTCGCTTGATAGCGCCGCAGTCCAGCGCGCCCGCGACGCACTAACAACCGCC
GCCGAAAAATCCCCCGTATCCAGAACCCAGGCCTACGAAATTTTCCGATCCGTAGACGTT
GACCCCGGCGAGCACAGAGGCCAACATTTACTCCGGCATTTCGGTGGCGAAGGTGACATC
GTACAAGGCCCGCCCATCGGAACGGAAGATTCCTTTGTGCTTCTCGATTCCATCTGCCCC
CTTTCCCTAGCACTTAACGGCGACGAAGCGCTCACAGAGATGACCCGTCGCTACTTCCAC
TCCCGTGGTGCTGCCACTGTGAAAGATCTGGTGTGGTGGACCGGACTGACTGTGCGTGAT
GTAAAGAAAGGCATCGCTGCCGTGTCTTCGGATGGACTGATTCACTCTGTTGAAGGCCCG
AATGGTGAAGAAATGTGGATCCCTACCTGGGCAGATGATGTCACAGACGCAGAGGTTTCT
GATGCACTAGCGTTGGAACTAACCCTCCCCGCCTTTGATGAATACCTACTTTCCTACACC
GACCGCAGCCACGTCATGGATCCCGAGCACCTTTTCAGCATCGGTCCCGGCAAAAACGGT
GTGTTCAAACCCTTCAAAGTAGTTCAGGGTGAGGCACTGCCGGTT

>RXA01313-downstream
TAGCCCAGCAAAATCTTCACTTG

>RXA01315-upstream
CATGTGCGGTTGTGTCCTAAGTCATTGATGTCACCTAACGCCCCTAAGTTCACTCGGTGC
AATATTGCACTGAGTGCAAGTTTACACTAGGTTTACTTCA

>RXA01315
GTGGATATTGAAGAGCAGCCCTCGTTAAGAGAAATCAAGCGCCAAATGACCCTGGAAGCG
ATAGAAGATAACGCAACCAGGCTCATTCTGGAGCGTGGCTTCGACAATGTCACAATCGAA
GACATCTGCGCAGAGGCAGGGATATCCAAGCGCACATTCTTTAACTACGTGGAGTCCAAA
GAGTCTGTGGCCATCGGGCACACAGCCAAGCTCCCAACGGATGAAGAACGTGAAGCATTC
CTGGCTACGCGTCATGAAAATATTATCGATACTGTATTTGACCTGGTAATCAACCTCTTT
GGCAACCACGACAACTCCAAGTCTGGAGTTGCAGGCGACATTATGCGTCGACGCAAAGAG
ATCCGGGTGAAGCATCCAGAACTGGCAGTGCAACATTTCGCCAGGTTCCACCAAGCACGC
GAAGGGCTAGAACACCTAATTGTTGAGTACTTCGAAAAATGGCCAGGCTCCCAACATCTA
GATGAGCCTGCAGATCGAGAAGCAATCGCCATAGTTGGCCTGCTGATCTCGGTCATGCTT
CAAGGTTCTCGTGAATGGCACGACATGCCACAAGGCACGCAAGCTGATTTCCAAGCCTGC
TGTCGCAAAGCAATTAAAAATACTTTTCTTCTTAGAGGTGGATTTTCAGAA

>RXA01315-downstream
TGACATCACAGGTCAAGCCGGAC

>RXA01316-upstream
AAAGCGCAAGGCTAAGAAGGATTCCCCAGAACCAGGCGATGACGATATCATCGATGGAGA
AGTAATTCCTCCGCAGAATTAAGGAAGTCGGTTTCACCCC

>RXA01316
ATGGATATTTCCATGCTCAACGTAATAACGAGCTACACCATTTGGGCCATTTTTGCCATC
ATCGGCATCTGCGGATTCGTTGGTGCCTTCTTGGCAGCCACCACCAGAGAAGATGCCTTT
GAGGTTGCTGATCGCCAAAAGAAAATGGTGTGGGTAGCAATCCTTATCGCATCCGGATTT
GTCCTCACCGCGCTAGGTCCATCGATTCCGATCCTGCCATGGGTCGCCATCATCATGATC
GGCCTGTACTGGTTTGATGTTCGCCCGCAAATCAAGAGCATCCTTGAAGGTGCCGGCGGC
TGG

>RXA01316-downstream

TAAAAGCTCCCTGAACTGCGAAA

>RXA01317-upstream
ATACATCCGCCTTAATGGCACAATTGTAGGTGCATTAGCAGGACTGGCCATTTACGCTAT
TTCCCATATCCTCTTCGGAGCTTAACTAGGAGTAACCATC

>RXA01317
ATGTCCGATGCAAAAGACGATTCCATCTTGTCCAAGTGGAGCAATGCAGCTTCCGAGCTC
AGCGGTGCCGTCAGTGGAGTAGCGAAGAAGCTCCGTGAAGAACTCTCTGAGAAGGAAACC
TTCAGCAAGCTTAAAACCGAAGCCAGCGAAGCCGTCGATCAAGCAAAGTCCGGCTCCTAC
CTAGATGCCGGTAAGGAATTCGCCCGCGACGCCGGATCCATCATCAAAGATGCAGCCAAA
ACCGTCAAAGGTGCCGTCAGTGATTCCGATAAAAACGACGTGAAATCCGCCTTCGGTAAC
GCCGTGGAAGCTTCCCGCGACAAGTTCGATGACACCCTCGAAAAGCGCAAGGCTAAGAAG
GATTCCCCAGAACCAGGCGATGACGATATCATCGATGGAGAAGTAATTCCTCCGCAGAAT

>RXA01317-downstream
TAAGGAAGTCGGTTTCACCCCAT

>RXA01318-upstream
GGACGCGTTCCAGAGAAAAGTGCAGGCATAACCCCTAAAATACCCTGATCTTCCCCCGTG
TCCTGCCCCCGTGTCCACCCCTGCGTACATAATAGGACGC

>RXA01318
ATGGGAAAACATGAGGTTGCTCAGCAGACGGTTCCGGGTCCTTCGCCGGAAATGGAAGCG
CAGCGGCGTAAAGAGTTGCGCAAGCACAAGGCCATTGCCACTGGCCTGTTGATTTTTGCT
GCCGCTGTATATTTTCTTTGCCGTTTCGTGGAGACCCGTCCGGGTGAAACTGCAGCGTGG
GTAGGTTTTGTGCGCGCTGCGGCAGAGGCCGGAATGATTGGCGGGTTGGCCGACTGGTTC
GCGGTCACCGCGCTGTTCCGTCATCCATTGTGGCTGCCTATTCCGCACACTGCGATTATC
CCGCGCAAGAAAGACCAGTTAGGTGAGGCCTTAAGCGGGTTTGTGGGGGATAACTTCCTA
AATGCCCAGCTCATTACGGAAAAAGTCTCTCAGGCGCGGATCCCAGAGCGCGCCGGGGAG
TGGCTCGCCCAGCCGGAAAACGGGGAGAAAGTTTCGCGCGAAGTCGGCAAATTGACCGCT
AATATTGTGCGCGCAATCGATCCGTCAGATGCTGAAGCGGTGATTAAATCTGCGGTGATC
GACAAGCTTGCGGAACCCACCTGGGGCCCACCAGCTGGGCGGTTGCTGGAACAACTCCTC
GCCGAAGGCAAAGCCGAACCAGTTGTCCAGGAACTCGCGCAGTGGCTGCACAAAAAGGCG
TTGGGCTCCGAGCCGCTGATTGATCGCCTGCTCAACGAGCGCCGCCCGATTTGGGCGCCG
AAATTCACTGCGCAGCTGGTCAGCGGCAAAGTCTATGACGAGGTCATAAAATTCACTGAA
GCCGTCGCTGCCGATCCTAACCACGAGGCCCGCAAATCGCTGCGCCGATTCCTTAATAAA
TTGGCGCAAGACCTGCAGCATGACCCAGGCATGATTATTAAAGTTGAAGAAATCAAACGC
GACATCATGGGCTCCGGCGCCATCGCGCAAGCCGCGCCAACCATCTGGGCGTCAGCCTCC
GAGTCGCTCATTGAATCCGCAGAAGATGAGTCATCAATTCTGCGTCGCAAAATTGCCGAA
GCAGCTACCAGCTGGGGTCAAAGATTGCTTGTCGACGACTCCCTCCGGCATTCACTCGAC
ACCCGGATTACCGGCGCCGCTGCTTTCCTCGCCGACAATTACGCCCCCGAAGTCACCGGC
ATTATCTCCGAAACCATTGAACGATGGGACGCTGAAGAAGCTTCAGAGAAAATCGAACTC
ATGGTGGGCAAAGACCTCCAATACATCCGCCTTAATGGCACAATTGTAGGTGCATTAGCA
GGACTGGCCATTTACGCTATTTCCCATATCCTCTTCGGAGCT

>RXA01318-downstream
TAACTAGGAGTAACCATCATGTC

>RXA01322-upstream
TGGCCTGCCCCTGAAACTTTTACGGCTTTCAGAGCGCAGGGCATCATTTTCTTGTGTCGC
CAACACTTGAGAAAAATTGCGGAAAAGGACACTGCTGTTC

>RXA01322
ATGAAACTTGCACCTCGTATGCGGATGAGGAGCCCCAAAACTTTCGCGGCCCTCGCCTCA
CTTGCTTTAGTCATAGGTCTCGGCCAGGTACCGATCGCCCAAGCTCAAACCGAGTATCGA
ACCGCCTCCGACGGTTCCCTGAACTGGGGATTTAGGCAATCGTTCCGCAATTACATCCAA
ACCGGCGTGGCCAAAGGTTCCATCACGCTTGGCGACGGCGCATCCGACAACGGTGGCAAC

TTCGCATTCACCCCACGCACCAACGGCACCACCGTGACCAGCGATTCCCAAGGCACCGTG
GAATTCAACGGCTCCGTGCACTTCCTCGGACACCAGGCAGAGGACAAATGGATCCTGGAC
ACCACCATGTCTGACATCAAAATGGTGTTCAACGGATCCTCCGCGCAGCTAGTTGTGGAT
TTGGTTGCCCGCGAATTC

>RXA01326-upstream
CCGGCTGGCGCTGAGGAAACCTTGGCAGGCGCCTCCCCGAAACT

>RXA01326
TTGCGCGAACGACTACTTCAAAACAATGGTGGCGAAGTCATCGACAATGAAAACAACGAC
TGGATTCTCCATCCAGTTCGTGATGACAGCGACCGAAAAAGGCTTGTCCGAACTGCCAAC
GACATCATCCGCGAGACCGAATCTGCACGTGAATGGGACAATTTCCCCGAAAATGCGATC
GCAATTGCAAATGACGGAACGGGCGACTTAATAATTCTGCTTCCCGACGATGATGCTTTC
TACATCTGGTCGCACGAAGATGAACCCCTGATCGAAACTGAACTTGAGGATGCC

>RXA01326-downstream
TAAAACAGCTGGACAGAATTCGA

>RXA01330-upstream
CCGTCCGTTTTCCTGGTGGGTCGGCCCCGCATCCAGCCCTAGAAATATCGGAGAGCTGCT
CGTTGAGGCCCAATGAAATGCCTCCGAAACAGAAACAGGC

>RXA01330
ATGTGGAAAGACTTAACCGAACCGCTGCCCGAAGCTTGCGCTGAGGGCTTAGAGATCCGG
GTGGTTAAATCTCCCGAAGAGCTGGCAGATTACGCTGCAGTTCTTTCTGCGAATTGGAAT
CCACCCGCCGAAACTGTGCAGCGTTTCTATACCGAAGCAGCTGAATACGCACTGAGAAAG
AACTCGCCCGCACTTTATCTGGTGGGTTATGCGGGCAACCGCGCAGTGTGTTCTGCGGAA
GCATTCATACACGCGAGCGTAGTTGGAATCTACAATATCTCCACCCTTGAGCACAAACGC
CGGCGTGGCTACGGCGGAGCCATCACCTTAGCCACGTTGCATACCGCACGTAACGCAGGG
TGTGACACCGCCGTGTTGCAAGCTTCCGAAGATGGTGAGCCCGTTTATCGCAAACTAGGA
TTCACCGACTGCGGTCGATTTACTGAATACTCTTTG

>RXA01330-downstream
TGATTAGTTAGGGACCGTATGCG

>RXA01331-upstream
GCCTCGGACTGGTTAATCCAACAGCCAGGTGGAGCTGAC

>RXA01331
ATGAACATCATGGGTGACCCCGCAGATGGTAACGGCTGGATGTATGCCTACAACGGCTTG
CACTCCGTGGCCCGCCACTATGCATGGCCAGCAGCAGGCGAAGGCTCTGCCACCGCGATG
CTGTTCTGGTGGCCTCAACTTCTAGGTGTGGGCACCGATGAAAACCCAGATCAAGTCAAC
GATGTGGATCAGGCTGCTCGTGATCTCAACGTCGGCTACTTCATGATCAGTCCGTGGACG
TTCTGGGATTTCCAGATCCCCAACTTCCGCCAGATCGATCTGCTGTGGCAAACCCCAGGC
GTGACACCGGTGTGCAAGAAGGGCGACTCGGTGATCTTCGCAGTCAACGATATGTTCACT
GACGCCGAACTGGATCAGATGCGTGCACCTGGTAATTCTCCAGAACCACTGCCAGAGCTT
CCTACCTTGGGCGAGCTTGGGTTGGCTGAAACTGAAGACGAGGTAGATCAGACTTATTAC
CATCGTCCAACGGTTCCTGCTGGTGTGAACTCAGAGATGCCTTCAGCCGAAACTCTGTAT
GCACCGGATCCAACGAAGCCGCATACGGTCCCTAAC

>RXA01331-downstream
TAATCACAAAGAGTATTCAGTAA

>RXA01333-upstream
CGCCCTTTAAGGCCCGTAAAGCACTCCACAACACTTCACGGCAGGCCGTAATTTCCCTGT
GAGGTACTTTCTTGCAAGTTGTAGCGCACCGCCGATACCA

>RXA01333
ATGCCTGGCGGGTGCTCCGGTAACATCGTCCGCATGCTGCCTAAATCCCGGATTTTCTCC
GCAATCTTGCTCGGAATTGGTGTGGCACTTGTGGTCTGGGGTCTGGTGGCTCCGCGCTTT
GTGCACGCTGATGGCCGTTTGCCTCTTGATTTGGAGGCGACGACGTACGTTCTCCATGAC
TCTGACGCTCAGACCACTATTAATTCTGATCCGTTGGCCGGTGTGGTGACTACGCCGGTG
ACTCGTCAGTTGCATTTTGAGGTGATGGATCCTGCGAGTGCTGATGATGCCACTATTCGT
ATTGGTGATTCGATGTTGCGTGGTAATCCTGATACTCAGGGTTTTGAGCAGGAACGGCTC
CTGTCAGCGACTGTGTCGAGTTTCCGCATTGATCGCACCTCTGGTGAGGTTTTGTCCGAT
ATTGCGCTGACTAATCAGTTGGCGAGCCCTACGGTGCAGTATTCGGTGGATGGCATTTGG
TTGAAGTTCCCAACTGACGCGCAGGAGACCACTTACAACGTGGTGGATCCGGTGCTGAGG
TCTGCGCTGCCGGCGGATTTTGTGGAGTCCACGGAGATCGATGGCCGTGAGGTGCTGCAT
TACCGTCAGGTGATTGATAACGTGAATGTGGCGGAGTATTTCGCGGATGCCAACAACACC
ACCACGTTGACTAAAGAGGATGGCGGTACCACGACGGGCTATTTTTATCACAATGTGACT
CGTGATTTTTGGGTGGATCAGCGTACCGGTTTGGTTGTCGATCTAGCTGAAAATATTGAT
GATTTTTACGGCGACCGCAGCGGCCAGAAGTACGAACAGAAATTGCTTTTCGACGCCTCC
CTCGACGATGCAGCTGTCTCTAAGCTGGTTGCACAGGCCGAAAGCATCCCTGATGGAGAT
GTGAGCAAAATCGCAAATACCGTAGGTATTGTGATCGGTGCGGTATTGGCTCTCGTGGGC
CTGGCCGGGTGTTTTGGGGCGTTTGGGAAGAAACGTCGAGAAGCT

>RXA01333-downstream
TAACCTGCTGTTCAAATAGATTT

>RXA01336-upstream
CATGGCATCCGCCTCCAACGCGCCGGGCGGGGGAGTCCACGGAATGCCCGGCTGGTGGGC
AGCGCAAGCCGTTTTAGCAGATCACAGGTAGAATTGCGAC

>RXA01336
ATGGAGCCCACCGTAAAAGCCAGCGCGCGCCACACCATCCACGTCACCGCCGACACCTGG
CGCATCCGCCTGAGTGCCTCAGCCCACTCACACCCCAACGACGCGTACGCGCGCCGGGCT
ACGGCAATTTCCGCCATAGGCAGCGTGCTTATCGACGTCCCCCTCCAAGGCGAACGCATC
TCTGAATCCACTGCATACGACGGCCAAATCAACGCCGACTGGAACGCAGAAGTCACCGGC
ACCGATGTGAACATCGCACGCGACATCATCTCCCGGCTCGCAGCGGTGCCAGACGTTCAA
GTCGACGGCCCGTTGTGGTCCTTGAGTGACAGTTTGGCTGCAGAGGCTGCTGTGGAGGCA
TTGCAAGGTGCTGCCGACACTGCGCGGAACACCGCGACCGCCATCGCAGAATCCCTCGGC
GGGCAGCTAGGTGCACTTCTCTACGCAACAACCGACACCCACAGCTCCACACCGATACCA
GCACGCGCAGAAATGATGGCAGCAAAAGCCTCCATACCACCGCGCACACTCGACCTAGAA
CTCGCCCCCTCTGACATCGAAGTCACCAAAGAAATCGCCGTGACCTTTGAATTCCTTGCA
GGC

>RXA01336-downstream
TAAACCGCGATTTGGTATTTCGG

>RXA01337-upstream
GCTGGCTATCCTCAATTCCGCTCGGGTCGCACTGCCACGCGGAGCGATTAGTGATTTTGA
TACGCAAGAAAAAGTTTCTTAGCAGGGTAACCTAAATGTC

>RXA01337
GTGACATTTCGAGGCGGAAACACTGGCGCAAAGCACGCGGTCGTTGTTGGTTCTGGCCCC
AATGGGTTGACCACGGCGGCGGTGCTGGCCAAAGCAGGTTGGCAAGTAGATGTGTATGAG
GCGGCGCCAACCCCTGGAGGGGCGGCGCGCTCAGAAAGCGTTCTGGGGGAGGGGACTATC
AGCGATTTGGGTGCCGCAGGGCATCCTTTCGGGGTGGCAAGCCCAGCTTTTCACTATTTG
GGTCTGGAAGATCACGGCCTGGAATGGGCGTATTCTCCCTTTGCGATGGCCCACCCGTTA
GATTATGGCAGGGCCGGACTGCTGGAAACGTCACTCCCAGAGACCGCCAAAAAGCTTGGA
CCTGATGCACGTCGTTGGAAGAATTTGCACCAGGGCTTAACCAAAAACATTGATAAACAC
TTGGCCAATCTATTAGGGCCGGTGCTGAAATGGCCAGCACATCCGATTCGGATGGCAAAG
TTTGGCCCATTTGCGTTGCTGCCCGCGAAACGTCTAGCCAGTGCCGCTTTTGAAACAGAA
GAAGCCCGATCCCTGTTTATCGGTTCGGCGATGCACTCGGTGACTCCACCACACAAGCCG
ATGACCGCATCACTTGGATTGCTTTTTGGCGCTCTGGGGATGTCGCGAGGATGGCCGGTT
GCAGTTGGGGGAAGCGGACGGATCGTCGATGCTCTGGTCAATGTCATAAACCATCACGGT

GGCACCATTCACTGCGATTCACAGATTGATTCCCTCTCACAATTCCGCGACACCGATGCC
ATTATTCTGAACCAAACCCCCTCACAGGTGCTGAAACTCAAAGGAACTGACCTTAATGCA
GGGCTTCCGCAACGCATGAGCACCTGGAAACACGGACCAAGTTCCTACAAAGTGGACTAC
CTCCTTGACGAACCAATTCCCTGGAGCAATCCCCAGGTAGGCCAGGCCACAACCGTCCAT
GTGGGCGGAAGCTCTGAGGAAATCGCTTTCGCAGAAGCAGAAGTCGCAGCGGGGCGGATG
CCCGAACGCCCGTTTATCATTTTGTGCCAACAACAAGTGGCGGATCCTTCACGCGCCCGG
GAGGGGCGCCACGTCGTGTGGGCCTACGCGCATGTGCCGCGGGGTTTCGTCGATAAGCGA
GCTGCTTTATTAATCACTGCGCAGATTGAACGCTTCGCCCCCGGTTTCCGTGATCGCATC
GTGCATTCAGTGGATACCAACGCGGAGGATTTAGAGGCGTGGAACCCCAATCTTGTTGGC
GGAGACATCACCGCAGGGTCCGCGCTGCTTCGGCGAATGCCGACCAAAATCGGCGAGAAA
ACGTACATGGCATCCGCCTCCAACGCGCCGGGCGGGGGAGTCCACGGAATGCCCGGCTGG
TGGGCAGCGCAAGCCGTTTTAGCAGATCACAGG

>RXA01337-downstream
TAGAATTGCGACATGGAGCCCAC

>RXA01342-upstream
GATGAGTATTCTCTCCGAGGCAACGAAGTTAATATGTCCATGAGGGCGAAGTTGTAGACA
ATATTTGGCCCATATGGATAATTGACAGGAGTTTAACGCC

>RXA01342
ATGGAAACCCCAACCCAAGACATGGATGTCCGCTGGTTATACACCCAAAGCCAGCTCAAA
CTCCGCGAAATTCTCCCCACAAACAAAACCTTCGATGTCATCCAAATCAGCGAACTCGTT
GACCCCACCGACTTCATCAGGCCCAACAGCGTGGTCTTATCCGTTGGCATCGCCTTCGCA
GAAACGCCCGACGGGCTTCGCGATTGGGCACACCGACTCGCCGACGCAGGGGTCATCGCG
ATCGGGTTCGGCTCCGGCCTCACCTTCCCACAGGTTCCGCAGGCGCTTATCGACGCCTCC
CTCCACCTTGGCCTCGGCCTCTTTGAAGTCCCCCGTGAAATTCCATTTATCTCGATCACC
TCCAGCGTGCGTGATGAGCAAACCCGCCGTGCCGGCCGCCTGCAACAAGAACTCCTCCTG
GAACAGGAACGGCTTAACTCCATCGCCATCTCCGGTGGCATCGAAGCCCTGTGCCGTGCT
GCCGCCGACTATTTGGGTGGTGCAGTAACCATCGTGGACAGCGACGGCCGCGTGGCTTGC
TCTATTACCACCGATGACCTAGACGCACTCCCCCAAGCTGTCTCGCGCCTGAACGGATCC
AGTCAAGCACTCACGGATGCCACCAACTTTGGATTCATCCACCGCATGACCCGCTACGGC
GACCGCCACCACGTGCTCTCAGTCCTTATGCCCACCCGCCCCACAGACCAACACCGCGCG
CTGATCAGACACTGCGCAGGCCTTGCCGATATTTTGCTCCAACGCCCCGAAGCCATGCGC
GACCGAGAAATCGAAGTGCGATCACTTGCCATGTCACTACTTCTGGGTCGAAGCGACGAC
CTGGCCACCATTCACCGCGTGTTCGCTGACATCACTGATGCTTCCGGAAATATCCGCCCC
ATCCTCATCACCGGCAACACACCCCAATCAGTACGAAAAGCACTCTCCAGTGTCGCCACC
GCACTGTACAAACAGGAACGAGCACTAGCTCATCTACGCCTCGCCGAATCCACCGAACTC
CTCTTCCTTCGCGGAAGCCGCAGCGTGCACAACATCGTGCAACTTTTTGGTACTGCCGCA
AGCGGAGTTCGCCTCTGCATTGGTCTGCCCACCCGAGCGGAAAACATCGATAAGAAACTC
ATCCGCGAACTCACTGCCACCGCAAAAACCCTACAACTTGGAACCCACGCCGAACCCCGT
GACGGCACCTTGCTGTGGCTCCAAAACCCCGAGCTGCGCAAAATCCTTAAGATCCGATCC
CGCGACACCTACGACCGTCTCCTCGACCACGACCGCACCAACAACACCGAGCTCGCCCCC
ACCTTGGTGTCTTTTACTCAGCACAGCGGACATATAGGCGACACCGCCAAAGAACTGGGC
ATCCACCGCCACACCGTGCGCACCCGCATGATCCGCATTGAAGAGATCTGCGAAATCGAC
CTCAATGATCCACTGACCAGAGCGGAGCTGCTCTTAGTGATCGCAACGAAGGAGGGAGAC
GTCGAAAAGCAA

>RXA01342-downstream
TAAAAAGACCCCATGCAAAGCAT

>RXA01348-upstream
ATGGGACAATGAGCACGTGACTCTACGATCTGCATTACTTGCGCTACTAAGTTCCGGACC
ATTGACTGGGTATGACGCCTCCCAGCGATTTGGGGCCTCG

>RXA01348
GTGGGCTTTGTGTGGAGTGGTTCCGATTCGCAGATTTATCCCGAACTTCGAAAAATGGAA

GCCGAAGAACTCCTCGTGGGATCCGATGTTCCCTGGGGCTCCAAAGGCGCCACCAAAACC
GAATACGCCTTGAGTGAAAAAGGCTGGGAAGCGCTAAGAAAAGCGTGGTACGAGCCAGTA
ACCTACGGTCCCACCAGAGATCCTGCCAGGCTTAAAGCCGCCTATTTTGAGGTCGGTACA
AATGGCGATGCACGCCGACATTTAAGGGCGCACATCGCTCATTTTGAACAGCAGAAAATT
CAATCAGAATCAATGATTGATGAGCTGAAAGCAAAAACTCATCCAACCTTGGCACGGCGA
CTTGAGCGCTCCCCGAAAAAGGAGCACGAGCGAATAGTCGCGTTTAAAGTGCTTGCCTAT
GAGGGGCAGATTGCACGCGCTCAGGCAGAGATTGAATGGGCGGAAAAGGGCTTGAAACTA
CTCGATACCCTT

>RXA01348-downstream
TAGTTTTCGAACACGTCCGTATC

>RXA01349-upstream
AGTTGTCAGCTGGGATTTGCCGATGGTGTTATCTTTGATATTTACCTTAACCCCGTTTCT
AATTCACGTTTTCTCGTTACCCGAAAGGAATTGATCGATT

>RXA01349
ATGGCGACATCACGTCGAGATGCCGAAAACATAGACCAGGCCGGTAGCGAATTCATTGAA
TCTGATTCAGGACACACCGCAACCCCTGAAGAGGTAGTAGCCACCGCTCTGACATTTTTT
GCAGAGGATGGTTTTAGCGAAACCAAATTGGAGAAAATCGCGAAGGCATCTGGCATGTCC
AAGCGCATGATCCACTATCACTTTGGCGATAAGAAAGGCCTGTACATCAAGGCTGTTTCC
TACGCGTTGCGATTGCTGCGCCCAGAGGCTGAAGCGATGCAACTTGATTCCGCGGTACCA
GTTGATGGTGTCCGCAAAATCGTCGAGGCTTTATATACCTGCATCACCAAGCACCCAGAA
GCAGTGCGCCTGCTATTGATGGAAAACCTGCATAGCCAAGACAGCGTGGATTCCACCGCG
GCATATTCCGATGAATCCAATGTGCTGCTCAACCTGGATAAGCTGCTCATGCTTGGCCAG
GATGCCGGCGCCTTCCGTCCTGGAATCTCCGCAGAAGACGTACTGGTTCTTATTAGCTCC
CTGGCCTACTTCCGCGTATCCAACAAGGTCACGTTGAAGAACCTCTACTCCCTTGATTTG
GAATCAGAGGCCAATATTGAAGGCATGAAGCGCATCGTCGTTGACACGGTGCTGGCATTC
TTGACCTCAAATATTCAAAATTCTGGCAACTCCAGCTACCTGGTTGTTGGTGGCAAGACT
GCAGAACCAGAAACTGATGACAGCGTCTACAGCTTTGATACGGACGTGTTCGAAAAC

>RXA01349-downstream
TAAAGGGTATCGAGTAGTTTCAA

>RXA01357-upstream
ACGGCGCAAGTCCCGAGCACAGATATAGTTATGCAAATGTGGCCAAGGCACACCAAGAAT
GGCTACACGCTGCAGATAATGACACGACGGAAGGTGGAGC

>RXA01357
ATGAGCGCTGAAGAACTCGACAACTACGAAGCAGAGGTTGAACTCTCTCTTTACCGCGAA
TACCGCGACGTAGTCAGCCAGTTTTCCTATGTTGTAGAAACTGAACGTCGCTTCTACTTA
GCAAATGCAGTGCAGCTTATTCCACACAACAGCGGAAACGATGTCTACTACGAAGTCCGC
ATGTCTGACGCCTGGGTATGGGACATGTACCGCTCAGCACGCTTCGTTCGCTACGTCCGA
GTGATCACCTACAAGGACGTCAACATCGAAGAATTAGATAAGCCTGACATCATCATGCCT
GAG

>RXA01357-downstream
TAGTTCTTAGGTTTAAAATCGCT

>RXA01359-upstream
GTTGGACCTTGTGCGATTTGGATGGGGAACAGCAGCCCAATCTTGACCATATTGCGCGAG
CCATGGAGCTTCGGGGCACTACATACAGTGAGGTAGCAGC

>RXA01359
ATGATTGACTCCCGCTTGCTGGCATGGGCGTATCTCTCAAAAGTGGTGGAGGGTCCCAAT
GCACACCTGCAAAAGCTCCTGAAAGAAGGTCATGATGTAGAGCGGATCGCATTTGGTATT
AAACACCGCGAAGAGTGGATTGGCGAAGGTCTGCTGAAAAACACCGATTCCCGGTACTCG

ATTGATACCGCGCAAACTGATCTGGAAACTATCGCCAAACTCGGTGGGCGGCTCATCACA
CCTGAAGACGACGAATGGCCGATGGAAGAATTAGACCATGCTTTTGGATTTGCCGCTTCT
GGCATGAGTGATCATGTGCGTACCTATCAAGATGATGCGCTGCCACCGCATGCGTTGTGG
ATTAGGGGAGGAAATCTCAGAACACTCAGTGCACAGTCCGTCACACTCGTGGGCACCAGG
GCAATAAGCCAATATGGCACGGAAGTAACTCGGGAATTCACCCAAAACCTTGTGTCTCAT
CAGTGGACAATCATCTCAGGTGGTGCCTTGGGAGTTGATAGCGTCGCCCATAGTGAAGCC
GTACGTGCACAAGGCTCCACCATCGCGATCGCAGCATGCGGATTGGATCGCTCGTACCCC
AGCCACAATCGAGATCTGTTCAACCAGATTGCCAAATCCGGAAAGGGGGCGTTGGTGAGT
GAATATCCACCGGGAACTCCACCTCAACGCCACCGCTTTCTCACTCGCAATCGTCTCGTT
GCTGCTCTATCTCAAGGAACTGTCGTGGTGGAGGCAGCCTGGAGGTCAGGCGCGCTAAAC
ACTTTGAGCTGGTGTGCTGGTTTAGGCAGGATTGCTATGGCGGTCCCTGGGCCGGTAAAT
ACTGCTGGATCACTTGGGTGCCACGAAAGGATTCGAAACGGCAGCGCACAAATGGTCACC
AGTGCGGATGACGTTCGGTCACTTCTGGGTGCAGTGGGTGCAATGGATAGCCAAACTCAG
TATGAATTAAACTTCGCGGCCACTCCAGTACAGGGTTTAACCAGAAATGAGCTGCGAGTT
TTTGATGCGTTAGACGACCGAGGAGAGGGGAGGGAAGCGGCGAGTATCGCTACCGAAGCC
GGGTTGACCTTGCAGTTAACAATTTTCCTTCTCATTGCATTGAACAAGCGCGGAATCGTG
AAACGCGACGGAACTGCTTGGTCGAGAAATGCGGAAATGCCA

>RXA01359-downstream
TAAAACCTGGGGGTTATATAAAA

>RXA01362
ATTAATGAGTTGATTCTTTTTGACGTACACGACTTGGTTAAATATGGCGTACATGTCTAT
GGCGCTCCGCAGGAATCTATTAACTTTTTAAGTGCTGCGTCGCTTTATCACCCACAAACA
GTGCTTGATTCATTTGATCATGACGGTTCAGGTAATCTCCCTGGTCTTAAAGACGACAAT
GGCAACTGGGACCGTCGCCCACACAAGGACCGTATCCAACTGGTCAATGCCGATACTTTG
ACGGTGTGGAAGTCCATCCTGGAGGATGAACAAACGCCATACTTGGATACCCGCATGGTT
TATACCGTCAACACGGAAGCAGCAGCAGCGTTGGAAAAGTTGGCTTCTGCACCTCGTATC
AAAGAACTCGGGCTGCAGTTCTCCAGTGGCTGGAATGAAACCACCGATAAGAAAAAGGGA
TACTTTGACGTTGGTTGGGGCTACCCAGCTTCCTGGTCTGATGCCATTTTGCAGGGGCCG
CACCTGGGTGTTGCTACACCAATGATCAAGCAGCCCAATCCGACAATGAAGCATAATCAA
GATTGGTCTGAAATTGATTTCGAGGCCATTCCTGCAAACTTCATACCTGCAACGGCGTAC
CAGCCCGATCGCCAAACAAAGCCCACTTATGATGCTGACTACGGCACCTGGACTTTCGGG
GACAAGCAGGTACCAGTTGCAGACACTTTCCGAATTGCATGGAGGGAGATGGCTGCCACC
ACGGGATTTAGGACTGTCTACCCATCAGTAATTCCACCGGGAGCCAACCATGTGCACACA
GTTAATAGCGCTGCATCACGTTCAAACTTAAAAACCATTCTCGTTGGAGCACAGCTTGGT
GCAATTCTAAGTGACTATTTTGCTCGGTCCTCGGGTTCAAGCCACATATTTAACGACATT
GTTCGCAAGATTCCACTTCCAAATTTCACATCCTTGGAAAAGCAGTTCGCCCGCACATAC
CTCCGCCTCAACTGCCTGACCTCAGCTTATGCCCCATTGTGGGAAGAGATCACCGGTGAG
CCGTGGGATGTTCAGGTGCCTTTGCGCAATGCCGAGCAACGTCGAGCAGCGCAAAACGAT
ATTGATGCCATGGTGGCATTGTCTTTGGGTATTAGTGCTGATGAGCTGTGCATGATTTAT
CGCACTCAATTCCCAGTGATGCGTAGATATGATCAAGAAGATCATTTTGATGCCAATGGC
CGTAAAGTTCCTAAAGAGATCATCAAGCTGCAGCAGAAACTTAAAGATGGCCAAGAGCTC
AGCGTGGAAAAGCGCACCTGGGTGCATCCCCAATCAGAAGTGTCCTATACCTTTGAATAT
CCTTTCCGGGTGTTGGATCGTGAAGCTGATCTGCGTGCTGCATATGCAAAATTTGAAAAC
CAGCTTAAGGAGCCA

>RXA01362-downstream
TAGAGCGCTTATGTCCTCACTCA

>RXA01364
ACGGGCACCCACCTTTATGATTCCCTGCAGCTGCTGTTCACTCTGGTGGATAAAGGCCAC
CACCCAACAGATGCTAAGGCTGTAGCTTTTGATGCCGAGGCTGGAGAAGAAGGCCTGCAC
TTCCGCAACCTTTCAGCGGATCTCTTCCTCCCTGCAGCCACAGAACTTATTGATCGAGTT
GGTCTTTCCAATGAAGCCCTAAACAAGGTCTTGGAAAACCTCCTGCTCTCCCGGGTGCAA
TCCGGTAAAGACCGCGGCTTTATCTCCTATGCCACCTTGGGTGTTACCGAGCTTGGCCAA
GTTTATGAGGGTCTGATGTCCTATACCGGCTTTATCGCCCAGGAAGATCTTTTTGAGGTT
GCACCACATGGCAAAGCCGATAAAGGTTCCTGGATGCTCCCGGTCTCAAAGGCTGATGAA
GTCCCTGCCGATAGCTTTATCGAAGTTGATCAAGAAGCCCCTGGTGGCGGCGTAATCAAG

GTGCGTAAACGCCACCCGCGCGGATCATTTGTGTTCCGTCAGTCCTCTCGTGACCGCGAA
CGCTCAGCGTCCTTCTACACCCCACAAGTACTCACCAGCTTTACTGTCACCCAGGCTATT
GAAGAACTCCAGGCATCAAAGCGCATCACCACAGCCAATGATGTTCTCAGCCTCACCATC
TGTGAACCTGCCATGGGTTCCGGCGCCTTCGCTGTGGAAGCAGTACGCCAATTAGCAGAG
CTTTATTTGGAATTGCGCCAAGAAGAACTAGAGCAGCAGATTCCAGCGGAAGACCGTGCC
AAGGAACTCCAAAAGGTCAAAGCGCACATTGCGCTGCACCAGGTTTATGGTGTGGACCTT
AACAGCACTGCTGTGGAGTTGGCGGAAATCTCGCTGTGGCTAGACACCATGAATGCAGAA
ATGGACGCACCTTGGTATGGCCTGCACCTGCGTAATGGTAACTCCCTCGTTGGTGCCACC
CGTTCGCTGTATGCACCTAGTCTGCTTAATAAAAAAGCCTGGTTAACTGCTACTCCAACC
CGCTATCGGCTTGATGATATCGCGCAGGCTATTGATGAAAACAAAGCAGAACCCCTCTTC
AACCACGGCATCCACCACTTCCTCTTGCCCTCTACTGGCTGGGGAGCCACTGCAGATGCC
AAAGATCTTAAAGATCTTATGGCTACTGAAATCAAGGAGCTTAAATCTTGGCGTACTTCC
ATCCGTGCGTCTTTGAGTAAAACTCAGATTAAGCAGCTCAATAACCTTGCCCTACGCGTG
GAAACACTATGGCGATTTGTGCTGATGCGTATTCGCATTGCAGAATCCCAGATCTCACGT
AGCACTACTCTCTGGGGTCAAGAGCCAGCTGAGGTTTCGGAGGTTGTCACACGTGAGCAA
ATTGAACAAGACCTCTTTGGCAATATTGATGGTGCATATAACCGTCTACGCTTGGTGATG
GATGCTTGGTGTGCGCTGTGGTTCTGGCCTTTGGATGCTGTTGCTACCGCTGAGCATCCG
GAGCGTCCAGCCCTTCCAGATCTTGATGAGTGGCTAGCCACCCTGACGGAGATTCTGGGT
ATTGATCTCCCTCTGAAGTCCAAAAACGAAAATCAGATTGTCTTAGGTCCAGATACCAAT
TGGCTAGCCATTAATGATGCCGAGGCTACTGATCTTGGTTTTTCTGGGGCATTGAGCTTT
GAGCGTGTTAGCGCGAATCACCCGTGGATCAATGTTGCCCGCCAAGTGGCTAAACAACAG
AGCTTCTTCCACTGGGATCTAGACTTCGCCCACGTTTTTGCCAAGGGTGGATTTGATCTG
CAGGTTGGTAATCCACCATGGGTGCGACCAGATGTGAACTTTGAGGATCTGCTTGCTGAA
CATGAT

>RXA01366-upstream
ATGCATGAAAACAAATTCTATGTGTGTTGAGCTGCCAAAAGGGGTTGGCGCGCCGATGAT
GACTGTCCAAACCTAAACCAAAGGTCTAAACTTTGGCTTC

>RXA01366
GTGAGTCAGTTTCGTCGTTGTTCCCGCCCTGGTTGTGGCAAGCCTGCCGTCGCAACCCTC
ACCTACGCATATTCGGATTCCACTGCGGTGGTTGGTCCTTTGGCGCCTGCAGCAGAGCCC
CATAGTTGGGATCTGTGTGAGCATCATGCCGAGCGTATTACTGCGCCCCTTGGTTGGGAG
ATGCTGCGGGTGAACGACATCAAAGTCGATGACGATGAGGATCTGACGGCTCTTGCTCAG
GCTGTTCGTGAGGCTGGACGCACTGTGAGTGGTCTGGTTCCTGAAGACGAAGTGGGCGGC
AACCATCCGGTGAACCGGAGTGCGCGGATCGCGGAACAGAAGGTTCACCGCAGGGGTCAT
CTCTATGTTGTGCCTGATCAGGACGAATCA

>RXA01366-downstream
TAAGGTTTGCTATTCGGATTGGA

>RXA01367-upstream
CGCGCCAACCCCTTTTGGCAGCTCAACACACATAGAATTTGTTTTCATGCATACGAGAAC
TTTCCGCAATCGGCACGGACGCGGTCTCCGCGGCCCACTC

>RXA01367
ATGCCCGTCGAAGTTCCCCGCCACGCCTCTAGACGCCAAGCCTTCGACCGCGCAGTCTTA
GAGGCCTACTCCCCTCTTTACGGGATTTACCAAAAAGAGCTCAGCAATCTAGACATCGCT
GTCGATACCGTTCCTCGCATGCGACTCAGCGCCGACCTTGCCATTCTCCCCGATGAAATC
ACCGCCGACGGCCCCGTTCCACTTGGTCGCGTCATCCCACCGGCGATCGATACCAAGGGA
AACCCCACGAGAGCGCGCATCGTTATTTTCAGAATGCCGATCGAGCAACGAGTCACCAAC
GCTGTGGAACGCCACGAGCTATTGACTCATGTTCTCACCTCTTTGGTGGCGAACTATCTG
AATATTGATCCACGAGACATCGATCCGGGATTCCAGGATCTC

>RXA01367-downstream
TAGCGTGGCCGGTGCACCATGGG

>RXA01370-upstream

CTGTCTGAATCGTGTGGGCGTTAGATGAATTGTTATAAACCGGATGTTTAACGGAATTTA
ATACGTGTCTTATTACGCGGACTAGAAAGGTTTTAGGGAC

>RXA01370
ATGGGTGCATGGGACGATGCAATCTTGACTGAGGAAGTCAACGTTGATTTTCTCGACGAG
ATCTCAGAATTAGATACTCAAGACATTCTTGAGGCGTTGGAAGACGCATGTTTGCTGGTG
GTTAACCAGGACAACGCCACTGAAGACGAACACCTCAACGGTCAGGCGGCTGCGACGATC
GCGGCCATCATGTTTGGCGCTCCATATTCTGCGGGCCAGGTGCTGGAGAATTACCCATTT
ATCCGCGAACTCGTCGGTGAGGGCTCTGAAGCTCTTCGCGGTGCTGCAGCGCAGGTTTTG
GAAGAGGCAGATGTGGAATATGACCTCGAAGCTTATTTAGAGGCCCTCAAC

>RXA01370-downstream
TAGCCCTCCACTAAACAGCTTCA

>RXA01372
CAGGACACCTTCGTCCTTCCCACCTTGCCCACGGCCGCAGGCTTGTCGCCTGCCCGCATC
GTGGCGTCGATAAGCACTCTTTTAGATCTTTTAGAAGCAGACCCCAGCATTATTTCCGAC
CGCTTGGAACACCTCGCCGACTGCATTGATGAGGAAGTGGAATCGCTATCGCCGGAACGT
GACGAACTAGTCAATCCCGGCCGAAAACTGCGCGCATACGTAGATCACGCACGGATCGTG
CATACCGGCCGAACTGATGTGGGACTCGCGATTGCCAACGTTATCGCCCCAATCTGGACC
CGACGAGGCCTGGTATCAGCCGTGCTGGATTTTCCCGAGCTCATGGAATCATTGCCGGAA
CTCCGCGGACCCGAGCCAATTACCGACGATATATTCCATGACCCATTCATAGATGACGAA
CCCGGGGGTGGTACCGTTTAGGGCTGTTGTCTGGGCCGAAGAGGAACCCGGAATCCCCGAT
GCCATGGCGCAAAGCTGCGACGGACCTAGCAAAGGGGCGCTGACACAAGCACTGCGTTTG
CTGGTGCGCGGACAGTCAGCCACGACCTATTCCATTGAAGAAAAGGACTTG

>RXA01372-downstream
TAAATGGAGCTATTGGAAGGCTC

>RXA01378
CATGTGTGGATTTCACCAGGTGCGAGCAATCCGATCAAGGATCGCCTCTTCCCTTGGACA
TTGGTGAAGGCTTTTCTCTCCTCCCCTGCAGCCTTGGGCGAAACAGTGTCCAATCGCCTC
AAAAAGGCCTCTGCACCAGAAGAAAAACGCGCCCTAGAAACCCTTTCACAACTTAATTCT
GCGATCACCCCGCAGACCTCACAGAAGTACCAATCTCTACTGAGCTACCTCGGTGACATC
GGAGTGAAGAAGAACTCCGATACCCGCGTGGTGATTTTCTCTGAGCGTGTCGCTACTTTG
CACTGGCTGCAGGAAAACCTCATCCGTGATCTCAAGATGCCACCCAACTCTATTGCTGTT
ATGCACGGCGGTCTCCCCGACCAGGAGCAAATGCGCCTGGTGGATGAGTTTAAAAAGACG
GATTCTCCCATCCGCATCATGATCACCGGCGATGTTGCCTCAGAAGGTGTGAACCTGCAT
ACTCTCTGCCACAACTTGGTGCACTATGACATCCCGTGGTCACTGATCCGCATTCAGCAG
CGCAATGGCCGTATTGATCGTTATGGTCAAACCCACAACCCTTCCATCGTTACCTTCTTG
CTCGATCCCGCCGAGGATTCCAAAGTAGGTGAAGTCCATGTGCTGGAGAGGCTCATGGAG
CGCGAACATGAGGCGCACTCTTTGCTCGGTGATGCCGCATCTCTCATGGGCAAGCACTCT
GAGCGTTTGGAAGAAGAAACCATCCGCGAAGTCCTGCGCGGTGCCCAAAACTTTAATGAT
GCAGTGGCTGATCCAGCGGAAGTCCTAGAAAACCCAGCAGGCCTAGATGATATTGATTGG
TTGCTAGCCCAAATCGCCCAAGCCGATGCCAAGGCAGAAACAGAAGCAGAAGCAGAAACA
GAAAACCAAACAGCACCAGATGCAGCTTCCAATAGCACGCAGCATGCACAACGCCGGTTG
TATGCACAGGAAAGCTCTTTCCTCTATGACTGCCTCCTCGAAGGTTTCAATAACGTACCG
GAGGATTCCATCAACCGCGGTGGCGTGGGGTTCAAAAAACACGATAATGACATCGTGGAG
CTCACCCCCACCGATGATCTGCGCCGTCGTCTAGATTTCCTCCCGCAGGATTATGTGGCT
GCTCGGAAAGTTAAGGAAGATCTCCTACTAGCTTCCACACTGATGCGTGGCCAAGAACGC
CTCAACGCTGCGCGCACTGGTGAAGATGGCAGTACCTGGCCAAGTGCCCACTATCTAGGC
CCCCTGCACCCAGTCACT

>RXA01379
CTAAATGTTGAAGAGTGGATCAGTGACCACTACCTCACCAATGACGATGCCAAAGGTGCC
TCATTTTCCAAGCGGGTGCGCGAGCGCATTAAAGAATGGAAAACCACCGAGGACGCAACC
CAGCAGAGTGGCCCTTTAACTCGTTTTTCCAGCAACCGCCTGCAGTTGCAGCATGCTCTT
TCTGAGCTTGACGACGCCACCACCGCCGCCAGTTTAGTGGCCTCTGCACTGGGGTATGGT

GTCCCCAGCGCGCGCCACGCGCAGCGCGGCTCCGACACAATATCCTATTCCTCTTGGGTG
GGAAATGCCGGCAGTGTGGAATTTCTTGCAGCGACTCCCGCTGAAAGCTTTGAAGAGAAC
TTCCGATCCCTTCCCCTTGAGCCAGTAGCGGTCAATGACAAGCCCCAGGATATCACCGCA
GCCAAATTGGTGGGCCAGATTTTCCTTAGTGATACTCCCCCTGCTTTTGTTGTTATCACC
GCTGGTAAATGGGTGGTTTTAGCCGAGCGTGAAACCTGGCCTCTAGGCCGCCACCTAGCT
ATTGATATTTCCCTGGTGGTGGAACGTAATGACACCAAAGCCCAGGGTGAGATGCAGCAG
ACGGTCGTAGCACTAGCCCGCGAAAATACCGAGCGTGCCGCCGATGGCACCACCTGGTGG
GAAGAAACCATTGAGCAATCCCGCGAACATGCTGTCAAGGTTTCTGGCGAGCTACGCAGT
GCGGTGCGTGAATCCATTGAAATCCTGGGCAATGACGTGCTCACACGCTATGAAGCTAAA
GAGCTCTCCACCGCTGAGATCGACGGTGGCGAGCTAGCTAAGCAATCTTTGCGCTATCTC
TACCGCATTTTGTTCCTGCTTTTTGCCGAGGCTTCACCAGAGCTTGAAATCCTGCCAACC
GGCACCCCGGAATATGACGAG

>RXA01380
TCGCTGATTTTGGGATGCGACACCAAGGCTCGCCTGGAGGATCTGTACCTGCCGTTCAAA
AAACGGCGCAAGACGAAGGCCGATATCGCTAGGGAGGCGGGCCTGGAGGGGCTCGTCGAT
AAGCTTATCGACGCCCCGTCCCTCGACGCCGCAGCGCAGGCAGCTGCATTTACGACTGAG
GGCTTTGAGGATTCCAAAAAAGTTTTGGATGGCGCTCGCGCCATTTTGATTGACCGCTTC
GCGCTCGATGCCGATTTGGTGGGCGAGGTGCGTGAGCAAATGTATCGCGCGGGTTCCATG
GCGGCATCGGTGGTGGCGGGCAAGGAGCAGGAAGGCGCAAAGTTCAAGGACTACTTTGAG
TTTTCCGAACCTTTTGACAAGCTTCCATCTCACCGAATTTTGGCGCTGCTGCGCGGTGAA
AACGAAGGTGTGCTGAGCCTCAACCTCGATGCGGGCGACGACATAATCTACGAAGGTTTG
ATCGCCGACCGATTCTCCCTGGACACCCACACTTCTAGCTGGCTGGCTGAGGCTGTGCGC
TGGGGTTGGCGCACCAAACTGTATGTGTCCTCCGGATTGGATGTGCGCATGCGTCTGAAA
GAAAAAGCAGAGGAAGGCGCACTCGATGTGTTTGCCACCAACCTCCGCGACGTTCTCCTT
GCAGCTCCCGCTGGTCAGCGCTCCACAATTGGCCTTGACCCGGGATTCCGCAACGGTGTG
AAAGTAGCTGTCGTGGATTCCACCGGTAAGGATGTTGCCACCACGATCGTCTACCCACAC
CAGCCCCAAAACCGCTGGAAGGAAGCCGTATCCGAACTGGCTAACCTGTGCGCGACCCAC
GGTGTGGAACTCATGGCGATCGGCAACGGAACCGCCTCGAGGGAAACGGAAAAACTCGCC
GGCGAAGTAGCTGACATGATCAAAGCCGCAGGTGGCACGCGACCAACCCCCGTGGTGGTC
TCCGAATCGGGCGCATCCGTGTACTCGGCATCACCGATCGCAGCCGAAGAATTCCCCGAC
ATGGACGTCTCCCTCCGCGGTGCAGTTTCTATCGCGAGGCGACTCCAGGATCCACTGGCG
GAGCTCGTCAAGATTGAGCCCAAAGCCATCGGAGTCGGCCAGTACCAACACGATGTCAAC
CAGGTTGCACTTGCCAAAACCCTTGATGGTGTCGTCGAAGACGCAGTAAACGCAGTCGGA
GTTAACCTCAACACCGCATCCGCACCACTTCTTACCCGAGTTGCCGGAGTGACCTCCACC
TTGGCAAACAATATCGTGGCCTACCGCAACGAAAACGGTGGATTCTCCTCCCGAAAAGAA
CTGAACAAAGTTCCTCGCCTGGGACCCAAAGCCTTTGAACAGTGTGCTGGCTTCCTCCGC
ATTTCTGGATCCACCGACCCTCTCGACGCCTCCGCTGTTCACCCCGAGGCGTACCCAGTT
GTTCGCAACATTGCGAAAGCCACAGGATTGGATGTCTCGGGACTGATCGGAAACTCTGCG
GTGCTCACCAAATTGAAGCCCGCTGATTTCGCTGATGAACGATTCGGCATCCCCACCGTC
ACCGACATCATCGCCGAGCTGGATAAACCCGGACGTGACCCCCGCCCAGAATTCAAAACC
GCCAGCTTCAAAGAAGGCGTGGAGAAAATCTCCGACCTCACACCCGGCATGATCCTGGAA
GGAACTGTCACCAACGTTGCGGCGTTCGGCGCATTCGTTGACGTGGGAGTGCACCGAGAT
GGCCTCGTTCACGTTTCCGCGATGAGCGACAAATTCATCTCCAACCCCCACGAAGTTGTT
CGCTCTGGTGAGGTCGTGAAGGTAAAGGTCATGGAAGTTGACGTCGACCGCAAACGCATC
GGCCTTTCCCTCCGCTTGACCGATGAACCCGGTGCCCCAGCTCCGCAAAAGCGCGGAAAC
CGACCAGCCAAACAGCAGCGAGCTCCGCAAAAACAGTCCGCTAAGCCCGCCACAGGTTCC
ATGGCAGATGCTTTACGACGCGCCGGCCTCGGTGGC

>RXA01380-downstream
TAAGGCAACTTTCAAACCAAGCG

>RXA01383-upstream
CTTCGAAGAAGACGATATCCCCTACGAAGTCGACGTGGATGACTTATTTATCCTCGGTGG
CTTAGACAACTTCATAAATCCCCTTGGAGTGATTGAGATA

>RXA01383
ATGAATCTCCACTCCTTAGAGATTCGCCAAATTTCATCCGGCACAATTTCAGAACGAAAA
ACTTGGATCTTTCCCACTGCTGCTCGCTCATTCAATCAAAATCTAGTACACCCGCAAAGC

ATTGAAATCGATGCACAAACCGGCGTTATTTTGGCTATGGAAAACCGACTACAACGTACC
GAAGTTGAATCAGTAGAGTACCCAACGGATCTTCCTAATCCTGCATGGACAGGTCCAGCC
ATTTCTTGGCCACTAAAAGACCCATCAATCGATTTCCCTGACCCGCTCCCCCACAGCATT
TCCGAATTACCACCTCAATCCGATAATCCTCGGCATTTGCGAGTATCCATCAGCTTAGAT
GCAGTGGAAGGTGCTTTTCCGCGCTACCGGATCGGAGATTCAATACGTATTCCGCTTGTC
TTTGCCCGGGACACGCCCTTCATGTCCGGCTTAGAAACAACACGTCGCGCCTGGATTGAG
GCGGCCACGGAAATGGACATCCATAACACATGGCCCATAATCCTCACCGGTGACGGCTGG
ACTGCACTCTCTCATTCAGACAAACCAATACGCCACGAAGCCGAGTTAAAGGGATGGTTT
TTCCACAGTTTGTTCGGCAGTGAAATGCCCTTGACTGATCTGAAGATTGAACGAATCTAC
GGAGGCCTGGGTACTTTCGACAGCGGAGCCACCCGGTGGCAAGAACTCACAGACACAGAT
GATGCCTACACAGAAAATGGCAGCTGGCTGTTGGAAGTTATCGTCGATGCCACCCTTGAC
GGTGCAATTCCACCACCACTTCAGCCACAACAGTTTGAAGCATCCATCACTCACATCGTC
GATGAGCAACTATGGGTCCTTGGGCAGATGCTTCCAGTTCTACGATGCTGGGATCTTGAA
ACCGGAAAATACCTGGGGCAAACCTATGTACCTATTTCGGTTTCTCATAGTTCTCGGCTT
CAGTTTTCGGAAGGGTTGATTCACGATTATGAAAATGCCTGGTCGCTGAATCCTGGGGTG
CGCATGCTTGCGGAGCCACAGCCGTGGATAGAGCCTGTCATTGAACTCGACGTTCCAGCG
CCATGGGAATTACAAGAAAGCTTCCCCGATGGGCTTTACTTCCTAACTGATGGCAAGCAA
ACA

>RXA01384-upstream
ACTGTCCCTCACTCTGCGAGCAGCCATTGCGCTATCGGCAGCTACCTGCAAGGTGCGCTG
GTGGGAAGCGTCGACAAGCATCTTTAAGTAGCGTTGATGT

>RXA01384
ATGCGCTCACTTCAATCGGTCCTTGACCTGCTGACTTCTAAGTCCAAAGTGGCTACCAAA
ATTGTGGTGGAACGAATTGAAAAGCATCCTGTTCATGGATTGGGATGGATGATGTATCCG
CCATTTCATCCATGGACTGATGCTTCGACCTTGACGATTGAGCGAAACGGAACCAGTCGG
CGCGCGAGTCAGAATGGCGTTGCGGTTCTTCATCAGCATGAGCAAGTTCAAACTATCGGT
CTAGCCAGCTATTTTATCGACTCCAAGATTTGGGTAAACGAGCTGGCTGGCCTTGATCGT
ATCAACATTTCTGAGAGTGAAGTTGCTGGTCGTGACGTATTAGTTCTGCCGTTATCTGAT
CTGACTTTAAGCATCGATGCGAAATACGGCGTGGTTTTGGCTGCGGAAGACAGCGATGAA
TCAGTGCGCGCGGTATCCGTGGAGTTCCTGGACCAGTGGGTAGATGAAGAAGAACCCCCA
GCGGAAGAAGTGCCTAAATATACGGAAACCAGGGAGGAACTTCCTCCACTTGAGATTCCT
CCGGCTCCTTCCGGAAATCGTAATCTCCGAGTTCTGTGCACGTGGGGAGCGATGGAAGGA
ATTATTCCTGAGTGGAAACCCGGCGATCAAGTTTCACTGTTTTTGTCTTTCGACCTCGAC
GATCCGCCGTTCGAACAGCTCAAAACCACTCGTCGCGGGTACACCGAACCTGGCGAGATT
TATGGAAACCAGCGCAGCTATAAATTTCACGCTGATGGTTGGAACGCTGTTATTTCCGCC
AAAGTGCCACTGCGCACCGAAGAAAACCTCACCGGCTACTTCACCCACAGCTCCTACGCG
GACACGAGCCGCCGCACGTCAGCGGTCATCACCGCAGTCTACCGCCACGGTAAGGACGCA
ATTATCGACGTGACCCTCGACGGTGCGAAACCTCCTAGATATCAAGAATCCTTGGATTGG
AGCAGCACCAGTACCTGTGACGGTGAAACAATCTGGCTGTCCGATAAGAGCTTGCCCTTC
GTCCGCGGTTTCAATGTCTCCACAGGCAAGCTAGTACACGAGATCTCCATACCCACCTTC
AATGAGATCGCCCTCGAATCCGGCAATAGAGCCCGCGCAGCGAAAAAACTTTGGGAACTT
CCAGATCTTAAAGAGGCAACCGACCCTGTCCCAGCGATCCCCGCGGGCTGGAAACTACAC
AAAAGATTCGGGAAAAACTTCCATATCGTAAGCGCTGACAACGGAACCTGGAAACAAACC
ATCCTTAGGATCAAACCCTTCAAAGCAATTGAGCTTGATCTTGGATACGCCAAGATTTCG
ACGATTTACCAATACGGTGAACGAATTTATCTGCGTTCCGATCTTCACCAGATCACGTTT
AATCAGGATCTTGAAATCCTCAGTGTAGAGGTCCACGGAAATCCCGATGCAGGTTATTGG
CCACTTTCCGATCTTCCACCAGGGGATTCTCCAACGCTGGGATTTCCTATCGGATCACTC
ATGATGTTCCACGAACAACAAGATATCTACGCTTTCCACGATCCTAAAACAACAAAGCAA
CTAACAACTGTGAACTTGCCCAAAAGGCAGTTTGAAGTGGAATATGCTTCTCAGAACAGA
ATTGTTATTTCGCTGAAAAATCCAGAAAGCCGCCTCATTGACAAACTGTTGGTGTGGGAA
CCACAAACCAGGTGGCGGGAACAAAACCTGGAGAGC

>RXA01384-downstream
TGAGCACGGTTTGATTAACGTCG

>RXA01390-upstream
CGTCCAGATAATCAATCTGCGAAGCCAGTGGCTTCCGAAGCTCCAACAACTATTACGCCG

GCAAGCTCTGGTGCATTAGCATCCGATGCTCCGACGTCTT

>RXA01390
ATGTTCAGGCGCAGCCTTCCCAGCAACAAGACATCCTCAGCAAGTTCCGCCAGCTCCGCC
GACACAAGTTACTCAGTCAGATTAGGCCGTCCTGAAGAGCCTGGTTACCAGCCAGAACCG
TCTTATTCGGAGCCTTACACTGACTCTGATTTCGCGCCAGCAGGTGCGGCCGCTGCGGCA
GCTGCAGTAGCTCCACCAATGATTGCGGAACAGCCACAAATTGTTGAAGATGCCCGCCGA
GGTACCCTCGATTTCGGCCTGTTGATTATCCGCGCAGTCATTGGTGTCTATTTGATCGTC
CGTGGAGTCTTTACATTCTTCACCCTTGGAGGATCTGCCGGTCTTGCTGGCCTCGAGGCA
GAGTTCGCTGGTTACCAGTGGCCTGAAATCCTCGCGATCCTGCTTCCATCTATTGAACTT
GCGGCTGGTGTCTTCCTGCTCCTTGGTCTGATGACCCCAGTGGCAGCAGCGGTAGCCACG
GTGGCGACATCCTTTACCACCCTTCACCAAGTCAACACTCATGAAGGTGGTTGGGGTGAA
CTTAGTGAGCCATTGATGCTGGCACTGATCCTCACTATCGTGGTTGTCGGACTTCAGTTC
ACCGGCCCCGGCAAGATTTCCCTTGACTCTGGCCGAGGTTGGCAAAGCGTCCACTGG

>RXA01390-downstream
TGAGCTCGTGGATCTTCGTGGTC

>RXA01391-upstream
ATGGTGTGAAACCATCATGGCTCGATCACAAAAAAGAACACCTGCTATCAGGTCAACCAA
AAAAGTTAAAAGTGTAATATCCAGCATCATCACGATTGCC

>RXA01391
GTGGCTGCAGTCGCTTTTGCAGCTTACGTTATAGATGGTGGGGTAGAAGAGGCGTCTGGA
ACACCGACGTCTTCGGAAAGCTCGGTAGCGGCAACTGCTCCAGCGGCATCTAGCGAGACT
GCGGCTGAATACCGTGCGATGCTCGCTTCCCTTGACGTTAAAGGTCGTGCGCCAGGAACA
GGATATGACCGCGAATTATTCGGACCAGCATGGACCGACACTGTTTCCGTGGAATATGGA
CACAATGGCTGCGATACCCGCAACGACATCCTGCAACGCGACCTGGATGACATCCAACTT
CGCGAAGGCACCAAGGATTGTATCGTCACGAGCGGCCTGCTCAGCGATCCATTTTCTGGC
GAACTTATTGATTTCGTTCGCGGTGAACGTTCCGGCGACGTGCAGATCGATCACCTGGTC
CCATTACATGACGCATGGGTCAAGGGAGCACAGCAGTGGGATGAGCAAACTCGAAAGAAC
TTTGCCAACGATCCCGACAACCTTCTCGCCGTTAAAGGTACGCTTAACCAGCAAAAAGGT
GCAGGCGATGCAGCAACCTGGCTTCCACCAAACACAGCTTTTAGGTGCGATTACGCAAAG
AAAATCATCACCGTTAAAGATCGCTACAACGTGTGGGTGACTGAGGCTGAAGCAAGCGCC
CTGGAACGCCAATTAGATACGTGTGCTGCA

>RXA01391-downstream
TAACAGTCACATAAGCATTTGGG

>RXA01396-upstream
TCACCAACCCACTTAACTTCGAGACCTTCGATTCCCTCGTCGTTCCAGTTGGTTCTTCTG
CAACCGCTGAGATCCAGGCTCAGCTTCAACCTCCCGCGTT

>RXA01396
TTGAAGGCTTTCAACACCAACTTCGCAGCCACTTTGGCTACCGGAAAGGTTGGCGATATC
ACCACCACCGTTTTAGTTGCAGGCGATGATGAAGACGCAAAGAACGCTCTTATCACCGAC
GTCAACGCTGGCGGCCTCGACGCCCTTGACGCTGGTTCCCTCAAGCGTGCACACGAGCTT
GAAGCAGTTGGTTTCCTGCAGCTCACCCTTGCAGGTTCCGAGAAGATTGGATGGACCGGC
GGATTCGGCCTGGTCAAG

>RXA01396-downstream
TAACACCCAGCCTCAAAAGCACT

>RXA01397-upstream
TGAGCTGCTAAAAGTCTCGCATTAAAGGACTGCTTCCCTTCGGGGGAGCATTTCTTTTTA
ACTAATTACTTGACACGTCAAGTAATTAGGGTCTAGTGTT

>RXA01397

GTGTTCATGATCAAAGAACTGCTCAACAAGCTCTTCGGAAACAAGAAGGCTTCCCCGGCA
ATGACACAATCTGAAACCATTTCACACAAGGAGAACAACACAATGACCACTTACACCATC
TTCGGCCGCGGCAACATGGGCACCGCAATCGCAGGCGTCCTCACCAAGGGTGGTGCAACT
GTAGAACACATCGGTTCTGCAGATTCTGACATCGCAACCATCAACGGTGACGTTGTTATC
CTTGCTGTTCCTTACCCAGCAGTAGAGTCCATCATTGCAAGCCACAAGGATGCTCTCGCA
GGCAAGACCGTTATCGATATCACCAACCCACTTAACTTCGAGACCTTCGATTCCCTCGTC
GTTCCAGTTGGTTCTTCTGCAACCGCTGAGATCCAGGCTCAGCTTCAACCTCCCGCGTTT

>RXA01397-downstream
TGAAGGCTTTCAACACCAACTTC

>RXA01400-upstream
GAGCAGCTATCACCCTTATGCATCGGCTCCGGGTGAGGCGGTGCCGGTGTCCTTTGATCA
GCAACGACATGTGGGTGCCGGCGAGCGACCGGGTAGTTGG

>RXA01400
ATGGCGATTAGTGTTTCTATGCCTAAGGCGATCAGCCGTGAGGAATTGGAGCGCGCGTGG
CTTGAAGTGATTGAACGGCACGGCACCTTGCGCACAGTATTTAGCACGGGAATGGGTGGG
GAAGTGCAGCAACACCGCATTGATGTGGGCCCGGGAAAATGGATTGACCACGCCGTTGCG
CCTGGTGAGAGCATTAATGAGGCGTTGCGGGCGGTGTTGAATCGGCAGTGTTCGCCGTAC
TCGAGGCCATCGCATAGTTTGTGCATTATTGATGCGCATCCGCGTCCCACGGTGATTATT
GGTAGTGATCATTCGCATGTGGATATGTGGTCCATGCTGGTGATTGTGCGCGATTTGTTG
GCTGCGCTCGATATGGAACTTCCCGTTGAGCCGCCGTTGGCGTTTGAATCGCACACCGCG
GAACTCCTCGCGGCTCCACCTGCACCGGAGCGGATTCACCAGCGGTGGCGTGAAATTTTG
GAAGCTGGTGGTGGAAAAATGCCTCAGTTCCCGCTTCCGCTTGGCGATGCCATCTCCATG
CCTGAACGCGTTGAAGTCCGCGACATTTTCGGGGTCAATGGCTTGGCGATTTACTCGGCA
CGCGCCCGCGCACAACAGGTAAGCTCCCTGGCCTTGACTATTTCAGTGATGGCTGATGTT
ACGGCGGCGCTGGCGGACCTTCCGTTGCGTGCTGTATTCCCAGTCCATAGCCGTTTCGAT
CAGCGCTGGCACGATAGTGTCGGGTGGTTTATCTCCAATTCGGTCATTGAGGTGCCAGAT
TCCGATCCTCACACTGCAGCCCAAGCTGTTCGCGAGGCTGTTTCTTTGGGAAGCTACCCG
CTGGCTGAGCTGCTTGAACCGTGGGGTGGCATGCCGGAAACGCCAGGAATGTTTGCTATT
TCTTGGCTTGACCTGCGCCGACTCCCAGTGAGCATTGACGATATTGGCCTCCAAGCCCAG
TATGTCAGCGCTTCACTGCGCACCGATGGTGTGATGCTGTGGTTTATTTTGGATCGCTCC
GGCGCGCACCTTCGCTGTCGTTATCCTGACTCTTTGGTGGCGCGGGAAAATGTAGGCCGC
TGGATTGATGCGATTGTTGCTCAGATGCGCGCCGAAGCTGGGACGGTGAATCTGCAGGCC
GGCGGGGAACAGCTGACACTTCGGCATGGAACTCGCGCCGATATTTCCGAGATCGCCCCG
CTACTTGCCCGAAACGCAGCTGACCCTTGTGAGCTGGTGGATCTTGAACATGCCCTTGAC
CTGCTGACACACGAGTCTTCGCATTTCCTGGCGGTGGTTCGAAACGCTCGTGGCAAGATA
ATCGCAGCGATGCAGTTGACTATTGTTCCGGAGTTTTCCCGCGGTGGTGCGCTTCATCTT
CACATCGAGGGGCCGTTCATTATTCCGGAATATCGCACCACCGATTTGGATAAAAAGCTG
CGCGCCTGGGCTGTGGAGCATGGGCGTGCGCGAGGGGTGAAGGTTGAGGAGGTGGTGGGA

>RXA01400-downstream
TAGTTGGTTTATTGGCGCCTCGT

>RXA01401-upstream
TGCCAAACGGAAGGTTTAATTGGTCTACATGTGTCAGTCTCATGGCACTATAATAGACCT
AGTATCTATAGATTGATAGAAAATAATTTAGGAAGTTTCC

>RXA01401
ATGAACTCTCCCCTACAACACAGCGCCTTCCCCGTCCCCGGCGCGCAACTCTCCACCTCA
TACAGCGACGAACACGGCCAAGCCGTCATCCAACTTCACGGCCTCACCTCCTCCCGCCAA
CGCGACCGCCTCCTCGACCTCGACCTCGGCCGTGGCCTTTCCGGCACGCGCCTTTTGCGT
TACGACGCCCGCGGCCACGGCACCTCCACCGGCCGCGCTGCCTCCACCGATTATCAGTGG
GACACCCTAGCGGGTGACCTT

>RXA01401-downstream
TAATGCTTCTCGACGCCCACTTC

>RXA01402-upstream
CGCTGCCTCCACCGATTATCAGTGGGACACCCTAGCGGGTGACCTTTAATGCTTCTCGAC
GCCCACTTCCCCACGAACAAGTCCACGGCGTCGGCCCCTC

>RXA01402
ATGGGTTGCGCCACCCTCCTCAAAGCCGCGGTGTTAAACCCCGACCGCTTCAGTGGATTC
ACACTCATGCTCCCACCCACCGCCTGGGAATCCCGAAAAGCCCAAGCCTCCGAATACCTA
TCCCGAGCAGAATTCCTAGAAACCCACGGCATGGACGCCTTCCTCAACGCCGAAAAACTC
CACGCCCAACCACCAGCAACCGTAGGAACCCCCGACACAGTCCCCGACATTTCCGCCGAA
CTCCTCCCCTGGGCTTACCGAGGCGCCGCCCAAAGCGACCTCCCCTCAAAGAAAGAAATC
GCCAAAATAACAGCCCCCACCACTATTCTGAGCTGGACCGACGATCCCGGACACCCCGTA
TCCACGGCAATCGAGCTAACCCGCCTCATGCCAAACGCCCAACTGCGCATTGCCACTACC
CCAGCGGAAGTCGCGCGGTGGCCACAACACCTTCGCGATGACCTGCAGTTGGAC

>RXA01402-downstream
TAAAAACCTTCATTATCTGGTTT

>RXA01403
CCGATCACCTACATCGACGGCCATCCATATGTCGATGGCGCGGTCGGGGAGACCGGCGGT
TTGATGCTACAGCCGGCCATCGATGCGGGCTTCACCCGCTTTTTCGTTATCGCCTCCCGT
CCGCGCGATTATTGGCGCAAGGAGATCGGGCGCCCGGGTTTCATCAAAGCTGCTTTACGA
CGTTTCCCCACAATCGCCGACCTCACCATCGCGCGTCCTGCACTGTATAACTCGGTAAAG
CAACAGATCCTCGACCTAGAGAAACAAGGCAGCGCCTATGTGTTCTTTGCGGACAACATG
AACATCCAGAACACGGAAATCAATCTGAAGAAACTCCGTGCATCTTTCGATGCAGGCATG
CAGCAGACCCGCAAAGATTGGCCGGAGATCATGAGCTTCCTGAACCAAACCAGA

>RXA01403-downstream
TAATGAAGGTTTTTAGTCCAACT

>RXA01405-upstream
AATTAGACGTCTGTCTCTAGGGATGCCGCATCCCGCCGGCGCTCCTAGAGTCCGTTTGTA
AAACCTAGAATTCCGAATACGTTCCGAATAGGGTGGGGGT

>RXA01405
ATGAGTAAGATAGTTGATCTGCGCTATGGGACCCGGCGTTCCTCGGAGTTGAGCAAACGC
TCTGCTGAAGTCTTTGCCGAAGCTGAAGAACATCCCATTACTGTGACACGTCGTGATGGT
GAAGCGTTGGTATTGATGTCGCAGCGCGAAGCTGACGGGCGAGCCCGCCTGCTGGAGTTG
GCTGCACAGTTAATTACTGTGGCCACTGATCATCAGGGCACGTTAGCCGAACGTATGGCG
AAAGTATTCCCGTGGATGCTGGCCCTGTCAGTGGCGGATCGTGAGGCGTGTGCCCGTGAG
ATTCTTGACGCTGCACGAGCATCGTTTGCAACCGAACAACCTCACCTCGCTCTTACTGAA
CTGACCTCATGGAAAGAAACAGCAGCAGCTGTTGCTGCTGGATTGAGTAACACTGATCTG
CAGTGGTACGACGATCCGCATCTGGTGGAGCGTCCC

>RXA01405-downstream
TAAGCGTGGCTGGAAAGAAAAGC

>RXA01409
GATTTCCCCGACGTCACCGCACGTTTGGGGTATGAATACATGCAGCTGACCCCTCATGTA
GATTTCGGTCCTTTCTTCCGCCACCCCAAGGCAGACGATGATCTCGTGGCAGCCCTGAAA
AAGCGTGCCAAGGATGCCGGAGTCACCATTCCTGCACTGTTGCCAGTGCAGCGTATTTCC
TGGCCGGAGGAAACCCAGCGTGTTGCAGCAGTACGCAACATCAAGCGCATCATCCAGTTG
GCCGTTGATCTGGAAGTAGACACCCTCAACACGGAGTTTTCTGGACGCCCAGAACGCTCC
GAGGATTCCGAAGATGCCTTCTACCGCTCCATGGAAGAACTCCTGCCAATCCTGGAAAAA
GAGGGCATCAAGTTCAACATCGACCCACACCCTGATGATTTCGTGGAAAACGGTATTGAA
GCATGGCGAGTCATCCGCGGTCTGAACTCCAAGCAGGTGGGCTTTGTTTACGTGGCACCT
CACTCATTCCACATGGGTGATCAGGCTGAGGCAATCCTGCCAGCAGTAGGCGATCGCCTT

GGGGCTGTGTACCTGTCAGATACCTTCGACCACCACAAATCCCACGGCCTGCGCTACATC
ACTAACCCTCCAGGCAACGCAGTGCGCGTGCACCAGCACCTAAAAATCGGTGATGGCGAT
GTGAACTTTGAAGAGATCTTCTCACTGCTGCGCTCTACCGGTTACCTTGACCGTGAAGAT
GCACTGTTGGTCTCCAACGTGTTTGCAGAAGATGAAGCAGCAGATGAAGTATCCCGCTAC
CAGCTGGAGAAAATCCGCTCACTCATCGAAAACGCA

>RXA01409-downstream
TAGAGTTATCTCGAAACTACCAA

>RXA01413-upstream
TTTGCCCTATTGGAAGAAGTAAATTCCACACCTTCACTTTCCAATACTTCTTTTGGTGAG
CGGGTTTCCTCAGCGTTTAACCATCTGAAACCATCTGAGA

>RXA01413
TTGACCCATCTGTTCTTAGAACTCGATGAGCGTTTAGTACTGGGTGTTCAGCAAGATGGT
TACCAATGGACTGAGCATTTGTTCCGGCTGCCACTGCAACATCTCCGTAACTCGCCCAAT
GACCTGCAGGGATTGAAGATACGATGGTGTGAACTTTATTCCACAACGGGGAAAGATCAA
GGGGTAGAACTTCTGCCTCAAGCAACCGTCGTTACCCCAAATAACTTCGAGGCTTCCACC
CTCTCCGGCCTTGAGAAGCTTGAGACCGTCGAGGACCTCAAGGAGGCTGCCCGCCTCATT
TATGAGCAAGGCCCCCAGTACGTAGTCGTCAAGGGTGGCATGGACTTCCCCGGCGAGAAC
GCCGTGGATGTGCTTTTCGACGGATCCTCCTACCACGTCTTCTCTGAGCCAAAGATTGGT
GAAGAGCGCGTTTCCGGCGCAGTCTGCACCTTCGCAGCTGTTATCACCGCAGAGCTAGCA
AAGGGTGCTGAGGTTGTAGACCCAGTGGCAACCGCAAAGCGTGTGGTCACCCGTGCGGTT
CAAGATGCTGTTGCATCCAACGCACCTTTTACCTCCGTATGGCTTGCTGAGGACAACAAG

>RXA01413-downstream
TAGAGTTTTAAAATACCGATCAA

>RXA01414-upstream
TATTGCCTAAGTAGACCAATAGGTCTATGCTTCATAGAACAACTAGTTCATAAGTGATTA
GTTTTAAGAATTTATTACCTCTCTACAGGAGAACCCAGCG

>RXA01414
ATGGCCGTTTTTGATTTCCCTAACCCCGTTAACGAATATGCAGCTCGCTGCACTGCGGGT
TTGGTTGTTTTGCTGAGCGCCGCCACGCTTTTTGCCTCTGGTGACCTTCGTATTATTTTG
GCAAGCATCTTGACCTTCGGCTTCGCATTGCGCGTGGCCGGCGGACCCCGTTACTCCCCC
TTTGGACGTCTTTCAGTACACGTACTTGTACCACTGCTGAAGAAAGCACCGATCCTGACC
CCTGGCCCACCAAAGCGCTTCGCGCAGACCATCGGCCTGGGCTTTAGCGGTACTTCCCTT
ATCCTTATGGCCTTTGGATTTAACGTTGCAGCTTCCGTAGTCCTAGTCATGCTCATCGCA
GCAGCCACCTTAGAATCCGTCTTTGGTATCTGCCTCGGTTGCTGGGGATTCGGCAAGCTC
ATGCGCTACGGCGTCATCCCAGAAGACGTTTGCGAGCAGTGCTTCCAGAAGGAATCCTCC
CGCACCGGCTGGCTCGTTAGCCTGAAG

>RXA01414-downstream
TAGCACTTCGAATCTAAGACCAC

>RXA01417-upstream
AGCCTCCCCAAGGCTGGTTAGTCCCACTATCCTCTCAGAGAGAAGCAAAACTGAAATAAC
TTCAGCCTCAGCTATCCCCGCAATTTAAGGAAAATAGGAT

>RXA01417
ATGACTGACAAGTTTGACAGAGTCCTTGCTGTAGAGGTGTGCATTCAGGAGTGGATCGAC
GAGCAAAACCTCACGCTAGAGGTGCCATTAATGATTGCACGTTTGCAGCTTAGAGACGTC
GCGAAGGATATCACTGCTGTTCACGAAGAAAAATTCTACGACCTCACTGATATCGATACT
GATGCCTTTGTGAAAAACATCAAACTGGGATGGAATGAACGCTTGATCAAGAAAAGCCTC
TTTCCACAACCGGACGTGCATAAACAACATTTCACAGAAACTGAACATGGCATTGACGCG
ACTGTGACGGTCTGGTCGAAGGGCTTCGATCCGGAAAGTGGCCCCGACTTCTTGGTTTCC
TATGTGGATGGTCTTTGGTCAGCCGATATTAGAAACCGCATCACGAAATTTCAGAATAGA
GAAATCGTTAGCAAATTCTATTTTACTCCAGAACATATTAAGGAGGATGGAGATTTCTCC
GCAGAGATTTTTATTAACCGACCAGAAAATGACGACGACTCACAAGATTTGGTCGAGGTG

TGGACTGATCAAGACACCAGATACTGCGGTGAAATGATCATCTATTTCAAATGGCTC

>RXA01417-downstream
TAAATTCCACTTTTCTGCATCAG

>RXA01421-upstream
TTGATGCACGTGCAGAAATCGTCGGCGGTCCGTGGCACCCATCTGTTAAGGGAGACTCGG
TTACTGCAGGGATCCTGCGAGATCGAGTAAACGCCTAAAG

>RXA01421
ATGACGTCGAAAAGCATTAGCGGCAAGCGCCCGAATCTGCCGTCGCTCACTGGAGCGCGG
TGGCTCGCGGCGCTCGCTGTTTATTTTTTGCATGCGTTGGTGTTTTTGTCGGTGTATCCG
TTCCAGCAGTCGGAACTGTTTGCCACAATCCATAAATTTGTCCCCATGCAGCTGGGTTCA
GCTGGTGTAACCTTCTTCTTTATCTTGTCCGGATTTTTGATCTATTGGTCAAATAGCCAG
CTCAAGGGCATGAAGAATGTGCTGTATTACTGCAAGCGCCGCATCACCAAGATTTATCCC
ATGCACTTGATTGCGTTGCCGATGTTTATTGAGGCGTCGGCGAAGTTCACGACTACAGGC
ATTACCTGGGTGCTGATTTTGCGCGAG

>RXA01421-downstream
TAAAGCTGTGGCTGCGGAATGCG

>RXA01422
TTCGGTGACTCCCACACCTCTGGCACCAATGCTCCATTCCGTACCGATGAGCGTGGCTGC
CTCAAGGGTGCAAACAACTGGGCAGATCAGCTGCAGTCTCAGCTGGGACTTGGCGCGGGA
GACCTCATTGATGTCTCCTGCTCCGGTGCATCGATCAACTCTGATGGATTCCACTTCTCT
GATGAAGTCCGCCATGCTGAAGCTCGTGGCGCAATCGGCCCAAACACCACCGATATTTTT
GTTCAGTTGGGCAAGAATGATCAGTGGGGCCTTTCCAATGTGAACCTTCTGCAGTCTGTT
CAGACCTGCTTGACTGATGTGTTCGCTGGTTGTGGCGATGCTGCGGTTGCTGCTGGCAAG
ATGCAGGATCCAAATGCAGTTACTGCTGAAAACTATGCAGAGCGCATGAAGCCAGTCATT
GACTACTTGAAGTACTACGCACCAAACGCAGAGATCACCTTGGTTGGTTACCAGGAATAC
ACCGCTCGCAGCGGAAGTCAGGTATGTGTTCGCCTTGGTGGAACCCCACTGGTGAAAAAT
GATGCACCTGCGCTGGTTTCGTTCATGAACAAGTTGGACATGGCGATTGATGGTGCTGCT
GGAATCCTCGGCGTCAGCCACGTTGATCTGCGTAGCGCGACTGAAGGGCACGACAGCTGC
TCCAACGATCCTTGGGTCAACGGTGTCTTTGATGCACGTGCAGAAATCGTCGGCGGTCCG
TGGCACCCATCTGTTAAGGGAGACTCGGTTACTGCAGGGATCCTGCGAGATCGAGTAAAC
GCC

>RXA01422-downstream
TAAAGATGACGTCGAAAAGCATT

>RXA01425-upstream
AGTCCCTATTAATCCCAAGGAGTTTCGACTCACAGTGCTCAATTTCATTTATTGGCCAAT
TTCGGCCATTCTGTGGTTCTGGCATAAAGCGTTCAGCTTT

>RXA01425
GTGCTGAGCCCAGATTCCGGAATTACCTGGGCCTTGTCGATCATGTTCTTGACCTTCACC
GTGCGTATGGTTCTGGTCAAGCCGATGGTCAACACCATGCGTTCACAGCGCAAGATGCAA
GACATGGCTCCAAAGATGCAGGCCATCCGCGAGAAGTACAAAAATGACCAGCAGAAGATG
ATGGAGGAGACCCGCAAACTTCAAAAAGAAGTGGGCGTTAACCCCATCGCAGGCTGTTTG
CCAATGTTGGTGCAGATCCCAGTGTTCCTGGGTCTGTTCCACGTGCTGCGCTCCTTCAAC
CGCACCGGTTCTGGCGTTGGCCAGCTGGAAATGACCGTTGAGCAAAACGCGAACACCCCG
AACTACATCTTCGGTGTCGACGAGGTTCAGTCCTTCCTGCGTGCAGACCTGTTCGGTGCG
CCACTGTCGTCCTACATCACCATGCCTGCTGACGCGTTCGACGCGTTCCTTGGCCTGGAT
GTCTCCCGCCTCAACATCGCGCTGGTTGCAGCTCCAATGATTTTGATCATTGTCGTGGCA
ACTCACATGAACGCGCGTCTGTCCGTCAACCGCCAGGAAGCTCGCAAGGCAGCCGGCAAG
CAGCAGGCCGCTTCCAGCGATCAGATGGCCATGCAGATGCAAATGATGAACAAGATGATG
CTCTGGTTCATGCCAGCCACCATTTTGTTCACCGGCTTCATCTGGACCATCGGTCTTCTT
GTCTACATGATGTCCAACAACGTGTGGACCTTCTTCCAGCAGCGCTACATCTTCGCCAAG

ATGGACGCTGAGGAAGCAGCTGAGGAGGAGGAAAAGCGCGCAGCAAAGCGCACTACCGCT
CCAAAGCCTGGCGTGAAGCCAGAAAACCCCAAGAAGCGTAAGAAG

>RXA01425-downstream
TAAAACTTCACTAAAAACCGCCA

>RXA01429-upstream
GGTAAGAAGAAGGGCAAGCTCGTGGTGGAATTCGGCGACAAGGATGATTTCGAGCGCATC
ATGTCCTTGATCCAGGGCCAATAATTTTAAGTTTGGCGCC

>RXA01429
ATGCTCCAGGCTTCCCTTTTCCCGATCGTGCAGGAACACATAGATTTCCTGCACCCCCAG
GCCCGCAAGTCGGTGTTTTGGGAGCTCGCACCTGAGGTTGCAGCTAAAGCTGATCCGGTG
TTTGAGAAGGAAGCCTGGCTGTCCACCACGCTGCTGGAATATGAATCCTGCGGTTTCAAC
ATTGGTTACCGCAATGGAACTCCGGCGTTGGCGTCGGTCATTTTCTGCGAGCGCGATGCC
GCCCCGGGCGCGAAGGCGCTGCCTACGGCACCGGTGTCTAGCGACGCTGCGATCATCAGC
AGCCTGTTCATCGACGAGGTTTTCCGGGGCACGGGCATGGAATCGGCGCTTCTCGACGCT
TCCCTCATGGAACTCATTCGGCGCGACTACCCAGCCGTTGAGGCGTTTGGATACCGCTCG
GAAAACACAGAAGCGGATGCGATCGCAGCTAGGCGTTTAGAAATCGGCCTGATTGATGTG
GAGGCGTTAGAATCAGCCGGTTTCGAAGTGGTTGCTGACCATCCCGTGTTACCCCGTCTG
CGGATGGAATTACCACCCGCAACGGTGCTGCTCACAGCTAAGGATGCCCAGCGACTCCTT
CAAGAGATGGGCGCGATT

>RXA01429-downstream
TAGCCAGCCTGCTCTGATTGCAA

>RXA01434
GTCACCGACGGCAACACCTCCACCGCATGGACCTCCACCGGCGGCGACGGCCTCCTAGTT
GACCTGTCCACGCCTGCCCGCCTCGACCGCGTCATCTTGACCACCGGCACCGGCTCCGAC
AGCAACGTGACCTCGACCGTGAAGATCTACGCATTCAACGACGCCTCACCACACTCCCTG
TCGGAAGGCATCGAGATCGGCACCGTGGATTATTCCGGCCGCAGTCTCAGCCACAGCATC
CGCGATTCCTCCAAGCTTCCGGGTCAGGTGGAATCCGTGGTGATTCTGGTCGATGAGGTT
CGTTCCTCACAAACCTCAGACACCAATCCACAGATGCAGATCGCTGAAGTACAACTTGTT
GGTTGG

>RXA01434-downstream
TAAATTACGCGTTTGTGATTGAC

>RXA01439-upstream
GTTAATCCACAGCGCCCTGTGTGCACTCTATTAGTGAATATCCGGTGAATGCTCGTCCCT
CGACTGTCTACTTAGTAGGTTTGCAGGCTAGTCTTTTGTC

>RXA01439
ATGACCCGATACTTTGCAGTTTCCAATCTTCAGGAGCTTGGCTCCCTCGAAGTACACAAA
TTGTACAAACTTCGTGTAGATATTTTCGTCCACGAGCAGCAGACTCCGTACGCGGAGATC
GATGACACCGATGCTGCCCCAACCACCAATCACATCCTGGTTTGGGAGCGCGCCGACGCC
ACCCCAACCAACCTCATCGGCTGCGCACGCCTCGCGCCCATCACCGCCGCCGAGCTTAAG
GCGTACACCGGCAAGGGCATTTCGCTTGACGACGCCACCCCGCTCTCACAACTCGGCCGC
GTAGCGGTGGCACAGGAAGGGCGGGGCTCGGGGCTCTCAGGTGAGCTCATGCGCAACGCG
CTGCGTCTTGCATATGAGCAGTACCCCGACCGCGATGTTGTCCTGACCGCGCAGAAGCCT
TTGGTAGATTTCTACGCAGAATACGGCTTTGAGGTCTTGGGTGAGGAATACCTTGACTCG
GGTGTTCCTCACCTTCCGATGTTGCTCAAGGCTGATGAGCTTGAAAGGTTCTCAGACCTA
GACGCC

>RXA01439-downstream
TAATCCGTAGTCACTGGAACTCA

>RXA01440-upstream
TTGATGGAACCACCCTCACGCTGACCACGCCTCAGGGGAATCAGTATTGGGCAAACACAC
ACGATTTTGGAGCCGGCACACACTAATTTTAGGAGCACTG

>RXA01440
ATGAAAACCAAGTGGTTAGCGATCATTCCATTCGTGGCGCTTGCGGTGGTTGCATGCTCT
GATACGCAGCCGCCGGTTACAGAAACAGTGACAGAAACCGCCCCGCAACCTACTTCTGAA
ACGGCAGCGCAGCCACCACAACCCACGACACCTGCGGAAACGACCACGCAGCAGGCAGAA
GGTATCAACTTGACGCCTCGCTACACTCGCCAAAATGTGGGGCACTTTTCCAGTGGTTAT
CAGCCTGGACAGGTGAGTTTTTCCTCAGCTGATGGAACCATTAAATGTGAGTTTCGCCCC
ATGGAACAGGACGCACCTATCAACCGGGAGCCCTCCACCGATTGGCGGTTGAGTTTCGTG
CAGGGTGCGTGCCAATTCGACGATGGTTACGTAGTGGCGGATACAAATGTGGAAAACAGA
CCAGGTTTTGCTGAGTACACCACGGCGATTTCTCATGTCATGCCGGAAAATTACACCACG
TTGCCGCCGGGAACCTACATCGATTTACACACCATGGCTTGTTTCACCGAGTCTGCCGAT
GAAATTTCCTGCATTAAGTACGCGACCAATGAAACATTCCGCATCAGCGCGCAGGGTTTT
GAGATGCTCTCAAATGCCCAGCGCGACGCGGAACTAACCACACAAGGTGGCTTGTACCAG
GCATTTTCCAACATCGCGGAATTACGGTTCAGTGACGGCAACGCCATGTCATGTTTCTTT
GACGCGCCGGGATCGCAAGATTTCTGGTGCCAAACACTCAGCACCCCCGGCTGGGACGAC
GGCAGCAACCTCATTCATTTGACGGTCACCGGCGGAAAACTCAGCCTGATGGGCACCCAA
GTGGGCAACCCCGGCCTCGACTATTTCCGCGGCCGCCAGCTCATTGAGGCGCCAAATTCG
CTTCTCGACGCCTCCCTCTCCGTAACACTCGACGGCGATCGGGTGCGTTTCCGCACCGCG
ACCGGCGAGGAGATGTGGGTGAGTTCCAGTGACTACGGATTAGGCGTC

>RXA01440-downstream
TAGGTCTGAGAACCTTTCAAGCT

>RXA01441-upstream
TTATAACAATTAGCCGTGAGGGTATTAATCAAGGTTTCGGGAGACTAACGTTTTAGAAAC
AAGTGGACTCCAGCACACCTCGTGAGATGGCAGGTTCATC

>RXA01441
ATGGCTAGAACGACAACAGCGCACGCAGTTCTCATGGCGCTTAGTTCAGTCGGGCTTTTG
ATGCTCCAGGCCTGCTCCGAACAGGAACAAACCCCAGAACAAACGCCAGCGCCCACCCTG
ACTTCGCAGGCTCCCGAGACTCCTCAAGCCTCAACAACCTCCTCAGCAAGCTCCACAGCA
ACTCCCATAGCAACTCCCATAGCAGCCACCGAGTTGGATTATCTCCACATCGATCCAGCA
ACGTATGACATCGGTGTCCAAGACCAAGAAACTGCCGTATTTACCACTGGCGATGGGATC
ACAGCGCAGTGTTTCTTCGAGGCAACACCGGGGGAGACCAGCTATCAGATCAAGGAGTTT
GATTTCGACGAAACTGCGGGAACGTGCGCTTTTGGTGATCAACACATCAGCGTCACCACG
GATGAAAATGTCCGGGAACGCTTTGCCGAATTGAGTGAAACCGAAGAAGAATTACCAGAA
GCGCAAGCGACTCTCGATGTTGGTGAGATGGTGCATCTTGGTCACATGGGTTGTTGGGCG
CCGAGTGTATCGGAGTTTAGTTGTCTCGATTTCGCCTCCAACCAGGCGTTCACCATGAAT
GAACAGGGCTTCCATGAGCTTGATCCTGCAAAAGCCACTGAGCAGCTAATTAATTCGAGT
GGCCAGGTTCAAACGTTATCGAAAATGACGAATTTCCAGTTCACCGATGGCACCAGCATC
ACCTGTGTCAGTGAGTTGCAGGCGGAAGAGTTCTTGTGCCACAACAGTGGTCCTGGAGGC
TGGTCAACTTCAGCTGGCCCTGCCAACACCCTGTGGTGGAATCTGAACCAGGCCGACTCC
GAGTTTGAGGGTGCTCGCCCCACGAATCCAACGCAAAGCGTTTATAAATCTCAACAAATA
TTCGGTCCGGGATCGTATCTCCTCGCGAACGGTGTGAGTGCAGAATTTGATGGAACCACC
CTCACGCTGACCACGCCTCAGGGGAATCAGTATTGGGCAAACACACACGATTTTGGAGCC
GGCACACAC

>RXA01441-downstream
TAATTTTAGGAGCACTGATGAAA

>RXA01445-upstream
GAGTCTCGAATGTATAACGAGTTTGTTCCTAATAACTTTATCATTAACTATGCCTGCAAT
AGGCTTGGGAAATTTTGGCATCCAGGTAATCGCGCTGTCA

>RXA01445
ATGATCCCACTTATTAATGTACGTTTTCCCGTTGCCGCCTTACCTCTCGCATTAGTGGCG

ACTGTATGGCTTAATGCTTGGGCAGACCATCTTCTCCTAACTGGTTTTATTGTTTATCTT
GCTGTGGAATACGCAACAAGCCGTGGGCGCTTCGCTCTCGCATTGATTTTGGGAGTTGAA
TGGATCTTAATTGCTTATGGGGTAGCTTTGGAAAGGCCTCTTGAGGCTAAAGACTCTCCA
TCTCTCATTACCGAAATTTTGCTCATACTTGTAGCAGCTGGCACAGGGGCAGGTCGGTGG
AAAATTTTGAGTGAACGCAAGCAACGTGCAATTACTCAGCAGGAAATCATCAAAAAAATC
CGTACTGATATAGCGCACTATTTGCATGACAGTATGGCAAGATCGTTGGCAATAATGATA
GTTCAATCAAAGCTGACTGAACTAGAGCCTGATCCAAAAAAGATTCAAGAAAAACTAAAC
AGTATTGCCAAAATTGGACAAGAGGCAGTGGCTGATTTGCATCAATTAGTTAGACACCTC
GTGGTCGAGGAGTCTGCTGAAAAAGCCACAGCGTTTGGAGCATGGGCTGCAGTTTCTATT
CATGACACGGTTAATTCTGCCATTCAGTTATTAGTAGATGCAGGACATGTCGTTTCCTTT
GACAGTAGAAAAAAGAACTATAAGCTGGACCATATTGCTGAAACGGCGTTTGCTTTAGCC
TTCAATGAGGCAGTCTGTAATGCAATTAAACATTCTCCGCCCAAGGCAAACGTTACTATT
CGCATAACAGAAAAAGCACAGTCTCTTCAGATTCTAGTAATGAATCCTATTGGAGATTGG
CATGCAAATGGGGAGTCCGCAATTCCAGGTGTGGGCATTGGCGTAGAAAGCTTAACCAGA
AGGATACGTAATATTAAAGGACAGGTCTGTGTGACTTCACTGCAAGGATACTGGAAAGTA
GTTATTTCACTACCTTTGAAATGTGAGGATTCT

>RXA01445-downstream
TAAATTGTCTCTATTTGTTGAAC

>RXA01447-upstream
TCCATGAAGTTGGAGTATGCACGCGTGTGCGCACACAGACGTTATTTCATCTTACTATCC
CATGTGAGGTTTTTAATCATCGCGATACTAAGCTTGCGGT

>RXA01447
ATGCGTCTTCTGGTTTTGCGGTGCGATGCCCCACACATCAACGAATTCCCTGCCCTTTCC
ACCTCTGTGGAGATCCACGATTTGCCTGCGGTGCCCACCCGAAAAGACCTCAAAATTCTT
GATGATGTGGCCTTTGATGTGCTCCCTCAGGATCCCACGCCTTCTCTCGATGAGATCGCC
AAGCAGCCTGATGTCGAGCATTTGAGCAGCCCTAAGTTTGCGCCACAACAGCCTGAAACC
CGTTTGCGCATCGTGGTGATCGGTTCGGATGCAGCGCTGTCTGCGGTCCTGACTCGTCTC
ATGCGCGCCGATAATTTGTGGGCGGAGATTGGATTCGTGCCCGTTGGTCCTTCAACGGCT
GCGAAGAACTGGGGTCTGCCCGCCGATGAGGCTGCCGCGCTTGAGCTCGCACTGACCGGA
TTGGTCAATCCTGCCCCGCTCATCCGCGATGACGTTGCGGTCGCCGTCGCCGGTTCAGCC
ACCATCACCAACTGGGAGCCGGGTGAGATCACCGGCGAAGTCATCGTCGATGATCATGTT
CTCATCCGCCACGAGGCTGCCTCGAAGGCCCCACGCCGTGGCGTCTACGGTGCCCGCTTG
GTGCCGATGCTTGACGCCCCAGGCATCGCTGCGGTCATCATGGACACTCCCCTGCCCGGC
GAGGTGCCCTCCCGCAGCCTGTTCCCTCGCCCCTCGGGCTCGGTTATTCCAGAGAGCTTT
TCGACGGGCCGTGCCATGCAAGCCGGCGGCCCCTCGCTACAAATCCGGGTTGACGGAATT
TCCCGCAAACGTAAAGTGGAGCGCGTTACCTTCTATCGACATTTGCGCGATCTCCAAATC
GTGCGGCCG

>RXA01447-downstream
TAAAACAAGGAGCCAGCATGGCA

>RXA01448-upstream
GCCTCGTTTGTTTCACCGGCACCGTTGGTGAGTAATCAG

>RXA01448
ATGGCCATTGGTGGCATTTTGATTGCCACGATGTTCCCGCCAGGTGATGGTGGAAGCATT
GACCGTATGATCGACGCCTTCATTGGTGGTGGCGTGGGAATTTTGGTCATCGCACTTCTT
CCCTCATCTCCTCTTGACGCAGGCCGGCATCAAGTGGCCAACGTTTTGGGGATCGCAGCT
AGTGTGCTGGAAGACGTGGCAGCTTCCCTAAAAGCCAAGGATGCAGCCAAACTCAACAAT
GCTTTGGAAGCATTGAGAAGGTCGCAGGCGTCGGTGAACAAGCTGGAAACTGCGGCATCT
TCAGGCAAGGAAGCAACCACCGTATCGCCATTTTTATGGGGAGATAGGGCCCGCGTGAGA
TCGCTGTATCGCATTCTGGCGCCAGTGGACAACGTCATCCGAAATGCTCGAGTCCTTGCG
CGACGGGCAGTGGTGCTGACCGAAGACAATGACACCGTCAGTGATGAACAAATCCACGTG
ATTGAGGAAATCGCAGACATTGCACTGCGACTGTCAGACCTTTATGAGCACCACAAAGAA
ATCAGTGAAGCACTGGAAATTCCTGAGTTGGTTAACCGACTGCGTCAACTGGGCAGTGAA
GTGGGCGAGGACATCGCCGAAGATCGAGTGCTATCCGCACAAGTAATTTTGGCGCAATCG

CGATCCATCATTGTGGACCTGTTGCAGATCTGCGGCATGTCCAGGGAATCTGCGGTGGCA
GTGTTGGTTCCGACCTCAGAGAGTCCGGCTTACCCTCCGGAGCTGTGGGATGACGAAGAC

>RXA01448-downstream
TAGCCTTTTATCGCGGTTCGGTT

>RXA01452-upstream
CCGCCAAGAAGGTAAGGACTACGTGATGGTCGATGGCGACGTTGTGGAGTTCCGGTTTAA
CGTCTAGCGTTATTGACGCTCCTCGTTATACGCTGGTCTC

>RXA01452
GTGATCAGATCGTTCGCCGACCGCGACACCGAGTTGGTCTGGTTGCGTGAAGGTGCGAAA
CGCGTCGATCCGCGAATACACAAAGTGGCGAATCGGAAGCTGCATCTGCTGGACGCGGCG
ACGACCCTCGATGCTCTGCGTGTGACTCCGGGGAATCGCCTGGAAACGCTCGAGGGTGAT
CGAGTCGGTCAGTACAGCATTCGAGTCAACGACCAGTGGCGGATCTGCTTCCGTTGGAAC
GACTCGGGCCCCGAAAACGTCGAGATCGTGGATTATCAC

>RXA01452-downstream
TGAGGAGGAGACGATGGCTCAGA

>RXA01456-upstream
AAGACAATATCCTTATATGTACGTGATTATGCGTTTCTCCCCCACTCTACGGTTTAATCA
CCTATAAAGGCCAACAAGTAGTTCACAAAAGGAAAAAATT

>RXA01456
ATGAACGATTCCATTTTTAGTCCCCAAGCACTGAATAAAGCGATGCTCGAAGCCGTCGAG
TTTATCCACGCCGAAGGTTGGGACGCCGGCCCTACCCTGTTCGCATTGGTCCCCACTGAA
ATGCTGGTGGATACTCTTGATGAGGCAGCTGACGACTCCCCACTAACCCTTGTTGTACAG
GACAACCTCCCTGACAACTTGCTGCCAGGTTCCGAAGCGTTAGGTGACTATGTGTCCCGT
TTGGCGTGGCCAGCAGAGATTGCCGGCGCGGTGTTGGCTCAGGAAATTATGTTCACCGAT
GCTGCCGTTGCAGGCTCAGAACCACGACCCGCTCGTCTTTTTTCCGGCGTTTTGCGCGGC
GAAGCAGAACTCACCCTTCTGCAGCTTCGCCCCACCGAAGAGGAATTGGCAGAACGCGGA
CCGTTTGCTGAAGATGAAATCGAACTGCGCGGCGGCCCAGGGGTTGCACCGGGTGTAATC
GCAGCACTGCGCTACACCCTCGAAGCGGACCCAGACGAAATC

>RXA01456-downstream
TAAAAACTGACTTTTCGTCCAGG

>RXA01457-upstream
GAAGCGGACCCAGACGAAATCTAAAAACTGACTTTTCGTCCAGGTTCGCTAGGATAAATT
AAGTTAACCCCGCCCACAATTTATTTGAGGAGTTCACACT

>RXA01457
GTGGCGTCCACCCCGCACAAGCATGTCCGCGTTGCACTGGGATTAGTGGCGCTCATTCCT
CTTTTAGCTGCATGTACGGGCGGCGGATCCACCGAAACTTCCACTGAATCCACGGCAGAA
ACAACTCCTGCGACAACAACGGAAGCAACGACAACTCCTGCTACCACTGCTTCGTCTTCA
GTAATTGAAACGACAGAGTCAAGCACTGCCGAAACGTCGACGAAAGAGAGTGGGGAGACG
TCGACAAGCAAACCTCGTATGACCAAGGACGTTGAAGTCGCCTATAAAGCTTTCTCCTCG
CTCGCGCCCGTCGAGCTTTTTGAGCAATTCGAAACCTGCGACCCGTCAGGGGTCGAGGAT
TCCTTCGCGTGCAACGGGCCGGAAGTTGGCCAATTCCAATTCTTTGACAATGCGTCGAAG
GCCACGAGCACGACGCAGCTGCTCACGGAACTGCGCAGCTCACGCGTGGTTGAGGATTCC
GGATCCAAGGTTGTGGGCTGGACCACGATTGGCACGATGTCGATTATCACGGTCGTTGAT
AATGACCAAGGCCTAGTGCTGCAGCAAATGGTGTCCTCCGACAAAATCGATCCGGAGGAA
CGCATCTACGAACTTGGGCTGTCGACACCGAAGGACACTGAAGAGTCCTCGGAAGAAACC
TCAGCGTCTAAAAAC

>RXA01457-downstream
TAGCCACACGTCTGGAAATCAGA

>RXA01459-upstream
GATTCGGCGATTCACGAATATCCACCCTACAACCTGTGTTCGCTTACAGCGTTGTTCGGA
TCGTAGCAATAGGAAATAGTTGCCTTGTAGATTGGTAAAT

>RXA01459
ATGAACTCTAATGGCTTTGGTTTCTCTTTTGGCAACAACGATGACGACGATGACAAAAAC
CGCAACAACGACCCATTCGGCCTTTTCGGTGGCAACTTCGGATTCGGAGGACAAGGTGGC
GCTGGTGGCCCCGGCGGATTAGGCGATATTTTAAACCAGTTCGGCCAGATGCTGTCCGGA
ATGGGAGATTCGATGAACTCCCCCGAAGCAGCAGGCCCGGTTAATTATGATTTAGCAGCA
CGCATCGCCCGCCAGCAGATTGGTCGCGTAGCGCCGGTGAAGGATTCTGAGAAGGAAGCA
GTCGAAGAGTCCCTTCGCCTTGCTGAACTCTGGCTCGATAACGCCACCCAGCTCCCCACT
TCCGGGCACCGCGTCGAAGCGTGGAATCCAGAAAACTGGTTAGAAAACACCCTGCCTGTG
TGGAAGCGTCTTGTCTCCCCTGTTGCGGAGCAAATGAACAAAGCCCAATTAGAAAACCTC
CCTGAAGAAGCCCGCGAGATGATGGGCCCGATGTCTTCTTTGATGAACTCCATGTCTTCG
ATGAACTTCGGAGTTCAATTAGGAAATGCGCTGGGCGACCTCGCAAAGCAGACCCTCACC
GGCTCTGACTTCGGTTTGCCTATCTCCCCAGTCGGCGTATCTGCCGTCCTGCCCGGCAAC
ATCGCCGAAGCATCCAAAGGCCTCAACGTGGCACCGCAAGAAATGCTCGTTTACATCTGT
GCCCGCGAAGCCGCCGCCAACGCCTCTTCAAGCACGTGCCGTGGCTTGTCGAGCGCCTCG
TTTCCTCCGTTGAGGAATACGCCGTCGGCC

>RXA01459-downstream
TAGAAATCGACACCTCACACATT

>RXA01460-upstream
GCAACATCGCCGAAGCATCCAAAGGCCTCAACGTGGCACCGCAAGAAATGCTCGTTTACA
TCTGTGCCCGCGAAGCCGCCGCCAACGCCTCTTCAAGCAC

>RXA01460
GTGCCGTGGCTTGTCGAGCGCCTCGTTTCCTCCGTTGAGGAATACGCCGTCGGCCTAGAA
ATCGACACCTCACACATTCAAGAGGCCATGGGCAACTTCCAAATGGACAACCCAGATCCT
GAACGCCTCCAGGAAATGATGAACGAACTCCAAGGTATGGACCTGTCCCCACGCATCGGA
TCCCGCAACGCCAACGCAGTATCCCGCCTGGAAACTCTCCTCGCACTCGTCGAAGGCTGG
GTCGACATCGTAGTTACCCAAGCCCTGAGCGAACGCATTCCATCACCGACGCCA

>RXA01460-downstream
TGAACGAAGCCTGGAAGCGCCGC

>RXA01463-upstream
ATTAGAACAAATATTCGTTAGAACACTTGTTTGTTTTGATTTGTGTGGTTAGGGTGGGTG
CTAATGAGTTAAAAAGGGGAAATTTAAACCATTAGGGGGC

>RXA01463
ATGGAAATGTCATACTTCAGCCATCAGGACCCAAATAATCCAGAGAGTCACATCAACTTC
ACCATGGCGCAAATGGAGATCCAGCGCTGGACTTTGCTGATCTCAAACCCAGAGGCGGAC
GCTAGCACTCTTGTCATGGAGTTGAAAACCGTCACGGGGGAATCCAAGCATTTTATCAAC
CAGGCTATTAACGCCATGTGGGCTTTAATGAAGCTGCCCATTTTAAGAGTGGTGGTAGAA
ACTCACTTCCACGTTCGGATTCCGTACCTGGCCCGCATTATGCAGGCAGTCAAGCAGGCT
AAACCGGAGTTGTGGGATGAGTTGGACCATCGCATTGCCGAAAAGCTGACACCGCGCATT
GCTGGCCAGGCACTGATGGAAGCCTCCGCACTTGCAGGGCTGATTACTCGCTGGATCAAG
GAACTGGATCCAACCTTCACAGGAAAGAAGCGTGGGCCAAAGGGGAGTGATGGCACCTTG
ACTTTCCGCCACGTGGACGGGCGTACGTACATCAGTGGAAATATTGACGGTGTCACCGGC
AAGCTGTTCCAAAAAGCTCTGGAAAAAGTGAAACAGAAGGGCGAGGACCTCGCGCGGGCC
CTGGTCACCTTCCTGGCGGGGCGGACCAAAGTGAAAATCGTCAGCGCGGTATACACGCCC
CTGGTGGGTGGCGTGTCCTGGATTCCGGGGGTGGGATTCCTGAGTCAAGAGGAGTCCCGG
AAGCTGGGTAAGACTGCCTCGAAGGTCATTGACCTGGATACGATCGCCACTCGTGTGGAA
AATGGCTACACCCCAAGTCCCGAGCTACGCCTTTATGTGATGGGGCGGGACGGCACCTGT
AGGCATCCGGGCTGCACGGTGTCTGCCGACAACTGCCAGATCGATCACGTGATCCCGTTC

GGTGAGGGTGGGTTGACTGTGGCCTGGAACTTGCAGTGCCTCTGCGCGCATCATCACAAT
ATGAAGACTGATGGGCGCATCCAGGCGGCGATTGATTCCATGGGTCGGGTCGCCTGGATT
GGGCCGTGCAATCGCACAGTGGTAACCGAACCTGTCGGACCGTTGGCGCAAGAGATGCCC
ACGGGGCAGTGGGGGCAGACTCTGGAAGCACGGATGGAGAAGACTTTTGAAAAGCTCCGC
AGTTCACTCGAGGTATTGGATGAC

>RXA01463-downstream
TAAACCCTTATGCACACCCCTAG

>RXA01469-upstream
TCCATCGCCGATCTTGCCGATTGCTGGGACGATCCTTTCGGTGACGGTGCATTTCACGTA
CCAGATGAGCAGCAGTTCACTGACTAGTATTCTGTAGGTC

>RXA01469
ATGGCATTTGCAGACATTGTGCGCAGCGTCGAAAACCGCACCAACGCAGCGACCCTCAAC
TGGTCCATCAAAAATGGCTGGAAGCCCGAAGTCACCGGATTTTCCGGGTACGGCTCCGGG
CGTCGAGTGCGCGTCCTTGCGCGCGTGCTCATGTCCAACCCCGAAAATTTGCTTGTCGAC
GCCCCCTCCCAATCAATTACCCAACAAGCACAGCGCGGTTGGCGCCAGTTCTTCACCATC
CAAGTGCCCAACCTGCCAGTAACTGTCACCGTTGGTGGGAAAACAGTTACCTCATCCACC
AACGACAACGGCTACGTTGACCTCCTGGTGGAAGACCACAACCTTGACCCCGGCTGGCAC
ACCATCCAGATCCAAGCCGAAGGTTCCACCCCCGCCGAAGCCCGCGTCCTCATCGTGGAA
AACACCGCCCGAATCGGACTCATCTCCGACATCGACGACACCATCATGGTCACCTGGCTT
CCCCGAGCACTCCTCGCCGCATGGAACTCGTGGGTTTTGCACACCAACACCCGCAAACCA
GTCCCCGGAATGAACCGCTTCTACGAAGAACTCCTCAAAGACCACCCCGACGCACCCGTG
TTCTACCTCTCCACCGGCGCATGGAACACCTTTGAAACCCTCCAAGAGTTCATCAACAAA
CACGCACTCCCCGACGGCCCCATGCTGCTCACCGACTGGGGACCAACCCCCACAGGACTA
TTCCGCTCAGGTCAAGAGCACAAGAAAGTCCAACTGCGCAACCTGTTTATCGAATACCCC
GACATGAAATGGATCCTCGTCGGCGACGATGGCCAACACGATCCCCTCATCTACGGCGAA
GCAGTCGAAGAACACCCCAACCGCATCGCAGGCGTTGCAATCCGTGAGCTCTCCCCCGGC
GAACATGTGCTCTCCCACGGAACAACTGCGTCACTGTCCACCATCACGACCAACGGGGGC
CAAGGAGTCCCAGTAGTTCACGGCCGCGATGGATATGAGTTGCTGCAGCGCTACGAGACG
AAGCCGTTCGCC

>RXA01469-downstream
TGAGTCCTACTGGGTGTCTCATG

>RXA01470-upstream
AAGACGAACCTCGTCTTACTTCCTTTAGTAACTGCACATATCTACTTGTATATGTGTGCG
GGAATTGAAGGCAGTTAAGTGTTGCCGAAGGAAACCGAAC

>RXA01470
ATGACGAACAATGCATTAACCGTGCCAACCCGGACCCGTCATCAGGCGGATTTGCTCACG
GCAGACTTCTGGGAAGACATGGGGTTGCCCCAACTGAAAACTACCATCGAAGAATCCATC
GACGATGTAGCCCTCCCAATGCATACCGCTGTTCTAGAAATCAGCGGAATGCCAAAGGAA
CTGCGTCAGACCGTGGAATCCGCAATGGTTGTGTGTATTCCGAGTCCTTCGGAGCTGTCC
GGCTCCAACAGGGACCCGCTCACCGCACGATGGTTCACTGCATGGCGCCGTGACCCATTC
GAACTTGGCCTCACTGAGTGTCGAGAGGTGATCACCGGAACTCCACGCGAACTCGACAAA
CTTCGAGGAGTGCTGGAATCTCTGGCTGATGAATACCGTTTTGAAGTTGAGCTGCGAATC
GTTGAC

>RXA01470-downstream
TAGAAAGCCAGTGATTCTTTAGC

>RXA01471-upstream
CCTCCAACCAGAGCTATAAAAAAGGTTGTAGAAGAAATTTCTTAACATACATCGTTGTGT
TGCCAGGGGTTTAACAGATTAGTTGCTAAGGTCTGTCTCC

>RXA01471

ATGCAGAGTTTTAAGACGCTTGAATCTTGGCCTGTCGACAATGTTTCGGCCAGTGTCATC
TCCGACGGCGCCGTGCACTTTTACGGCGACGTCGATCGTGTTTTTGAACTCATGAGTGTG
ACAAAACTCCTGGCCACCTACGGTTTCCTTGTTGCCATCGAAGAAGGTGTTTTTGAGCTC
GATTCACCGATGGGTCCTGAAGGATCCACAGTGAGGCATCTGCTCTCACATGCTTCCGGC
GTGGCATTCGATAAGCCGGTAGCGGAAAAGGGAGTGGGGGAGCGCCGCATTTACTCCTCT
GCTGGCATGGACATCTTGGCGGATGCTGTTGCCGCTGAAGCTGAAATGCCGTTTGCAGAG
TATCTCCGCGAGGCTGTGTTCGAGCCTTTGGGAATGGAGAACTCTGAACTATGGGGTTCT
GCGGGCCACGAGGCGCGCAGCACAGTGGCTGATCTGACCAAGTTCGGCCAAGAGCTCACC
GCACCAACTCTGATCTCACCAGAAACCCTTGCAGAGGCTTTCCAGGTGCAATTCCCGGAA
CTGATTGGCACCGTCCCCGGTTATGGCATGCAGAAGCCGTGTCCGTGGGGATTGGGCTTT
GAAATTAAGGGACAGAAGTCGCCGCACTGGACAGGTGACTTGATGCCGGAGAACACTGCT
GGACACTTTGGACAGTCGGGAACATTCTTTTGGACTGTTCCAGGCTCAGGTCAAGTCGGG
GTTGTTTTGACTGACCGAAATTTCGGTCCTTGGGCTAAACCGTTGTGGACTGCCTTCAAT
GACGAAGTCTGGGCCGAGTTAAATTCA

>RXA01471-downstream
TAAACTTTTGCCGTAATTACGGT

>RXA01472-upstream
GCACGTCCACGCGCCGGACTTGCGCGCCTATTTACAAGCACGCTTATCGACGTAATTACA
CTCGGTGGAAACCGTCGCGGAAAAATGGAGGATCCTCGCC

>RXA01472
ATGAACCAAGCAAACCTGCCTGCCGAAATCGCGGACCTCTCCGATGAAACCGCACTGTGG
GAAATCATCAACGAATACAACTGGGACGACGGCTTCGCGGTTCCCCTTGCAGTAGTCCGA
CACCCCAAATGCGACCGAGCGCTAGCCCTTCGCCTGTTTTGGGACATCGATGAAACCGCC
CAAATCCACCACTCCGACGAAGAATCAGCGATCGCCGAGTTGTACGCCAGCACCGCAGAA
AACGACCCAGCAGAATTCGACAGAATCATGGACTACTGCACCACACTGGTCGAAGGGCTC
CGCAAGCAGACCTATCCTCGGGGCGCCAACCGTTTCGACACGGGATTTTTCAACCTCGAG
GACCCTTCTTTGACCGACCGTCAGCGCAAAATCCGCGCCGGGAAAACCAAATTTGCGCTC
AAGAATTTCGAGGAAGCTTTCCTCCAACCAGAGCTA

>RXA01472-downstream
TAAAAAAGGTTGTAGAAGAAATT

>RXA01473-upstream
CGTAAGCAATTCCCACCAATGCAGTTTCCTCGGTGCGTTATAGTGTCGAGTAGGGCCAAA
AACCAACAATATCCTGGTAGCCAAGAATAAGATCGTGCTT

>RXA01473
ATGACTGACATCGGTGATGTCGATCAAATAGTCTGGGAATTCATCCATTTCCACGATGAC
TCGATAAATCCATTCTTTGAGTTCATCAAGAGTGATTGCATCAACGATGAGGCAATCGAA
CGCAAAACCCAGATCCTCGGAATCATCTTGGGTAACGAGCCATGCGGGAGTGTTATTCAC
GCCCGCCAGAATACAATAAAGCCCATGAGCCATACGGTCTCTTTTGGCGACGGCTGGATC
CAAGTCCTTGAGGATGCTGCAGAAACCGTGTCGATCACCGACACGTTGGATGCCCTCCGA
TTTTCTCCCGAGCAAGCGGAATGGGCTGCAGAATTCGGACCACTACTGTGCGGCCCAGCG
AACCAACCGCCGGCGTATCTCACGGCTTTAGACGGGCACACAAAGCTACCGCTTAGCCCG
CAGCTGACGGAGTTCTATAGCTACGCCCGATCCTGGACAAACAGTGAGGCCTTGGGAAAC
GTCATTGATCCCGATGACTACCTCGATCATCTCACCGACCCTCGCCTTCATTTGCAGGAT
CTTCTGGATAATGAGTTTGAACGGGTGGGGGTGCTCGTCGATAAGCAAAATCGCCCGCTC
GACCCTGCCCGGTGCGCGCTGTTCTCGCTCGACGCACTTGCACGCGCGCCCTACAACCGC
GCCTACTTCGTCTTCGCCGCGCCCGAGCCTGAGATCTGGGCGTTTGAGAACGAGCACGTC
CACGCGCCGGACTTGCGCGCCTATTTACAAGCACGCTTATCGACG

>RXA01473-downstream
TAATTACACTCGGTGGAAACCGT

>RXA01474-upstream

CATCACCGATGTCAGTCATAAGCACGATCTTATTCTTGGCTACCAGGATATTGTTGGTTT
TTGGCCCTACTCGACACTATAACGCACCGAGGAAACTGCA

>RXA01474
TTGGTGGGAATTGCTTACGCCCGTTTCCCTGATACCCGCGACGATTCCATCAGCCGCGGC
AAAGCACGATCAGCGTTGGAGAAATCCACGGGCCTTAAAGAGCGTTTCGCGCGTCATTTT
CCTGCAATTTCCATACCTGTCGATACGGGTGATGCTGCAGATATTCTCGTATCGGGTTGG
TGGCTTTCAGGTTCTAAAAAGAAGATCCTGACTGCAGCGGAAATCCAGACCTTATTTATC
AACCGATTGGCCACAGGTCCATTGAGCACTCAATTGGAAACTGCTACCGGGTTGAAACTG
CAGGTGGTGACCAATCGAGAGCGTATGAAGATCACTCTCATTGAACCCAAAGGCACATCA
GGACATGCCATCGACCCCCAAGCTGGCAAGGGTTCAAGGGGTGGCTTCCTCCTGGACAAT
GGCCAAGAAGATGAATACGACGATGTCGACACCGTCACAATCCCCGATGCACTCAATGTC
ATCGGTTACATTCTTACCCATGGAACTCCACCTCAAGAAGGCTGGAAGGTAGACGTGTTG
GAGCGT

>RXA01474-downstream
TAGTCCTCGATGAATTCTTCTCC

>RXA01475-upstream
TGGATCTCAATGTAGTCGCAATACGGCTTTTATTCGTCAGGCAGTTCTGCGAATAGTATT
CGTGCACATTGGATTCACACCCGTAGTAGTTTTTGGGGGA

>RXA01475
ATGAGCATCCAAGGGTTTTCCGCAGGTGACTATTCTGCATGTTTTGAACCGCGCATCGAT
GCGTGGGTTGATATTCGCGGTCCGCGGAAGCCCGAGTGGTTGGCGGAAAATATCGATAAT
CCGCTGAGACACTGGGGCGATAATCCTCATATCCCGGTGTCTGCTGCGAAAAAGGCTGGA
AATATTTACAAAGAGACCCTTCGAACCATGAGAGCCTCAACAAAGACCCCAGACCAGGAT
CCCTTAAAAGAAACCCTGCGCAGCTTCATCGCAAGCATCAACCAGCTCGCCGCAAAGAAG
AATTTCATTGATGCCGGGGTGCGCGAAGATATCGTTGTTGCGCTGGAAAAACTATGCGAA
GCAGCAGAAGCTAGCCCAGAAGAAATTCAGCAGGCGATCGTGATGGGAGAAGAATTCATC
GAGGAC

>RXA01475-downstream
TAACGCTCCAACACGTCTACCTT

>RXA01476-upstream
ATCCAAGAAATTTCGCACCTCAGGAGTAGCGATACTTCGTAAATTTGGGAAGAAGGAGTA
GCCACATGACGTTGATCGACCTCACTGCTGGAGTGAGCGC

>RXA01476
ATGAGCGATTCACCGTGCACCGTCGTCATCCTGAACCGCACAGCTACTGCGACTTCCATC
CTGAGAGATATTAAAGCCCTCACCGGTTACGGCCTGTCTGAGATCAGGTCGCGCATCGTT
GCGGGACTTCCCGTCGTGATCGAGGAGATGTTCTCAAACGCCTGGTACGACGAACGCGCA
CAACTGTTGCTGGCACTGCTGACCAAATGGCAGAACGAAGGAATCACATTCGAGATTCGG
GAAGTCGCTGAGGATGATCCCATCGAAGCAGGGGCATTGATCTCTCTAGAAGTGCTGCGA
AACATCATTGAGCCAGACGATAATGAATCGAGGGACGGTATC

>RXA01476-downstream
TAGTGGTGAACGTAAACCCCCGG

>RXA01479-upstream
GCCATAAATTTCGAAGAAGCGCGAAACAGGTAGAGTCTAAGGTGTCATTCTTGGTACAAG
TTTTATATTTAGGGAGAGTTATCCACACATGATCCAGTTA

>RXA01479
GTGATAGGCGCTGCAGCAGGCTACGTGCTTGGCACAAAGGCCGGCCGCAAGCGTTACCAC
CAGATCAAAAAGGGATATGAGGCAGCGATTAACTCCCCTGCCACCAAATCTGCAGTAAAC
GCCGCCCGCAAAGCCATTGCCAACAAGCTGGATCCGCAGCCCCGCATGAAGGAAGTAAAA

AACCTGCGGACTGCGGACGGGCATGAAGTCCTCGAGCAAGACCAGGAC

>RXA01479-downstream
TAAATTACCCTCTAAACGCCCGG

>RXA01484-upstream
GAGTTTACTCTTAACCGCAGTAGTGCAGCCAGCCCTGAGGGTGGTGGCGTATTCGATGCT
CAGAACGCCTAATAATCGGCACAAAATTGATTCAATTTTG

>RXA01484
GTGTTGGGCACAGCTCAATATGATGGAGTTCCATCGAGGCAGTTTGCTGCTCGTTTGAGG
CATGCCGCGAAGCTGTGGCGTCTTCATGAAATCCAGCATGTATATACTGTCGGCGGAAAA
CTTCCTGGCGATCGTTTCACCGAAGCAGAAGTCGCGCGGGAGTATTTGATCAAAGAGGGC
GTGGATCCGGATCTGATTTTTGTCTCTGCAGTTGGCAATGACACTGTCTCCTCCTATGAG
GCGCTTGATCCGGAAAAGCTTGGTCGGGTGCTGATTGTTACTGATCCGAACCATTCGTAT
CGGGCGGTGCGCATCGCGCGACGCATGGGCTTTGACGCGAAACCTTCCCCGACAACCTAT
AGTCCCGCGAAGTTTCCGTCGATAGTTTATTTTCTGACCTTGTCCCATGAGTGGGGCGGG
GTAGTAGTACAGGACGTGTCGCGGCTCTTGGGTGAACGGGTGCCCGATAAGGTGAAGCAT
CTTTGCGCGCAATCCAAGGTCTGCTGCGCCCTTCGCGGCGTGCACGCCATGAGCAACTTC
GGAGGC

>RXA01484-downstream
TGAAAAAGTAGATGTACCCCTAT

>RXA01485-upstream
CTCAGGGCTGGCTGCACTACTGCGGTTAAGAGTAAACTCTTGGCTAAAAATCTTCTCACG
TTAACTAGTGTGCCAGCTGGACTCGTCTAAGGTGGGGACC

>RXA01485
ATGAACTTTAGTTTGGTGCATCTTCGGGAAAACGTCCGCCGTGTATCGGTCACTGTGGCA
ATTGGAGCTGGCGCGCTCCTTATCAGTGGACCATTTTTTACTGCTCACACTGCAGAAGCC
ACAGAAACATATGTCTTGGCTGAATCACCAGAATTTTACCAAGACAATGTCACTGACTAC
ACCGGCCAGATTTCCTCGTCCGATATCACCAACATTCAGGCTGCCATCGATGATGTAAAG
GCATCTGAACAAAAGGTTATTTTCGTTGTTTTCCTAAGCTCTTTCGACGGAGTTGACCCT
GAAACGTGGACGCAGCAAGCACTCCAAGCCAACGGCGGCGGAAACGTCTTGATTTATGCA
CTCGCTCCCGAGGAACGGCAGTACGGCATCCAAGGTGGTACTCAATGGACCGACGCTGAA
CTCGACGCCGCCAACAACGCTGCTTTCCAGGCACTTTCCCAAGAAGATTGGGCAGGCTCT
GCACTAGCGCTGGCAGAATCAGTTGGTTCTAGTTCTTCCAGCTCTTCGGGCTCGTCCAGC
TCTTCCGATTTTTCCGGCGCTTGGTTGGCTGCTGCGGGCGTTGGCACAGTGGCCGCTGGT
GGCGGAATTTGGGCCTATTCCCGCAGCCGCAAGAAGAAAACAAGTGCTGCAACCTTGGAA
GATGCACGCGAAATCGACCCGCGCGATACCAACCGCCTCATGCAGCTTCCCATGGAAACT
CTCGAACACCTTGCCCAAGAAGAGCTCACCTCCACTGATGACTCCATCCGTCGCGGAAAA
GAAGAGCTCGCTATCGCTACCTCCGAGTTCGGACCAGAGCGCACCCGCAGCTTCAACCGC
GCCATGAACCACTCCACCGGCACCCTGCAAAAAGCCTTTGAGATTCAGCAGCGCCTCAAC
GATTCTATCCCAGAATCCGAAGCCGAACGTCAATCCATGCTGGTAGAAATCATTTCATCC
TGTGGCCAAGCCGACGATGCCCTCGACGCCGAAGCCCAAAACTTTGCCGATATGCGCAAC
CTGCTGATCAACGCGGGCAGCAAATTGGATGCTCTCACCCAAAAATCCGTCGACCTGCGC
ACCCGCCTCCCCAAGGCCCAAGAAACACTCGCTGGCCTGCGCACTCGCTACTCAGCAGAG
GTCCTTGAAAGCATCGACGACAACGTCGACCTCGCCAGCGCTTCGCTCGACGAAGCAGAA
GAAGTCCTGCCACAGGCGTACGAGATAGAGTCCATGCCCGCAGGCGAGCAGGGCGGGCTT
ATCGACGCGATCCGTCACATCGAGCACGCCATCACTACCGCAGACAAACTCCTCGCGGGC
GTCGAGCATGCCGATGAAAACATCTCCACAGCCAAAGCAAACGTTGCCGATCTGATCCAA
GAAATCTCAGACGAAATCAACGAAGCCGGCCAACTCAAACAAAGCGCAGGAGCCGACGGT
GCCCGTGCCGACTGGGCCTCCCTCGACGATGCTGTCCGCGCAGCCAGCGCAGCACTAATC
ACCGCATCAGCAGACGCCGAAAAGGATCCGCTCGGAACCTACACAGAACTTGTCGATGTC
GACTCCGCCCTCGACACTCAACTTGACACACTTCGCGCCACCGCAGCTGATCAAGCCCGC
CAGCTACGCGTATTCGACCAACAGCTGCAATCTGCAAGAAGCCAAATCCAAAAGGCCGAA

GACCTCATCTCCACCCGCGGTCGCATCGTAAAATCCGAAGCCCGCACCCACCTGGCCAAC
GCACAAAAGCTGTACGCCATGGCACAACAAAACCGCACCCGCGACACCCGTGCAGGAATT
GATTACGGACGTCAAGCAGCAGTCGCAGCCCAACGCGCCAGCAAGTCAGCACAAAACGAC
ATCACCACCTACAACAATCGCCACAATTCCGGTGGCGGAACCACCGGTGCGATTGTCACC
GGCATGGTGATCAACTCGATTCTCAACAGCGGCCGCGGTGGCGGTTTCTGTGGAGGCGGA
GGCTTTGGTGGAGGCGGTGGCGGCTTCAGCGGTGGTGGCGGTGGCGGAGGAGGGTTCCGC
GGAGGCCGCTTC

>RXA01485-downstream
TAGCCTGAAACGAGCAAAACCAA

>RXA01488-upstream
CCTTGATATCGCCACCGGCATCGATGATGCCCTCGCACTTGCCTACGCACTGGGCTCACC
TGAACTAGAGCTCATTGGTGTCACCACCACCTACGGTAAC

>RXA01488
GTGCTACTCGAAACCGGTGCAGTCAATGACCTGGCACTGCTTGATCTGTTCGGTGCACCA
GAAGTACCTGTGTACTTGGGTGAGCCACACGCACAGACCAAGGATGGCTTTGAAGTTCTT
GAGATCTCCGCGTTCATTCACGGACAAAACGGCATCGGCGAAGTCGAGCTGCCAGCAAGC
GAGTCAAAGGCACTCCCCGGCGCAGTGGATTTCCTCATTGATTCCGTCAACACCCACGGC
GATGACCTGGTGATCATCGCAACTGGTCCCATGACCAACCTGTCTGCGGCAATCGCAAAG
GATCCAAGCTTTGCTTCCAAGGCTCACGTGGTCATCATGGGTGGCGCCTTGACTGTCCCA
GGCAACGTCAGCACATGGGCAGAAGCAAACATCAACCAGGACCCAGATGCAGCAAACGAT
CTGTTCCGTTCCGGTGCAGATGTCACCATGATCGGTCTTGATGTCACCCTGCAGACCCTT
CTTACCAAGAAGCACACTGCGCAGTGGCGCGAACTGGGCACTCCAGCTGCTATCGCACTG
GCCGACATGACTGATTACTACATCAAGGCATATGAGACCACCGCACCACACCTGGGCGGT
TGCGGCCTGCACGACCCACTGGCAGTAGGCGTTGCAGTGGACCCAAGCCTGGTCACTTTG
CTCCCCATCAACCTCAAGGTAGACATTGAGGGCGAGACCCGTGGACGCACCATTGGCGAT
GAAGTCCGCCTCAACGATCCAGTGCGCACCTCCCGCGCAGCTGTCGCCGTAGACGTGGAT
CGTTTCCTTTCTGAATTCATGACCCGCATCGGCCGAGTCGCAGCACAGCAG

>RXA01488-downstream
TAAAAGCAGCTCTGGTGAAGGTT

>RXA01492-upstream
TGAAGTGGGCGCGTTAGCTTCGGCGCGTGGCAAACCACATTTGCTGGACTGCAGGCATAA
TGGACAAAGACTTTTAGCAACAACTATGTGGAGGTGACAG

>RXA01492
GTGACCACAACTCTGTGGGCGGTTTCTGACCTCCATGCAGCGGTGAAAGCTAACGCTGAT
CCAATTGAGAATATTCAGCCTAAGGATCCGTCTGACTGGTTGATTGTTGCAGGTGACGTG
GCGGAACGTACCGAATTGGTGCTGGAAATTTTGGCACGTTTGCGCAGGCGCTTTGCCAAG
GTGATCTGGGTTCCGGGTAACCATGAGTTGTTTTCTCGCTCCGCGGACCGCTATCAGGGG
CGCGATAAGTACTCTGAACTCGTTGAAGGCTGCCGCAAGATTGATGTGTTGACTCCGGAG
GACCCTTACTTAACCTTTGGTGGGGTTACTATCGTTCCGTTGTTTACACTCTATGACTAC
TCGTTCCGTCGACCTGGTTTCACCGTGGAGCAGGCTGTGCAAGCGGCGCGGGATCGTCAA
GTGATGATGACTGATGAGTTTTCTATTGCGCCTTTTGTTGATATCCGAGCGTGGTGCTGG
GATCGCTTAGCCTATTCCATTAAGCGTTTGAGCAAGATCAACGGGCCAACAATTTTGATT
AACCACTGGCCGCTGGTGGTGGAACCGACTTATCAGATGCGCTGGCAGGAACTTGCATTG
TGGTGCGGTACTCGCCACACCAGGGGATGGGCCGAACGCTACAACGCGGAAGCCGTTATT
TACGGTCATCTGCATATGCCCGGAATAACCAACGTCAACGGTGTGAAACACATTGAAGTG
TCGTTGGGTTATCCGCGCGAATGGGAGCATTGGTCTGGGCAGCATGTGTGGCCATATCCA
GTGATGGAGGTGGACAATGCTGGA

>RXA01492-downstream
TGAGTCTTTGTTTCCAAATTCGG

>RXA01494-upstream
GCGATGAGGAGCTGGCTAAATTGCGCGAAGGTGCAGCGCCTGCAGGTGATGCAGATCCTT

ACAAGACTTCATCCAAGTCTGAATCTGAGGAATAACACCA

>RXA01494
GTGACGGATAATAGTCAGTTTCATGCTGCTTCAGCATTAGTCCAGGCAGCTCACACGGTT
AGCGTTGTGGGGCATCTGCGACCCGATGCTGATGCAATCGGCAGTGTAGCTGCCACAGTG
GCGGCACTACAGCAACTTGGTAAAGACGCCGTAGGTGCAATCGGCCAGCTAGATTCGATG
CCCGAGAACTTGTACACCATTCCTGGGGCATCAAACATTAAGTTTGGCGATTCACTGCCG
GAATCTGACCTCATCATTGTTGTTGATTGTGGGTCAATCGAACGCACCGGTGCGTTTGAA
AGCATCATCGTCAACAATCCTGACAAAGTATTGGTGGTTGATCACCACGCCACCAATCCT
GGGTTTGGTGCCGTCAACTTAATCGATGTGGAGGCAGAATCCACCACCACGATTTTATAT
GACTGGTTTGATGCGATGTCGGTGCAAATTACTCCCGATATCGCCCACGGCCTTTATGCT
GGACTGCTCACCGATACCGGGTGCTTCAGGTGGGGTCGACCAGTCATGCATGACATGGCT
AAAGAACTCATGGAGTTCGGTCTAGACATTCGTGCCATTTCATCAGCATTGCTTGATCAA
ACCTCCGTGGATGATTTGCGTCTTGTTGGCCAGATTGTCTCTCGGATCGAGCTGCGGGAA
GCAGGGCCATATACTCTTGCTGTTCTCGTGGCAGACTTCGATACCATCAACGGCCGTTCA
CGCGCCGTTGTGGAAGGCTTGATCGAAATGGTTCGCGCTGTGGAAGGCGCAGACTTCGGA
GCAGTATTCAAAGAATATGAACGTGGCGTCTATACCGTGTCACTGCGTTCCTCCAATTTG
AGTGTCGCTTCCTTGGCAGTGCATCTTGGCGGTGGCGGACACATTCCTGCTGCAGGCTAT
ACCGCTCGTGGTACGGAAATCGAAGCCCTCGATACGTTGATTGAAGCAACCGTTACCTTG
GGGGAGTCTTTGCGAAGCTCGGCGCATGTCGATGTC

>RXA01494-downstream
TAACAACGACTTTGAGCATGAGT

>RXA01497-upstream
CGCCCACGGGCAAAGTTTTCAAAAACTCTGATCCATATGGATCAGAGTTTTTTCGTATCT
GCCACCAGAAAGACGCCCCTTTGGCACGCCGAATTAGTCA

>RXA01497
ATGGTGGGTAAACTTCCCATCATGGCTGAAACCAACGAAAATGATCTTCCAGTTATCGAC
CTTGCCCAAATCGAAGGCTATGTTGTAGATGACTCGGATGAAGATGATCCAGTACTTCTG
CGTCCAGATGGAACCCCCATTGAAACCTGGCGCGAAGACTTCCCTTATGAAGAGCGCGTC
ACCCGCGAAGACTATGAGAAGGTCAAGCGCTCCCTCCAGATCGAGCTGCTGAAGTGGCAG
AACTGGACCAAGGAAACTGGCCAGCGCCACATCATTTTGTTCGAAGGGCGTGACGCCGCT
GGTAAGGGTGGCACCATTAAGCGCTTCAACGAACACCTGAACCCTCGTGGTGCCCGTACT
GTTGCGTTGGAGAAGCCATCACCACGCGAATCCACCTCATGGTACTTCCAGCGCTATATT
CAGCACTTCCCAGCTGCTGGCGAGATCGTTTTCTTTGACCGCTCTTGGTACAACCGTTCC
GGCGTGGAGCGCGTCATGGGTTTCTGCACCGAATCACAGCATGCAGAGTTCCTGCGTGAG
GTTCCAATGCTGGAAAACATGATCCTGGGCTCTGGTATCAGCTTGACCAAGTTCTGGTTC
TCGGTGACCCGTAAAGAGCAGCGCACCCGTTTTGCTATCCGCCAGGTTGATCCTGTGCGT
CAGTGGAAGCTTTCCCCAATGGACTTGGCTTCACTTGATCGCTGGGATGATTACACCCGC
GCTAAGGAAGAGCAGTTCCGTTACACCGACACTGATGAGTCCCCGTGGATCACCATCAAG
TCGAATGACAAGAAGCGTGCGCGTATCAACGCGATGCGTTATGTATTGTCCAAGTTTGAT
TACACCGACAAGGATTACGAGCTCGTTGGTGAGCCTGACCCTAAGGTTGTGCTTCGTGGG
CGCGACCAGATCGGTGAC

>RXA01497-downstream
TAGTCACTAGGCGGGCATGAAAA

>RXA01501-upstream
CTAACGAAATCGCCGGACTCCTCGCAATCACAAGAAGCGACGACTAGCCTGTGGGGACAA
ACTATTTCAAGAATTTATTCAACAAAGGAGTTCTTCACAA

>RXA01501
ATGAAGGAAGTAGCAGTCAACGAAGTCCCAGCAGGCGCACAGTTGATCGATGTCCGCGAG
ACCGATGAATACGCAGAGGTTCGAGCACAGGGTGCCGTCAACATTCCTATGAGCGAGTTC
GTTGGCCGCATCGATGAGATCGATCTGGACCGCGACATTTATGTCATTTGCAAGCTGGGT
GGACGCTCAGCTCAGGTTGCCGAATACCTTGAGCAGCGCGGAATTGAAGCCATCAACGTA
AACGGTGGCACCGACGGCTGGGTTGCTGCAGGATTGCCAACCGAGGCA

>RXA01501-downstream
TAAGAACCCGCCGCAAAAGATCC

>RXA01504-upstream
GCATGTAGCGAGTTTGATGAAGTTGTCGCGATAAGAGGAGGGGCGTGTCGGTCTGTAGGA
TTGGCTCGTACCGAACTTAGAAAACTCATGGGAGTTTCGC

>RXA01504
ATGAATATCACGTGGCTTATCCTGGCCGGTGTTTTAGCCATCATCGCTGTCGTGTTCTTT
TATCTTTCAGCACAGAAGAAAAAGAGCGAACCGCAGCCTCCTCGTCAGCGTCAAGATCCT
CTGAAATTTGCCGACGGATCCGACACTTTTAATGCCCGCATTTTGGGTCCTGGAGCAATT
ATTTCCCGCGGTGGCGTGGATTATGTCTGCCGCGGAGCCATCCAGTTCCGTCAAGGCCAA
TACATTTGGCACGAGTATCTACTCGACGGTGGCAAAGGCAGTGAGTACCTGAGCGTGGAA
TACGATGAGGGCCAACTCAACCTCGGATGGTGGATTACCCGCCCTGACCTGGCACAACAG
CCCGCACATGATGTCACCGTGGAGGGCGTTCGCTACCGTAAAACCGAATCTGGCGTGGGC
ACCTTCACCTCCGAAGGCACCACCGGCGTGGCTGATCAAGGTGAATTTGAATACTGGGAT
CTCGCCGAAGTTGGCGGAAACAGGTTGCTCAGTTTTGAACGCTACGGCAAAGACAGTCCA
TTTGAAGTATCGCTCGGGTGGACGGTGCTGCCCGGCGAACTCACCGTTTACCCAGCACCA
GAGGCCTCA

>RXA01504-downstream
TGATTCATCACATCGATTGCATG

>RXA01505-upstream
TCAGTTTTGAACGCTACGGCAAAGACAGTCCATTTGAAGTATCGCTCGGGTGGACGGTGC
TGCCCGGCGAACTCACCGTTTACCCAGCACCAGAGGCCTC

>RXA01505
ATGATTCATCACATCGATTGCATGCCTACAGATGTCTCCGCCGAAGCGCTCGGCGTGAGC
TGGAATGGGGAATCGCCGGAGGTGCTCGTCGATAAGCTTATCGACGCATCCCCACACCCC
AGCACCTGCCATTTAGCGGTGATTGGCGGCTCGCATGTGGTTACCGTTGAAACGCCCGAT
GGGCGTTTCCGGGAAGAAATTTCCTGCCATGCACAAGAAGCGGAAGATTCCCGCTGGCCG
CTGCCCGACAGCATCACGCGGGAAAACTACCTGCTGCAAACCAACGTCGCCGTGCTGTCT
GAGGAAGATTTTGCCCGCGCAGCCGAAGAAATCTCCAACGGCGACGACGACTGGTTGATC
GCCAGTTTCCCCGGCGCCGGCGAACACCACCTCACCGCGCTGACCGCAGAATTTCTGGAA
GACGTATGGGAATGGTTTAGCCACCACCTCTACCCAGAAGAGCTCACCATCGTGAGCACG
AGGAGCATTTACAAACCA

>RXA01505-downstream
TGAGCTCCCGAAACTACCGAAGC

>RXA01506-upstream
CGCTGACCGCAGAATTTCTGGAAGACGTATGGGAATGGTTTAGCCACCACCTCTACCCAG
AAGAGCTCACCATCGTGAGCACGAGGAGCATTTACAAACC

>RXA01506
ATGAGCTCCCGAAACTACCGAAGCATAGGATTCATCCTGCTGTTTTTAGCAGTGTTGTGC
CTGTTCGCTGCGGTTTTTGCCAAGCCTGCGGTGGGAAGCCAAGTCTCCGACCGCTGGCCC
GGAAACAACGGCACCTACTCATGCGCTGGCGAAAGTGGGGTGGTGGATGAAATCGTGAAC
ATGTCCACCCCAACCGACCGCGCCACCGACCCCGCAACTGGCGATACTTACCTGCGATAC
AGCAAAAACCTGATCATCATCTCAGGTGAAGGCACGCCGGAATGCACCATCACCGTCGAA
GGCCTTGACCGCGTCAACAGTGGTGCGTTCATCTGGCTCGGCGGCGGTTTCGGCCCATCC
TCACCAAGCAGTTCCAGCGGCGGATCCTCCGGTTCCGGCGGTGGCGTGAAA

>RXA01506-downstream
TAGAAAGAACACTATGAGTCAAT

>RXA01507-upstream
GCGTTCATCTGGCTCGGCGGCGGTTTCGGCCCATCCTCACCAAGCAGTTCCAGCGGCGGA
TCCTCCGGTTCCGGCGGTGGCGTGAAATAGAAAGAACACT

>RXA01507
ATGAGTCAATATCTTGTCGACGGAGTGCTCGGCACCCTTTCATATTTCGTGTTGGCCGCA
GTGATCCTCGTGGTCGGTTTTGTGATTTTGGACTTGATCACCCCAGGTAAACTGCATGAA
CTCGTGTTTGTGCACCATCTGCCCAACGCCGCTGTGATCACCGTGGCGCAGCAGGTTTCC
ATCGGAATCATCGTGGTCACTGCTGTGCTGACCTCCTCAGATATTTTGAGTGAAGGTTTG
CTGGAGACTGCAGTGTTCGGTGCCCTTGGTCTGGTTATCCAAGTGGTGGTCATGGCGGTG
TTGGAAGCTGTCATTCCGGGACGTTTCCGTGATCTCGTGGAAGATCCCAAACTCCGTTCC
GGTGCCGTCGTGGCCGCCGTCATCTTGATCGTGGTGGGAACCGTAAACGCTGCATGTCTG
ATT

>RXA01507-downstream
TAGGACCCATCTGGCGCTGGCTG

>RXA01518-upstream
AGCAGAACCTGATGCCGTCCTGCACGGCACGACCATTGCAGAACATGTGGATAATCTTGA
TCCCACAGACATTGAAGGTGTCACCAAGATTTAAGGAGTC

>RXA01518
GTGGCTTTCATGCAGAAAACGTCAGCGGGTTGGTTGATCGCAACGGGAGGTTTCCTCGCC
GCTGTGTCCGCCATTTTGACGTGGCGTTTTTATGGATCCATGACCTCTATTTCCATCACG
GTATCCATCACTTTTTGGTTGTTGGCCGTGGTGTGTGGTTTCGCAGGTGTGAAGGTCCAA
GGTCGCCTCGATGAGGGGCTGATCGGCCAGGACAAATCCCAAATGAACCCCGTGACCATT
GCCTATCTGGCCATGCTGGGTCGAGCGTGTGCGTGGGGTGGCGCAATTTTCGGCGGCGTT
TATGTGGGAATTGGCAGTTATGTAATCCCACGCGCCGGTGAGTTGTCCGCAGCATCGAAT
GATCTTCCGGGAGTTATTGCCTGTGCGCTGGGCGGAATCGCACTCTCAGCTGCCGGACTT
TATTTAGAGCGAAGCTGTGAGGCTCCGCCTCCCCAATCTGGCGAAGCGATCAGC

>RXA01518-downstream
TAGATTGGAATTCATGAATCAAG

>RXA01519-upstream
CTGGGCGGAATCGCACTCTCAGCTGCCGGACTTTATTTAGAGCGAAGCTGTGAGGCTCCG
CCTCCCCAATCTGGCGAAGCGATCAGCTAGATTGGAATTC

>RXA01519
ATGAATCAAGACCTGTCACACGAGGATTCCGGCGACGGCAATTCTGTCGACCGTGGACAG
ATTCTGCTAGCAGTACTCATTGGACTTGCCCTGATTGCCAGCGTCATCATGCTGCTGGCC
AACAGTGACGGCGCCATGAAAATAGCACTTCTTGCAGCGCTGTGGGCGGCAATCATCGGA
TTCTTCCTTGTTTATCGGTCCCGCAAACAAGTCGAAGCTGCTGCGCGGGAGAAGGAAACC
CTCGAATACGCACACCAATCTGAACTCAACCGACTAGAAGCTGAACTCGTCCAAGAAAAA
ATGGAGATTTCTGAATCCCGTCGTGCACGCGATCAGGAAACCCTTGAGGAAATCAAACTT
CAACTGGAGGAAATGCGCACCCAGCTGTCTGAGCTTTCTGGCCGTGAATGGGGCTATGAG
CCAACCATGCTGCGTGCCGAAGCCCGACGAATCCTTGAGTTGGAATCCCAGCAGCTTTCC
CAGCAGTTCCAGGCACCGCAGCCAGAAGTCCCGGAGCCTGTTGCAGTTCCAGAGCCAATG
CCGGAACCTGCACCGGTGCCGGAACCAGTACCAGAACCTGAGCCAGTTGAAGTTGCTGTC
GAAGCTGAGGAAGAACCAGCACCAGGTCGCAGAAGGCGTAGGCACGCAGCTCCCGAAGAA
ACTGGCGGACGCCGACGCAAAGATGAACGCCAAGGCGGTTTGAGCGTGGCTGATCTTCTG
GCAGCAGCAAGGAAAAAGGAAAACAAC

>RXA01519-downstream
TAATGCAGGCTCCTCGCCTTCGC

>RXA01520-upstream

CTGCATACCTCGCTCACGCACGGCATCACTGTGATGGATCCGCTGCAGACGTCCGGCAGG
CATCGTGATGTCTGCGCACCCGATTGGTCAGGACCGGTGG

>RXA01520
GTGGCGTCCGCGTTGGATGAGTTGGGGGAGACCATCGTGGGGCTTTTGGTGGGGGAGCTC
GGTGGCTCGATTGTCGAGATCGCCGATGACAAGCGCGCACAGTTGGCTGCAGCGCTGACC
TATGCCGGATTTTTAAGCACCTTGCAGCGCGATGCGTCGTATTTCCTGGATGAATTTCTT
GGCGATCCCGATGTGACCTCTGACATCGTTATGGATTCCGCACAGCAATTCCAGGCACTG
CCTTCGTTGGATGAGGTCATTGCCCAGTACGATTCGATTAACAACCCCGGCAGGCAACGC
CTTTTCCGGGATTTGGCGCGCAGGCAGGCAGAGATTTCCCGCGCGCAAGATATTGAGCTG
TGGGCAATTCAGAAGGAGGACCGT

>RXA01520-downstream
TGAGTTTCACGCATGGTCAGGGC

>RXA01523-upstream
AATCCTCCAAACCTGTGGATAGAACAATCTATCCACAGGTTTTCAGTTTTCTGCAAAGTT
CATCCTTGGCTTCTTATGCCTTCGGATCCATAGTGGGGTC

>RXA01523
ATGAAAAACTGGCAAGAAGAATTCCAACTAGTCAATCTCACGAAACTTCTGCATAGCGAT
ACCGAGACTTCTGCGGCAATCAGTAATGGTCAAATGATTAAACTCACTCATGAAGTCGCA
ATCAATGCTGAAAAGTACCGAAGCCTTCCTGCATGGGATAAAGCAGCCGCCCGAGCTTTT
GCAGTGGGTATGACTGTGGACAAAGCAGTGGTAGCGGGGCAGTCTGCGGCGAGGTTATGG
GGATACCAAACTTTGACTGTTGAGAAAACCGTGTTGTGTCTGTTGCCGGAAAGGCTACGT
TCAAAATCCTCCAAGCATTGGCCGTCCGGGATGCGATATAAAGATCGTTACCTCTCGTCG
CGTGATATTCGAGAGGTTCATGGGATCCGAGTTACGGGAGCGTTCCGCACATTTTTGGAC
ATCGCTTTGGATGATGGGGTGGTGGCGGCTGTGGTCACTATTGATTCAGCTCGAAGACAG
AATCCATCGCTTACGCGTGAGAAGTTAATGCACAGTGCGGAAAGTTTCCCGAGGCATCGG
GGTGTGAAGGCGTATCGGCAGGCGATTGAGTTGTCGATTCCCAATTCGGATAGTGCTCAG
GAGACGAGGGCTCGGTTAATCCTTCGGGAGGCCAAGCTCCCGGAAATCCAGTCAGTGAAG
GTGCAGGCCCGTTTCGATCAATCGCACAACAAGTATTTCCTCGTCGATTTCTTGATCAAT
GAGTGGATCATCGTGGAGATTGATGGACGTTCGAAATATGATTCCCCGGAGCTCAATGAG
GTGCTCATGGCTGAACGCGATCGGGAGAAATTCTTCCTCAATCAGGGCTATGCGGTCTTA
AGAATCGATCCGAAACAGTTAGACCTCAACCAAGATGGGGAGTGTGAGTTCATCGGAATC
CTCAAAAACACTTTGCAGAAGACCCCACCTGAGCACCTCAAGCAAGCCGCC

>RXA01523-downstream
TAAACACTCCAAGAACCACCATT

>RXA01525-upstream
GTCTCTGTAGAAATCTAGGGCTTTCGACGCTTGAGCCCCGCGCACCTGCAAGGTGCGCTG
TAGGGAGGCGTCGACAAGCATCTTTAAGTAGCTTTGAAGC

>RXA01525
ATGCGTTCCTTTCAATCGATCCTTGACCTGGTAAATTCAGCATCCGAGGTGGCTACCAAA
ATTGTGTTGAAGCGCTTCGAAAAACGGATAACCAGCGAAACTGACTGGGTACCGTATCAG
CGGTTTAGTCTTTGGTCGGTTGGTTCTCCGCTAACGATCGAACGCAAAGGCCCCGATGTG
CGTGTGAGCAAGGACAACACTGCCGTTCTTCAGCGCTATCAAAGACCGGAAGCAGAAGGA
CTGATCAGCTACTTCATGGATCCAAAGCCATGGATAACTGAATTGGCAGGCCTGAATCTG
GACGATGTTTCCGAAGATACAGTTGCAGGTCGGACAGTATTAGTGGTTCCCCTATCCAAT
GTCATTCTCAGCATCGATGCGGAATTTGGGATGATTCTAACTGCGGAAAACGACATAGAA
AAGATCCACGCAATATCTGTCGAACTCTTAGAAAAATGGAGATCATCCCATTACCCTGAG
CCGCATTTTCCTGCAGCGGTTCTCCCACCTGCGTCGACTGGAAACCGCAACCTCCGAGTT
CTATGCCCTGAGTTTTCCATTCCAAGTGTCAACGTTGGTGATCAGGTTTTACTATTTTTA
ACATTTGATCAAACCCTGCCACCAGTAGATCAGCTTGAAACTACTCGCCGCGGATACACT
GATCCAATCCAGCTTGACTACGACCACCGCCAATACAGGTTTCACGCCGACGGTTGGGAT
GCCATCATCTCCACGGTGGAGCCACTACACGACGAAGAAGAACTCACAGGTTACTTCCTG
CACCGCCTTGACCCAGATAGCGCGTACCCAACCATTGCAGTCGTTACAGCAGCGCACTAC

CACGGTACGGACGCAATTATCGACGTGACCCTAGATGGTGTGCATCCACCCAAAAACCAA
GAAACTCTTGAAGGCATCAGCACTAGTACCAGTGACGGTGACATATTTTGGCTCTCCGAT
GAAAGCTTGCCTTTCGTCCGTGGATTCAGCGTGTCAACAGGCGAACTATTACACGAGATC
TCCATCCCCACGTTCCAAGAGATCGTCCTCGATTCCGCTAATAGAGCCCGCGTAAAACAA
AAGCAATGGCCTCACGATTTCAGTGATTGCAAGGGAAAAACATGGGAGCTTCCGGATCTT
AAAGAAGTATTCGAAGCTGTCCCTTCGATTCCAGCAGGTTGGAGATTGTTAGACAGCTTC
GGGAAAAACTTGCACAATGTCACACGCGAAAACCCTCGTCTTAATGACAACTTTTGGCTT
CAAACAATCCTTAGGCTTAAACCATTTAAAGCAGTAGATCTTGATATCGGCCGATCGATA
ATCACAGCAATTTACCCATACGGTGATCGAATTTACTTACGCGCTAGTAACCACCACATC
ACGTTTAACCAGGACCTCGAGATTCTCAACGTAGAAGTCTTTGGCGACCCTGAGGTTCCC
GAATCTGGTCTAATTTATCTTCCACCTGGGGATTCTCCAACACTCGGTTTTCCCACCGGA
ACACTCATGATGTTTCATGAGCAAGAAGGCACATATGCTTTCCACGACCCTGAAACAACA
GAACAAATAACAACTGTGAACTTAGACAGGAATAGTTTTTCAGTGGCATATTCTTCCCGA
ACCAAAATTGTTATTTCACTGAAAAACCCAGAAAGCCGACCTACCAACAAGCTGTTGGTG
TGGGAACCACAAACCGGGTGGCGAGAACAGAACCTGGAGCGC

>RXA01525-downstream
TGAGCACGCTTAAGGTGAGGTGG

>RXA01527-upstream
ATTTGGCTTTTGCGGATGAGCGGAAGTTGGCTAGGCAGGCGCATGATTTGTTGCCTGAGT
TTGCTTTGAAGGAAAAGGCGGAGGGAAGGTCCACCCCAAG

>RXA01527
GTGATTCCGAACCCCAACCCGAACCCCAAAGCCAAAACTCTTCGCCTCGTTTCAGCGCTG
ACCGCCATCACTGTGGTGGGTTTTAGCGCTTCACCTGTTCATGCGTTGCCGATTCCGTTG
GATCCTTCTGATCCGGCGGTGTCGGAGTTGTGGGTGAATCCGAATGCGCGGGCTGATGAT
GAGCTTTCTGGTGTGGATGTAGAGATCTCGGATTTTGTCATGCCGAATAGCAATCTAACT
GTGCAGGTGGGGGAGTCTTTTAAGGCGCAGGTTCGGGTGACTAATCGTTCGTCGGAGACG
TTGAGCAATATTACGTTGCAGGCGCGTCGTGCGGAGGCGTCGTTTGATATGGCGAGTGCT
CGGGTGGCGGCGACGGATAATAATTATGGCTACTTCGGCGCGATGGTGACTCTTGATGAT
GAGTTGGAGCCGGGGGAGAGTGTTGAGACTGAGGTGGAGATTTCTACCGATAGTTTGTCG
ATTTCTCAGCCGGGTTCTTATCCGACGATGTTGGCGTTGTCGGGGCAGCTTGATGGGGTG
GCGCAGCATTTGGATTCGCAGCGTTTCCTTCTGCCAGTCCTCAGCGATACAACTGATACA
GAAGACACCGCCACCCCCACGACGATGATTTACCCGATATCAGCCCAGACGAATGTGTTG
GGTGGTGAGACCGGCGAGGCGCCGGAAGAGCCGCCTTTGCTGGTCAGTTCCGACGCGCTT
GCGGGCGAGTTGGATGAGGGCGGTCGTTTGCAAAAGCTTATCGACGCCTACCTCCAGTCT
TCACCCGCCGTGCAGCAAGCCACGTGCCTTGCTATTGATCCGCAGCTTCTTGATGTGGTG
GATCGCATGACCGGCGGTTACACCGTGACCGATACTCGTCCCAGTACGGTGCGGCAGAAT
CAGCGGCTTCGTGAGTTGTGGACTGCCGATAATCAACCCACCAATGGTGTCGCGGGCACG
GGTGCGGAAAACGCTGCCATTTTCTTGGAGAAACTCCGACAGGCCACAGCCACCTCGTGC
ACCGTGGCGTTGCCGTGGGCGAATGCTGATCTAAATGCAGTGAGCCAAACCGGTAATCAG
TGGTTGATGCGCGAGGCGCTACAGCGAGGTGTCACCACCTTTGAAGAAGTGTTGGGTGTT
ATTCCGGAATCCAATGTGGTGATTCCTGGAAATGGTTTTGTGGAGCCCTCCACCGTGGGT
GATCTCGGATGGGCGGAAGTAACGCTTAATCCGGATCAGGCGTGGGAGGTGCAGTCAGAG
GAGTTGGTTGCTGCCCCTGATGCCACAGAGCAAAGCGCATTGGATAACCCTAAGCCAACG
CCAGGCACGGTGACGCCGCCAACCCCTATGTCAACGGTGTCCGTGTTGGTTTCTGATAAC
ACGGTGTGGCGCACAACGAGCGCGGATCGGTTCCACTCTTTGGCTCCGGGAATAACTGGG
GTGTCGTATCAGGGATCGTTATCGGCAACCTTGGCTACCTTGGGACAAAACCCTGAGACT
GTGGGCTATTCCAATCCGGATTCGCGTTATGACTACGCCATGGATTCTGAGAGCGCCCGC
AATCTCACCGGCCAGGCGGCGCTGCGCTTGACGGTGGACAACGGCGATGAAGACTCTCCC
GTGTTGATCATGCCGAGCGCGGTGCTGGGCGCCGAAGACGGCGCGATGTTGCTTGAGACC
ACCGGGGCTTTGCTTGCCGACGGCTCCGCCCGACCTTTTTCCCTGCAGCAATATGTCACT
GCCAATGCGGAACAAAGAAATACTTTGGCCACAGCAACAACTCCACCGGATGACACTGCT
TTTGGTGCACCCTACGACGATCCTGCGTCATTGACGGAAACCGAAATTCTGCGAACCACT
CAGCAGGCGGAGTACATCGATGATCTCACTGGCATCATGTCCAATGATCCCAGCATTGCA
CTGACCCGTTATGGGTTTACAGCACCGCTGCGGCAAGATCTGCTGCGCGCGTTGAGTATC
AGTGAGCGTCGTTCGTTAGCTCGCCACACCCAGGCAACCTCTGCTGCCGATAAATTACTT
AATCGCAACCGCGATACTCTGCAGAAGCTGCGTAGCTCTGTGGCGTTGTTGCCGCCGGGA

AATGTGTATACCCGAACCTCGGAATCGTCTCCGTTGTTGATTGTGGCGCAAAACGGTTTG
CCATTGCCCGCGGAGACTCAGATTTTGTATTCCGGAAATCAGGATGCGCACATCAATACT
CCGGGTGTGGTTCGTATTCCGGCGCAGGGTTCCATCACCTTGCAGATGACTGCGGATTTG
CCCGATGACAATCTGCGCACTGATCTCACGTTGTGGTTGGCATCCCCAGATGGGGCCACC
ATTAGTGAACCTGTGGAAATTACTGTCCAGCCTCGCCCGAATTTGGGCACCACGCTGTTT
TTCGTGGCAGCGGGCATTCTGGCAGTAGGAGGGTTGTTGTTTATACGGAAGAAACGAAAC
GTCGAAAAGCGCTCGCCCGGTACGGGATCGCCCAAACCGCCACCAACCCAC

>RXA01527-downstream
TAACGTATCGCATAGTTATTTTC

>RXA01536-upstream
AGCATAGATGACTTGACACTGTTGCAGCAGGCGGTTTTCACCTGGCCTCTTAGGATTTGG
TCAAATGGTTGCAACGACGCCAGGGAAGGAGGCGCACCCC

>RXA01536
ATGGCATTTGGATTTTTTAGTAGACGTAAGAAAAAGAACAAAGACAAAAACCCGAATGAA
AATTCAGCAGTGCCCGCACACTCTGAAGATTCACCTCAGGAGGTTTTTGAGGGTAATGGT
CGTCAGGTAGGCGACCCCATTGAACAGCAGGTTGATCGAGATGCTAAAGGTCGTCTCACA
GCGGCGGATTTCTTGCCGGACGCTGATCTGCCACAGCTGAATCGTTCGCGTGCAAATATG
CTGCGCCGTGAATTGGAGTACCGTTTTTCACTCCAGAATGCCCACATTAATATCGATGGA
AACACGGCCATGATTCAGCGTTCAGATGGCGGGGCAGCACATGTCTCGTTGCGCACCCTC
GCGATGAATGCAGCTGGCCTTGATAACTTTGATCAACTCCCTGAACTGGTGGAAAGCTTC
GTTCACGGCACGCTGGCCGATGCAACATTAAACGATCTTTCTACTGCTGACCTGTATAAA
GCACTGCGCCTTCGCCTGCTGCCAACACCTGGCGAAGGCGACGATCTAGTTGAGCATGGA
CTCGACCGGGAAAGCCAGATCCGCGACGATTCAATCCTGCGCACCTTCACCTCTGACATG
TCGATCGCGCTGGTGCTCGATACCGAGCATGCCATCCGCATCCAGCCACTCAAAGAGCTC
GAGGAGTTCGATGACCTCAGCGCCCTAGAGCGGGCTGCGGACCGCAATACCTGGCAAGAG
CTTTACGACGCAAACGTTGACGCTTCCTTCGTCGACGCTGAATCAGACAGCGAAGGGTCA
TCATTTTGGGCTTTCGAATCTAACTCGTACTACTTGGGTAGTGCACCACTGTTCCTCAAC
GATCTGTTGGCAAAGTGGGCACCTGACCTGGACCAAAGTGATGGCGTCATCTTTGCTGTC
CCTGATCGTGATCTGTTGATTGCGCGTCCTGTGACCACCGGCGAAGATCTGATGAACGGA
ATCACCGCGATGGTGAGGATCGCGATGCGCTTTGGCCTCGGGAACCCGACGTCGATAAGC
CCGCGCCTGCACCTGCTGCGCGACAACCAGGTGACCACCTTCACCGACTTCCGCGTCGTC
TCTCCTGAAATGGAAGCTGAATGGGAAGACAGCGCGTTTGACGCGCCACCGGCCGGCGCG
ATCGGCATTGAGGTGCGCCCAGATCCGTATCTGATGGAGCGCCTCCAACAGGGCGGCTTT
GGTGATTTCGGAGATTTCGGCAAGCCCCGCGATCTAGATATG

>RXA01536-downstream
TAGCGAAAAAGGGACCTTCACTT

>RXA01539-upstream
AAATGAACAGGTAGAAGAGGTTAGTGTCGAGGTATCTTCTGTCCAGTCATTAACCCAGCC
TAAGACGTTGGGGCAGCTGCATGACCCAAGGAAAAATGTC

>RXA01539
ATGAGTAGCAGCGACTTGGCTTCTATTATTGGTGTAGAGCAACAGCCTGTTGCTTATGGT
GAGTCTGAGGAACCAGAAACACTGCGTGATGTGTTGCCTCGGCGAAAGCTTCACCCATCT
GAGATAACACCGAGTTATGAGGTTGCTGATGGTGAACAGCGCAGCATTTTTGGTGAATCA
GCTCCGTCTGATTTTGATGACCTCAGTGATGTCGAAGAATTTGATACCAGTCATTGGGTG
CGTGCTGGACAAGATGATCGTAGTGATGATGATCGACTCGCTGATGAGGCTGGTGTACCG
CCTAGTGGCGCACAAGATGTAGCTGATAATGAGGCTAATCTTTCTGGTGTGGATGAGCAG
CTGCACATGCGTGAAGTCCATGCACAGAGTTTTGACCCTATTGACGTTGCCAAAAAGGAA
CGCAAAGCAGCGGAAAAGAAGTATGCCAAGCCACCAAAAAGTGATAATCCGTACCTAGCA
CGGGATGCCAAAGATGCAGCTGCTCGTAAGCGGAAGATCAATGCAGCTCATGATAATTTT
GCCCAAGAGATGGCACAGGCTGCGATGGGACCACTGCGCAAAGGGGTCAACACTCAAACG
GTGATGGCCGCGTGTACGACTGCTGCGGTGATGTGGTGCATGAGCCCACGTATGACCGGT
GTGAACGTGGATATGAAGCGCAAGTTTAACAAGGATCTGGAACAGGCTAAAGACACTAAG
TTGTCGAAGTATGTGTCCAAAGATTTTTGGAAGTCAAAGCTGACGCGCGATAAGACGGAG

AAGGAAGCGAAGTCGCTCTCTGATGCGTTCATGCAGCAGAAAACAGCGATCATCAGCAAC
CGTGAACGAATCCCCATGAGTGTTGCTTCTGCCGCGCAGACCGTGGTTCGGTTGTCTGAT
CAAGCGTATGAGGCGATGCGTGAAGTAGATACGGATGGTCAAGCGATAGTGGATGCGAAG
GATGTCTCTGCACAGGTGGCAGAAGATATTGACATGGTGGTCAAGCAGGGTGAAGAGCAT
GGCCTGAAGTCGAAGGATATTTATGGCGCTGCCCGCGATATTGTGGGTCGTCGCATGGAG
CGCGATCCAGGCTATGCTGCCCGGTTTAATGAGACGGCTTTTGGCACCGTGCGCCTGGGT
GAACAACGACGTGGCATGGTGATTTCAAAGACCCCGACATGGCAATTCCCTGATGGTGCA
GGTTTGAGTAAAAACGCCGGCTGGTTTAGTGTTCGTGAGCCGATGGGTAATGCGCAGAAC
TTCGCTGACAACCTGGCTGCGACTTTGGCGACAGAAATGCGGGTAGCTGGTGAGCAGTAC
GGTTCCGATGGCGTTCGTGATGTAGTTGCCGGCTTCATGACAGCGACTGATGTCTCAGAA
AGTGGCCTCGCCTCTGCGAAGAAACTGTTACCTGACTTTGATACACGTGGTCGCAGTGCT
TCTCGGGTGCGCCAGATTGCTATGGCACAGCGCACACAGGCAGCGATCAAGGTGTTGCAG
GATGATGGTAATCAGACCGCGATGACGACTGAGCAGGTCAAGGAGGTTCAGGTATGGGCG
ATGGATCAGGCTGAGAAGGTGATGCAGCGTGATCATCCAGCGATTCTGGATAAGTTTGTG
CGCAAACATGGGCAGACATTTGGGCAGGATGCGGACGCTTTTGTTAAATCCATAACTATG
GAAAAAGACACGAGCAGCGAGTACACTGATGCTATGGTTCGACCTCAAGAAAATCGTGGA
TCAGGTCGAGAACTGGCAGCTCGTCGTCGTGTACAAGCAGCGCAAATCAATCAGGCAGCA
CAGCTGGATATGAATGTTCATGATTTCCGTGAATCGAATCTGCCAGAGGAACGACCCGCG
AATCCTTATGAAGCGTATGTTCGTGAGACTGAAGCGAAAACCAATGATCCGCAGTACGGT
TAT

>RXA01539-downstream
TAATAGAAAATGATAGAAAGAAG

>RXA01540-upstream
CCATGCAGCACTATGGGTTCCCTGATCCCGATGCGTACTTTGACCATGCCACTATCGCAG
GAAAACACCACACACTCATCACAAGAAAGTAGGTCTCACC

>RXA01540
ATGACTTTTGCAGAACTTAGCTCACCGCGTACCATCATCGCTTTTAATGGCCGTGCCGAA
TCTGGCAAAGATACTGCAGCACAGTATCTCACCCATATGCACAGTTTTCACCGCATCGCC
TTTGCCGATGGTGTCCGTGACGCACTCTATGCGCTTAACCCACTGGTCTGTGTGGAGCAG
GCTATCACCACACATGGTGCCATTTATGACCGCGTGGCCACTGTTGTGGACACACTTGGT
TGGGATACCGCAAAGCAAATCCCCGACATCCGCGCACTTATGCAGCGTATTGGTACCGAA
GCTGGTTGGCGCATCCACGGCGAGCATCTGTGGGTCAATCTTGCTATCAAAAAGATCAAT
GAACTGCCCGCTGACCACGCCATTGTCATCACTGATTTGCGATTCCCCAATGAGATTGAG
TGGTTGAACAGCCTCAAAGCCAACCCGATGAACACCATTCAGACCGTCAAAGTCATCCGA
CCAGATCATGAATCGACCTTGACTGCAGGATCATTCGGTACTACCTCACATATTTCCGAA
AGCTTTAATCTCACTACCGACACTGTGCTCCGCAACGATGGCACCATTGACGATTTGCAC
TCAAAGCTGGCTGATTTTTTGAGCACTTCCCCGCAGCCCGTGCTCTCTCGTAACGCCCCT
GTACCAAAACACAACGCACCGGCACCAACCACTGATGCCATG

>RXA01540-downstream
TAAATAACCCCCGTATCAAGATC

>RXA01542
TGGGGTCAAAAAGATCACTGGGGCAAAGCTCCACTGGGTGATCACGATGCTGTGCGTATC
TATAGGCAAGCAGAAGCCTTGATGAAACAGCGCGCAGCAAACAATAAGGGCTTAGACCTC
AATGATGAAGCGACCTATGGCGCCATCATGTTTGCGTCTTTCGATGATGCCTTCGCCGCT
GATGCCGAAGCTCATGGCTGTGTACACCGACCACAGTTCGCGAAGGTAACTAGGCGAAAT
ATTCTTAATTCACCGCAATACACGGCGATTAAGTCATCTTATGACGCGCTGGTGCAGCAG
GATCTCGTGGCCCAACAGCAGCAGGCACAAGCGCTACAGCAAGCTGCTTATGAGCAAGAG
CAGGCAGCTATTTTCCAGGCACGTGATCAAGCAACATTCCAGGCTGAACAAACGCTCGCG
CAAGAGTCCGTTCGCCAATCAGAGGGTGTGGGTTTACCTGTCATTGATCCGATGGAGAGC
TATTTCCGGGAGTACGCCTTCTATGAAGGTGTCGAGATGTTTGGTACCTGGGGTACGCAC
GTTGATGCTGGTGTGTCGCAGTTTAGCACCTCTGATGGCCGTGCGATCCGAGCGCTTGTT
GATGAGCATCTCGCAACCTATGAACCAGTAGAGCAGCGGGGGAGTACTCAGGCATTCTTC
GCCTCTGTCAATGCTGCCTTTGCTGAGGTGGCACCTCACGCAGCACCCATGTTTAGTGCG
ATTGCTCGCGAGGGTGAGGGTTCAAAGGGGTACCAGGCGCTGCGTCACCGTTTCGACAAG

ATGGTCGGCACTGCAATTGGACCTAATGGTTTGCCTGAGGGACCTGATCTGGGTGGTCGT
CGTTTACCTATTTCGCCTTATGATCCACGCTGGTCAGACCGCGAAGTAGTCCGTGTGCAC
GGTACCAAGCTGCTATCACTGTCCGAAGAGAGTGTTGGCATGATCAGGGACCTTGATCTA
GCAACGATCCACCTACAAGATAATGATGTTTACGAGGGCACTCATCGAGAAGACGACACT
AAAGGCGGTGTGCGACCGTTGACTCAATGGGTCAATGGTGAAGCTATTGCCTGGCGCACT
ATCACCGAGAATGACCAGATGCGACTGCCCAATATTGGTCAGTTTATGACGGCTAAAGAA
TACCGTGCCGCAGCGTCATGGCTGCGTGCTGGACTCATTGATACCGCAGATGTTGCGAGT
CAGAAAATTGACCCCAACAAGGTCATGTCTGATGAGGGTATCGCGCGCTCGGAAGCTATT
TTGACGTATCTGTCGGATGAGGGTGTGGATTTTAGGATCGAGCCAGATCGTGAGCCGGGA
CAGCTTAAAGTGCGTATTGAGGGCACCCGTATTGATATTCGTCTCACTGATACTCGCGCC
AATGAACAGTGGGTGGGTCGTGTCTATGATTCTGGCACTGTGATTAAGTATTCCGCCGAA
CAAACAGCGGAAGAACGTCTACGAGCTCGTGAGCGCATGGAGAACGGTGATGGAACGTGG
ACACCGGCTACTGATTATGAACCAAGCCCAACTGAAGTTGTCGATCTCGTGAAATTTGCT
CTCGGTCGAGAGGTTGAGCGACAGGATGGCAAAGGTCTTGTTGGTGTGCCTAATGCTCGA
CACCCACGTGCTTTAGAGCAGGCACAGGATGCATATTTCACTAAGAATCGTTCCGCATTC
ATGGTGCGTGAAGGGCTCTCGATCGTTCAGGATGCACGTGATCGAAGTGCTGGTCCTGGA
AAGTGGTTTGATAATGAAGCGAAAGCATCGGAGTGGCTTGGTAACAATATCGCCCTTACT
CGTGCGCGTGTGGCCGAAGAGCTCGGCGTTGAAGAACTGATTGCGCTTTCTGCACAGTAC
GCCGATGATCCTGACTTCATGCCGGCTTTTGCTGGTGAGGATGAGCTCATGGCGATAAAG
CAGGACTATTGGGCGATGCTGCGAGGTGAGGAAACCGATCTGCTTAACCCTGGGGTTAAC
CGCGATGATTATATGGCTGCTATCCGCGATGGTGATCATGAGCAGATTGCTGCGATGACC
TCAGCAATGAATGCTGTGACCGTGGAGGATCGTGTGCGTCAGCACGCGGCCCTTGTTCTT
GATGATTATGTCGGCACGGTGGAGCCTGATCCTGTTACCGGCTTGCGTTTTAATCCGGTG
ACAGTTGCTCAGCACATGCCGAGTGCTAAATCCCTGTGGTCAAACCATGACGATATTATT
GCCGCGTTGCGAGCGACTTCGATTACTGGCGATGAACTGCGCGGTGACGAATTCTATAAC
GATGTTATTAATCAACAGTTGCTCAAATTTAATCCTGAGACCGCGCAGAAAATGGTTAAT
AACCCTGATCTTGACCCGCAGTTGGCTCGATTTGGCACTGTCATTGCCGAGACTATTTCC
CGCAATGGTGCTGATGTGGTCGATATTGCTGTTGACGATAACGGTGTGGTGCGGTGGACC
GCACAGCGACGTGTTGGTGCGAAGGATAGTCGTGCAGTAGATAGTAAGGGGCAGGTTCGC
GGTGAACGCACCCGTCATGTGCAGGGTGAGATAGGTCAGATTTTTACTCGCGGTGAGCAT
GGTGAAATTGTCACCAAATTTAATGGTGGCGAGAACTATATGTTTGCCCCTGGCTACACC
GCGTCTGTGGTACCACAAAAGCCTGGTGAGACAAAGAGTTTAGAAGAGCGTACCAAGCTC
AAAGGCTATGAGCAGGTGATGTCAGAGGCGTTGGTGTACCGTGTGCGAGAAGATTTGATG
TTCACTGAGCGATCCCGAGTGGGTGCTACAACCAGCATCAACAGTGCATATAAGCGACTG
TATGACAATCGCTTCCCTGTGGACTTCTTCGAGCGCAGCGCCGAAGAAGGTTTGAGCGAT
GAGTGGCGTGCTGCGTTGCTTGAGACTGCGAGTTTGCGTGTGCGCTACGACAACTCTATT
CGTGATGGTGCGAATGTGATGGAGGATATTCGAGCACAGCAGCGTGGTTTTGATGCGCGT
AATGATAACTCCCGTGATGCGCTGGTGCTTACCGGTGGGCGTAACATTTCTGTACTTGAT
GTTGATGCGGGTAAAGGTTTCTTTGATCCCATGATGACTGGTATGGCGGCGAACCAGGGT
TCTGTTCGCTATTTGTTGCCTTCTGCGAAGGTGGGCGCTGATGGCATGATTACCCCTGGT
GATCCGGCTGATCGAGTACCTGTTGCAGCGCATCCAGAATCATGGGCGATGGGCTTTGAC
CCACATGACCGTCAGAACATGACTTTCTCGAACATCATGCAGGCTAGCGCTGTGACTGGT
GGTGCACGCACTGCGATGATACAGCTGGGCGGTTGGAACTTTGAAGATGGCATTATTGTC
TCTGCCGATTTTGCGAATACCCATGTTATTCGCGATACGGAAGATGAGATGCGCCCCTTG
GTTGCCGGCGATAAGCTGTCTGATTTTCACGGTAATAAGGGTGTGACCGCTCTTGTTGTT
GATCCAGCGATGAGTGATGCTGATGCACGTGCAGCAGGGCTGGAATCAGAGGTGGCGTTT
TTCCGAGACAACCCTGATCTAGAGGTTGTCATGAGTCCGTTTTCTGCCATTTCTCGTTTT
AATGGTGGCACGGCACGTGAGCTCATGACCAACCCGCAGGATGTGGTGTTCAGGAATAAT
GATGGTTCTACTCGTGTTCAACCAGGTGCCTCTGGTGATCTCAACTTCATCGTCACGCAT
ATGGCTGTTGATGCGAAAACCAATGTCTATGATGAAGAAGCTGTTCGTGAGGGCCAAGGA
CGTAAAGCGTCTTCTCAGCTGGCGTGGGTGCTCCAAGCCCAGGAATGTCATGAGATTATG
GAGCACTTTTATGGCAACAACGTCTCTGCATTGGCTAACTTCCAGGAATATCTTCGCGTC
ACGGGGCTTGATGTCACCCCGTATGGTGAGTTGCGCGAGGGGTTCAGCGAGTCCAATGAG
CAGCGCAATATCATCGAGATGCCAAGCATTTACGATGAGAACGGTGAGCTGAATAATCGT
GTTAATCGTGCACAGGTGCGCGAAGCTTTTGTTGAGCAGATCAGTCGCGCTGGTGGTGTT
ATGGAGATTCCTTTCCAGTTACAGTTGCGCAATGGTGCACAGCTAGAAGAGTCACCTAAT
AATCCAGACATGTATCAGTTGCCACTACTGAGCCCGCATTTGCGCAGTGATGAGGATTTA
GCGGACGGTAGTACCTCTCGACATGAGTACACCACGCGGTATATGGCTATTTTTGATACG
TGCTACAAGCTGGCAGAAGAGCAAGCCAAGATTGACGCATTGCGCCAGGAGGAAGCGCAG
CACGGCACGTTGCCTCGTGCTGCGGAAAAGCGACTGAGCGAGTCACAGAAGTTTGTTGAT
CAAGCACAGAAAAAGGTGCAGGCAAGCTTTGATGGAATTGCTAATGATATTGTCGCCAGC

CGGATCGAGACCAAGAACAATGTGTTCAAGGACGGCTTTATGTCGGCGCGACAGTCACAC
TCCGCTACTGCTGTGTGGACAGGTGATCCACGCCTGTCAGTTGATGAAGTAGCCATGAAC
TCTTCGATGGCACGTGAACTCGGCGTTCTCGATAACGGTTATGCAATGGTGTGGCGTGAT
CCGGTGATCCGCGATGGTGGTGTGCGCTATTTGCGTGTGGTTATTAATGATGATCTGCAC
GGTGTGGCAGTCAACCCTGTGTCGGTGAAGAGCTTTGACGGTGACTTCGATGGTGACTCT
GTAGGTCTGGTCGGCAATCTGCCGAAAAAGGCGCATGAGGAGGCATTGTCCAGGCTCACA
GTTGAGGCAAACATGCTTGATCTTGGTGATGGTAAGCGTATGGAGGACGGCACTATGTTT
TATGGGCTAACTCTGCATGACAGCCTCGATGTACAGGTAGCGCAGCACCATGATCCGGCA
ATGGCCGAGAACATGAAGGTTATTGTCTCTGAGCTTAACCGCTACCAGCGTGAATACGAG
GCCGGCGAGATTAGCCGCGAAGAATTGCTAGAGGTCAACCGTGCACACATGGATGATCTC
AATGAGCACTATGCACAGGCT

>RXA01543-upstream
GTGCTTTAGCCAAGGTGAGGCATCAAGAGAAGCAACAGCGTCGTTACCGTTTTTTTGGTG
GGGGCGCTGTTGTTGTAGTTAAAGAAAGAGCGGTGGGAAA

>RXA01543
ATGAGTTTGAAACAAGCCATTATCGTGCGCAATGAATATACGATTAAGCAGGCAAATGGC
AAAGGTTCACGAGGATCATCGCCAGGTAAATATATCTCTGGCTATATGGCACGCAGCGAT
GCGGTAGAAGCAGTAGCACCTATTGTGCGCAATAAATTAGATGATTTCATCATGCGGTAT
ATGGCACGTGATAGTGCCGTGGAGCAGCTCACCACGGACAGTAACGCAGACTATGACCAG
CAACCTGAAATGAACTCTCGTCGTGGCCGGCAAGGTCGCCGCGCGACCTTGAAACAACGT
CGTGCAGAACGCAGCGCCCGGCGAGCAGCATTGCGAGCGGGCGTGAATACAGACTCCGAC
ACCACCAACCCATCACAACCTGTGCACCCGAGGGAACTCGCGGAATTTACTACCCAGGAT
GGGCAGCGCGTTCATGATCTCATGCTGAGGGCTCAGGGTAATGGGGGAGTGGCCTTTGGG
TATGGCGATGTCTCGCTGTCACATGATGATCTTCATGCAGCAAGTAATAACGTCCAAGAG
CTCTATGAAAATAGGCATACCGTGATGAAAGTGGTCCTATCTTTTACCCAGGATTACCTG
ACCGCGCATGGCCTTATTCCAGAGGATCTCGATATTAAGCGTGCTGGTGATTATCGCGGC
CAGGTTGACCAAATGAAGCTACGCATGGCTGTCATGCATGGTGTGGATCGTCTAGCCCAG
CGTCATTATGATGATTTGCGCTATGTCGGCGTGATTCAGGTTGATACGAAGCATGTGCAC
GCCCACTTGACCATGGTGGATGCTGGTTATGGACACCGGGCTGCTGATGGTACGCAAAAA
GGCAAAATCAATAAGCCAGGTAAGGCTATTTTGCGGCGTGGTATTGACGCCTGGCTTGAT
CAGCATCAGCATATGGCGCACTTGTCAGCAGCAGTGGGGTATGAAAAACGCAATGTCACC
AGCTACGTCAAGCGCTGGGCGTTTCATCAGCTCACCCAAGAAAGTGCTGCGCAATTTGTG
GTCGCTTGTTTGCCAGAGGATAAGCGACTGTGGCGTGCATCGACCAATGCCAAGGAAATG
GATAAGCCGAATAGATTAGTGCGCGAGTTGGTGGAGGCGCGACTTGGTGAGACTGATTCA
CCGATGCCGGCAGCACTGTCGCAGGTCTATCAGTATGCGCAAAAACGCCGCGTTAAAGAA
GGTTTAAGCAAGCAGGACACCCAGCGTTTGATTGATAATGGCCGCGAAAAGATCATTGAG
CAGGCCATGAACGGTGTCTACAGTGTCCTATCCGCGATTTCCGATGAGCAACGCGATGTC
TCTACGGCCATGTTGACAGTCATGCGTCAAGACTATGAGGATTTGCTCGATGGTATTGCG
CGGAAGAAGAGCAAGGATCTAGACGAGCAGGGTAGTAGTGGATCACAAGAGGTGGGGAAA
GAAGAGCCTGAGCCAAGTATTGAGGAATTTGGGCTGCGTTTGCGGTCGTATTCAGCACGC
TTGAATCATCACCGAGAACAACGAGAAGCCTTTGCCGTGAAAAAACGCTCGTGGGAGGAC
GCTAACTCTCAAGGTTTGGCTGATCCCACCTCACAGGTAATGTGGAGTTTTTATGACACT
GAGGAGCAGTATCATGCGATGTGCCAATCCAAGTACCAGCACTTTTTGACCTTTGCCCCA
CCTGTCGGTCAGTGGGAGAAGCAATGGGCTGAGGTTGCTGATTACGGTAAAAGGGTTGTG
GGTCTGCGTGCACTGCGGGCAGATCGTTCTTTGGCACGCATGAGCGATGAACGTGCAGCT
GAAGCTTTGGGTCGGCAACTTTATGACCAACCCGGTGGTGGGTTATTGGCTCGAACAGGC
GCTGAGGGTAAAGCTGGGCGTGCGGTCCTGGATGGCCGAATTGAGCGCATGATGGTGACC
TATCAGCAAAAAATTGATGATTTGCGACGAGAATGGGCACAGCTCGGTGCACGTTTAGAG
GTTGAAGGTGATGCTGTATTGATGGATGCAGCAGATCTACGTGAATCTGGGGGAGAGGGT
GCAGATGAACGCCAGATACAGCAGCAAACAATTGAGTTGCCGGTCGCTGATGTATCTGAT
TCTGTGCGCACATACCTTGACGAAGAGTTACGTGATAGTCGTGATGTGAGCGCTCATGAT
CCAGTGCACACCTTGCGTGGCAGGTTTCAGGTCGTGTTTCGACCGGAGCATGATTTTGAG
CAGGTGGGTGGCCCTGACCTGCGCGATCTTCACTATGCCTGGTTTAGCGATCAGAAGGTC
AGTCAGCCCATTGTGTGTAGTTACGGTGAGTTAGTCACCCAGCGACGTTATGCTTTTGAA
CGCGCTCGGGAGTGGATGATCAGTTCGCAGCAGGAACCAGAAGCAGTGGCAGAAGAGCTT
GATCATGCCGGCGCGGACATAACTCGCATGGAAGCAACCAGTAGTGAGGTATCCCGTACA
GGTATTTTGCGTAGTGCCATGCTTGCCAGAATTAGAGAGCAGGCGCGACAACGCGCTCAG
CGTGCAGCGGAAGAGCAGGCTCGTCGTGAGCGTGAGTTGGTAGCACAGCGACAACAAGAA

ATTGATCAGGAGACCACGCAACCAGCGTTCGAGGTGGTGCAACGACATGTACAACCGGAG
TCGGTGCAGATTAAGCGGGGTAGAACAGTTGCGCTAGATAAGCGAGTGCAGCCACTGATT
CGTGATGCTGTGGATCGAGCTGTGCTGGATTCACAGCTGCGGAGTACCCGTGATGGTGGA
TTGGGG

>RXA01543-downstream
TAGGCGGTTGATTAAAAAAAAAG

>RXA01544-upstream
CTAGATCTATAACGAGGATCGGCGCTACTTTAAGCATGTTTGTGCTGTTGGCGCCGATTT
TTTCATAGCTGTACACACATAAGGCAACAGGAGAAATACA

>RXA01544
GTGAAACTTGACGACGCTATGGTCATGATCGAACAGCGCCTGGTCAAAGGTCGCGGCGCA
ACCAAGACGCAACTAGCACCCTATGAGCATATCCAGCGCAATATTGCAGCCCGAGGGTTG
AGAGCCGATGACGGAGGCTCGTGCTTCGGTTATGGGGATGCGTCGCTGAGTAATGACGAT
GTAGCAACTGCTGCAGAAGATATTCAGGATTTGTTTGCGTGCGGGCATACGGTTATCTCA
GCGATTGTCGTTTTTGATAAGAGCTATCTCAGTGAGCATGGAATCATGAGCTTTGATCCG
AACTATTTTGGTCAGGATATTTATGCGGACACCCATCCAGAGATTGATCTCATGGAATTG
CGTTTAGCCGTGATGAATGGGCTCTTGGGGCTTGAGGGAACGTTTTTTGAGGATATGCGT
TATGTCGCATCTATCGAGGTGAGCCGGAGCTATGTCTATGCGCACATAATGATGGCGGAT
GCAGGCGTTGACGATGCACGCGGTAATGCACAGGTGAAGATTACGGACACCGAACGAGTG
CTGTTTAGACGTGGTGTTGAATCCCGGTTTGTGGAGCAAGAGGCACGCAACGTCGTGCTT

>RXA01544-downstream
TAGCCAAGGTGAGGCATCAAGAG

>RXA01545-upstream
ATAAGAACCGACACGACGCCCTCAACGACGCTGTTGCAGCAGCTCGCAACTAGCTAGTTA
CCACGCCTGACACACGATACGTAGAGAAAAGAGAAATGAT

>RXA01545
ATGAAGCTTGCAGGTTTTAACACCAATTCACCCGCAGCGCAGCGGGTTGCCGAACAGGGT
GAAAAGGTACAGCTCGATGCACCGGTGTACGCGGTGTTTACCCCAGATGTTGTTGAAGTT
GAGTTTATTGGCACGCAGCATGAGCCGGTATTGCACGTTGAGGGTGCCATCGACAGCGTG
ACTGCATTGTCGCAGCTACCGTACGACATTCAAAAAATTACGTTTGATTCAGAAAACCAA
CAGCGTTTTAGTGGATTTTATAAATTCAGTCCACAGCAGCATAAAGAGCTCATTGATAAA
GGTCTGTATCTAGAAGGTTTCCAGCCACCGCGCGAGATGATGACGAGCCTGCCGTGGGAA
CTACCCATGAATGCCGATGTCACTGTCGTGGCACCAGAGTCGCAGGATGCGCCACCGATT
GTGCTTGTGGGCTTATCTGAGATTCATGGTGTGGATTTTAGTCAAGAATCCTCTGGCTAT
GAGCTCACCAGCATGTTTGAGGACTACCGTAGCCAGCGTGAAGCGGGCGAGGCGGACAAG
GATTTCTCTGAGTCAATTTCTCGTGCAGAGATTGAAGGCAAAGATATTTTCGCTGATGCT
AACCGCACCCGTACCGGTGTCAGTGCACATGCACAGCGCCTTGAGCAGGAGCGAGCGCTG
AGCGCAGCACAGTTGATGGCGAAACTTGCTGGCATTTCCTTCCAGACTGAACCCGTGCTT
GTTGGTGCGGAAGAGAGCTTTGATGCTGAGCAATTCCTCGCCCATGATCTTGATGACACC
GCTGGTATGAGTGAGTGGGAGCGCGAGGTTACCGAGTTCTACAACGAGAAGATTCGCGCC
CAGGAGCCTGTGGTGGAGCGGGAGGCTGAGCGGGATAGCGATATTGAGACTGAGGTTGAT
GCAGCACCAACTGTCAGTGCTGCAGAGATTAACGATGTTATTCATGATCTTGATGAGCTT
GAATTCGATGACGTGATTGATCTTGATGCAGATGATGTTGTCAATACCGCCGAGGTAGAG
GCGCCAGCAAGTGTCAGTGCTGCAGAGATTTCTGCGACAGAGCTTGATTTTGATCGCGAG
TCACGGGCTAAGACCGCGCAGCGAGAAGCCAGCCGACGTGTTGCACAGAAGATTCAGACT
CAAGAATCTGTGCGTGAGGCATATATTCGCGAGCAAAAGCATGGCTATGACGCATCACCT
GCGGAGGGGCGCAAGTTTGATGAGAAAATTGCAGAACGCGGGCTAGATCTA

>RXA01545-downstream
TAACGAGGATCGGCGCTACTTTA

>RXA01546-upstream

ATAGTTAGTTGGTGACTAGCTATTGGGGGTTTTGTCTTTTAATATTATAAAAAGAAAGTG
ACAAACATACTTGCATTAAAAAGGAATTGAGATAGGCACT

>RXA01546
ATGGCACGAGCGAAAAATAAGAAACAGCGTCAATTGCAGCACGCTCATGATGCAGCACAG
GCTGAGATTGCAGAAGCGGTAGCGGTTAACACGGTTGAACCAATTAATGCACGCACCGGT
GGATGGCCTTCGTGGGTCGATAAGGTCTGGAAGCTCACTGGTTCACTTGGTGGTTGGTTT
GCTTTCCTGGTTTTTGCCATCGCCGTGTGGCCGGTAGCGATCCTTGCAGCTGGCACTGTG
GTCACCATCATCGGTACGTGGGGAGTATCAGTACTGCCAAGTCTGGTTATTTCCAGCATC
GGCGCTTCTGCTGGTGTGATTATCTCCACTACTGATGGGTTCCTCTTTAGCTGGGTCATC
CCGGTGCTGTTTCTCATGATTGTGCTGGCACTGGTGGTCATGAAAGTGCTCAATCTTATT
TTTGGTGCATTGTGGCGCTTCACCATGACTTTGCGACAGGGGTTATACGCAGGTCGTGAA
AAGATTTCTCGCGACGACGCGAAGCGCGCACGAGCAGAAAAGAAGCTGACTAAGCAGCAG
GCTAAAGAAGCCAAAAAGCAGCGCAAACTTGATGCCATTTACTCGGCTCAACAGGCTGAA
GAGACTCTGGCGCAACAGGCACAGTCTGAGCCAGAAGAGTCAGACGATAAGAACCGACAC
GACGCCCTCAACGACGCTGTTGCAGCAGCTCGCAAC

>RXA01546-downstream
TAGCTAGTTACCACGCCTGACAC

>RXA01547-upstream
TGCAGCGGGCACTAGAGATCGCTCAGCTGAACAAACAGGAGAACAGATAATGACGACACG
AAATGTAGATAACCAGAGTGGTGTAACTGAGGACGAGCCG

>RXA01547
ATGTTCGATCAGGTCAAGCGCTTTTTTGTTCGCAATATCGTCATGATCATTGCGTTGATC
TTGGCAGTGGTGGTCATTATTGTTGCCACCAGCACCTCTGCGGATCGACATGCTGTACTT
AAGCGTCAAACTGGTGAGATTATGGCCTTGCAACAGGAACGTGATGCATTAAACAGTAAG
CTTGAGGGCCAACTTGAGCAGGTGGTGCGTGACGCTACCGGTGGTATGGATATTGAACAC
AAGGCTGCAGATGATGCTGTTGTTCGAGAATTTTTGTCCATGGCGCTGACGTGGGACAGC
GTGCGCGACTACCTTGATGTGCGCGAGCAAGTGATGCGGGTTTATGACCTGGATGAAGAA
TCACAGTTTATGTCGGTGTTTATGCCTGGTGAAATGGCGGGCATTGCTCGCACCGATCCA
ACTGGCGAAGTGCACTATGCCTATGATGCAGATCTGTCCAACCGCTTTAGCAGCTTAGAA
TCCGTGGTTACTCGCATTAATGGTACAGAGTACAGCTATGTATCCACGGTGACGATGAAG
TCGAAGCGCTCTGGTGGTGAGGCAGAAACAACCTCTACCTCACGCCTTGCCTATGACGTG
ATCGACGGCAAAATTCGTAACCTCGAAGCACGTACTGTCCCCGGTGGTGTGAAATACTCG
GGC

>RXA01547-downstream
TAAAAGTTTCTGGGGCAACCCCC

>RXA01548-upstream
GGCGTGCGAGCTGCTGGTTGGCGCTTGTGCACCCCGTTTTTGTGTAATAACTTATATTCT
AGAAACTTCAATAACTTAGTAACTTTAAAAGGGGTTTAAT

>RXA01548
ATGGCTGAGAATAATGGCGGGTCGGATGACCTTAAGCCCATCTCTGTCGATGGGGTCGTC
AATGGGGAAGTGCGCAGCGACAAAGAAAAGCAGGCGTTCGAGAAGATTACCGGTGATGAT
CTGCGTCGTCGTGCAGAACAAATCCGTAAACGTCGTTTAGCAAAAGCGCAAGAAGATGCA
CGTAAGCGTAAGCCATTGTTTGGTTTGGGTCGTATCGCTGTCACAGTACTGGCTGGCGCC
GTATTTATTGGTACAACGTTGTGGATCAGTACCACCTCGGGCGGCTTTGACGACAAGGTG
AGTGCAAACAATGAGCAGATTGTCACTCTGCGTAATGAAGTCAACGACTTAAAAAACACT
GCAGAGACAATGCCCAAAAAAGAGACTCTTGCTAGTCAATTTGACGCAGCAACCTCACGT
GCACAGAATGTGGCTGACTTACAGAATCAGTTAGCCGGCATTATTACCAGTGTTGATGAT
GATGCCGCGACCGAGCAGTTCAAGACAATTGTTGATGAGCTGAAACCGAAATTCACGGTC
TCTGCTGGTACGACAGGTGAATTTCCTGCGGCGGGTCGTTGGTACCAGCCACAAGAAGTT
GTTGTCGGAGATAACAACCGACCCACCTGGGCGCCGATGGGGGCTGAGTCCTGGGGATGG
ACTGTGACCCCTACACTGTCGATGTCAGATACCGAGCACGTTGTGGTGATGTGGGAGGCC
CGCTTGACCGGAGGTGAGCGTTACGGTGCGCTGTTGGCGTGGGTGACAGCCGATTACAAC

ATCAACACCGGCGTGTTTAGCTCGCTGGCGTTGGCGCATACCTATGAAGGACACCAGCGT
ATTGGTGCAACCACCTCACCAAGTGAATTTGGTGCCCACGGCACAAATGCAGAGGCGAGC
GCTGCACGTGCTGGCAGTGAAGGCGGGGGGCTTGAGGGCGAGGCTATTTTCGTTGATGAG
CTGCAGCGGGCACTAGAGATCGCTCAGCTGAACAAACAGGAGAACAGA

>RXA01548-downstream
TAATGACGACACGAAATGTAGAT

>RXA01549-upstream
CAGCTTGCATTTGCTATTAGTGGCGATAATGAAAGCGATCGCAAGGTTTTTCTGGAAA

>RXA01549
ATGGTTGATAATAAAAACTCCAGTAGCAATAGCCCCACCGCAGCGTCCGAGTACTTCCTG
CGTGAGTGGGAGCGCCCGGCAGATGTCGCAGGTAATGCACCCATTCGTGCAGAGCAAGCA
TCTAAGTGGTACGCGCAGATGGGTGGTTGGCAAAAGAACTCAACCTTGGGTGAGTCTGTG
ATCGCTATGGCTGATGGTGCAGCAGCAAAATCCACGGCGCGTGATGAGCAGGATGCTCTT
AATGATTGTCCTGAAGAGGACCGCACCTCAGGTGGAAATACGTCCGCTGCAGAAGCAATG
GTGACTATTTCACATCCTTATCTGGCTGATTCTCGTGGCAATGACGGTACTGATATTTAC
CGCTATATCCATGATGAAGTGCTCACCGGTGATCCGTATTACGCATCCTGTGACCGTGGC
GTTGCTACCGCTATTCGCTGGTCGGGCACGGATGATACGTTCCCAGCAGGTCCAACAGCA
GCACAGTATGAATACGTTGTGGGCACAGGATCGGGCCGTTGGGAGGAAATCGGCAATCTT
GCCACCATGTCAGAGAACGATTTGTTACCTGGCGATGTGCTTCTTGGTGCACCGAATCAC
GTTGCGATGTATGTCAGCAATGAGGTTGTTGTGGACATGTTGGGCCCTGGTAATGCAGAG
CCTAATGCAGCTATTGGTCATGCATCGTTGAATGACCGCTCACCTGGTCTGGATACCTTG
AGTCTGGATGGATGGGGCGTGAACTTCAAGGTGTTCCGCAACACCCAGGCTGAGACAAAC
TCAGTGTTCTCTGGTGTACAGATTCCGGCTGGTAAAGAAATTGGCGAAATGACTAACCCA
ACTCGAACTACTCCTGCAGGA

>RXA01549-downstream
TAAGTTTTTTTCATCGCTGGGTT

>RXA01552-upstream
ACTTTGCTCTTTTTATGGCGCTGCACGAGATTCAACTCAAAGTGAAGGTCAGCTATTTGA
ACTCAGTGCAAAAGATGATCGGCATACCAAACTAATGAAG

>RXA01552
ATGTATCTGGGAATGAAAGAAGATTCCCTAGCGCCACCCCAAAATAGATTCGAGTCTCAT
AAGACTGTCTTTTCCCTAAAACAGAAAAACATCCCAATTAAGGATGCTGCTAAATCTGAT
CAGGTGAATCTCACTTGGCATGATTATCCAGGTGAATGGTTTGAGGGTGGAGCTGTAACG
GACTCGGAAAAGCAGGATAAAGTTGAAACGTTTAGAAACCTGCTGGGCTCAGATGTAGCG
CTATTTTTAGTTGACGGTCAAAAGCTGCATGATTACGCCAATGAAGAGGAGCGCTATCTT
AGCTATTTATTTGATGGATTCATTGAAAACCTAAATCAGATCAAAGATGCAATCCTGGAG
GGTGGGAAACAGCTCCAACAGTTCCCACGAATTTGGGTAATTGCTTTATCCAAAGCTGAT
CTATGGCCAGATCTCCAAGTAAAAGATTTTGAGAATCTACTTAATAAGAAAGCTGGCAAT
GAAATTATTGCGCTGCGTTCAAAGCTTTTGGAGTTTATCGATAACGACGAAGCTTTCTCC
TTCGGTAAAGATTTCCTTTTGCTCTCTTCGGCGAAGTTCACTCCAGGCCATATTGATATA
AGCCAGCGCAAGGGTGTTGATGTCCTCCTCCCGTTGGCTTGTGTATTGCCCATGCAACGC
CATTTGTGGTGGCAGGAGCTGAAAGTTTTGCCAATTAACCTGGCTGATATACTTTTGGGA
AATGAAATTGCCCAAATGGGTTTCAAGATCGTTTCCAAAGTTTTGAAAAACAAAGTATCT
GGAACAAATAACAAGGCGATGGCGGCATTGGTTTTCGCTGAACTTGTGAGGGATATGGTT
GATCAGCCAACTGAATTGCTTCAGAAGGCTCGTGAGGAAGCCGTCGGAAGGCGTGAATTC
CTTAAAGCGATTACTGCAGAATTCACCAGGAAGCTGAATCAAGCCGAAGCTGATCAGGTT
TTAGTTCGGGACTTTGCA

>RXA01552-downstream
TGACACTCATGTGGGCAACCCGT

>RXA01554-upstream

TGGCTTAAACCTTATTTGTAGTTGTCAATAAATATGAAATTCCTTAGCAACTTGTTTAAA
TAGACGTATAAACAAGTTTGAAAAAGGAAGGTTATCCATC

>RXA01554
TTGAAAAAGCATGTGACCTCAGCCGTTACCGCCGTGGTGACGGCTTTTTCAACGGCTGCG
CTTGGTTTAAGTATTGCCGTTTCTCCTGCTGTTGCCCAAGTGGCTAATCCAGCTCCAGAT
CTTTCTGCGCCGTATACATGGGTGGAAGAGTTTGATTCCGAGGATGCTCTCAAAGGGTGG
AACATTTTCCGCCAGCCAGATTATGGCAGCGACAAAGTTCTCTATACCGAAGATGCTTTA
AGTATCGAAGATGGCAAGCTCACCATCACCACTCAGCGCCACTGCGTTGACGAAGACTTC
GCGATCAGTGATCCTGTCAACCGCGGAAAGCTCAATGACAGCACCGCGCAAGTTGAACCT
TGTGCTCCAGGTCAGTTTGAAAAGTTCACCAGTGCGCGCATCGTCACTCCGAAAATTGCT
CGTGGAGAGTTCGACCTTTCTGTCACTGCAACTCTTAACACCGGTGGCGTCGAAGGTGTC
CGAAGTGCCATTTGGATGCAAAACGGTGAACAGGCGTGTTCCTCAGCAACCAACAATGGC
CTCTACGGAGAACTAGACCTGGTAGAGCACTTTTCTTACGATCTTCGCTCGCCATGGTCT
CCATCAAACACCCACTTGGGTTGTGATCCTGAAAGTGTCAACGGCACCAACCGTGCACCT
CGTGAACTTAAACTAGATGAGTCACTCGATGGCGTGGAGCACACCTGGACTGTGAGCACC
ACCCGCGACGGCGTTGAGTACTTCATTGATGATGAGGCGATTAACCGCCAGTCATGGCGC
AACGATGTCACTTTGGGGCATGCCGAAATTGATGATTTCGGGATCTCCGCGCAGACGTTT
GATGAGATCGTCGACCGCGAATGGACTCTCACTCTTAATCAAAAGGTAGAAAGCGCCGAC
TGGGCAAAACCACGTTCCTCTGAGGAAGATTTCCCAGTCCGGTCCATGGTGATTGACCGC
ATCGAGGTCACCGGATCTCCCGCAGTATCTGAAGACACCCCCATGCCAGATACCACCCAG
CTTTTGACCCAAGACACTCTGGAATACCTCGGTCGCATGCCAGTGCTGGAACGCTACGAG
CCAGCAAGTGCTGATTTTGCCGATGGCCGCAGGCCTTCCTGGAACTACTTCAATTTGAAG
GAATCGTGGCAGAATCCAGAACTCGAGCAACGCCCAGAAGCTGTCGAATTCGTTGATGGA
CGCATGGATATCGTGACCCGTCGCCACTGTCTGGCCACCACTGATGACATCGCCACTCCG
GAAAACGCACAGGAGGAACCGTGCGCGCCGGGTGAGGTGACACGCTACAGCTCAGCGCGT
GTCCACCTTCCAGAGATCCCCGCCGGCAACTTCCGGCTCACCGTGCGCGCACGGGCGCAG
TCCGAAGAGCTTGTCGACGGCGTCCGCCCCGCTATCTGGATGCAGAACAATACCAACTTC
TGTGCTGACAACGATGGACGCCCTTATGGTGAACTGGATATTACTGAGTTCTACAGCTCT
CGTGTGAACACCCAGTACTCGGCAGTACACCTTGGATGTGCTGGCAACCGCCCAGAGATG
AAGCTTCGCCAAATGGAAATGGAAGAGTCCATGTTTGGGGATTGGCATGACTGGGGCGTC
GAAGTCTTCGACGGCCAGATCGTATTCACCATTGACGGCAAGGCAGTAACTTCCTCTGGC
AAAGATGTCTTTGGCAACTCTGTTACCCCAGCCGCTGCACCTCTTCGCCCCGCGCACTTC
AAGTTGTCGGAAGAGGAATACCGTGAAGTCATCGGGCAGCCTTGGCACCTTATTTTGAAC
ACCATGGTGGAGCAGTCTGGCAAAGACAGCTGGATTACAGCGGTCGACAATAACGAGGCG
TTCCCAGAACACCGCTTCCAAATTGACCATGTGGCAGTAGATATCGAGTCTGACTCTGTG
GACAATGTATGGCCTGACGCTGCGAATGAAATCCCAGACAATGTTGGTATTGAAGACTCT
GATGATGGCAGCGACCTGGAGGTTGGTTCGACCGGAAGCTCTACAGCTGAGACCGTGAGC
TGGATCTCGTTGTTCACCGCGTTGAGCTCGCTGGTCTTCACACTGGCTCTCAATCAAGAA
GCATTGCAGAATTTGATTAATCAGTTCATGAGACAGTTCAAG

>RXA01554-downstream
TAATCCTTGTGGGCGCTTTGTCT

>RXA01557-upstream
TAAAGGTGTGAAAATAGTTCCTCACGTGGGGAACTATACTGATCCTTGATGCGTTAACTT
GATTGACGACGAAAAATCAATTGAAAGGATCGGGGACTCC

>RXA01557
GTGCGAAGCAGCAATCCCGTTTTTAGTTCCCTTAAGGAAACTCAACGTCCACAAGGCCAG
AACCCATACGGTGGTTACGACAACTTCGGTGGTGTCTACCAGCAAAACGTAGCTCCACAG
AAGGCGGAGCGCCCAATGACTGTGGATGATGTGATCACCAAGACTGGTATCACTCTCGCG
GTTATTATCGTTTTTGCATTGGTCACCTTTGGCGTGTGGTTGGTTAGCCCCGGCCTCGGA
ATGATCTTGACCCTTGTTGGTGCCATCGGTGGTTTCATCACCGTTCTGGTCAGCACCTTC
GGCAAGAAGTACGGATCTGCGGCAGTCACTTTGATTTACGCAGTATTCGAAGGCCTCTTC
GTCGGCGGAATTTCCCTTCTGCTGTCCGGCTTCACAGTTGGTAACGCCAACGCAGGTGGC
CTCATTGGCCAGGCAGTCCTTGGCACCATCGGTGTATTCATTGGCATGCTGTTTGTATAC
AAGACTGGCGCTATCAAGGTCACTCCTAAGTTCAACCGCATCCTCACCGGCATGATGGTT
GGCGTCCTGGTTCTTGTCCTGGGCAACGTTGTATGGGCACTGTTCACTGGTGGCGCAAGC
CCACTGCGTGACGGTGGAATCATCGCGATTATCTTCTCCCTCTTCTGCATCGGCCTGGCA

GCATTCAGCTTCCTCTCCGACTTCGATGCAGCTGACCGCCTCGTCCGCGAAGGTGCACCT
TCCAAGATGGCATGGGGCGTTGCGCTTGGTCTTGCAGTGACCTTGGTCTGGCTCTACACC
GAAATCCTACGTCTGCTTAGCTACTTCCAAAACCGC

>RXA01557-downstream
TAGTTTACGCAGCACAAGACCCC

>RXA01560-upstream
ATGGGAGCAAGGCTCATTTAGCTACTTCGACGTGGAAGCGCACATCGTTGAGTTGATTCC
TGCATCAGTAAGCGATGCGTTTTAGGCACATCTGCGATCC

>RXA01560
GTGGGCGTGTCCTACATCATCGCCGGCGATGAGCAGCTGGATATGGCAGAAGCCGTTCGC
AAAATTGGGGAGACCTTTAAAACTGAGGAAATTATCCTTGGTGGCGGAGGAACCCTGAAC
TGGTCCATGCTCCGCGACGGTTTGTGCGACGAGGTTAGCATCGTGATGATGCCAATCGCC
GATGGTGAAAAGCACACCCACTCTTTGTTCGAAGCCGATGAAAAATACTCAGCACCGTTG
CCGATCGGTTTTTCACTCGCCAGCGTTGAACCACTAGAAGATGGAAGCGTTTGGATGCGT
TACGGGGTCAATGGCCCAGTGGACGCGAAC

>RXA01560-downstream
TAGGTAGCAAATACTCGCTCTTT

>RXA01574-upstream
AAAAATCCGCACACCCCACATTGCTCAAAGGAATTGACAAGGCGCTTCGCAAGGCCGAGT
AAGGTGGGCAACGAGTCGGTGAGAGTATGAGGAATATTTG

>RXA01574
ATGAGCAACAAACGCATCGGTGTAGTGATCGTTTCCTACGGACACGAACAAGATGTTGCC
AACCTGGTAGACACATTTGCAGATCAGCTGAAAACTGGTGACCGCGTAGTTGTCGTGGAC
AACCGCAAACCTTGGGTGTTAAAAGACGCCGTGGGGGAGCGCCTGGAAAAACACGGCGCA
GAGATCATCAACCACGACAACGGTGGTTTCGCCGCTGGCTGCAACGTGGGCGCAGCGCAC
ATCGTGGATGACGTTGACCTGCTGTTCTTCCTCAACCCCGACACAGTGATCGACGATCCC
ACCCTGTTCAATTCGCTGAGACGCGTCGATGAACAGTGGGCAGCATTCATGCCGTACCTG
CTGCTTCCTGACAGCACCATTAACTCCGCAGGCAACGCCCTGCATATTTCCGGACTGTCG
TGGGTGACTGGTCTGGATGAAAAACCAGTTGAAGGCTCATCTGAAGTTACCGATATTTCC
ATTGCCTCTGGCGCCTGCCTTGCCGTGCGCGTGGACTGGTGGAAACGCCTCGGTGGCATG
GAAGAACTGTATTTCATGTACCACGAAGACACTGACTTCTCCGCCCGCTTGCTGCTGGCC
GGCGGTCGAATTGGTCTCCTGCATTCCGCGTATGTCACCCACCATTACGACTACGCCAAG
GGTGACTACAAGTGGATTTACATCGAACGAAACCGACACGTTTTGCTGCTCAGCGTGCTG
CCGCTTCCATTGCTGTTCGTGCTGATCCCGCAGATCCTCGGTGTGAACCTGGGACTGTGG
GCGATTGCCGCAAAGGAAAAGAGGGTCGGACTCAAGGTGAAGTCCCTTCGCCTCCTGATC
CGCGATCTACCAGCGATTTTCAAACTGCGTAGGAGCACGCAGGAGCTTGCCGAACTCACA
CCATCGCAATATCTGGCAAAAATGGAATGGCGCCTAGACAATCCCAACCTAGGCAACATT
GGATCCAACAAGATTGTTGCGACTGGATATAAGACCTATTACAAGTTGTGTATGAGTATC
CTGAAATTGCTCGCT

>RXA01574-downstream
TAACACCCCATAAAGAGGGTGAA

>RXA01575-upstream
GCTGTTTTTTGATGCATCCATGATAGGAATAGAGCCTAGTGCATGATGGCTGATTTTCCT
GTTAGGTGCCACCGACCCCAGTGATGATAACTTGATTGTC

>RXA01575
ATGAAATCCATTGATCTTGAGCAGCTGGCGGGCACGCAATCGCGCACGTATCAATCGCGA
AAGATCACCGATGAGATGGTCGCCCGGCCGGTGCATGTGGCGATCGCGCTGTGGGAAGTG
CCGTGGGAGTCGGCAAAATCCGGCAAGATTGAGGGTTGGGTCATTGCCGTGGATTCGCCG
CGTGGGCGGTTTGTGCGCAGCGGGCAGACCAAAAATGGCGACGCCGTCAACCGGACTGTG
TCGATGCTGAAATCAGCGTTGAAAGGGGTCCGCGGGAAGGCGTGGATTGTAACTGGGCGT

CGACAAGCAGCTTTACGCGCAGCCCTGGTGCGCGAAAACTACCTGGTCACCGGAAGCTTC
GCCGAGCAAAATAGGGCCGGCGTGAAGGCGTCGGCGATCTCGCGCCGCGCCGAACAATCC
GCGCTCTACAAGGCGAAAAAAATCGGCGAATTCGCCGAGCGCGCCCCACGCGTCAAAGAG
CGGCAAGAGGCACATTGGTGGCCACGGTTGTCACGCACGCAAGGCACCGCAGGCGTTTTA
CGCTTAGCGACGGACGCCTCTACCGATGGGGTCTTCCGCGGCGCCATGTGCTTCGTAGCC
TCAAACGGCGACTACCTCCTGGAGACCCAAGACACCACCGCAAGCTCCGACGAATTAGAA
CTCGAAAGCATCACCCACGCCCTGATCTACCTCAAAACCATCGGCGCGACCCAAGCCATC
ATCGAATCCGACAGCAAAGCCGCACTTGAAGCCATCGACTTCATCCTCAACAACCGACCG
CGCCGGGGCAGGTGGCGCGGCATCACCGCATGCGCCCGCAACCGGTTCCGGGATGCCTGG
GAAGCGCTTATCGACGACTGCGTTGTGGAATTATCCCGCGTACTAGGGCACGCCGGGGAT
CCACTGAACCAAGCAGCCGACCAAATCGCATACATGGGCATGCGCGCCGTAATTTTTGAA
CAAAAATCCGCACACCCCACATTGCTCAAAGGAATTGACAAGGCGCTTCGCAAGGCCGAG

>RXA01575-downstream
TAAGGTGGGCAACGAGTCGGTGA

>RXA01577-upstream
CCGTAGACATCCTCTACACCGAATACTCCATGAGCAAGGGGCAATCCCTGCTCAACGGCG
TAAACATCCTGGCCGACGGCTTCCTAGCGAGGAGACTCCC

>RXA01577
ATGACGCAGACCACCACCCAAATCATCATCCAGATACTGCTTCTCCTGGCAACCGCAGCA
CTGGCACTATATTTCCTCCGAAACCGCCGCAAAGCCCGCGCCAAAGCATGGGTGAAAATC
GGCTTCGTAGTATTCATTTTCGCCGCAGTATGGGCAGTGCTCCGCCCCGATGACCTCACC
CAACTAGCCAACTTTGTGGGCGTGGACCGCGGCACCGACCTAATGCTTTACGCCCTGGTT
GTGGCATTTATGTTCACCACGCTGTCCAGTTATGTGCGTTTCCGTGAACAAGAGCTGCGT
TATTCCAAGCTGGCCCGCGCTGTCGCTTTGCAAAATGTGGTGCTGCCGGAGGATTCCCAG
GGTTCTGACCCCGCT

>RXA01577-downstream
TAGGAAAGCGCTTGGCCTCTGGA

>RXA01579-upstream
TGGCAGCATCCTGCGCAAGGTTGGGCAGCAGACCATTCATTACGGCGAATACACCGGTCA
TTGTGAGAAGGGTGCTCAGCAGCAATGCCCAGGTGCGTCG

>RXA01579
TTGACCGAGGTATTCAACACTGACCAGCGGGTGCTTAACGCGCTTTTCAATGTTGTAGAA
GAAGATGACTCCGGCGATACCGATGATGAACAGCACAACCACCAGAATCCAGTTCGCGGC
ACCGAGTTTGCCGGCCTCGTTGAAAGCCATGAGCAAAGATCCAATGGACACCGCCAGTGG
CAGCACACCAAGCCAGTCCATCTTCGGGGTTTCTTCAGCGGTGGATTCCTTCACGCTGAA
AGGCAGTGCGAGGGCAGCGACAGCGCAGAAAGCAGCCATGACCCAGAAGATGGAACGGAA
ACCAAGTGTTTCAGCCAACCAGCCACCAGCAAGCGCGTCCACGCCGCCGATACCACCGTT
GACAGAGGTAACAATTCCGAGAAG

>RXA01579-downstream
TAGCGCATATTGCTTTTCATTGG

>RXA01585-upstream
TGCAGACTGCTGCGCCCCGTTCCATCAGCAAGGTGGAGCGCAAGGTGCTGACCGCTGTCG
CTACTGATGAGGTGCAGTCGCAGGAAGCTCTAGAAAAGTA

>RXA01585
GTGGTTGAGACTCTTTCTATCACCTCAGGTGCGGCTGGCCTGCAGGCGCTTGTTGCGCGT
GCGGTTGGTTTGAATGAGTTGGCGAGCGCGCGTTTCCGCCAGCTCACGCCAGAGGTCGTT
GATGTTTTTGTCACCACTCCGTTCAACGTGACGGCGTCGCGCCGGGTATTTGGTGTGGCG
GGTCGCGATGGCGCTGCAGTTGGCGCGAAGGATTTGCTGCAGGCACTCAGCGAGGGCCGG

GAAGACGTAGGCACCTCCCGCGACGCCAGCTGGCCGGGCTCATTGCCGCCAGCCACGGGC
TTTACGCTTGTCGACGAACTCCCCACCCACGTGGTGCGCACTTTGGCTGATCAGGGTCAG
GCATTGGCTCGCCAGTTCTCCGGCCCGCTTGGCCCTCCGGCTTCGTTGATGGATCAGGAA
GTTATTTCAGCAGAAGGCAATGGCAAGAAGGCCGGAATCCCGATGCGCACGGTATTTACC
TGCACTTCGCTTGGTTTGATCCCAGGTTTTGAGGCAGCCAATGATGTGCCGAGGCACCTG
CGGGTATCGGTGAATGGTCGTTGGACCCGCGTTGATGCTCCCTATGGCAGTGTTTATCAC
TCGTCAGGTTTGGGTCTGAGCGTTTTC

>RXA01585-downstream
TAAAGCAAGACCCAGCCTGCAAG

>RXA01586
AACAACGCGGCGTTCATTGAGATCGCGCAGGAAGCTCGATTGGCGTTTGCGGAGGATCAG
TTCCGTGAGCGTGGCTATGAGATCCCTGCTGTGTTTGTGCGCCACTTGGAAGTTGATTAT
TTGCGTGCGATCTTGCCGGATACCACCCAGGCTGTCGTGGAGACACAGGTGACCAAGATC
GGTAATACTTCCTTCAGCACTCGTCAAGAGGTCAAGGATCGTAACGGTCGTGTGTGCTGC
GTGGTTGAGTGCGTGCAGGTGGCTGTCAATGTGCAGACTGCTGCGCCCCGTTCCATCAGC
AAGGTGGAGCGCAAGGTGCTGACCGCTGTCGCTACTGATGAGGTGCAGTCGCAGGAAGCT
CTAGAAAAG

>RXA01586-downstream
TAGTGGTTGAGACTCTTTCTATC

>RXA01587-upstream
CATTTAGACTGGTCGGTGGACCCGTTCTTAGAATACTAACAAGACATTCACTGAGAATAT
GGCTGGTGGGCAGACCACAGAAGGAACACCGCTTGGAGGA

>RXA01587
ATGACTGATTTCTTCGGGTTGATCTATAACTGGTCAGTGACTGTGGGCTGGCTCATCGGT
ATTCCTGTCTCCATTGGTCTGTTTATGATGGGTGCGTTGATGTTTCGACGCATGGACAAG
GGATCAGCGTTTAAAAAGGTTGTTATCCGCGTCGTGTACGGTGTCGTTGGCCTGCCACTG
CTTGGTGTCTCTTATACCGGTGCGCTGGATTCCTTCCTCGACAGCGGTAGTTCCACAAGT
GCTGGATCAAATGCGACAAAGATTGTGTTGTCCACCTACGTGGATTTCCAATCATGGGCA
GAAAACACCCGTATGCGTGTTCCTGACAAAGTAACACTGGCGTGGAGTCTGGAGGATCAG
GCGCCAACAGGGCAGTCCATGCGGATGGTACGCAATTCGGCGTTGGAAATTAATGCTCAA
TCAAATGAGAGTTTTACTACTTTTAAGAATCCAGGTTCCATGGATCTAGGCTATAGCATG
GACTGGATGGAAAAGATGGCGGATCCAGCCAATTCTGGCACCGATGGGACCTCATCAAGT
TCGGCGACGACTATTTTCCAGGGAACCATCGCGCTACTGAGTCGTTATATCGACAACGAC
AGTATCTCCTCTGGCAGTTTCGAAACCTCTATTCGAAGTGCGATGGAATCTTTGACCTCG
AAAGAGGGAAGTGGCGAAGCTGTTGCCGGTGGTGATGTAATGGCCTGGGTTACTGGTTAC
AACACAGCCTCTGGTCTTAATGAGATCACTGCTGCTGAATTAGCTGATGCGAACAATCCA
TTGCTTGAGGTCAGCGACTCAGCTGGTCTGCAGGGACGACCTATTGACCGCAATGCGGTG
TCATTTAAATCTGGTGATGCGACAGCGTCATGCAACAACTCAGTCGTGACAGGTTCTCGT
GCTGTGGTCGGGGACTACCGAAGTGACTGCAATATGTCGCCCTTGACGATGTACAACTTC
CTCAACACCTCATTCCATCCAGCTGATGCAAGTGTCTTTTCTACGTCCACTTCTGCGTCA
AGCTACACCCGTGCATCGCATAGCGCAGTGAGTCTTATCGGTTCTGGTGCCATGAACTTT
GTGTACTGGTTCTCTGCAATGTCCCTGATGGGTAGCTTCATCGTGATCGGTATCGGTTAC
GCCGGTGCCATGCTGTTTAATACGATTCGACGCACGCTGTCGCTCATTGGTGCCGTTCCT
TTTGCTGCGATGGGCTTTATTGCTGGTGTTGCCAAGGTCATTGTGTACACCATCGCTATG
CTCGTAGAGGTTATCGGAACGATCATTTTGTACCAGCTCATTACCCGGTTCTTGATGGCT
GTACCAGCACTCTTTGAACAACCTTTGGCTGATTCCTTAAGTAGTAACGAGAGTGCTGAG
CTGGTTGCCGGTGCTGGTATGGGGCTAGTCGGTATGGCACTAGCTACCTCAGGCAACTGG
GCGATTGCCGGCATGGTGATCACAGTGGCCTCATCCATGGGGGTCATCATCTTCACGATT
ATTGCGATGAAGGTGCGCGGATCTTTGGTATCAGGTGTCGATGAAACCGTGACCAGTGTT
ATTAACCGCTTCTTGGATACACAGGTCTCTTCTGCAGGTGCTACCTCTGGTGACGGCATG
ATGCGTCGTGCAGCCGCAACGGGTCTTGGTATTGGTGCGACACATATGGTACTCAACCGT
GATGGTGACGGTGGTGGATCTGATTCAGGCTCTGGTGGATCAGGTGGCGGTAGCGATTCA
GGCTTGGGTGAGAAGGCTGCTGGTCTGGCGAAGGTTGTCACAACTGTGGCTGGTGCCGGA
TTAGTCGGTAAGTATGCTACGGATGCGCTCGATAATTATGCAGATGGCGTTATCAACGGC

GACGGTGATGGTGCGTTCGCAGCAGGTGGTGACGCTACCGTTGATGGCGACTATGTAGCA
GATGGAGATGCAATTGCTTCTGCTGATGCTAACGCTGATTTTGTAGACGGGGTTGCTGAT
GGT

>RXA01590
GGCAAGTTGAAGGAATATGCCACCTATATCGGCGCTGATCCGGCGCAGGGTTTTAAAGAC
GTAGGTCAACCAACGCCAGAAGCGCTGCGTAGCCACTATGAGGGTTCGCAGAAGGCGACT
GCAATTAAGGTGCTCTTTACCGGTGTGGCTGGTAAAAAAGAGCAGGAAATGGTGGCATTG
TGCCGCAATCTTGGTCTGACCAAGGAAGCTATGGCTGCATCAGCACCGGCACAGCAGTCG
ATTCTGCAGGCGAAGCACGACCCGATTGACGCGCTCTATCGTGCAGAAACTCTTATGGGA
CCAGTAGGTGATCTCTACCAAGGTCGCAAGATGCGTCGTGGTGAGAATGAGCAAGGTCGC
TATGAGTGGGAAGTCGTTAGGGACGAGAACCACCAGCCTATCCAGGCCACCAAGGATGAA
TGGGTACAGCAGTACATGGAGATGTACGCCGATGACAAGGGTATGGGTGTCTCGGTTGGC
GTTGACCAGGTGGAGAAGATCGCGGAAGAATTCTCTGATGAGCAGGGTTATATGCGTGTG
CTTAGCCATGATGAGCTACCCACTGAGATTAAGCCACTAGCACTTGATCAGCTTGCCTAT
GGCGATAAGAAGAACCGCTTTGATTTGTTGTGCGAGATGGCAAAGCAGCAGGTCAACATC
TACGACGGTGATGCTTATGACTTTGCCCCTCGTGTGGTGCGCGCCAATATGAAGGCAATG
GAGGATGCAGCGCGTTTTGGTATCCCTGATGTGGAGATTCAGTCGATTTCTGCACAGCAG
TCATTGGCGAGCTTTGAGCGAGTCCCACAACGTTCTGGTTTCCGTATTGAGCGTCGTGTG
CCGGCAGAAGTAGGTACAGGGATTGCTGCACCAGCACCGTTACCTGATGCAGGTGTACAG
GGGAATTATGTTCAGCAGCAGGTGCCTGCGACCCCGCCAGTTATGCCTGTCACACCTCCG
GCACAGCAACCTGTTTCGCCTGCTCAGACGGACTTCCGGGGCGTTGGTCAGCCACTCGAC
CAGGGCGGAAAAATCGGGAATTATGGACATCAGGGACCTGCAATGGGGGCGCAACAGCCA
GTTGTGCCTCAGCAGCAGAATATTCCGCCTGTGCATAATCCGGTACCACAGAATTCTGTT
CCGCCTACTCCGGTTGTGCCGAAGCCAGGTACAGGAAACCCGTTTACTCATGGTGGTGCG
AACAATCAGTTTATGGGTCGATTTGATACAAGCCGTTACAACCAACAGGAACCACCACAA
CGACAGGATGGCGGGTTTGAGCTC

>RXA01590-downstream
TAAATAATGGCAGTAGATTTCAG

>RXA01592
AACTTCGACCGCTCTCGTGACAACGATCGCTCAAGCGCCCGCACTCCTCGTGGAGACCGC
GGCGATCGCGGTGGCTACCGAAACTCCCGCGGCAACGATGACCGCGGAAACTACCGTCAA
AACCGAGATGGTGAATCACGAGATCGCGGCGGATACCTCGGTGACCGTCGCGACAACCGC
TCAGGTGAATATCGTCAACGTGACGATAGGCGTGACGATCGTAGGGACAACCGAAGCGAT
GACCGCCGCGGTGGTTACCGCTCCGATCGCAACTTTGACGATCGCAACAGCAACATGCGT
GATGATCGTCGCGGCGGCGACCGTTCATACAGCCGTAATGATCGCTCCGATCGTGGCTAT
CGTAGCAATGACCGCTACGACCGTAATGATCGTCGCGATGACAACAGGGACACCAGGGGT
GGCGATCGCGGAGACCGTCGCTACGACAGGCGCGATGACCGACGTGATGATCGTCGCGAT
GATCGTCGTGGCGGACAGGGCCAGGGGCGTCCAGGTGGAGATCGTCGACATGCGAACCGT
GCAGGTGCAGGTCGCGATCAGCAGCGTGATTCGCTGCATCCACAGCGCGCTGGTTTCCGT
GAAGAGCGCTTGAACACTCGTCTCAATGAGCCTGATTTGCCGGGCGATATTGATATCAAG
GACTTGGATCCTTTGGTCCTGCAGGATTTGAAGGTTTTGTCTAAGGACAACGCAGATGCC
GTCGCAAAGCATATGATCATGGCTGCGACCTGGCTGGCCGACGATCCTCAATTGGCACTG
CGCCACGCCCGTGCTGCGAAGGATCGCGCGGGACGCGTGTCCGTCGTGCGTGAGACGAAC
GGCATTGCTGCTTACCATGCTGGTGAGTGGAAGGAAGCTCTTTCGGAGCTTCGTGCTGCG
CGCCGCATGTCGGGTGGTCCTGGTTTGATTGCTGTGATGGCTGACTGTGAGCGTGGCTTG
GGTCGTCCTGAGAAGGCGATTGAGCTGGCTCGAGAAGAGGATTTGAGCTCTTTGGATCAG
GATAACCTGATCGAGTTAGCGATTGTTGTTGCTGGAGCACGCCATGATTTGGGTCAGCAT
GACTCTGCGATTGTGGAATTGCAGAAGGTTAATCCAAGCTTGAAGAGCACCGGTTTCACC
CATTCTCGTTTGTCTTACGCTTACGCCGATGCGCTTGTTTTGGCTGGTCGTGGCGATGAA
GCACGTGAGTGGTTCCAGCACGCTGCCACCTTGGATGAGGACGGCTACCTCGATGCAGAG
GAGCGTATCGAGCAGCTCGATAATGGGAACAAC

>RXA01592-downstream
TAGACTATTGGTCTAGAGTGTAA

>RXA01595-upstream

AATACTTCCTGTGGCTGGTTAAAGATGGTGGCGCTTCAATGCCGGATGACCAGCAATTGT
CGGCAATGATTGACACGGCTGTAAAGGAAGGTCCGCAATA

>RXA01595
ATGACTGCACCCACGAACGCTGGGGAACTCAGGCGAGTTTTGCTGGTTCCACACACCGGG
CGTTCTTCCAATATTGAATCCGCCATCTTGGCAGCCAAGCTGCTCGACGATGCTGGAATC
GATGTGAGGGTGCTGATCAATGATGCAGATGATCCAATTGCAGAGCACTCCGTTTTAGGC
CGTTTCACCCATGTCAGGCACGCTGCAGACGCCGCTGACGGCGCAGAACTAGTTCTGGTG
CTGGGTGGAGATGGCACCTTCCTCCGCGCAGCAGATATGGCCCACGCTGTTGATTTGCCT
GTTCTGGGCATCAACCTAGGCCATGTGGGATTCTTGGCTGAATGGGAGTCTGACTCACTT
GAAGAGGCACTCAAACGTGTGATCGACCGCGATTACCGTATTGAAGATCGCATGACCTTA
ACTGTCGTTGTCCTAGACGGCGGTGGAGAAGAAATCGGCCGAGGCTGGGCTCTCAATGAG
GTCAGTATTGAAAACTTAAACCGCAGGGGAGTGCTCGATGCAACCCTCGAGGTAGATGCA
CGACCAGTTGCTTCCTTTGGTTGCGATGGCGTGCTGATTTCCACCCCAACCGGCTCCACC
GCTTATGCATTTTCCGCCGGTGGTCCTGTACTGTGGCCAGAACTCGATGCCATCTTGGTG
GTTCCTAATAACGCCCACGCGCTGTTTACCAAACCGCTGGTTGTGAGCCCAAAATCCACC
GTAGCTGTGGAATCCAATTCAGATACTTCAGCAGCGATGGCCGTCATGGATGGTTTCCGT
CCCATTCCTATGCCTCCAGGATCCCGTGTTGAGGTCACCAGGGGTGAGCGTCCCGTGCGT
TGGGTGAGGCTTGATTCTTCACCGTTTACCGACCGACTTGTGAGCAAATTAAGGCTCCCC
GTTACCGGTTGGCGGGGTCCGCAAAAACAGGCGGAAAATAAAGATCCCAGGTCAGCGGGG

>RXA01595-downstream
TAATTCGAAAACCATTCGAACAA

>RXA01597-upstream
GAGTAGAACCACTTCTCGCCGCCAGTGCATAAGAGTTTTCTTGGAATTTTTTAGGCGCGC
CTCCACCAAAGGTTGAGACTTTGGTTCCACAATGGGCTGC

>RXA01597
ATGAGTCTGTTCAACCGCAAAGCCGACCTGCCCGGCCTGCAAGGTGCCACCCGAATCTGC
ACCCCGCAGGGCAAAGGGCTAAAGCGCCTGTCCGAAGGCGATCTCGCAATCATTGATGCA
CCAGATCTATCCAGGACCTTCGCCCAACGATTGCTAGCAGCAAAACCCGCCGCAGTCCTC
AACGTTTCCCGGTTCACCACCGGATCGGTGCCCAACTTTGGACCGCAAATGCTTATCGAC
GGCGGCATCCAGCTCGTGGAAGGCTTTGGCCAGGAGCTGCTCGACGGCACCAAAGACGGT
AAGAAAGGTCGCCTGACAGAAGATGGACAGCTCTTCTACGGCGAACGACTGATCTCTAAC
GGCAGTGTTCTCAGTGGACCTGCGGCTGAAAATGCATTTGCAGACGCCCAGCAATCACTG
CTGGACCGCATGGAAGCCTATTTCGGCAACACCATTCAGTTCATTCACTCAGAAGCACCG
CTCCTGATCGATGGCCTCGGCATTCCCGATACCGGAAATGCCATTGAAGGCCGCAAAGTT
CTCATTGCCTCACCAGGGGATAACCACCGCAGCAGGCTCAAAGAACTCCGCAGCTTCATC
CGCGAATACGATCCAGTACTCATCGGTGTCGATGGGGCAGCAGACACCTTGGTGGAATTG
GGGTACAAGCCCGCGCTGATCGTCGGCAATCCCACTGGTATCGGCGCAGATGCGCTGCGC
AGTGGCGCCAACGTAATTTTGCCAGCTGATCCAGACGGCCACGCTGTTGGTCTGGAGCGC
ATCCAGGATCTTGGCATCGGTGCGATGACCTTCCCATCCTCAGTAAATTCCTCCACGGAT
CTGGCGCTCCTGCTTGCGGATTTCCACAACCCGCAGATGATCGTCAACGTCGGCGGTCCT
GTCACCCTTGATGGTGTTTTTGAAAACCGAGAAGATTCCGATCCCGCGGCGCTTTTGACG
CGCGCCAAGCTAGGCACCAAGCTTGTCGACGGATCCGTCATCGCAAGTCTTTACACAGTG
CGCAGCTCCAGCAACCTTGGATGGATGTGGGCACTGTTAGCCATTTTGGTGGTTCTTGCA
GTCGTGATTGTTATCGCTGGCACCGCAGGATCAGGCTCTTTTACCGACAACCTCATTGAC
ACCTGGAACAGCTTCGCGCTGACAGTGCAGGGTTGGTTCAAA

>RXA01597-downstream
TAGGAAGGCAACATGGCTAAACG

>RXA01598-upstream
CGCTGGCACCGCAGGATCAGGCTCTTTTACCGACAACCTCATTGACACCTGGAACAGCTT
CGCGCTGACAGTGCAGGGTTGGTTCAAATAGGAAGGCAAC

>RXA01598

ATGGCTAAACGACGTGGAAGAGGCGCCGCAACCTTCGCCGCACTGGGATTTGGTGCAGCA
GCCGGCATTGCCTTTGGAACTTATGTGCTTGCACCCAACCTTCCTGAAAACATTGACCCA
AATGCACCAACATCAGCTGAATTAGTCGAGGCAGAGACCTTGGCTGAGGTTAATGCGGTG
CAGGCCGATCAAGCAGACAGCATCATTGACCACATCGTGGAAGACGTGGTGGCTGGCACA
CTGACCGATCGCCCCGTACTGGTGATGCGCACCGCTGACGCTGAAGAATCAGACGTTGCC
GATGTGTCATGGCTGTTGCAGCAAGCAGGAGCTATTAATGCTGGATCCATTACACTTGAG
GAGAATTTCTTCTCCCAAGACGGCGCGGACCAGCTGAAATCAATCGTGGCAAATACGTTG
CCTGCAGGCGCTCAGCTTTCTGAAACCCAACTGGATCCAGGAACTCACGCTGGCGAGGCA
CTTGGTGCCGCTTTGCTGCTCAACCCTGAAACTGGTGAACCACTAGCCAGCACTGCAGAG
CGCGGACTATTGCTCAACGTGCTGCGCGACAACGGTTACATCTCGTACGAAGACGGCACC
ATTTTGCCAGGCCAGGTCATCGTGATGATTACTGGCGATAGCGACGGCTCAGGTGATGGT
GCCTTCGCTGCAGAAACACAATCGCTGTTTGCTCGCGCACTTGACGCCCAAGGATCAGGC
GTGGTGGTTGCAGGACGTATTCACACTGCTGCTGATACTGGAGTTATTGGACGGCTTCGT
GCCAACCCTGATGCTGCAGAAAACGTCTCTACAATTGATTCCGTGAATCGTACTTGGGGC
AAGATGGCTACCGTGCTATCAGTTCGTGAGGAACTAGCCGGTAGGTCTGGAGCGTTTGGT
TCCGCTGCCTCCGCAGACGCGGCAAGTCCGTCTCTCGATGGAACTGCAGCAGCGCCAGCG
CAG

>RXA01598-downstream
TAGGTTTTCCAAGCCTTTAAAAC

>RXA01600-upstream
TGAGTACAAATCTCGTCCAACCCATGCTCATCCACTGTTTTACGGCCTGGTGAAGACCGC
TTTGGAGCTGCGTGTCCACCCTTAGATCTACAATGTGATC

>RXA01600
ATGGTTTCGAAGATGCACATTCCCGGTACCCATGAGTTCACGGTGACAGATACTGAACTG
TTGTTAGAGTCCCCAATTTTGGGCGTTCGTCGAGATTCATTGATCATGCCGGGTGGTTCC
ACTGCCCGCCGTGAAGTGGTTGAACACTTTGGGGCGGTCGCAGTGGTTGCCTTTGATGGT
GAAAACATTGCGATGGTCAAGCAGTACCGTCGCAGCGTGGGGGATTCCTTGTGGGAGCTG
CCTGCAGGTTTGTTGGATATTGCTGATGAGGATGAACTCACGGGCGCGCAGCGCGAGCTC
ATGGAGGAGGCTGGTTTGGAGGCCAGTGAGTGGTCCGTGCTCACTGATTTGATTACCTCG
CCTGGTTTCTGCGATGAAGCGGTGCGTGTCTTTCTAGCCCGAGGCCTCACAAAGGTTGAG
CGCCCGAAGGTTATGGGCGATGAAGAAGCGGACATGATTAACCAGTGGGTTCCGCTACAT
GAGGCAGTGGGAATGGTGTTTAGTGGCCAGTTGGTTAACTCCATTGCCATTGCGGGTGTC
ATGGCTGCTGATGCTGTGATTGCGGGTCGTGCGTCTGCGCGTGCCGTCACCGCGCCGTTT
ACCTATCGCCCTACGGCGTTGGCGCAGCGTCGAAAAGCGCACGGCATTGTTCCTGACATG
AAAAAACTA

>RXA01600-downstream
TGAAGGCTCGCGTTTTAGCGAAA

>RXA01602-upstream
TGCAGGCCACATGCCTCCCAGTGCCGTCTCTGCACGTTGATTTTCCCCTGCCACGACTGG
TCGCAGGGCGACTTTCTAGCACTTTTAAAGGAATTTTTTA

>RXA01602
ATGGCTAAAACCCATATTCGGTTACAGGACCTTTCCCTGTCATACACCTCAACCCCGTTA
ATTACGAAGCTCAATATCACTGTTTCTTCTGGACAGTGCGCAGTGATTGTTGGTGAGAAT
GGTCGAGGTAAAACCACACTTCTGCGAGCACTGGCTCGAGAATTCCCGCCATCTGCAGGT
GAGATTCTCACTCATGGCACGGTAGCAATTGCTCATCAACACATGCCTGCAGGTGATCTG
TCCGTCGGAGAGATCTGTGATGAGGCAATTCGTGATTCAAAGAATGCTCTCGAAGAGCTT
GAGAGAGCTGGAGCTCTACTTGAGACAAACACTGCGCACGCACTTGATGGATATCAACAA
GCCCTTGATGCCGCTGAAGTGCTTGACGCATGGAACGCTGAACATCGATTAGAAAAAGCT
CTGCGCAGCTTTGGCGCGATCACCGATAGATCCCGTGCACTCAGTGAGCTATCGATCGGG
CAAAGGTATCGGGTACGGCTGGCCTGCCTCATCGGTGGCGATGCTGATATTTTGCTTCTC
GATGAACCCACCAATCATCTTGACCGGGGCGCGCTTAACTATCTCACCGAAGCCATAACC
TCCCACAAAGGTGTGGTACTTGTTGTTTCTCATGATCAAGCACTGATCAAAGATGTCGCG
GATTTCATCATCGATATTGATTCAACCCCAGACGGCCTACCACGGATCTATCATGAGGGT

TTTGATTCTTATCGACGCCAAAGGAGTGCGCTTCTTGAAACTTGGAGGCAGGATTATGCC
GCTGCACAAACTGTGCAACAGCAATTGCAGGAGGATCTAGAGCACGCACGCCAGCGGGTG
AATTCTTCGTGGAAACCTCCAAAAGGAACGGGAAAACACACTCGCGCATCTCGGGCTCCC
GGAGTGGTGCAGGCCTTAAAGCGAGCACAGGATGCGTTGGATAGCAAAGCGTTGGACGTT
CCCCCGGCTCCGGCCCCATTGCTTCTGCCTACCTTGAAAGTGCGACCAGATAAACCCATG
GTGGACTTTTCGGACCTTTTTGTACCCCACCGCTTGCGTCTGCCAGGCTCACATTCAGTG
GTATCAGGTGACAAAATAGTGATCACTGGTGACAACGGCGCTGGCAAATCAACGCTCATC
GAAGTCTTGTCTGGGGTTTTGACTCCGGCAAGTGGTTCGGTTGCAAACCATGCCCGAACT
GGGGTTCTCGGCCAAGAATCACTTGTCGGCGAGGTGCCATCAATAGCACGAGATCACGCA
GTTAAGTGGGGACTTTTAAGTGTTGAGGAGAGCCGATTTGCCCTACAGGAATTCTCAATT
GGTCAACGCAGAAGACTAGATTTGGCCATGTCGTTAGCTGGCAATCCTGAACTGTTGCTT
CTCGATGAACCTTCGAACCATCTGTCTATGCACTTGGTTTCCGCACTTACAGAGTGGCTG
GACACGACCGCGGCTGCAGTGATCATGGTAACGCATGATCGACAGCTACTCCGCGATACG
GCTCATTGGAGGCACATCGAGTTGAAATCT

>RXA01602-downstream
TAAGAATTCGCAAGGGCTTTCAC

>RXA01605-upstream
AGTCAAGCGCCGAAGAAAGGCCCGNGAAGGNAATCAGACGACGGGCACCTACTACTTCGG
CATTGAAATTCCGAAGAACTTCAGCGATTCTATTGCCAGC

>RXA01605
GTGACCAGCGATTCACCCGCGCCAGCAACCGTCAACGCGGTATTCAACAACAGCAACGGC
TTCATTGCCTCCATGCTGGGCAACCAGGTGGTCAACACTGTTGTGGAGACCATGGACACG
GAATTCGGCGTCCGCATTGTGGATAACATGCTCGTCGGTTTCTCCACCTTGGGCGACGGC
ATGAACCAAGCCGCCGAAGGTGCCACTACGCTCAGCGATGGCGTCGGTTCCGCCAACGAC
GGTGCAGTTCAGCTTGCCGACGGCGCGGTCACCCTGCGCGACGGCATCGCAAGTGCCAAT
GAGGGTGCGCAATCGCTTGCCGACGGCGCCAGCCAGCTCGACACCGGCCTCGGCTCCGCG
GCTACAGGCAGCCAAACGCTCGCCGACGGTCTATCCAGCCTGTCTGCGGGCACCGCCCAA
CTAGGCCAAGGCGCAACCCAGGTTTCAGATGGCGTGGGCCAACTTGTCGACCAAGTAGCA
CCACTGACCGCCTATGTTCCAGACATCAACTCTCAGTTGATCACCCTGCGCGACGGCGCA
GCCACCATTGCCTCTGAACTATCTGATCCCTCCAGCACCTACCGCTCCGGCGTGGACTCC
GCTGTGAGCGCATCCCAGCAACTAGCAGCCGGCCTGCAAACCCTGAAAGACGGATCCAGC
CAACTCAGCATCGGTGCACGCACCCTCGCTGATGGCACCAGCCAATTGGCCGCAGGTTCC
GAACAGCTAGTTGTTGGCGCACAAGCACTGCGCGACGGCACCGTCCAGCTTGATGAAGGC
TCCAGCGAACTCGCCCTCAAACTCACCGACGGCGCAAGCCAAGTACCAACCTTCGCTGAC
GGCGCAGACACCACCATCGCAACCCCAGTTGAAACAGAACAAGCAGGAGACACCACACCG
CTCTTCGGTATTGGTCTCGCACCATTCTTCATGGCTGTCGGCCTGTTCATGGGAGCAACC
GTTGCCTGGATGATCCTGCACCCAATCAGTCGCCGCGCACTCGACTCCCGCATGGGAGGC
TTCCGAGGCACCCTGGCAAGCTACCTTCCATCAACAGTCTTAGGCCTTGGCCAAGCAACC
ATCATGTGGGCAGTACTGTACTTCCTGCTCGACCTCAATCCAGCTCACCCAGCTGGACTG
TGGATGGCGATGGTCGCCATCTCATGGGTATTCATCTCCATTACCCATATGTTCAACAAC
GTGGCAGGACCCTCCGCAGGCCGTGTGCTGTCCATCGTGATGATGTCCTTCCAGCTAGTC
TCCTCCGGTGGCCTATACCCACCAGAAACCCAGCCAGCATTCTTCCACTGGTTCCACACC
TACGACCCGATCACCTACGCAGTCAACCTCGTGCGCCAAATGATCTTCAACGAAACCCCA
TCCAACGACCCACGCTTCATACAAGCAATCTGGGTACTGCTCTTCATCTGGGCACTGATG
CTCGCCATCTCCACCCTGGCGAATAGAACAAACAAGGTTCTTCGCATGAAGGACTACCAC
CCAGAACTGAAGGTC

>RXA01605-downstream
TAAAAGCTTTTCCCGCCCGGTTC

>RXA01610-upstream
CATTAATCACATGTGGTTAATGCCTTTTTTGATTGCGTAGACTAGGAAGGTACGTCAACT
TCCATATCTTTAGTTTGCGAAAGCGATCAACTTAAAACAC

>RXA01610
GTGTCCGGTTTTCTTACTCCCCCAGCTACACCCCATATTCGGACGGCAACTGCCAGTATT

GCTACCGCAGTTGCCGTAGCACTGTCAGTGTTCGCTGCTGCACTCATTCCAGGAAGCGCT
CTGTATTCTGTGCTGACCGCTGGAGGGGTGGCACTTGGAGCAGCATCAGGCGTTGCCGCG
TTACGCCATCGCGGAGGGCTTCGCATTTTTCAATGGCTGTCTGCGCTTGGTGGAATCGTC
ATTTTGCTGATCGGTATCGTAGTGGCAGTTGCAAAGTTTGGGGCCTCGGCAAAACTTGCC
ACGTTAGGCCTGGTGACCTCGTATTATCTCATGCCGTCTGCGGCATTGGCCTGTTATATC
GGAGGGCTTGGCCAGCTACCAGCCAAATGGATTGCGCCAGCGTTTATGGCTACGGCTGGT
GCAGGTGCTGCGGGATGGTTTTCATTGGGGGCAGGCACCGGTTTTGAACGGTTCCTCATT
GCTGTTGCAGCGGTGTTTTCACTGATGGGATGTGTATACCCAGTGTGGGGATGCGTCGTA
AAGCGTCCACGTCAAGTGGCTGCATGGCTGGTCGCGCTGGCGGCCCTGGTGCTTGGGGCG
CTCATGCTTTTTATGGTGAGCATGGTGGTGGCGCCGGGTTTGCTGTGGCTGCAGCCCACG
ACGGTCGCATGGGGTTTTATGATTGCCGGGGTTCTTGCGACGGTCGCAGGCTTGTGGCCT
AGGCGTTTT

>RXA01610-downstream
TAGACGGAATCGTCTGGGAGGGT

>RXA01611-upstream
CCCGCTTACAACTACTTGGTTTACACCGGTGTTATCAAGGGCTAAATCGCCTAACCTCTA
TCTTCATCTATAGCTTAGCTTTACTGAAAGGCTTTTCATC

>RXA01611
ATGCGTAAATTCCGCAACACTGCAATTGCACTAGTTTCTGCAGCTGCAATCACCTTGGGT
GGCGTTACCGCTGCTACCGCTCAGGAAGACGAAACTCCTCCTGCAGCAGAGACCGAGACC
ACTTCTCCTTCCGGTTCCTCAGGCTCTTCCTGGAACGACTACAACGAAGAGTACGAAGGC
GACCAAGAGGGCTACGGAATCGACGGCTTTGGTTCTTCCCGCGATGACTCCGGAGAAGAA
GTTCCACGTTGGTTGGAGACCTGGGGCAAGGTATTTGACGCTTTGACCATTACCTCCGTT
CTTGGTCTTGTTGTCTTCCCTGTTGTTAACTTCCTGAAGTACAACGGCCTCATTAAG

>RXA01611-downstream
TAATCTGCAATTTCCTGTCAAAT

>RXA01612-upstream
GAAAAAACGACGTTGGTTCGTAGTCGCTGGAAATTTAATAATTCCTCCGTCCCCTTCAAC
TAGGGGGTGGAAACCCGACTATTTCCGAAGGACTATTCTC

>RXA01612
ATGCGTTCTTTCCGTACCGCGGCAGTTGCAGGCCTTACTGCAGTTGCACTTTCCGTAGGT
TCCGCCACCGTGGCAACTGCGGAAGAATCTGATCAAAACCTCTCATCCGGCTTCTCAGCA
CTTTCTTCCGGTGGCGCAGCGGCCGTAGGTGAGGACTGGGATGCAGACCAGCCCGTCACA
GGTGAAGACATCTTTGGTGAAGAGCACGAGCGCGATAACGAAAACACCCCAGCGTGGGCT
AAGAACATGTACGATCTAACCGTCTTGGGTGGCATTGCTTCCCTTCTCGGTGTCATCGTA
TTCCCCGCTTACAACTACTTGGTTTACACCGGTGTTATCAAGGGC

>RXA01612-downstream
TAAATCGCCTAACCTCTATCTTC

>RXA01618-upstream
GGCCGTGCGCGCCTCCAGCGAGCCTGGCCGTGCCGGAAAAGTGCTCATTCGTTTCTAAAC
GTTTAAGGCCCATTAGACCCCTGATTTAAAAGGATCTCAC

>RXA01618
ATGATCATTATCGGAGCAGTTTTCGCCATCCTCGCAGTTCTACTGCATGTTTTCATCTTC
TACATGGAATCATTCGCATGGACTAGTGAGAAAGCACGTGGAGTTTTCGGCACCACCGAA
ATCGACGCCGAAAACACCAAGGAGATGGCCTACAACCAAGGCTTCTACAACTTCTTCCTG
GCAGTCATCGCCGGCGTGGGTGTTGCGTTCCTCTTCGCTGGTTCAACTGGCATCGGCGCA
GCCCTCGCACTCGCTGGCACCGGTTCCATGCTGGCAGCCGCTGCAGTGTTGGCTTTGAGC
TCACCCGACAAGCGTGGTGCAGCCTTCAAGCAAGGCACGTTCCCGCTGCTCGCAGTGGTG

TTCCTTGTGATTGGATTGCTGGTT

>RXA01618-downstream
TAAGCAGTTTTTTAAAGGAACTT

>RXA01619-upstream
CCTGCAAGTTTACTGCTCGGCCGTCACGGGGGAATGGAAAAAGTACGCTTGGTGTTCATA
TAGCGAACCCATTTTCTATTGCGATGAGAGGAACACCACC

>RXA01619
ATGCGCGCAATCACTCACAACACTTTCGGCGACCCCGCCGACGTCCTACAGATTACCGAG
AAGGAAATTCCCACTCCCGGCCCAGGTCAGGTTCGTATTCAAGTGACGCTGGCAACCATC
CACAACCATGATTTGTGGACCGTGAAGGGCTCTTACGGCTTCGTCCCAGATCTGCCGGCC
GCCGCAGGCACCGAGGCAGTCGGCATCGTCGACGCCCTGGGCGAGGGCGTCGAAGGTTTG
CAGGTCGGTCAGCGTGTTGCGTCCGGCACCAGCTTTGGCATCTGGGCGGAGTACGCGCTT
GTCGACGCCTCCGGCCTCATTCCCGTACCAGAACAGCTCTCCGACGAAAGCGCAGCTCAG
CTCGTCGCAATGCCTTTCAGCGCCATCAGCCTTCTTGATTTCCTGGATATGAAACCAGGG
GAGTGGCTGATCCAAAACTCCGCAAACGGTGCCGTCGGCCGCATGCTCGCACAGCTGGCA
GAATCCCGCGGCATCCATGTCGTTGGTCTCGTCCGCCGTGACGCCGGTGTCCAAGAACTC
GCTGCTCAAAACATCAGCGGCGTCGTTTCCACTGAGACCCCAGGCTGGGAAAAGCAGGTC
GAAGACATCACCGGTGGCGCAAGCATCGCCGTCGCACTTGATTCCGTCGGTGGATCCTCC
GCAGCTGACCTGGTGAAACTGCTTGGCGAAGGCGGCACCCTCGTCTCCTTCGGCGCCATG
GGCAACCCAATCATGGAAATCCCATCCGGCCCCGTCATCTTCAAGCACATCACCGTCAAG
GGCTTCTGGGGAAGCAAAGTCAGCCGCGAAATGCCAGCAGAGAAGAAAACCCAGTTGTTC
GGCGAGCTCATTGCGCGCATACTTGATGGAACATTGACCCTTCCAGTTGATTCCACCTTT
GATGCCGCTGACATCGTCTCGGCCGTGCGCGCCTCCAGCGAGCCTGGCCGTGCCGGAAAA
GTGCTCATTCGTTTC

>RXA01619-downstream
TAAACGTTTAAGGCCCATTAGAC

>RXA01622-upstream
AAGGCGTGGGCGTTTTTGAAGGAGCTTCGTTTGGAGCGCGGTCCTTTGGATCGTGAAGTT
GCCATCGCAGAGCTGAAGAGCTGGTGGGAAGGAGAAAACA

>RXA01622
ATGAGTGATTTTTATGCCGACAGGTTGTTTAACGCGATGGAGCGCAATGAGGTAGCTCCA
GGCATGTTGTTGGTGGCTGCGCCCGATATGGCGTCGGAGGATTTTGAGCGCAGCATCGTG
TTGATCATCGAGCATTCTCCTGCCACCACTTTTGGTGTGAACATTTCTTCACGTTCCGAT
GTTGCTGTGGCCAATGTGTTGCCCGAGTGGGTGGACCTCACCTCGAAGCCACAGGCACTG
TACATCGGTGGGCCGTTGAGCCAGCAGGCTGTGGTTGGTTTGGGCGTGACCAAGCCGGGC
GTGGATATTGAAAATTCCACCAGCTTCAACAAGCTCGCCAACCGCCTGGTGCACGTGGAT
CTGCGTTCTGCACCTGAAGATGTGGCTGATGATCTTGAGGGCATGCGCTTTTTTGCGGGC
TACGCGGAGTGGGCTCCGGGCCAGCTCAACGAGGAAATTGAGCAGGGTGATTGGTTCGTC
ACACCTGCGTTGCCGTCGGACATTATCGCGCCGGGCCGCGTCGATATTTGGGGCGACGTG
ATGCGTCGACAAGCAATGCCTTTGCCGTTGTATTCCACGTTTCCGTCGGACCCTTCAGAT
AAT

>RXA01622-downstream
TAGATGAGTTCCGAAAATTTAAA

>RXA01623-upstream
CGCGCCGGGCCGCGTCGATATTTGGGGCGACGTGATGCGTCGACAAGCAATGCCTTTGCC
GTTGTATTCCACGTTTCCGTCGGACCCTTCAGATAATTAG

>RXA01623
ATGAGTTCCGAAAATTTAAAAGAAATTCGCGGCGGAATCGGTGAGACTTTAACGGTCGGT
TTGGGGCTGATTCCGCTGGGTTTGGCCTTTGGGCTGTTGATGGTCCAGACAGGTTTCGCC

TGGTGGTGGACGCCGATTTTCTCCTTCGTGATCTATGCCGGTTCGATGGAATTTCTGGCA
ATCGGCATGGTCACCGCAGGTATCGGCCCGTTTTCGGCGGCGGTCGCTGGTTTCATGGTG
AATTTCCGCCACATTTTCTACGGTCTCACCTTCCCACGCCACCGCATCAAGTCCGGCGCC
GGCCGCGCCTATTCCACCTACGCGCTTACCGACGAGTCCTACGCCATCGTGTCAGCCCGC
CCACCTGGCGATATCAGTGGCACGCGGGTGCTTACCGTTCAAATTTTGTGCCAAGCTCTG
TGGGTTATCCCAGGAATTATTGGCGCCTTGGTTGGTCAAGTGCTGCCCGATGATCTAAAA
GGCATGGATTTTGCCCTGACCGCGCTGTTTGTGGTGCTGGCGTGGGAGGCATTCAAAAAT
AACAAGGATTATTCGCTGCCATTATTCGCGGTGGTATTGGCTCTGGTTTCCGGTTTTGTG
GCGCCCGAGCAGATGCTGGTTATCGCTTTGACCACGTACTTTTTGATCCTTCTTCTCCGC
GTCCGCTTCCCCAACCTGGACAAGAAACTGGAGATCAGGACTTCCCATGAG

>RXA01623-downstream
TGAGTTTGGCCTGCCAGAAGGCG

>RXA01624-upstream
GAGCAGATGCTGGTTATCGCTTTGACCACGTACTTTTTGATCCTTCTTCTCCGCGTCCGC
TTCCCCAACCTGGACAAGAAACTGGAGATCAGGACTTCCC

>RXA01624
ATGAGTGAGTTTGGCCTGCCAGAAGGCGTCACGCTGCTCAACGTCGCCGCCGTGTTGATC
CCCATCGCGATCATCACCTTGCTGCTGCGCATCTTCCCCTTCGCCGCGATGAAACGCGTC
AACAGCAACCAACTCATGGGAGTTTTGGGGCGCACAATGCCAGTCGGAGTGATGGTCGTA
TTGGTCATTTACACGCTCTTTGGCCAGGTCAGTGCGCCAGGTGGTGTGGGTGCTTCACTG
ATCGCGGTGGCATTCACCGCGCTGCTGCACTGGTTGAAAGGCTCCGCCGGGCTGTCCATC
GTCGGTGGCACCTTGGCCTACATGTTTCTGGTCAACGTCGTTTTT

>RXA01624-downstream
TAAAAGATGCTTCTCGACGCAAA

>RXA01627
CGCACCTATTCACCATCCCTGAAGGATTACAACTCTGATGAACCCTCACTGTTGGGGCCT
GCAGAAGACCCCAACATGTATCAAGAATTCGAAGTGTCCTACGAGCAGCTCGGCATCAAA
CCAGAGGGCCGCACCCTGATCGGCGATTCCTTCAGCGCCGATTTCTTGACCTCCAATGAA
ATTGGAATAGTTGATGAGGTTCCTTCTGGAACGATCGCTTTCACGAACTGGAAGGACGTA
ACCGAAGGTCGCCACAGTTGGTATGTTCGCTCCGAGGATCCTTTCGGCGGCGTCGAGATT
TCACCCGTGCAGTCCTTCATTGCCGGGGAAGAGGCTGGCGGGAACGCGCCCGGCACTGGA
AGCTCCAATGGCGGTTCATCCCACGGATTATGGGGTGCGCTTGCGGAATTCTTTGCCGGA
GCGGCAGCCCTGGCTGGAGCTGCGATCGCATTTGTCCCCGGAATTTGGGACTATGTGACC
AACGCATTCAAGCGA

>RXA01627-downstream
TAATTATGGATAGGTAAACGCTC

>RXA01628-upstream
CTTCCCCTTTCAGCCCGTTGAAGAACCAATGAGCCCTGCCCGCACCCAGCCCCGAGCGGC
TTTCCTAAGGAAGCTCCGACCCATCACATGTAGCCTTTCC

>RXA01628
TTGGTTCTCGTAGGGTGCAGCAACACGGCAGAGTCCACGACCACCGATACGGCAGGCTCC
ACTGAAACTTCATCACAGATTTCACCCACCACTCCAGTCAGCACCACCGAAGCAGCGCCG
CCTGAAGATCCAAGCGCAAACGCTTTGGAAGAGTATGCTCAGATCCTTGCCAATCCAAGC
ATCTACCCCTTAACCGAAATTTCACAATTCGTCCCCACAGGCACATATGCCTACACACTT
GTTGAAGCAACTTCCGATTCCATCCCAGAACTACTACTCCGCGCCGATAGTCACGAATTC
GCGCCAATTTTGGTTTTCACCTATGACGAAAACACACAATCCGCAACCCAAGCTGGAGGA
GTCCTAATTGACGGTGTCGCCAGCGCCGGCGGTTCACGAGTCAAGGTCAGAGCTTCAAAT
TCAGGAGCAGGAATCTACCAATTGAATTGGTACTCGATACAACCAGTTGGCGAAAGCTCT
TTGTACGGAATCCAAGGAAACTCCCTGACACAAATCGCAGACCCCGAGGATTTCATGGTC
CGTGAACTATTACCTGACCACCACGAAATTACCTGGGTTGATTCCAACGACCCCTCCGGC

CTATCAACCGTTCAGACTGGTGGAGCCAACATTCAACAAGCAGCCCCAACTCCCGTTCAA
CAGCCTGCGTCAAACCTGCACTACTTCTCTGGTGTAGTAACGATGCAGACCGCCGGCGAA
CTCATGCGAGGTGAACGAACTCCCAATGGTGAGCCTGCCACTGATCTCTATCTCGTACTG
GTCCTTGATTCCCCAATTGAAATCACAGCACGAAACGCAGCTACAGACCCTCAGACTCGT
ACCATTTCCGAAGTCAGCCTCGGCCGATACATCCCCGCTGATGGTGACAATGATTGGATA
GGCTACCTCGACACCCACGTGGAAATCACTGCAACAACGGATCAGGTCTGGTTCCCAACC
GACACCGGTCTACCTCTTGGAATGCTTCGTCTAGCGGACTACAAAAGCATCTCA

>RXA01628-downstream
TAAACCGACGCAGCACTCGTCGA

>RXA01630-upstream
GTAGGTGAGTCTTCGTGAGATACCCCCGGCCAGTCATACAGTTCAACCAAGCTCCACCAC
CCAGATAAAAACCTGCGGGTTGCGTTTTAGGAGAATTCCC

>RXA01630
ATGAGTGATCAAAAAATTGTTGTTGGCCTGCTAGGCATCACCCACCCGCATGCGTCGGCG
CGGGTGCGTGCCCTCCGTGAAATTGATGGGGTAGAGGTCGTCGCCGCCGCGGATACTGAT
TCCCGCCTCCAGTACTTCACCGACAAATATGATGTTGAACCCCGCGAGATCGATGACGTC
TTGAACGACGATCGCATCAACGCCATCATGGTTCACTCCAAGAGCAAGGACATGGTCCCT
CACGCCAAGCGCGCGCTCGCGGCCGGAAAATCCGTCGTCGTGGAGAAGCCCGGCGGGGGA
ACAGTGGCGGATCTTGAGGAGCTCCTGGCCCTCAAAGAAGCTGCCGATCCTCAGCGAATC
GTGCAGGTCGGGTACAACGTCCGCCTGTCTGAATCGGTTCAGAGATTAAAAGAGCTTCTC
GACGCCGGCCTCATCGGCGAAGTCGTCAGCGTGCAAGCACGCGGCGCCGCAAAAGTAGGT
GAGCATATCACCGAGCACCTCAACCAACCCGCAGACATGGGCGGTGTGTTGTGGATTCTT
GGCTGCCACATGCTCGATGCATTGGTGGAAGTCTTCGGAGCTCCAGAATCCGTGAACGCC
CGAGTGCATAAGACCGCAAAACTCTCTGACGACACCAGCCGCGAAGACTCAGCCTCCGCA
CTGCTGTACTACCCAGATTTCTCCGTCAGCTTCAGCTTCGACGGCCACGATGATCTGGAA
TGGTTCGAAAGCTCCCGACTCACGGTCTATGGAACCAAGGGCATGATCGAAGCCGGAATC
CTCCCTCAGACACTGCGCGTATACCTCAATGAGTCACGCCAGGGCTGGCCACAGGGTTGG
ACCGAGTGGACCCAGAGCTACTTCACCCCACCGTTTGCTCGCACAGAATCCAACAAATTC
TCAGAGCTTCCAGAGCTAGAAAACATCAGCAACTTCCGCACAGAAATGCAGGGGTGGGTG
AATTCCATTCGCACTGGATCCCGCAATGTGGCGCCAGTTGAGGATGCTCTCACAGTCGCT
CGCATTGTCAGTGCATGCTACGAATCCGACAACAACCAGGGCATTTCCGTAAACATC

>RXA01630-downstream
TAAGAGGAGCACTCCATGAAACC

>RXA01634-upstream
ATTGGATCTAGGAAAAATTATGAACATCTCAAAGCTCGGACTGAGGATCGCGGTCACAGC
AACGGCGACCACAACGGCGCTTGCCCTCGGTGGCACGCAC

>RXA01634
ATGGCAGTTGGTCAAGAAACTGATCTGCTCAACGCTATGGAAACACTCGCTGGGGTTCCC
TCAGACTTGGTGGTCACTGAAATCCTCCCCGATACCACCAGCTATGACAATTTTGAATTC
TTTGAAGTTCACAACACCGGCAGTGCACCCGTGACCATTGGGGAAGGGGAGTACACCTTC
GCCTATTCCTTTGACGATTCCGCCGATACGTCCCGCGACAAGGCACTGGATCTTGGCGGG
GAAGTCACGGTAGATGCAGGCGAAACCATTGTGGTGTGGATTGAGTACTCCAGTTCAACT
GTTGATACCGCTGCGTTTAGTGAGCAAGACTTCCGTGATTTCTACGGCATGGATTCCTCA
GCCCGCATCTTCCGAGCAACTGGCCAGGCGGGTCTCGCTAACGGTGGTGATCGTGGCATC
CGAGTTCTGTACAATGGTGAAGTTTCTGGTTGGTCCCACTACCCATCAGATAGCGCAGCG
GTTCAAAAGGGAATTGACTTCGCGCTGCCAAAAGTAGGGGAGCAGGCCAGCATTGCAAGT
GCGCACCAAAAC

>RXA01634-downstream
TGATCCAACTCCAGGATCAATTA

>RXA01635-upstream

AGGGAATTGACTTCGCGCTGCCAAAAGTAGGGGAGCAGGCCAGCATTGCAAGTGCGCACC
AAAACTGATCCAACTCCAGGATCAATTACTTCTGATCAAG

>RXA01635
TTGATTCCTGGCGGATTGGACACTCCAGAAGAGCCTGAAGCCCCTGAAGACTCTCTTTTT
GAAGGGCGCACTCCCCCTAGGGATGCAAGCACCCGCTTGATCCTCACTGAACTAATGGTC
AACTCCACCAACATGGGCAGTTCTGATGGTTTTGAGTATGTGGAAATCACCAACACTACT
GCCGAACCCATCGATTTTTCCGATTACACCTTGAACTACCTGTACCCGCAGGATGAGTTC
ACCAACACCAACGAAGCCGTCTGGGCTGCGGAACCTGGTGATGTCATTATTCAGCCTGGA
AAATCTCTCGTGTTTTGGATCAAAAATGGCCCCAATGATGAGGCAACCGCAGCAGATTTC
AATGCAGAATATGGCACCAACCTGGAGGCTGGAAAAGACCTTGTTGAAATCTCCTCAGGT
GGGATGGCCAATGGTACTGCCAGAGGAATGCAGATTCAGACCAACACTGGCCACATAGTC
AACCGTGGTTTCTACAACATGGCTGGCGCTTCTGATGTGAAAGCCAACGAGGGTCTTCAT
TTCGCAGTGGATGAGTCTGATCTTCTGAAGCAAACGCTTGTCGGCAGCGGTGCGCCAACC
CCGGGCACTGTGTACACTTCGCAGATTCCTAATCCACTGTCTGCCGTTATCGCTGATTCT
TCTGTACCACTCATCACAGATAATACCGCAACCAGTATCAACCCTGCGGAGCCGTTTACC
TTCGCCTTCAAATATCACCGA

>RXA01635-downstream
TGATGTCCAGGTGCGCACGGCAA

>RXA01636-upstream
GCTGATTCTTCTGTACCACTCATCACAGATAATACCGCAACCAGTATCAACCCTGCGGAG
CCGTTTACCTTCGCCTTCAAATATCACCGATGATGTCCAG

>RXA01636
GTGCGCACGGCAACACTGCATGTTACTTCCAGTGCTGGCGAAGCCGCGACAACCATCAAC
CTCACCGAGGATGACGGCTCTTTCAATTGGGCTCTGCCTGCAGCGGATCTCACCGGAAAA
TCCTGGTTCGAATACACCGTAACCGCCACCGACGGATTCAACAGCGTTACCACCGAGCCG
GTACGCGTCACCGTCGACGGCGCCAACACCGACCCGCTGCGCCTCAACCTGGAAGAAAAC
CAATGGGTCAGTGGCACCACCGATGTTATCGGTGCTTCAGATGTCTTCGGCGACAAGCTT
GAATTGCTTATCGACGACGCGCCTGCAGTCACCAACTCCAGCCTGTCTGCGGCCCCGACG
TTTGCGATGGAAGTAACCCAAACTGATGTGTTCTTCCGCAACGGCATCCTTGCCGGTGGG
GAAGAACTCCGCATTTTCGATCAAGGAACTTACGCCAACACCGAAACCATCTCCACACCA
GTCCCGCTGTATCACATCAATGAGGACGGTACCCTCACAGTCAGTGTGTATGCGGGAACT
AAAGCAGCACCAGAAATTGACCTCAACGAGAAC

>RXA01638-upstream
TTTCACTGGGCCAGTGGACTCACGGCCGGTAGATAAGGTGGCGGAGATTTCAACGCAGGG
GGAGACGTCGATAAGCAATCAACCCCAACCCCAGCCCACC

>RXA01638
GTGCTCGTGACCGAGGACCTGCTTATTGAGGCGCCATTTGGTTTTGAAATGCGAAGCGAC
GAACAGTCGCGCTACCTGGAAGGCCCCGACCCGAATCTGCGCATCCACGTGGGCGTCGAT
CCGCTGCACGGCGCGGACGCCGCGCTGGTTGCCGAAGAGCTGCGCCGCCTGATCACCGAG
GATCCTTCGCTGGAGGAAATTCCCGCAGGGGAGTGGGGCGAGAAAACCACCATCGACTAC
CGCGAAACACCCGGCGATGGCTCTCATGTGCTGTGGGTGACCTGGTTTGACACCGACCGA
CAACTCAACGTTGGGTGCCATAGCAAAGCCGCCGAAACCCTTGTTCACAAGGCACAATGC
CGAAATGTGATTGAGCATCTGACGCTGAAA

>RXA01638-downstream
TGATGCCGGTTTCTATCCGGAAT

>RXA01639-upstream
AGGCATCAAACCCACAGCACAACCACCAGGACGTGCCACGATGTCCATCCGTGGTGAAAA
CATCGGTGTTGCACAGATGGCACCGCATAGGTGATGACTC

>RXA01639

ATGAGCACCCAAACAATCACCATCACAGTCCTAGAAACCGCCACCATCTTTGACGGCCCT
GAAACCATCTACCGCTATGACCTGGCTGCCGAAGGCATCCTTGATGGATGGGCTCACTCT
GCTGTGCTGGATCAAGTGAAACAAATAGCAGGTGAAAACTGGCCGACTGTTGAGATCGTG
GTGGATGGCACCGACAACGTAGTCAATGCACTCACCTCCATGTTTGCTTCCAAAGGCGTG
ACCTGCGGTGGGGTTGGAGTAGAAGCACCTCCCGTTGCGGAGGAACCACCGAAAATTAAA
CGGCCCACGAGTGGAAAACAAGTCCGCCAGTTCTACGGCATCAAGCCACTACACCTGTTG
TTGGTCAGCATATTGGTTGGTTCTATTGCTGGTATTTGGGGATTTCGGGTTTCACTGGGC
CAGTGGACTCACGGCCGG

>RXA01639-downstream
TAGATAAGGTGGCGGAGATTTCA

>RXA01641-upstream
GTGAAATTAGGGGAATTCTCACCAACGCTGCTCCCCGTCCCCTTTTGCTGGCATACTCAA
AGACACATTTGTTGGGGGGACAATTTTGGGGGTTGGTTATT

>RXA01641
TTGGCAATCGATAATGCGCTGCGCGTGAGCATCCGCATAGATCTCACCGTTGGCGATGCG
CCCGCTGCTGTGGCTGATGTGGCGCTACCTGCAGGTTCGAGTCTGGCGGACATTTTGGAT
GAAATTTTAGAACTCACCGATGCACCCCGGATTTCCAGGCCGTGGGTGGCTCACACTGCT
GCGGGAAGTCCCATTGATTGCGGGATTCCGCTTGCAGAAACACAAGTGGAACAAGGCAGC
GTGGTGGTCCTTTCACCCGAAAGGGACTTGGAAGCCCCCGTGTTGCGTGATGTCGCCGAA
GCGTTGGTGGAGTTTTCTTCCACGAACCGCGCCGGGCACCTCGTGGAATTGATGACTTTC
GCGGGGCTCATCGGGGCTGCCGTGTTAATGACAAGTCCTGCTGCCTCCGGAATTATTGTG
CCCGGCCGCATGGGAATCTTCGTCGCAATCTGCGCTCTACTGCTTCTGTGGCTCCCACCC
GCGCACACCCCGATCCTTCGAAACGTCCTGCCGATTACCCTGATCTTGGGCGCAGGCGGA
GCGGTATCAGTGCTGGTTGCAGGCACTTCTGGGACTTCTCCCGGCGCGCTTACCTGGACG
ATTTTCGCTGGCGCGTGCACTATTCTTGCCAGTTCGCTGCTGGTTCATGTGGTGTATCGT
CCAGCAATTCTTCTGGTGGCAACACTGTCCACATTGGGGCTCGGTCTCTTAGTCCTTGCA
GCAACCACCACTCTGTGGAAGCTCAAAGCTACCGAAGATTTCAGCGGTCCAGCAGCGATC
ACGGTCACCGCTTCCACCATCACCATGTGCTTCGCCCCGAAAATCGCAGCATCGCTAGCA
GGCCTGCGCGTCCCATCGCTTCCCACCGCCGGCGAAGATCTCTCCGTCAGCGACCTCACC
ATGACTGATCCCGAGAAAAGAATAAAAACAACAAAGACGCTTTTCGACGCCCAGATCCTT
GGCCTTGGCGTTTTGAGCGGGCCTTTGGCGTTGTTGTCGGTTACCCCGGGCACCTGGACA
ACCACCGTTTTTAGTTTATGCATCGCGGTGGCTTCGCTGCTTCACGCTAATCGTCATCAA
GCACCAATTCCCACGTGGACATTGATGGGGTTATCTGCCCTTGGTTTCATTTCCATGGCG
TTATCCGCAAGCCGATCAGGTTCACTAATTGCACTGATCGGTTCTGTGGTTATCATCGCT
GTGCTGGTCAGCGTGGCATTGTGGATCAGTACAGTCCCCACGCTGGAACCCACCACCATT
GTGTGGCTTGAAAGGTTGGAATCACTGTGTCTTGCAGCTAGTCTGCCACTCGCACTGCAT
TTGCTGGATGTATTTGGAATGCTGCGCGGTCTTGATATTGGATTCGGTGGA

>RXA01641-downstream
TAAGATGCGCAGACTCATCGCGG

>RXA01642-upstream
TTGGAATCACTGTGTCTTGCAGCTAGTCTGCCACTCGCACTGCATTTGCTGGATGTATTT
GGAATGCTGCGCGGTCTTGATATTGGATTCGGTGGATAAG

>RXA01642
ATGCGCAGACTCATCGCGGTTAGCTTGGCCGCTCTGTTTATGTTGGCTTCCACTCCAGCG
ACGAGGGCACAGGAAGTAGAAGCTCTCGCTTGCCCCGAGGTAGCGATCGCCGATCCTTCC
TCCGCAGTTTTAGATGAACACCTTTCGCAGTCATTATCCCAAGCTCACCAACTAGCAACT
GGCGCCGGTGTGATGGTGGCAGTCATCGACACCGGAGTATCCCTGCATCCACGTCTGCCC
CACTTAATTCCCGGCGGTGATTTCGTGGGCGCCCACCAAAGCCCCGATGTGCCAGGTGAA
CTTATCGATTGCGACGGCCACGGCACCATCGTCGCCGGAATCATCGCCTCCCAAGGAAAC
CCCGGCACCGGCTGGCCATATGACGGCAGCTCCGATCCTTATATCGGTGTCGCCCCAGAT
TCCGGAATCATCTCCATTAAACAAACCAGCTCATATGTGCGTACTCGTGAAGATTCCAAC
GTCGGAACGCTGAGCACCCTGGCGGAATCCATCCACCGAGCTCTCGATTCCGGTGCCCAC

GTGATCAATATTTCCGTGGTGTCCTGTTTGCCCCAATCACCCGACGAGGCCGCATCGTTC
CAGCCTCTGACGGATGCTCTTAACAGAGCAGAACTTCAAGGGGTGATAGTGGTGGCAGCA
GCAGGAAACCTCGGGCAGGATTGTCCAGTTGGATCTACCGTTTATCCTGCACATTCAGAC
ACTGTGCTCTCTGTGTCGGCACGTTTTGATTCTCACACGCTTGCAGAATATTCCATGCCT
GGCAACCAACAAATCCTCTCTGCACCAAGCCACATTCAGGCTGGTCTATCACCGCGTGGC
GACGGCTTCGCCAGCCACATGATCACCACCGCTGGCGAAAGCCCCTTCGAGGGCACCAGT
TTTGCCGCTCCAGTTGTCAGCGCCACAGCTGCACTGCTTCGCCAGCATTTTCCCTTTGCC
ACACCCTATGAAATTCGTGCACGAATCTTCAACAGCATCGACCCTGCAAGAGGCGCTATT
GATCCCTACCTGGCACTTACTCAAGAAATCTATCCCACCACTCCCCTGGTTCATGAGATC
GCACTAAGTGTTCCCACGCCGCCGGATGATTCTCCACGGGAGCGGGGCATCCTAGTTACC
GCAATCATTGTTGGGTTGCTCGCAGTGTTAGCTGTGCTGATGGGACTACGCCGAATTCAT
CATCACTCGGCCTTTCAAAAAGCTAGCTCAAGTGTTATCACT

>RXA01642-downstream
TAATCTATGAGGCACCGTTCAGA

>RXA01643-upstream
CGGATTTCAACACTTTCAGGATGCATCTGTAACTATGCCCATGCCACACCCCATGTTTAT
CGATGTCTCCTTCCCACCCGCGGAGACCTGTAGTTAACCC

>RXA01643
ATGGGCACGATGCGAGAAATGGTCAGTGACCGCATTGACCGACTACAAGAAGCACACGCG
CGATCAAAGCAGAAGAAGTTCGGCTTCTTAGTTCGGCCAGGCACCCTGATCCTTGGATGG
TTGGTCACGATCATCGGTCTGATCACCATTCCACTTCCCGGCCAAGGCTGGCTGACCACC
TTCATTGGTGTGGGCATTTTGTCTCTGGAGCTTAAATGGGCGAAGAACCTCCTGGCCTGG
GGAGTGCATCAGTATGATCGCTTCTTCACCTGGTACGGCAAGAAATCATTCCGCTTCCGC
ATGGCGATGTTGGCACTGATGATTCTGCTGATTTGGGTGGTGTTCATCGTGACATTTTGG
TTGATGTGGCACGCCGGAACTATCCCGTGGGCAGATGAGTTCTTCACCTGGCTTGGGTTG
AGCCGC

>RXA01643-downstream
TAGCAACTATTCGCTTTGAAGGC

>RXA01645-upstream
AGAGGGCATCACCTATGACCGCCTGACAATCCGCGATTACATCTGGCGCTGGGACACCGA
CTGGTTCTGGTGTTCACGCGCATTCGGCACCCAAAACCCC

>RXA01645
GTGGTGCGCAAACTCTGGCCCAGGGATCTGCTGCGCTCGAGTTTCTATTGGAAGATCATC
GGCTGGGATCGAAAATACTCCATCGCTGATCGCCTGGAAGAGCGCAAAGGCCGCCCGGCT
AGGGAACGGGTGGTCCAAGACGTGGAAGTTACGATTGATAAACTGCCAGAATTTTTGAAA
TGGTTCTTTGAAAGCAGCGACATCGAGCCGCTGTGGCTGTGCCCGATCAAGCTTCGGGAG
GTACCAGGTAGTTCGGTTGGTGCTGGAGAAATTTTGAGCTCCGCTGAAGCAATCGACTCC
GGTGCTGCTGAACACCCTTGGCCGCTGTATCCCTTGAAGAAGGACGTGCTGTGGGTCAAC
ATCGGATTCTGGTCCTCAGTGCCGGTTGATCTGATGGGCTCCGATGCACCAGAGGGAGCA
TTTAACAGAGAAATCGAACGCGTCATGGCAGAGCTAGGCGGACATAAATCGCTGTACTCC
GAAGCGTTCTACACCAGGGAAGACTTTGAAAAACTTTATGGCGGAACCATCCCGGCGCTG
CTAAAAAAGCAGTGGGATCCCCACAGCCGATTCCCCGGTTTGTATGAAAAGACAGTAAAA
GGCGCC

>RXA01645-downstream
TAGGATCGCTCACTGTAGGTAGA

>RXA01646-upstream
GGTCGTGCCGTGGAGCGTGCTGCGATTGTTGCCGCAGGGAAGTGAATTAGCAAAAGAGAC
AGCGCTCGCGCCCACCTATTAAGGAGTATGGTGGCCTTAC

>RXA01646
ATGAGCGGATTAGTTGACCCGGATAGTACTTTTTTAAAGACCATCGGAAAACTGAGCAAC

AGCTTGTCCATTGGTCGTGGAGTAGATCAAAAAGAGGTAATCCCCAAAGGCTGGAACGCC
CATTGGGAGGCAATTACAAAGCTTAAGAGAAGCTTTGACGCGATTCCTGCTGGGGAGCGG
GTGCGTTTAGCTAAGAAAACCTCCAACCTGTTCCGTGGACGCTCCGATGCAGGTCACGGC
CTAGATGTGGCAGCGCTTGGGGGAGTGATTGCCATTGATCCGGTCAATGCCACCGCCGAT
GTACAGGGCATGTGCACGTATGAAGACCTGGTAGATGCCACTTTAAGTTATGGTCTGATG
CCGTTGGTTGTGCCTCAACTGAAAACCATCACGCTTGGTGGCGCAGTGACCGGAATGGGC
GTGGAATCCACATCCTTCCGCAACGGTTTGCCACACGAATCAGTGCTGGAGATGGATATT
TTTACCGGCACTGGTGAGATCGTGACTTGCTCGCCCACAGAAAATGTCGACCTTTACAGA
GGTTTTCCCAACTCTTATGGTTCGCTGGGATACGCGGTGCGGCTAAAAATTGAGCTGGAA
CCAGTGCAAGATTACGTCCAGCTGCGCCACGTGCGCTTCAACGATTTAGAGTCTTTGACC
AAAGCGATTGAGGAAGTCGCGTCTTCTCTGGAGTTTGATAACCAACCCGTCGATTACCTT
GACGGCGTGGTGTTTTCACCCACGGAAGCCTACTTAGTTCTTGGCACGCAAACCTCACAA
CCTGGCCCCACCAGCGATTACACCAGGGATTTAAGCTAC

>RXA01646-downstream
TAACGCTCCCTGCAACACCCAGA

>RXA01647
ATGCCGCGCGGAGTGCCGGTGGGGGTTCCTGATGCGCCGGGGCTTTTCAGCAGCACCGAA
GAACCCGAGCAAGATTGGTTTGTGTGCCAGGATGTCGGCACTGGGGATCTACACATTACG
GTTCCTAGGGGCGGACTAGGGCCCACCCTGATTGCGGAAGGAAATGGGTGGCTGGGGGCG
TCGAAAAGCGAAACCGGCGAGGTCACCTGGAACCTGATTACCGCGGACGGGCGCCGCGAA
CTGCCGGCGTGGGGCAGCGAACATGGGCGCATTATGCGCCGCCACCTGGGGATTTCCGAG
GACACCCCGCGCGTATACCTGACCACTGAGCTGCTCAACGCGATCCCCGAGCACGACGCG
GTCCGCTTCCCAGCCCCGCTGCCCGAGCTTGTCGACGCCTCCACCCGCAACTGGTTACGG
CTCGACGGGGCGCTCGCCGAAATCACGCCGCTACAGCGCGGGTTGCTTATCGACGCCGGT
TCCGGTGTTTTCCCCGACCCCACCGCGCTTCTTGGTGTGCATGAAGAAACAGCCAACACC
TTGACGCTGCCCGAGCAAACAGTTTCTTGGCAAGATCTGGACGGTGGTTTTGCCTGCGCG
GATGGTGAAGGCCAGATCGGTTTCCTGGAAACTCTGGAATCGGGGGTGGCGCTATCTGGT
GATTCCAGGGCGAAAAGTTTCAGCACAAACGCTGGTGGGGCAGTGGGCGTGGACAGTGGC
TTTGGCTACTATGTGGTCTCTGATTTTGGGCTGATGCACCCTGTTTCTACTGGTGAATCG
ATGGTTGCCCTAGGAATCACTGACGTGCAGGTCGTGCCGTGGAGCGTGCTGCGATTGTTG
CCGCAGGGAAGTGAATTAGCAAAAGAGACAGCGCTCGCGCCCACCTAT

>RXA01647-downstream
TAAGGAGTATGGTGGCCTTACAT

>RXA01656-upstream
TCGGCAAGCATGGCTTCATCGTCCTCAAAAAAGTGGTCTAATGCAAGTGACTGAAAGTGG
ATCTACCGCTAGTCCACTTTGTGGCGTTGGATCATCTGTC

>RXA01656
ATGACCGAAACTCAAGAAACTTACCAAGCAACCACTCGTGTGAAGCGCGGCCTTGCCGAC
ATGCTCAAGGGTGGTGTGATCATGGATGTGGTCACCCCTGAACAAGCGCGCATCGCCGAA
GATGCAGGTGCCAGCGCAGTTATGGCACTCGAGCGCGTTCCCGCCGATATCCGTTCTCAG
GGCGGCGTTGCTCGCATGAGTGATCCTGACCTGATCGAAGGAATCGTCAATGCGGTCTCC
ATCCCGGTCATGGCGAAAGCTCGCATCGGTCACTTCGTGGAAGCTCAGGTTCTGGAAGCT
CTCGGTGTTGATTTCATCGACGAGTCCGAAGTTCTCAGCCCTGCCGACTACACGCACCAC
ATCAACAAGTGGAAGTTCGACGTTCCTTTCGTCTGTGGCGCGACCAACCTCGGCGAAGCT
TTGCGACGCATCACCGAAGGCGCTGCAATGATCCGTTCCAAGGGCGAAGCCGGCACCGGC
GATGTCTCTGAAGCTGTCCGTCACCTGCGCACCATCCGCGGCGACATCAATCGCCTGCGC
TCCCTGGATGAGGATGAACTCTTCGTCGCCGCCAAGGAATTCCAGGCACCATACGACCTG
GTCCGCGAAGTCGCCTCCACCGGCAAGCTCCCTGTGGTCACCTTCGTTGCAGGTGGCGTC
GCAACCCCAGCCGACGCTGCACTCGTGCGCCAAATGGGCGCCGAAGGCGTCTTTGTCGGC
TCCGGCATCTTCAAATCCGGCAATCCAGCCGCCCGCGCCGCAGCGATCGTCAAGGCTGCA
ACGCTTTTCGACGACCCCTCCGTCATTGCCGACGTATCCCGCGGCCTGGGTGAAGCCATG
GTGGGCATCAACGTATCCGACGTTCCAGCACCACACCGACTCGCCGAGCGCGGCTGG

>RXA01656-downstream
TGATCGTTGGAGTTTTAGCTCTC

>RXA01658
GATCCACAGATCCTGTCACCAACCTTCACCCAGCAACAGCAGCTGCGAAACTTCTACGGT
TTCCCAGACCAGCTGGCGATGGACCGCTTTGAAGTAGATGGCAAACTCCGCGACTTTGTT
GTGGCAGCACGTGAGCTCGATCCAAACGCCCTGCAGCAAAACCAGCAGGACTGGATTAAC
CGTCACACTGTTTATACCCACGGCAACGGCTTCATTGCAGCTCAAGCAAACCAGGTGGAT
GAGGTCGCCCGCGACGTCGGATCCACTCGTGGTGGTTACCCTGTCTACACCGTCTCTGAT
TTGCAGTCGAATGCTCGTGCTGCAGAAAGCGAAGATGCTGAGGAGCTTGGCATCAAGGTT
GATGAGCCTCGTGTGTACTACGGACCACTGATTGCTTCTGCGACTGATGGTGCTGACTAC
GCAATTGTCGGTGACACCGGCGATGGCCCAGTCGAGTACGACACTGACACCTCCAGCTAC
ACCTACGAAGGTGCTGGCGGCGTGGACATTGGAAACATGGTCAACCGTGCGATGTTTGCA
TTGCGCTACCAGGAAATGAACATGCTCCTGTCTGATCGTGTTGGTTCCGAATCCAAGATC
CTATTTGAGCGCGATCCTCGTTCCCGTGTGGAAAAGGTTGCACCTTGGTTGACCACTGAC
TCCAAGACCTACCCAACTGTGATTGATGGTCGCATCAAGTGGATCGTCGATGGCTACACC
ACCTTGGATAGTCTTCCGTACTCCACGCGCACCTCACTGACGGAAGCGACTCAGGATGCT
GTCATGCCTGACGGCACCCCACAGCCACTGATCACAGATAGGGTCGGTTACATCCGCAAC
TCCGTGAAGGCTGTTGTTGATGCGTACGACGGAACTGTTGAACTCTACGAATTCGACACC
GAAGATCCTGTTCTGAAGGCATGGCGTGGCGTGTTCCCAGACACCGTGAAGGACGGGTCG
GAGATTTCCGATGAGCTTCGCGCACACCTGCGTTACCCAGAAGATTTGTTCAAGGTCCAG
CGTGACATGCTGGCCAAGTACAACGTTGATGATTCTGGAACATTCTTCACCAACGATGCG
TTCTGGTCTGTCCCAGGTGACCCAACTGCAGCGGAGGGCCGCCAGGAACTTAAGCAGCCT
CCTTACTACGTGGTGGCAGCAGACCCAGAGACCGGTGAGTCCAGCTTCCAGCTGATCACC
CCGTTCCGTGGACTTCAGCGCGAGTACCTCTCTGCACACATGTCTGCGTCGTCTGATCCA
GTTACCTACGGTGAAATCACTGTTCGTGTGCTGCCTACCGATTCTGTGACCCAGGGTCCA
AAGCAGGCCCAGGATGCGATGATGTCATCTGACCAGGTTGCTCAGGACCAAACACTGTGG
CGTGGATCGAACGATCTGCACAACGGAAACCTGTTGACCTTGCCAGTTGGTGGCGGAGAG
ATCCTCTACGTTGAGCCGATTTACTCGCAGCGCAAGGATCAGGCA

>RXA01659
CCAGAAGCTGTGACTGCTGTGTGGATGGAATCTGATTGGGTGTTGGCGGAAACCATCAAG
GGTTCCACGCCTTCCGATTGGGAAGAGATTTTGCGGCCGTTGGCGCTGCTCACGGACGCG
TCTTTCACGTTGCCACCTCGTTCCACGCGTGCGCAAACCTTGGATTTGAAGCATTTGGAA
CCAAGCCGTCTGAAGCCGGAGCAGCCAGAAAAGCCAGCGTTTACTCCCAATGCTTCGGAA
GAAGATTTGTCTCAGCCGTTGGTGATCCGCCCCGAGGAGCCGTTGCAGATGCCGGTTCGC
GGTGTGCAGGAAAGCCGCGGAGTGGTCGAGCCACGGTCATTGGGTGCGGATGATGTGGAG
TCGATTGCGGAGGGCGATCCAGAGCGTCCGAGCGATCTTTATGGCACGCGTGTGCTGCGT
GATCTCAATGGTCAGTCCAGTATTTTCCAAGATTCCACCGACGCGGATGAGCCACCAAAA
AAGTGG

>RXA01659-downstream
TAGAAAACTGGTGTTTTTCGGCC

>RXA01663-upstream
TATTTTGCTGGTTGGTCACAGTGGAGCGCTAACCCCGAGAATCCTATCGAGGCCTAAAAT
CGTGGCTTGAGTACGCACTGCCAGTAAGGTGTGTGATGTG

>RXA01663
ATGGAAATAAGTGTCTTGATCATCGCCGCACTGATCTTGGTGGCAGGCATCGTACTGTGG
CGCGCGGACTCGTCTAAACAGGCAGCTAAAAAGGCTGAATCACCTGTGGGCTCAGTCGCA
CCTGCGCCCGTGCTGGTTGAAGAAGAGCCGGACCCTGAGTTTGAGCCAGAACTGGACCCT
GAACCAGAAGCGCAACCAGAACCAGAGCTGGAAGTTGCGCCTAGATTTGCGCCAGAACCA
GTTCAAGATCTTGAGCCGGATCAGGCTGAGGACATTTATTTTGATGATTCCCCTGAACTC
GATGCTGATGTTGAAAATGCCTTGGCTGAGCTTACTGAGGTAGAAGACTACCCGGAAGAG
CCAGTGCAGTCTGAGCAACCTCAAGCCCCTGCCACGGCGGAGGTAGCTGCGGACGAGGAG
CAACGGGGCGTCGAT

>RXA01665-upstream

AGGATTGGCGCCCGTGACGCTACTGAAAAGGTGGAGGGGCGCGTCGAAAAGCGTTGGCCG
GTGCTTGAGCGAAAACCCGTGATGATTAGCATGGTTTGTT

>RXA01665
GTGAAGATCGATGAATTGATTGCTCTCGCCGCGGAGCAACCCACTCGCATCTCCAGGCGT
TCCGGTGTCTCGCGCTCGACCCTGAAGCGGGTCGGCGATGGCACCAGCGAGCCCACCCTG
TCGACGCTGCGTGAGGTCGCGTTGGCGCTCGGGCTTGATATTAAGGTCGCCGCGCACCAC
GCCTGCGATCCCTTTGCGGCCGCTGCAGCGCGCACGCTTATCGACGCCTCCGTCCCCGAA
AATCCCCACAACCAGGAAATTCTCGCTTGGTTGCACCGTTTTGAGCGGTGGAATATCAAC
GATCCGCTCACCCTTGTCTCTGAAGCCGGAACGCTTCAGGGCATCACACATCGCCAGGAT
GCGCAGTTTGTGAAACTCAATCCACGCGGCATCGCTGAGCTACCGGAGCTTTTCCAACAG
CACAAAACCAAATGGGCGCTGTCGGGCGCTGCGGCTGCCACGGTGATCATGGGACAAATT
GTGCTGGGGAATTCGATTGTGTGGCACGAACCTGCCCACGATCTCGATGTCTCAGCGCTG
GGCACCATTGTTGATGTGGCAGAAGACGCCGATCTAATTCTCCTGCCCGCAACGGTCACG
GAACTGGTGGGAAGTTACACCCAGGACAGGCTAAATTTTGTGGCACCTGTGCAATTAGTT
ATTGATCTACACAGCCTCCACATGTTCGAGGAAGCCGATTACCTCACGAGCGGTTGGCGC

>RXA01665-downstream
TAAAATACTTAGCGTACGCACCC

>RXA01669
CACAACCTTTCCGACGCATTGACTGCGATTCCTCTTTGGATTGCTTTCATACTTTCCCGG
CGCGCAGCGACTCAAAAATATACGTATGGATTCAATCGTGCAGAGGATTTAGCGGGGTTG
TTTATTGTCGCGATGATTGCTCTTTCGGCGATTGTTGCTGCATGGCAGGCGATCGACCGG
ATGATTAATCCTCGCCCGATGGAGAATATTGAATGGGTGATTGCGGCAGGTGTTATTGGT
TTCTTAGGAAATGAGGCTGTGGCAATGTATCGCATTCGGGTTGGTAAGAGGATTGGCTCG
GCTGCTTTGGTTGCAGATGGCGTTCATGCTCGCACGGATGGTTTTACTTCACTTGCAGTT
GTCGCAGGTGGTGTTGGAGTTTTTCTGGGATTCCCCCTGGCTGACCCAATTATCGGATTG
ATCATTTCTGCGATGATTGCCACCCTTCTTGTTGGTACGATCCGTTCGGTTGGCAGACGC
CTCATGGATGGAATTGAGCCGGAGTTGGTAGAGAAGGCTACGCACGCGATCTGGCATGTG
AAGGAAATTGAGTCGATTGATCGACTGAGGTTGAGGTGGGTTGGACACCGTCTTCACGGC
GATGCCACGGTCAGCACTTCTACATCATCGCTATCGGAAGCCACCGCAATCGCCCTTGAG
GCTGAGCTTTCCGTCAAACAACATCTTCCCAATGTGGATGAAATGACTGTGACCATCACC
CCTTCCAAACCT

>RXA01669-downstream
TGAGTCCCGTGATACAATTGTTG

>RXA01671-upstream
TCTAAAAACACATTTTTAAGCCCTCCCGGCGCAGCTGAAAACTCAGTCGCCGGGAGGGCT
TTTTTGTACCCGAATTTGTACCCGAATTTAAGGAATCGCT

>RXA01671
ATGAATCATGTTGTTAATTTTGCTTCACATTTGGAAGACGCAGCCCTGAAGCAAGCCGAA
GCTACTGCCACCATGCCGTTTATTTACCCGCATGTGGCGTTGATGCCTGATGCTCACTTT
GGGCTGGGTTCGTCGGTGGGAACGGTGTTCGGCACCAAGGGTGCGATCATTCCGGCGGCT
GTGGGTGTGGATATAGGTTGCGGAATGATAGGAGTGTGTACCAATTACACGGCCTCTGAC
CTGGAGGGACGTGATTTGGTGACGCTTCGGGATTACATCGAGCGGGTGATTCCGTTGTCT
CCTGGAAATTACAATTCCACCACCTTGAAGGAAACCGCGAAGGTGAAGGTCGCGGAGTTG
GAGGAACTCGCGGAGCGCGATGGTGTAGATTTGTCGCACTCTCCGACGTGGAAGCGCCAG
TTGGGTTCGCTTGGTGGAGGTAATCACTTCATTGAGTTGTGTCTTGATGAGTTGGATCGG
GTGTGGATGTTTTTGCACTCTGGTTCCCGCGGTGTGGGTAACAAGATTGCCCATAAGCAC
ATCAAGAACGCGCAGGCCCAGTGTAAGAATGAGGAGCTTCCCGATAAGGATCTTGCGTAC
CTTGACCGAGGGGAC

>RXA01671-downstream
TGAGGAGTTTGAGTCTTACATCA

>RXA01672
TCACCACTAGCAACCTTCCGAGTTGCACTGGCAATGTCCATCATCGGACTCGTGGCGTGG
ATCATCTGCGTAACCGTCCTCTATTTCGGACTTAACGTGGCTGGCGTCTGGCAGAACTTC
AACGATGTCATCGGCGGTGTTGGTGCAGAACAAACCATCACCTTCGGGCTCGTCCTGAGC
ATTTCCGCACTTCTGGGAGCTATCGGAGCGATTACCGTCGCTGTGCTTGCACCATTGTGT
GCAATCATCTACAACTCGATTGTTGACCTCTTCGGTGGACTGCAGATTCAACTGCAAGAA
GAAGTAGAC

>RXA01672-downstream
TAACCTCTGAAACACAAACCCCT

>RXA01673-upstream
AGTTTGCAGGTTCGGCCACCCATTATCCATATCAACATTATATGGGTGGATATGAAAGTA
CCGTCTACCGCGTTCTTTTCAATTAGCGCAACCTTGAAGC

>RXA01673
ATGTCTACAAACCTTCTGGAATCGACGCCGCCCTTTACCCAACTTCGCACCGGAGTCCTC
CAGAAGTACACCCCGGGCCTGCTCTTATGCTCCATTGCGGTACTCATCGCTATGATCGTG
AATCACTTTTTCTCTGGTGTGAGTCCGCTTATCGTCGCGATCATTCTTGGCATCATCCTG
ACCAACCTGATTCAGCTCCCAGCATCGACCTCACCCGGCATCACGTTGGCGTCGAAAAAG
CTTTTGCGGCTGGGAATCGTCTTCCTTGGTCTGCAGTTAGTTTTCTCAGATATTTTGTCA
CTTGGTTTCCCCATGCTGGCGGTGATTGTGTGCATCGTTGCCGGTGGTATTTTTGGGACC
ATCCTCATGGGACACCTGCTCAGAATGAAACCAACCCAAGTTCTGTTGATTGCTTGTGGC
TTTTCTATTTGTGGCGCTGCGGCCGTGGCAGGTGTTGAAGGAGTAACTGATTCCGAAGAA
GAAGAGGTCGTTACTGCGGTTGCACTTGTTGTTATTTTCGGAACGCTGATGATTCCTTTT
ATCCCATTCGCAACCAAAGTCTTGGGGTTATCCCCTGAAATCGGTGGGATGTGGGCAGGC
GGATCCATCCATGAAATCGCCCAAGTAGTAGCAGCTGGAGGAGTCATTGGTGGTGGAGCA
TTAGGTGTTGCAGTTGTGGTGAAACTCGCCCGAGTACTCCTACTTGCACCCATTGCTGCC
ATTTTAAGTTTTCGCCAGCGCCGCCAGGGTTACACGTCCCCCGATGGAAAGAGACCACCG
GTCGTTCCCCTATTTATCCTTGGATTCTTGGCGATGGTAGTTTTGCGCTCCACTGTTGCG
CTCCCAGACGAGGTAATTGCGGCTGGAGGTTTCCTACAGACAGCCTTGCTCTCTGCAGCA
ATGTTTGGTCTCGGGTGTGGCGTAAAAATCCAGAACCTGATCCATGTTGGGGTCAAGCCT
TTCATTCTGGCTTTCGGATCCACGACACTTGTCACCAGTATCGCACTTGCAGGCACCCTA
CTCACCCACCTCGGA

>RXA01673-downstream
TAGAACCGAAGACCCAGTTGTAC

>RXA01675-upstream
TTGCCGATTCTAGCGGGAGAATTAGTGTCCATCGCATCGAACCACATCTGATTTTGAGCC
CTGGCTAACGGATTGTTTTTGACAGATTGGAATGACAATA

>RXA01675
ATGAACGAGATTCCAGAATGGTTGACTCTTGTATCTGTTGAAGCAGGAAAGAGACTTGGG
CGGCCTGGGCCATTGGTGTTTCCGCCGGAGTTGGTCACTTTGGCAGTTGAAGGGATTGAG
CTTATTGAACTTGAGCCTTCATGGACTTCTGATTTGCCTCTGCCGGAATTCGGGTTCCTA
GCTGCGGATATGGTTGATTTCTATGATGATTATGAGTTTAGTGAATGGATTCCGGGTGCG
TGGCCTCTTGCTTTAGATGGTGGAGGAGGTTTCTTTTGCCTTGATCTCCGTGCTGCCAAC
GCTGATGGAGAGATTCCTGTTGTGTGGGTGCATGCCAGCAACTTGGGTTGGGGTGATGAT
GAGGCAGTACGCGTAGCTGCCTCGTTGGCAGATTTGTTGAGTCCGTCGAAA

>RXA01675-downstream
TAGAAGAATTAGCATTTACCGGA

>RXA01676-upstream
AGTTACAGCTTTTCTCGGTGGCACACTCGCGCTACTTAGCCCTTGTGCCGCACTCCTTTT
ACCAGCATTTTTTGCATCCTCAGTGGGTGCTGGCCCGCGC

>RXA01676
ATGATCCTTCACGGTGTTGTGTTCTACGCAGGACTTCTAGTACTTCTCGTGCCACTTGGC
CTTGGTGCGGGAATCCTCGGCGAGCTGTTTATCACCCAACGCCAGACCATCATCGTGGTT
TCATCGATCGTGCTGATTATCCTAGGTTTTGTCCAGATCTTCGGCGGCGGATTCGACTTC
GGAAAAGCACTCCCAGGATTAGATCGTCTGCAATCTAAGGCCACTGTGACCTCAGGTCTA
GGAAAGAGCTTTTTACTAGGAATGACCAGTAGTATTGCCGGTTTTTGTTCCGGACCAATC
CTCGGCGCCGTTCTTACTTTGGCTGCCACCAGTGGAAACTCCATCACCTCAGCACTCATT
TTGAGTGCTTATGGTGCGGGAATGGTGCTGCCCCTGATGGCTATTGCAGCGCTCTGGGCC
AAACTCGGACAGCGTGGACAGCAGATGCTCCGCGGCCGGGAATTCACCTTCTTGGGCAGG
CAGTGGCACATTGTTTCTGTCATTAGCGGTGCCCTGATCATCGCTGTCGGAATCCTCTTT
TGGTCCACGAACGGCCTTGTCAGCATGCCGGAGCTCGTTCCAATGGACACCCAGATCTGG
CTACAGGAAGCCACATTCTCACTCGGGTCACCACTCTTTGACATCGCATTGATCATTGTC
GCCGCTGGCTTGTTCTTGTACTTCTGGAACAAACGACAAAAGCGAAAAGAAGAAGCTCAG
CGACCCAAAGAAAGTGGATGGGTTATTAACCCTCGC

>RXA01676-downstream
TAATTATTAGTTTTGGAGCGAGG

>RXA01677-upstream
GTCGCCATAGTTGAGTTTTATTCATGGCTTTTAGCTAGGCGACTTTAGTTGAGGGCTTTT
AGTTGAGGGCTTCCCAGCAGGGATGGTTAAGGAGAATTCA

>RXA01677
GTGAACCAACAGAGTAAAAAGTGGCTCGTACCGACACTGGTCGTCATCATTGCAGTGCTC
CTCATCGCAGTTGTTCTGTTGATGTACCGAGGAAATGCGAGTGATACGGCCGAGGGCGTT
TCAGCCGCTGCGACTTCGGACTCGGCTGCTGCTTCGACTGCTGCTTCGGGTTCCGCTTCT
GGTGCTGCGGACTCCGATCTGACCAGCGTGGAAGCACGCGACCCTTCCGACCCTGTTGCG
GTGGGAGACGTTGATGCACCTGTTGGGTTAGTGGTGTTTTCCGACTACCAATGCCCGTTC
TGTGCAAAGTGGAGCGATGAAACCCTGCCACAGATGATGAAGCATGTGGAAGATGGAAAC
CTCCGCATTGAATGGCGTGAAGTGAACATCTTTGGAGAACCATCTGAGCGTGGAGCTCGC
GCGGCATACGCTGCGGGTTTGCAGGACGCATACTTGGAATACCACAACGCACTCTTTGCC
AACGGTGAAAAACCCAGCGAAGACCTGCTCAGCGAAGAGGGACTTATTAAGCTTGCTGGT
GACCTTGGACTAGACGAATCGAAATTCACTGCCGATTTCCAATCCCCTGAAACTGCAGTC
GCAATTGCGCAACATCAACAGCTGGGAATCGATCTTGGCGCCTACTCCACCCCAGCTTTC
CTCCTAGGTGGCCAGCCAATCATGGGCGCTCAGCCTGCTTCTGTATTTGAAGCCGCCTTC
GAGCAAGCACTGGCAGCGAAAGAA

>RXA01677-downstream
TAAACCGTGGATGTCGGCCTAGT

>RXA01681-upstream
CTTTAACGAAAGACTTGTCGTTACTTTAGTAATTAGACCAACATGGTGGTGAGTGGTTGA
AATCTTGCCATCAAAATTATCGAGTGAGTTGAAGCATTCC

>RXA01681
GTGGAAGTACTACTACTTATCGCAATCGTCGTTGGTGGTGGCGTTTTTGTCGCCTCAAAG
ATGGGATCCAATAACAATAAGAAGCAAGAAGAAGCCAAGTTTGCTGACGCACAGGCAGAT
GCGCGTCGGTGGATTGAGCGTCTTGGTTCCCAGGTTTTGACCATCGCAGGTACAGATGCT
GCGTCGACCCAGGCTATTGCTGACGCCTCAGAGCGCTATACCGCTGCGTCTTCTCAGATT
TCTTCTGCCACTACTCCTCGTCAGGCAGAGTTGGCTCGAGAATCTGCACTAGAGGGTCTG
CATTATATGAACGCGGCTCGTGAGATCATGGGTATGACTGCTGGCCCTGAGCTGCCTCCT
CTGGAAGGTCAGCGCAATGCTGGTCGCGTTACAGAAAAGCGCACCATTGAGCAGGAGGGT
CGCCAGATCACTGCTTCCCCCGTCGCAACAGATGAAACTCCGAACTACTACCCTGGCGGT
AACGTTGCGGGTCGCCCAGTCCCTGCTGGTTGGTACTCCGAGCCTTGGTGGGCAAGCGCA
TTGCGTTCCGGTCTGTGGACTGCAGGTTCGGTCATGATGTTCTCAGCAATGTTTAACGGC
ATGGCTGGTGTCGGCTACTCCGCTGCAGACCTT

>RXA01681-downstream
TGAAAAATGGCTATGGCGAGGGC

>RXA01685-upstream
CAATAATTAGGTGAGCAACCCTAATAAGAAACCTTTAGATCCCGCACAAAGATTCTCCCT
CCCCACCAGATGGGCGATGTTCTTTGTCGGGATCTTTATT

>RXA01685
ATGTCCTTCGCCATCGGCATCACCGTCCACGCAGGACTAGGAACCACCACAATTTCATCA
CTTCCCGTGGTGTGGACTGCTGCCAGCGGATTATCCCTGGGCTGGACCACAATTTACTTC
AATGGCTTCATGATTCTGTGCCAAATAATTGTGCTGCGTTCCCAGTTCAAACCACAAATG
TTAGTCCAAATCCTGTGGGCATTCCTCTTTGGGTTTCTTTGTGATTTAAGCCTGCAACTA
ACCACCTGGGCGCAAACTGACAATTATTTTGTGGCCTGGATCTGGGTTATTGTGTCCACC
ATTTTGATGTCGATCGGAGTTTTTATTCAAGTACTCCCCAACATCACTTTCATCGCTGGT
GAAGGCATTGTCTCTGCGCTGGTGAAGAAATTTCCCAACGTGGAATTTGGCACCATGAAA
CAAATCGTCGACTGGACTTTCGTCTCCGTCGCTGCCATTTTGTCCTGGATCACCATGGGT
GGACTTATTGGCGTGCGCGAAGGAACAGTGTTCGCGGCGTTTTTCATCGGATTCTTCGTC
CGCCAGTGGCGCAAACTCTACCTCCGCTCCATCGGTCAC

>RXA01685-downstream
TAAAGAGCTTGTTCCAGGAAGAG

>RXA01686-upstream
GGAGGAAGGGTTGCAACGCTTTTTCAAGAGAATGACCGTGCGTCCGCTTAAACGAAGCGT
CGAACGCCGGTCTTTTCTCATTTCACTTAAGATGTAGAAC

>RXA01686
ATGACTTCACTCAGGGACTTACTTGTTTCCACCAATGCCGACGCAGCAATTGCAGATATG
TCAGCATTTATCGAAGAAACCGTGGGCAAGCAATCCGGCATCAGCGGCATCGCACTCAAA
GGCGCAATGGGTGCTGCAACCAAGATCGACTCCGACATCGTAGCCAAAGGCTCCAGGCGC
CTCCTCCCGGAAATCGCTGACTCCCTCGACGGACTCTGGCAGGAATACCAAAATGGTGGC
ACCGCCGCAGATTTCGGCGCCCACCTCGAGGCCAACAGCTCCACCGCACTCGACGCGATT
CTCAGCGTTGCTGACAAAAACGCAGAGAGCATCAACGTTCCAGGACTTGGCAAGGTCTAC
AAGGGCGTGCGCGGCAAGGCTGCCAAAGTAATCGAGCAGGAACTTCCTGCAATTGGCCAG
TTGATCGAAAAGAACGCACAA

>RXA01686-downstream
TAATTAGGTGAGCAACCCTAATA

>RXA01693-upstream
AGGAGACTGGCTGGATTATTGGCTGGTTTTCTTGGGAAATCGTCATGGGCATTAATCCTA
GTCCCAACAATTGCCAGAACCCGAACACTAGGCTTGAACC

>RXA01693
ATGAATACTGCACCTTTCAAACTCGAAGCTGACTTCGCATCAGCCCTGCCCACCATGGCA
GCCCCCTGGCAAGGTGAGGAAGCCCCCAACCCTGAGCTCGTGATTTTAAATGACGACCTC
GCCTACAGCCTCGGGCTTGATCCGACATGGCTTCGCACACCTGAGGGCGTTCAATTTCTT
CTCGGACTCAACCCCGAGCCCTTAACAAAAGCAGTTGCGCAGGCCTATTCCGGCCACCAA
TTCGGACAGTTTGTGGCAAGCCTTGGTGATGGCCGAGCGCTTCTTCTCGGCGAAGCCCGC
TCAGCTGACGGCGTACTGCATGATATCCACCTCAAAGGATCTGGACGAACCCAATTCTCC
CGAGGAGCCGATGGACGCGCCGTCCTTGGCCCCGTCTTACGCGAATACATCATCTCCGAA
GCGATGCATGCACTTGGTGTTCCCACCACCAGGTCACTTGCAGTAATTAGCACCGGTAGG
AAAATCCAACGAGGAAGCGTAGCCCCAGGCGCAGTCCTTGTTCGAGTAGCAACCAGCCTC
ATTCGAGTCGGATCCTTCCAATACTCCAACATCTCTGGTGGCATCGAACTATCTCAACAC
CTGGCGAACTATACGATCACCAGGCATTTCCCTTCGTTGGTAGCTGAACTATCCGCACCA
ACCCCCGCAACTTATGTATCACTGTTTAAAGCGATTCTTCAGCGCCAAGCAGACACCGTT
GGAAAATGGACCAGGCTGGGTTTCGTTCACGGAGCCCTCAACACAGACAACACGTTGATA
TCCGGAGAAACTGTTGACTACGGCCCATGCGCTTTCATGGAGCGCTACCGTGGCGACGCG
AAATTTAGCTCCATCGACACTTATGGTCGCTACAAATTTGAAAACCAACCTATGATCCTC
GGATGGAACATGGCCCGCCTCGTAGAAACCCTCCTCCCACTCCTGGGCGCCACACCAGAC

GAAGGCATGACAGCAGCCCAAGAAGCTCTCGTAGAATTCGATGACCTCTGCGAACAAGCA
ATCCGAAAAGAATTCGCCACTGCACTGGGCCTTGACGAGTCAGACACCGGCACGGTAGAG
CAGTTCCGTGAACTGCTCTACCTCCATAACCCCGACATCACCACGCTGCTGCGCGCACTC
ACCGACAACACCGCACCACCGAGTGGCTTTGAAGCATTCGTTCACGACTGGAAAACCCAA
GACCCAGATATCGAAGCAATGCGAGCAGTAAATCCACTTTTCATTCCACGCAATCACCTC
GTGGAAGCTGCTCTCGCAGACGCAGTTGAAGGGAATCTAGAAAAGTTCCACGAACTCCTC
GCTGCTGTCACCAATCCTTTTGATCCAACTGCGGGCCCCGATGAACTACGCCTGCCAAGC
GAAGAAGGATTTGAAGAAGACTACATGACCTTCTGCGGTACC

>RXA01693-downstream
TAGGACAGATGGTGGGGCAGACG

>RXA01694-upstream
CGACACCAATAATTTATTGGGTATCCACCAATTACCGCTGTGAGCACTGCAAATTACGTA
TTCGAAAAGCCATGTCCACCACGTGTTCTATCCTGGCGGC

>RXA01694
ATGCAAAAAATCACCCCAAACATCTGGTGCCAAGGCACCGCAGACGAAGCAGCCGAATTC
TACGTCAATGCGTTTTCTGAGTTTCCGGGTGGCGCAGAAGTACTCACCACAGTTAAGTAT
CCCGAAGCTGGCTTGCTGGACTTCCAGGAGCCTTTCGCAGGAAAAACCTTGACGGTGGAA
CTCGCTATCTCAGGCTTTAAGATCATCTTGATCAATGCTGGTGAAGAGTTCACTCCCAAC
CCATCGATCAGCTTCATGGTGAATTTTGATGCGGTGCGTGATGAAAATGCCAAAGAGCAC
CTTGATGCGGTGTGGGAAAAACTCCATGAAGGCGGCAGCACACTGATGCCAGTCGATACT
TACCCATTTTCGGAATACTACGGGTGGGTACAAGACAAATATGGTGTGAGCTGGCAATTG
ATGCTCAGCCGCCCAGAAGAAAAGCCAGGTCCCGCAGTAATCCCAACGCTCTTATTTGGT
GGGGCAGCTCAAAATCAGGCAGGCCCAGCTCAAGAAAACTACGTTGAGGTGTTCCCGAAC
TCCCAACTTGGTGATCGTGCACCTTATGGACAGCAAACAGGTCCTGCCACTCCTGAGGCC
CTCATGTTTTCCCAGTTCCAACTCGACGGTCAGTGGATTTTCGCGATGGATTCCGGAGTT
GAGCAAGATTTCACCTTCAGTGAGGGTGTCTCATTGATGTATGAAGCTCATGGTCAAGAA
GAACTCGATGCCATCTGGAATGCACTCTCGGCAGTTCCAGAAGCTGAGGCTTGTGGTTGG
TTGAAGGACAAGTTCGGCGTGAGCTGGCAGATTGTTCCCGACAACATGGAGGAGCTCATG
GCTAAACCCGGCGCGTATGAAAAGCTTCTTGCGATGAAGAAGATCAATATCGCGGAGTTC

>RXA01694-downstream
TAGCAGTTCTAAGCGCTCCACGC

>RXA01696
CACTCCGACCCAGTACTCATGGTGGAGGCCTACCGCCAGCTCGCTGAACAAAGCGACTAC
CCACTGCACCTCGGTGTTACTGAAGCTGGTCCCAAGTTCATGGGAACAATCAAGTCTTCC
GTAGCATTCGGCGCTCTGCTGTCCCAGGGCATCGGCGACACTATCCGTGTGTCTCTTTCT
GCTGACCCAGTGGAAGAAATCAAGGTTGGCGACCAGATTCTGCAGTCCCTCAACCTGCGC
CCACGCAAGCTGGAAATCGTGTCCTGCCCATCATGTGGCCGCGCACAGGTCGATGTGTAC
TCACTTGCTGAAGAAGTCACCGAAGCACTCGACGGCATGGAAGTTCCACTGCGCGTCGCT
GTCATGGGTTGCGTTGTTAACGGCCCAGGTGAGGCTCGCGACGCTGACCTCGGTGTTGCA
TCCGGTAACGGCAAGGGCCAGATCTTTGTCAAGGGCGAAGTCATCAAGACTGTCCCAGAA
TCCCAGATCGTGGAAACCCTCATCGAAGAAGCAATGCGTATCGCAGAGGAAATGGACCCA
GAAGTCCTCGCTGCAGCAAGTGCTTCCGGTATGAAGGCTGAAGTGAAGGTAACCAAG

>RXA01696-downstream
TAAGTTTTGGTTAATTAAGGCAC

>RXA01697-upstream
TAGATCAACTAAGTATGAACGCGAATCCGACTTTGGTCGTACTGCAAGAATCGACCAGAG
CCCGATTAAAAAATGCCCCCGCGCAACGAAACTAGTAATC

>RXA01697
ATGTTTCAAGGACTAAAAGAACTCACCGCAGCAAAAGGCCGCACGCTGCTGATCACCGTC
ACCGTCGGGCTGATCGCCGTGCTGGTTACTTTCCTCTCTGCCCTCACCGCCGGGCTTGGC

CACCAATCAGTATCCGCACTGAAATACCTAGCGGGTGATAATGAACTTATCCTCGCCGAT
TCCGGATCCACCACGCTTTCCGCGTCCACGCTTTCTGATCAAGCAGTTGCCCAACTCGAA
GACGAAGGCGCACAGATGCTGTGGCAGGTCCGCGACCGAGTAGCAGACACCCCCACCATG
CTCCTCAACTCCCCTGACCTTGCGCCTGGTGAAGTATCCCTTCCTGCCGAACTCGCTGAT
TCGGAACTCGCTACTGCGCATGATGTAGTGGATTCTTCCAACGATCTGTACCTCGATCAC
CTGCCCGTGGTATTGATGAACACCTCCGATTTAGCCTCACTCGCGCAAGTCCGAGGCGTG
ACAGGACCAGCAGGCGCATTCGCCTCTGACGTTGCGCTCCCCTCCGACACCGTTGCGCTC
TCTGGATCCGAACGGTGGAACGCATCCGCCTCCTACCAGGGCGAACAGATGTCACTCAAC
CTCATGATCGTCATGCTGTATGTCATCTCCGCACTCGTGCTCGGCGCATTCTTCACCGTC
TGGACCATCCAACGCCTCCGCGGCATCGCCATCTCTAGTGCTTTGGGAGCAGCCCGCCGA
GTACTT

>RXA01701-upstream
GCCGATCAAATTCATTGATTGTTAATCGGAAGTTTTTTGAACAGGTAAAGCTAGGGGACC
TGTTCAGTGCCTGTTGGCGGATGTATTAAGGAGAATGCCC

>RXA01701
ATGCTGAGCCACGAAGAAATTGTTGCGATCGCAGAAGATTTGCTGTCTAAACGCTACGGC
GGTGTACAAACTCTTTCTGACGTGGAGCAGCTCAACGGTTCCGGCACCTCCGCGGTGCTG
CGTGCCAGGGTGGCTAACTCCCCATTCCTCCAACAGCGCTCCGTGGTGCTGAAGTACGTG
CCCAGCACCGGAGACGTCTTTGATGATTCTGCGCTGGTGCGTGAAATCGTCTCCTACCAG
TTCACCACCTCCTTGTCGGAAGATGTCCGCCCAGGGCCAGTCATTTTGGCCTATGACATT
GACAAGCGCATCCTGGTCATTTCAGATTCCGGC

>RXA01703
CTCAAATACTTTGCACACATCCACGCTGTGGTTCAGGCTGTGTCGCGGAAGATGACCAAC
TTCCACGGCGTTATTGATTGGGACACCGGTGACGGCGACGGCGGTTTGTTCAAGGGCATT
TTGGTCCGCTATTTAGCTGATGTGGCCATCCGCCTGCCTGACGATTCACCAACCAACCGG
GAAACCAAAAAGATTGCAGCACGCCTGGTACTGGAATCGGCGGAAAGCGTATGGAACCAC
CGATTGGAAGTTGATGGCCTTCCGGTATTCGCCACAGACTGGACAACGGATGCACGCCTG
CCACAAAACTTTGGTTTGAGTTCCTCTAGTTTGAGCGATCTGGTGAGTGTTGTGCGCGTG
GATGAACGTGATCTGTCCGTGCAATTGTCCGGTTGGATGCTCATGGAAGCAGCAGCGAAA
GTGGCCGAAGAACTGGAAAACAACGGCAATAGTTACACCGGTCGCTCCCGA

>RXA01703-downstream
TAGCCCCGATAGTGTATGTGCTG

>RXA01709-upstream
TTGTTGTCTGCAGGG

>RXA01709
ATGCGCTCCGGCGTGGACATGATTCTTAATGAAACCGGGGGTGAAAAGATGCTTGCACAG
GCAGATTTAGTCATCACTGGAGAAGGACGCATTGATGCACAGACCCTCAGCGGGAAAGCT
CCTACTGGAATCGCCAAACGGGCACGTGCGAAAGGAATTCCAGTACTGGCGGTTTGTGGG
CAGAGCCTATTGGGTCCAGCAATCTCAAATGAGCTATTTGAAGACATCTACAGCTTTACC
GATTTCGAATCTGACATCAATGAATGCATTCGAAACCCGCTCCCAATTTTGGAAGGTATC
GGTTTTAACATCGCCAAACATCATCTGAGT

>RXA01709-downstream
TAGCGATATTTCAGCAAACCGAT

>RXA01711-upstream
TCTCGTGAGTTTCTCCCCGGTAGCACCTTCTATATCAGCCCCCACGCCGCGTCGGAGCAG
GTGGGATAGCATCGGCAACGCGGTTGCATGGCCGTTGGCC

>RXA01711
ATGTTGTTGATGGCGCATCGCTTCTTCGTGCTTGCGATTAACGGCGCAGTCACCGACGAT
TTCACGACGGTTTATAGTGCTTTACGACGTTTCGTTGAAGGTATTCCGGTCTACAACGAG

GTCTACCACTTCGTCGATCCGCACTACCTCTATAACCCGGGCGCCACCCTCCTATTGGCA
CCATTGGGATATATCACCCATTTCACGTTGGCTCGGTGGATGTTCATCGCGGTGAACCTC
CTTGCCATTGTTTTAGCGTTCGGGCTGCTGACCAGACTCTCCGGTTGGGCGCTGCGCAGC
ATGGTGTGGCCGATTGCGATCGCCTTGGCGATGCTGACAGAAACCGTGCAAAACACCCTC
ATTTTCTCCAACATCAACGGCATCCTGCTGCTCATGTTGGCGATTTTCCTGTGGTGCGTG
GTGCACAAAAAATCCTGGTTGGGCGGACTAGTCATTGGTTTGGCCATTTTGATCAAACCC
ATGTTCCTGCCACTTCTCTTCCTACCTTTGGTGAAAAAGCAATGGGGATCGCTCATCCTC
GGCATTTTAACCCCAGTGATTTTCAATGCAGTGGCCTGGTTCTTAGTTCCGGGAGCATCT
GAATACGTCACCCGCACGATGCCCTACCTTGGTGAAACTCGAGATTTTGCCAACAGCTCA
CTCCCAGGCTTGGCCATCTATTTCGGAATGCCCACCTGGATGGAAATCACCTGGTTCCTC
ATCTTCGGCGCAATGGTCGGCCTCGCAGTGCTGGCACTCCTGAGATTCCGTAACACCGAG
CCATACTTCTGGGCAGCAACCACCACCGGTGTACTCCTGACTGGCGTATTCTTCCTGTCC
TCACTGGGACAGATGTACTACTCCATGATGATCTTCCCTATGATCTTCACCCTGCTCGGA
AGCCGATCCGTATTCCACAACTGGGTTGCCTGGGTCGCCGCCTACTTCTTACTATCCCCT
GACACTTTCACCTCCCAGCGACTACCCGATGTAGCCCGCTGGATGGAATTTTTCAGCGCG
ACCGTTGGTTGGGGACTATTGATAGTGGTTACATTTGTCTCGGCGCTAATCTGGTTTATT
GGTGATATCCGAGCCAAGGGAACTCCGAGCTCACCCATTACCACTGATCCAACGCACGAC
CATCTTGAGAGGACAGCA

>RXA01711-downstream
TGACAGACTTCAAACTCATCAGC

>RXA01714-upstream
CATTGGATAATTAGCAGGAGTGAAGTTGCATCAAAGGACAAACATAAAATAAACGGCGCG
CCTCCCCAGAGTTACCCCAATAATTAGTAAATTGCAGATT

>RXA01714
GTGATCGATTCCGAAGCGACCTCTCAGCACAAGACCTCAGCTACCCCGGCAGAGAGCACT
CCCGCGGAGTTTTCCGAAGCGGTTGAGTCTATGCACAGAGCGCGCCTGCGCCCAGAACTT
ACTTTGGGCACGATTAGGCCGCCTCAGCGCCTGGCGCCGTTTTCGCACGCCATTGGACTC
GAAGTCGGAAATCAAGAAGAGTCAGACGATGTCTCCACCAACAGCGAAGGTGATTCCTTT
GGTCGTTTGATTCTGCTCCACGATCCGGGTGCCGAAGAAACCTGGGAAGGAGCAATGCGC
CTTGTCGCCTATATTCAAGCTGACATGGATCACGCTGTTGCTTCCGACCCGCTATTGCCG
GAAGTAGCGTGGCAATGGCTTAACGAAGGTTTGGAACAAGCCGGCGCAGGATTTACCAAC
CTAGGCGGAACCGTAACCTCCACAACCTCGGTGCGCTTTGGTGAAATCGGTGGACCGCCA
AGTGCCTACCAAGTGGAAATGCGTGCGTCCTGGACCGCGACTGGCACCGACCTCACCGCG
CATGTTGAAGCGTTCGCAGCAGTGCTTGCCTCTGTTGCTGGACTTCCCCCAGAGGGCGTC
ACCGAACTACGAAGG

>RXA01714-downstream
TAGATTGGACACCATGGTTTCCG

>RXA01715-upstream
ACATGTTGTTGGAACATGCCGGCAGAGCCGACACTACGATTCATTCGCTAAAGGGTCTGG
CCACTGACACTGGCAAAGATCCACGAAAGGAAGTTACCCT

>RXA01715
GTGAGCGAGCTCGATATTAAACAGCTCAACAAACTGCAGCGCTACTCTCAGTGGGCGGTG
TTCCGTGCTATTCCTGGAGCGCTCGATGATGATCGCACAGAAGTCACTGACCAAGCAGCC
AAGTTCTTTGCCGACCTTGAAGCAGAAGGCAAAGTCACTGTCCGTGGCATTTACAACGCC
TCCGGCCTGCGCGCAGACGCTGACTACATGATCTGGTGGCACGCAGAAGAATTCGAAGAC
ATTCAGAAGGCCTTCGCTGATTTCCGCCGCACCACCATTTTGGGTCAGGTTTCTGAGGTC
TTCTGGATCGGAAACGCTCTCCACCGTCCATCTGAGTTCAACAAGGCTCACTTGCCTTCA
TTCATCATGGGTGAAGAAGCAAAGGACTGGATCACTGTTTACCCGTTCGTGCGCAGCTAC
GACTGGTACATCATGGAGCCCTTGAAGCGTTCCCGCATTCTCCGCGAGCACGGACAAGCT
GCTGTGGAATTCCCAGATGTTCGTGCCAACACTGTGCCGGCTTTCGCACTGGGTGACTAC
GAATGGGTGCTGGCTTTCGAGGCTGATGAGTTGCACCGCATTGTCGATTTGATGCACAAG
ATGCGTTACACCGAGGCTCGCCTCCACGTCCGTGAGGAGCTGCCATTTATTTCTGGACAG
CGCGTCGACATTGCAGATCTGATTAAGGTTCTTCCT

>RXA01715-downstream
TAAAAGCTGCTTTTCTAAACGAT

>RXA01729-upstream
TCAAGGTCCGGCGATTCTTCAATTCTTCGAGTTCAGGAAATCGCATACTCTCTAGGCTAG
TAAACTTTTCTACGAACCTATTACTAAGAAGGAGCCCGAA

>RXA01729
GTGAAGTTGAGGACAATCCCAGCCCTGTTAGCCGTCGCACTTCTTGCAGGCTGTTCGGGT
GAAAGTGCTGATAGCCAAGCCGTTTCCGCTGAGGAAACCATGGAAGTAACCACTACCTCA
ACCCCGGTGTTCGAAGCCAAAGAGGTAAGCCCAATCACAGTCCCAAGCGGCGATATCAGG
GTTGAAGACCCAGGTCTCAATGTTGAATTTATCTTCCGAGGCACCCGCTACGGCACCAAC
GGTGGCTCAATTATTCACATCGCGGTGAAAAACCTAAACGACGTAGCCCTGCCAGCCGAC
GCCATCGATCCACCCACCCTGGACATCGAAGACTACAACGGCAACAAAACCAACATCGAA
ACCCTCTCCGGCGACGACAACATCCCACTCGACCTACCACTGGGTGCCGGCGCGACAACG
AACCTGCAATACGCGTTCAACACCTCAAACGGCTCATTGTCGAATGCTAAATTCCAGATC
GGAAACGTCATCTACTCAGGCAATTTGAACAGCTTGGCG

>RXA01729-downstream
TAAGTTCAAAAAATAATTTGAAT

>RXA01731-upstream
GCTTTTGCAGCTGTGGGGTTGGGCTGGGGGCAAGTGTTCATGTAGGTGTCATTGATCGTT
CACTCAAGGTTGGACGTTGTGTTCATGAATAACTTTTATG

>RXA01731
ATGAACGCATCGTCCATTTCTTCCCGATTCAAGGATCTTTTTGTGACACCCAGTATTGTT
TTTGATTTCGATGGCACGCTTGCCATTGGCCATGGCCCTGTCCTTGCGTATGCATTGTGT
GTTGCACCGGAGGGTTCCAAGGACTTTCTGGAGCGTGTGCGCAGGGAGCTTCGGCGCTAT
GACGATGGTCAGAGTATTTACCGTGATGGGTATGACATTGTGGCTAAGTTGGCGTCGGAA
TTGGGGATTGATGATGGCACGATGTCTGTCGCTTATGGCGAGAGCCGGAAGTTGCTTGGT
TCGGATTTAGCGCCTGTTGAGCATGTGCGGGGTATTAAGGATATTTTGTCCTCGTTGAAA
GGTCATGCTCGGTTGGTTTTAGCTACCAATGCCCCGGAAAATGGCGTGCATGATTTGCTG
CGTCAGTGGGGTGTTGCTGATTTGTTTGATCAGTTGCATTTTGTGGTGGGTAAGCCTGCA
GGGTTGATTTCGATCATTTCTGATTTGCAGCTTGATGGTCCGGTGCTTGCGGTGGGCGAT
ATTTATGAATTCGATCTGAGTCCTGCAGCGCAGTTAGGTGCAGATACGGCTCTGGTTGGA
GCTACAGCAACCATTTCTGAAGCGAAGGTCTCCATGCGTGGAGATTCTATCGCTGATCTC
CCTCTCCTTGCCTGGGTTTGTTCCCGGGTCTCCTCTTCT

>RXA01731-downstream
TAACTTTCTTGTCTCATGTCGCT

>RXA01734-upstream
ACGATCTGCCGGAGAATCTCAAGAAAGTGCTCACTGCGCÀGCACACCGTCACCGTCCAAG
ACACCGGCACCGGGCGGATTTCACTCCTGGATGTGCAACC

>RXA01734
ATGACAGATCCAATTGAGCAGGCATTTGAACGCATCCGCGCCGAAGCCATGCGCAGAAAT
GGATCCGTTCCCGACCTCAATAAAAACGATGCTTTTCGACGCCCACCTGCGCCGAAAGGG
GGCGTCGAAAAGCGCAAAAAAGGCCGTGCAAGCGGCCTAGACGGCCGCCAGAAACGATAT
GTGCGCGGCGCGGAGTCGCTGGGATCGGTGCTGAACAAGGAAATTCAGCGTCGTGGCTGG
GGCAAAGACATTGCCGGCGGTTGGGTGACGTCCAACTGGGAAGAGCTTGTTGGCGCGAAG
ATTGCGCAGCATACGCGCGTGGAAATGATCAAAGATAAGAAGCTTTTTATCACTTGTGAT
TCCACAGCGTGGGCCACCAATCTGCGCATGATGCAGCGGCAAATCCTGCAGGTAATCGCT
GAAAAAGTGGGTCCAAATATTATTACAGAGCTGCGTATTTTTGGGCCTCAGGCCCCAAGC
TGGCGCAAGGGGCCGTTGCACGTAAAAGGACGCGGTCCGAGAGACACATACGGA

>RXA01734-downstream
TAGTTTGGTGATAAAAACCGTCG

>RXA01738-upstream
GTGAGCTCTACCGCATCGACTCCCCAGAAGCAGAAACTGTAGAGCCCGGCGATCGTCTCC
TTTACGTTCGCCGAGTATTTAGCGAGGAGGTAAATGACAA

>RXA01738
ATGAGAATTCTTCCCATCGGCCCCCACGATGAAATCGCCGTCAACGGATCAATAGTCCTT
CTATCCGAGCACGACGGAGACATCGTATCGGTCGGCCCCGACCTCGGCACGGTGCGAGTT
ACCCTTGAAGAGATCGAAAGTTTAGGTACACCGACGGCACCCCGCGATCTGGGTTCTCGG
GAAGTCGACGCATGCGTATCGTTGCTCCGCAACCGCGAGTTAGTGCGATTCGATCCCCAC
GATGGCAGTGAATTAACCTATCGGGAACATAGCGTTGCTTACGGTGCGAGTGGCAAGCCA
TTGTTTCCCCGATTGGATCCAGCGGTGATCGGCATTGTGGAGCTGCGAGGTGAGGATCGT
TTGCTTCTGGGCATGAATGCGCAGAAACGCCAACGCTATTCATTAATCGCAGGTTATGTT
TCGCATGGTGAGTCGCTGGAAGACGCATTCACCAGAGAAGTGTTCGAGGAAGCGGCGCGC
CGGGTATCTGAGATTTCCTATGTGTCGTCTCAACCATGGCCGATCTCTGGTTCGCTGATG
CTGGGTATGAAGGGCTTCACGGAAGATGAGTTGCCTCAAGGCGAAACTGATGGTGAATTA
GCGGAGACAATCTGGGCTTCGCCACTAGACATTATCGATCGTAAGATTCCGATCGCCCCA
CCCGGATCGATTGCCTACGACATGATCAACGCCTGGGCGCGAGATAAACAAAAC

>RXA01738-downstream
TAAGGGAGCTTTTTACAGTGATC

>RXA01741-upstream
GCATCTCTGGCTTTTCCTGCATGACAGATGATTGTAACTGTGATGAAATAAGGCCAGATG
AAGTAACTGTGTCGATTAAGTTTTGGGGGAAATTTTTCAG

>RXA01741
ATGACACACATCGCTTTAGCCAACTCTGCCCAAGTTCTGATCCGCCCGGATTCTGCGATT
CAATTCGGCATCGACGCCACCCGCGCTGGCGTCTTAAATATCGATCCATCGCTGTCGTCG
CGAGTCGTCCCGGTGCTGCGGAATCTGCGGACCGCCCGACCGATCGTTGATGTCATCGCC
GACCTCACGACTGCAGGCCTCGCACCCACCGCTGCGAGCAGTTTGCTCGAGGACCTTTTA
GAATTCGGTGTGGTCCGCGAATCGGCGGCGGCGCAGGTGTTGCTGTTCGGGGACGGTTCG
CTTGTCGACGTCACCTCCTTCCTTTTGGAAACCTCCGGCTTTGTTCCCAGACCCCAGATC
ATCGATGAGTCGCCTCGAGAGTTTTTCGAGCTTCCCTCCAGCCACATTTTGGTTCTCAAC
AAGCTCGCACATTCCCAACGTCTATCCCCGCTGCTTCACAAATATGCGCCGACGTATCTG
TGCGCCGCGATCGTCGATAATCGTGGCATCATCGGCCCGGGCCGGAGATCACGATCGGGG
CCGTGTTTGATGTGTGTGGATCTGCATCGCTGCGATATCGATCCGCATTGGCTCTCTATT
ATCAATCAGCAACCCAACGGTCCCACCTTTCCTGATCCCGTCACGGAGATGGCGACGGCT
GCCCGACTCGTCGCCTGGGTCACTGCCGATACATGGTTGCCCGGCGTTGTGGAGGAAGTA
AACCCCCACGATCGAACAAACTCGGTACGCACCCTCCCTGTGCATCCAAAATGTCCGATG
TGTTGGAGTTTAGGTTCC

>RXA01741-downstream
TAAAGTGCTCCCAAAATCGCGAG

>RXA01742-upstream
TGGCTAAAGCGATGTGTGTCATCTGAAAAATTTCCCCCAAAACTTAATCGACACAGTTAC
TTCATCTGGCCTTATTTCATCACAGTTACAATCATCTGTC

>RXA01742
ATGCAGGAAAAGCCAGAGATGCCAGCGATTGAGGTCATCCGTTCAGCGAAACGCACCAAA
ACTGTTCAAGCTCGAATTGTGGACGGGCAAATCCAGGTGCGCATCCCTGCGAGGATGTCT
AAAGCGGAGGAAGAAAAAGCGGTGGGGGAGATCGTCGCAAAGCTAAAGCGACGCACCCAA
TCGGCCGTCTCAAGCGACGCTGACCTGATTGAGCGCGCCCATAAGTTGAACAAGACTGTG
TTGGAGGGGCGGGCGCGGGTGGAAAGTATTCGGTGGGTGAGTAATCAGAAGGGGCGGTGG

GGGTCGTGCACGGTGGCGACTGCGGAGATTCGGATTTCGGATCGTTTAAAGCACGTGCCG
GATTATGTGTTGGATGCGGTGTTGGTGCATGAGCTGACGCATACGTTTATTGCGGGGCAT
TCGGCGGAGTTTTGGGAGTGGGCAGACAAAACGCCCCTGGCAGAGAGGGCCAAGGGCTAT
TTGGAGGCGTATCAGCGGTGGGGC

>RXA01742-downstream
TGAAGGTTTAGTTCTTGTCGGAG

>RXA01748-upstream
ATCACCAAATGTGGCGGTTTTGCGTCGAAAAGCGTGCTCTTTCTACACCTCTTTGAGGTT
CATTTTCGCGGTTTCCTCACAATCGCCTATTGTTAAGTAC

>RXA01748
ATGGCAGACGCGAAAAAGCAGGCGGATAAAGCCGCCAAGAAGCAGGTAAGAGCAGCCAAG
AAGGCACAGCGCAAGGAGACTCGCTCACAAATGTGGCAGGTCTTCAACATGCAACGCAAG
CAGGATAAGGCTCTTATTCCGCTTCTGTTGCTCGCTATTCTTGGTATCCCGCTGGTCCTT
TTCCTCATCGGTTTGATTTGGGGTGGTCAGTGGTGGATGCTTCCGATCGGCATTGCTGCA
GGTGTTGTAGCTGCAATGTTTATTTTCACCCGTCGCGTTGAGCGTGACGTGTACAAGCGC
GCCGAAGGTCAGCAGGGTGCTGCTGGTTGGGCTGTGGAGAACCTCCGCTCTGGCGTGGGC
ATGACCTGGCGCACCAAGACCGCTGTTGCAGTGACCACTCAGATGGATGCAGTGCACCGC
GTCATTGGTCTGTGTGGTGTTGTGCTGGTCGGCGAGGGCTCCCCTCACCGCCTGAAGCCA
ATGCTTGCGCAGCAAAAGAAGCGCCTGAACCGCGTGGCACCTGGTGTTCCAGTGTATGAA
ATCATCACGGGCAACGGCGAAGGCCAGACCCCTATCGCGAAGCTGCAGCGTGAACTGGTC
AAGCTGCCTCGCAACTACAAGAAGAACGACGTCGCTGCCCTGGCCGCTCGCATTGAGGCT
ATGGACAATGTCGGAAACGCTCCTGGCGGATCTTTGCCTAAGGGTCCATTGCCAAAGGGC
GCAAGCATGTCCGGTATGAACCGCCGCGCTCGCCGACAGGCTGAACGCAAGGGCGAGGCT

>RXA01748-downstream
TAAAGCCTTTTCGCTTTCGCGTC

>RXA01749-upstream
GGTTTTTGCGTGCTCTGGTTTAGGGACTGGTTTTGGGAACGTGCCCAGTTCCACATCAAA
TAACGCTGAGGTCGTACTTAATCCATGAGATCATGAATGG

>RXA01749
GTGAGCTTCCTTGTAGAAAATCAATTACTCGCGTTGGTTGTCATCATGACGGTCGGACTA
TTGCTCGGCCGCATCAAAATTTTCGGGTTCCGTCTCGGCGTCGCCGCTGTACTGTTTGTA
GGTCTAGCGCTATCCACCATTGAGCCGGATATTTCCGTCCCATCCCTCATTTACGTGGTT
GGACTGTCGCTTTTTGTCTACACGATCGGTCTGGAAGCCGGCCCTGGATTCTTCACCTCC
ATGAAAACCACTGGTCTGCGCAACAACGCACTGACCTTGGGCGCCATCATCGCCACCACG
GCACTCGCATGGGCACTCATCACAGTTTTGAACATCGATGCCGCCTCCGGCGCCGGCATG
CTCACCGGCGCGCTCACCAACACCCCAGCCATGGCCGCAGTTGTTGACGCACTTCCTTCG
CTTATCGACGACACCGGCCAGCTTCACCTCATCGCCGAGCTGCCCGTCGTCGCATATTCC
TTGGCATACCCCCTCGGTGTGCTCATCGTTATTCTCTCCATCGCCATCTTCAGCTCTGTG
TTCAAAGTCGACCACAACAAAGAAGCCGAAGAAGCGGGCGTTGCGGTCCAGGAACTCAAA
GGCCGTCGCATCCGCGTCACCGTCGCTGATCTTCCAGCCCTGGAGAACATCCCAGAGCTG
CTCAACCTCCACGTCATTGTGTCCCGAGTGGAACGAGACGGTGAGCAATTCATCCCGCTT
TATGGCGAACACGCACGCATCGGCGATGTCTTAACAGTGGTGGGTGCCGATGAAGAACTC
AACCGCGCGGAAAAAGCCATCGGTGAACTCATTGACGGCGACCCCTACAGCAATGTGGAA
CTTGATTACCGACGCATCTTCGTCTCAAACACAGCAGTCGTGGGCACTCCCCTATCCAAG
CTCCAGCCACTGTTTAAAGACATGCTGATCACCCGCATCAGGCGCGGCGACACAGATTTG
GTGGCCTCCTCCGACATGACTTTGCAGCTCGGTGACCGTGTCCGCGTTGTCGCACCAGCA
GAAAAACTCCGCGAAGCAACCCAATTGCTCGGCGATTCCTACAAGAAACTCTCCGATTTC
AACCTGCTCCCACTCGCTGCCGGCCTCATGATCGGTGTGCTTGTCGGCATGGTGGAGTTC
CCACTACCAGGTGGAAGCTCCCTGAAACTGGGTAACGCAGGTGGACCGCTAGTTGTTGCG
CTGCTGCTCGGCATGATCAATCGCACAGGCAAGTTCGTCTGGCAAATCCCCTACGGAGCA
AACCTTGCCCTTCGCCAACTGGGCATCACACTATTTTTGGCTGCCATCGGTACCTCAGCG
GGCGCAGGATTTCGATCAGCGATCAGCGACCCCCAATCACTCACCATCATCGGCTTCGGT
GCGCTGCTCACTTTGTTCATCTCCATCACGGTGCTGTTCGTTGGCCACAAACTGATGAAA

ATCCCCTTCGGTGAAACCGCTGGCATCCTCGCCGGTACGCAAACCCACCCTGCTGTGCTG
AGTTATGTGTCAGATGCCTCCCGCAACGAGCTCCCTGCCATGGGTTATACCTCTGTGTAT
CCGCTGGCGATGATCGCAAAGATCCTGGCCGCCCAAACGTTGTTGTTCCTACTTATC

>RXA01749-downstream
TAGCATTGACCCCTTAAGCGCAG

>RXA01750-upstream
TCGCCCCCGAGGATTGTGTTGCGAACAGTCCTGAAGATCATGTCAGACCTACATTGAGCC
AATGATCGACATGTGGACGAGGGAAACTCGACCGAACAAT

>RXA01750
ATGTGTATCAACGACCCTAAAGGCGAGTTGCTGAAGAAAAATTATGTTCGGATGTCTAAG
CGCGGTTTTCAGGTTGTTCAGTTTAACCTGATTAACAACCTGAAAACTGATATTTATAAC
CCGTTGGGATTAGCAGCCGAAGCAGCTCGCGAAGGTAACGGGATGAAGTGCGCAACCTAT
GTGGAAAATATCGCAGAGGTGTTCTTTCCGGTGGACGGTGCCGATGATCCGGTATGGCCG
AATGCGGCCAACAATGCCTTCAAGCGTGCAGCCTATGGTCTTATCGACTTCTATTTGGAA
GAGGAGCGCGAGATGCGCAAGCAGGCTGCAGCTGAGAATTGGGATGCCAAGGTGCTTGAT
ACACGTATTGATCAGATGTGGGGTAAGGTCACGCTCTACAACTGCTACCAGCTCTTTGTG
CAGCTTTCGGCAAAGAAGCTGAAGAATCCCGTTGAGCGACTCAATGAACGTGCACGTGCC
GGTGAATTCGGTAACTTAGAGACTGATGAAAATGCAGCCATGATGTTCCAGGATGCTGTG
ACAGAGGCCGAAGAGAACGAAATGTTTCTGTGGGAGGGTGAGAAAGAAAAAGACATGCTC
ACCTTGTTCTTTAGTGCCACAGACGGTCTGCCAAAGTCCAGTGTTCGTACTCTGGTGGGC
AACGCAGATAAGGCCCTGAAAGCAATGGGTGGCGCTGAAAAAATGATGGCGTCGGTCTAC
GGTATCGCGATTACAGCGATGTCCTTCTTTACAGACCCCACAATTTCAACGTTAACCTCA
GGCACACTAAGTCAGAACGTTGACTTGGCCGGATTGTCGTTTCCACGGCGCATGGGTGTT
CGTTTTGCGGCCCCCTATGTGAAGCGCTACAACCTGGTTGGATCACAGGTGAAATGGGAT
GCGTATAGTGACGCCAAGTTCACCAAGCCGTTGGGTAAGAATTTTGTTCATGATGACACG
CTGTCGGTTGAGGGTTGGGCGCGGTTCTATATTAAAGACTCGTTCCCGAGTAATACTGCG
TACCTGCGTTTGCGGATTCTCAATGGTACTTCTGGCACGTTGATCAAGACTCTGTACTTC
AAGTTCACCAAGGGCTACCAAACGAACCTTAAAGGCCGTGCGTTTATTACTGATCCGGTG
ACCGATGAGAAGATCATTAAGAATGGTCTGCTGATCGAGCTGGTGAAAAACGATGCTGGT
GACTTTGTTCCAGGTCATGTGCAGTTTAAGACGAAGAAACTGAATCTTGACCAACTCACG
CAGGAACAGATCAATATGCCGGGTCATGACATGATCAAGCAGGTTGATGCGATGGTTGAT
GCGGTGTCGGCTCTGAATGTGCGGTATTCGGAGAAGCCTAAGGCAGTGTTCTTCGTAACG
CCTCCGCATCTTATGAAATATGCGAAGTTGATTTTGATTCTCATCAAACAGCTTGTGGAT
CTGAACTTCGATTCCTCGTATATGACGCGTGAGAATCAGAAGCCGGATTATAAGACTCGT
TTCATGTTGGACGAGTTGGGAAACCTTCAGAGTGAGGGTCATGGTATTGCGGGATTTGAA
ACCATGCTCTCGATCGGTCTGGGACAAGAACAACAATTTAGTGCGACCAGTTGCGTAGCG
AAAAACTACGCTCTTGCAGCT

>RXA01750-downstream
TAAAGTTGCAAGAAACTGTTTCA

>RXA01752-upstream
GAAATGACGTGACCATCGATACCAATACCCAATTGAAAGATCTTGACCTGGTCAGCCAAG
TTGGCCGTCAGATCGTGGCAGAACAACAGGTGGGGAGGTC

>RXA01752
ATGATGGAACAAGATCTCAGCTACCGTGAAATTCTTCCCCTCAACGCGAGTGAGGAGAAG
AAAAAGGCTGCACTGATTGATGCCATTGAAGGGTTAAGGGTGCGCGATCCGCTACTCTCT
GCCTCGATTGCATTTACTAGAGGGCAGAAAGTCGCCTTCATTGCTGTGGTGGTGGGCTTT
ATCTTGATGCTCATTTTTGCTCGGCAAGCAGCACTTATTGGACTGTCAGCAACGTGTACG
TTCATGTACCTCATTACATTGTTGGACAGATTTATCATGTTTTCCAGAGGTATCCGCGCG
GAATCCATCATCCAGGTATCGGATGAAGATGCGCTGGCTTTCCCTGAGGACAAGCTGAAA
ACCTACACGGTGTTGGTGCCCGCCTATGGCGAACCTGAGGTGATTGCGCAGCTGCTGGCA
TCCATGCACGCTTTTGATTACCCCAAGCATCTTCTGCAGGTATTGCTCATGTTGGAGGAA
GATGATCTGCCCACGATCGCCGCGGCAGAGGCAGCGGGAGTGGATCAGGTGGCAACGATC
ATTAAGGTGCCG

>RXA01753-upstream
CTGATTGTCGCAGCCGTGGTGTCAGTGTCCAGGCGTTCGCAAAAAGGATACAAATGATTT
CTTCTTTACCCAGTAGAACGCAGGGGAGGAGGTTGGGTCC

>RXA01753
ATGAGTAACCCGTCGCTAGAACCTCTAGAACCGATCGAGCTTTCTGACGGTACTGAAATT
GAAGTTTCAGACGTTGATCCAGAACCGCAAGCTGGCAATGCGCAGATGGAAGTACCCAGC
TTACGGACATATGTTTTTCGCGGAATCATTGCCATTGCCTGTTTGATCATTGGTTTTTAT
GAGAGCTTTGTGCTGATGTGGCAAAACCTCCGAATCGGCGTGGCCAACTACTCACTACTT
GTGGTGCTCATGGCGATCGTGTTGTTTATCGGACTGGACCGCAAGCGTGCTCGTGCATTG
AACATTCACGACCGCGAAGTCGACTACATCATTGGTGGCATTGTCGTACTGATAGCCATC
ACGATTAAGAGCCAGCTTCTGCCACGTTTTGTGGACTGGGAAACTCTGCTGCGCTTGGAT
ATGTTCGCACTGTTATTCTTTGCGTTTGGTATTTCCGGCCTGGTGTTTGGCATGCGCTCT
ACCTTTTCTTTTGCACCCGGCTGGATTTTGCTGTTTGGCTACAACGCGGTGGCACACCTG
ATCATCTCGGTGATTTTCGGTGGTGGCTTTTGGGGCCCGGTGATGGCAAACATCATTGGA
CTGTCTCTTGCGGTGTTGGTGTCCTCCAACAGGGACCTGGTTCAGGCCACCTATTTGGCA
CTGATGACGGTGTTGTTTGGCGTCATTATTGCCATCATCGTGTGGGCGCTGACCGATGGC
AGTAAGTTCCTCACCTTGGTCCCAGCAGTGCTGGCAACCATCACTGTGGTGTTGGTGTCT
TCGCGTTGGAGGCTTGGTCAGTGGAAAATTCGTCGTAGACAACCCACGGTGGAAAAAGCC
GGACCCGCGCTTATCGCGGTCGTGGTTGCGACAGCACTCTTGGCGTGGATTCCTACTCCT
TATGTGGAGCGCGTCAACAACCTCCCCGGGCTTCAAATGCTGGCAAAGCCTGCCCCAGGT
GTTATCGCACCTATTGGTTGGCACATCGACGATGTGCAGTATTACAACTGGGCTTCGCGC
TACTTCGGCCCCGGTTCCTCTCTGCTTAGGCAGACGATGACGGCAGATCATTACAACGAG
GCGTGGGATCCAGATGGACTCGACCGAACTGTTGTGGTGGATACCCTCCAATCGGCGGAA
CGGTTCCAGCAGCGTGCCTTTGGTGACGAGACGCTGTATTCCACTCTGAGAGGTCGAAAG
TCAGATACCGTCCAGGTGGATCTGGGATACGGCGTGGACGGACGCGCCTACACGGTGCTC
GATGAAACTGACTTCTTGACGTACACCAAGCTGGTTTTTGAATGGCAGACCACCAACAAC
ACCGTGGAGAAGATCTCCGTCATCGCGGTGGATGATCACCGCGCAGAAGCGAAGTTCCCG
GAGCTTGCACCATCGGTTACCAGAATGTTTATCCAGGTGGCTACCATTTTGTTCCGTGGA
AATGACGTGACCATCGATACCAATACCCAATTGAAAGATCTTGACCTGGTCAGCCAAGTT
GGCCGTCAGATCGTGGCAGAACAACAGGTGGGGAGGTCA

>RXA01753-downstream
TGATGGAACAAGATCTCAGCTAC

>RXA01754-upstream
TGTGGCTGAAGACAAGAATGAATAGCATTCATCTCGTCGAATTTCATGTAGAAATTTGTC
CCCCTTTTTTTTGATGTGAAAGTTGAATCGGTAAGCTCCT

>RXA01754
GTGAAAATTAAATCCGTATTTTTGAGCACCGCTTTAAGCGCTTCCTTACTGCTCGGAATC
ACCCCACCCGTGCTGGGAGCAACGATCAACCCCAGTTTGCCTCTTTCTGCGTTGAGCTCC
TCGGACGATATCGCCGTACCCAACTTCGCCAAAGAATTACCGTTAGCTTTTGATGTACCA
GCAGGCACTGTTCCCCAAAGCTTGAGTGGAACGCTGCAGATTCCTGCCGAGTTTTCTGGC
GGCGTCGTGGAGTTTTATGACGGTGACCGGCTCTTTCACACCCTGCGCCTAGAAGTTAAT
GATTCCCGAGCACACATTGAGGTTCCGCTGCAAAGCGTTCCTGTCGAAGACGGCCGCGCC
ACCTTTTGGTTGCGCGCCATGTTGGATCCTGTAAACAACCAGTGGTGCTACGAGGAGCAG
GAAGTCCGCTTCTTAGACGGAAACGTCACCTTTGAAGGGGCGACGATTAACCCAGCTGTG
GTGGCTGATTACTTCCCGTCAGTGCTGCGCGCGTTGACAATTTACGTCCCGGAAAACCCC
TCTGAGGCAGTACAAGAAGCCACGTTAGAGGTTGCGACCTCCCTGGATTCGGTGTACCGA
AGATCAGGTCTGGATGTCAACGTAGAAACGCTTCCAACCGGCACCGATGCTCCTCCTACA
CGTCCTCAAGATTTTGAACGCCAGATTGTGCTGGTTGACGAGGCAACAGAAAGTAACACG
CAAAAAACCGAATTGGTCAATCCCGGCCAAGACAATGCATTCTTGCGCCTGAACGGCAAC
GCCGACGAGCTTTACGATCAAGCGCGCTTGCTTACCGACGCAACCCTGCCACTTGCCGTA
GACACCGAAGTAACGGCCTCAGGTTTTGGTGATGTGCCCAACCTTTCTACAGATGTGGCC
ACCCTCCAAGAACTGGGTATCACGCAGCTCACCTCTGAATCAGTTGCGCGCACAAGCGTC
ACCTTGGGCATTGAACGCTCCCGCCTGCGGACCTACTCGCAGTCCATGGACCTGCACATA
ACGGGAACCTACACCCCATTGCCACCCCAAAATGCAGGACAGATCACGTTCTCCATTGGT
GACACCGTGTTGGACTCCTTGACCACCGATGACACTGGCATCATTGACCGTGAGTTCAAC

GTTCCTGGAGACTTGGTCAACCGCTACACGGCGATCGTCGTGGAATTCACCAGCACCGGC
GACGTTAATTGTGGGGTCACCCAGCCCGTAGGCCTCAACATTGATTCCGACAGCCTTGTC
ACCTCCCAACATTCAGATGTTCCTGTACTCAACGGCTTCCGGTCCCTACCGCAGTCCTTC
CAACCTCGTGTGGACGTGGCGTTTGCTGATCCCAGCGTGCAGGAACTCTCCCGCGCTGTC
AGCGTAGTGTTGGGAATTCAATCTATGAGCTCCCAGCGCATCCGCCCACACCTGGTTAAC
TGGGATGAAGCCGTAGCCAGCGAGCGCCCAACAATTTTCATTGATGCTGCGGGCGCAAAG
ACTGATCAAGTGCCAAGCTACCTCGCCCAACAAGGCCAAACCCTAGAGATCACCAGCAAG
AACGACCAAAATGCGGACGGCGAACAACTCACCCGATCCCTGCAAACCAACGCTGCGCTT
GTTGTCGGTTCCATTCAGGCCGTGTGGGATGCCGATAAGAAGCGCACGGTGATTGTGGCA
AGTTCCCAGGACAACCCCCCCGATTTGGATGCCTTGATTTCGTGGATGGGAGAAGACCGC
GAACGCTGGAGTGATCTCAACGGCGACCTGATTGTCAAAGTCCGAGACCGCGAACCTGTG
CAATTGACCACCGTGGAAGCCCCAGATCAGCCTGGTCGATCGGCCACAGCCTTTATTGCG
ATCGGCGTCAGCCTTGTGGTCATTGCCCTGATTGTCGCAGCCGTGGTGTCAGTGTCCAGG
CGTTCGCAAAAAGGATACAAA

>RXA01754-downstream
TGATTTCTTCTTTACCCAGTAGA

>RXA01760-upstream
ACCTACTCAAACTTTCCTCTGCGCCATAACGTGAAGTGAGTGCCGGGGCAGTCCCGGCAG
CACCCAAAAGCGCATTTTTGATACGAAAGTGAGTCATACG

>RXA01760
ATGGCAGCATTTCTAGAGATCACCTTGAAAATCAATGACGAAGGCCGCCCATCAGCAGCT
GGCGTCTACCAGGAATACAAGCAACCATTCCTCAGCTCAATTGCTGGCGCTACAAGCAAA
GAACTCCTCATCCGAGAAGAAGACGTGCAGGTGCTCCACGGCTGTGACACCGTAGCTAAT
GCTGAAGATTATCTTGTCAGCGAACTGTTCACGGCCGATGTTGTCGGTGGTCTAGCTCCA
CTATTGCAGGCTGATCCAGAGATTCGTATTTACCAGGTCGCG

>RXA01760-downstream
TAACTGCTGTGGCAGGCTCATCG

>RXA01761
GCTGATGCTAACGCTGATTTTGTAGACGGTGTTGTTGATGGTGCTGGTCGCGCGTCATTT
AGCAATGCTGCGTATAGCTCCGATGGAACCACTCTCGACGGTGAGGGTGCGAGCGTTGAT
GCACAGGGTAACCCGCTTCATGCTGATGGCACACCAATGAGTGCTGCTGAAGCTGAAATG
AAGATGGCTGGTCTGAGCTCGTCAGGAACCATGATGGAGAAATCTGGTGTGAAATCGAGT
GGCATTACCACTGCAGCGGATGTCATGGACGATCAGTCTCTGGCAAGCAGTGTCACTGAG
TCTGGTCTGTCCAAGATTCCAGACACCTATGGTGCAGATGTCTCGGGTGCTGCGGGCACA
GTCGGAACTACCGGTGCTGATTACAGTGCGACCGATTCAAGCGCAGGTCTGAACATGAGC
GAGGCTGCATTGCAGAGTGGCACCCCAATGGGCGCTCTCGCTGGTGGATCTGTGTCGAGT
TCCGATCAGGCCATGAATGACGCAGCTCTTCAGATTGCAGCGTCTCAGGGTCTTGCACCA
GCAGGTTCCATAGCTGGTATGGAGCAACTTAGTGCTCAAGCCACTGAAGCACCTGCTGGA
AAGGCCGGCAAGCAGCTTGGCGATCTTTCTGGCTCAGCGCTCAATACTCAGCTGGCGTCC
ATGGGACAGCAGGTAGGTGACAGTGTGAACAGCGCTTATGCTGCAGGCGGTATGGGTGGT
GTTGATGTGGCTGGCAAGGTCACCGAGGCAGCACAGCACTTGTCTCAGGTTCCAGGTCAG
ATTCAGAATGCTGTGACCAATGCGGATGCTGGTTCCTCTGGCGCAAGCTTTGGTCAGATG
GCACAGGGGGCAGCTGGTATTGCCGGTGTCGCAGGTGTGATCGGTGCAGCGGGCGCAGCA
AGCTCTGCAGCACAAGGCGCAGGTACTGTCCAGGGTGCGATGGGTAATGCTGCAGCTGGT
GCGGGAATGATCAACAACGCTGTTTCCGGTGGAGCTACTGGCTCAACAGGTGCCGCACAT
GTGGTCAATGCATCACATGGACCAGTGGCGCCTGGTCAGGCTCACTACCAAGAGTCTGGT
CATGCACAAGCATTTGTGCAGAACAACCAGGCCAACACCGCGCACACAGCAAACACGCGT
GCACCGTCATCAGCTCAAATTATGGGCGCGAACGTTGCTGGCTCACTGGCATCACAGGCT
GTACGAGGAATCGGTCAGCCTGGTCAGATGGGTGCTAATGTTCGCGACGCGATGGGTGGC
AGCGGACGCTCTGGTGGCCGTGGTGGAGCAACTCAAGGCGGTCGAGGCGCACAGCGCAGC
GGTGTCAGTGCTAAGAACGGTATCCGTGCACAGCGAGGTCAGAAGCCTTCTGTGACCGGC
CAGGCGATGAATGCAGCAATGCGTTCAGCAGCGGTAAGCGGTCGCATGGCAAACATGGAC
GGCAACAGTGTAGGTGGCACTGAAGCAGATCCACAGCAGGGGAGTGGCGTAACCGAGAAG
GGTGATAAAGGCGTTAAA

>RXA01761-downstream
TAGCGTGTAAAACACAATGACCG

>RXA01765-upstream
GCAGTCCGTCGGTGTCGTTTTCCCTGAACTGCCGGCAGAGCTTCAGCCACAAATCCCAGT
CAAGGCATAACACCGCACACCAAGAATTTTAGGAGGGGTC

>RXA01765
ATGAGCAACAACGTAGTGAAATATGAGTGCGCGGTCGACGCCGACAACATTGTCGCAGTC
GATATGCATGTGCACTTGGAAGTCGACAGCTGCGGACACAAATCGATGCCGGCAGACATC
ATGGCGGCATCCTCGAAGTACTTTAAGACCGCGGAACGAACTCCCTCAGCAGATGCCATT
GCTGATATTTATAGGGAACACAAGATGGCGGCGGTGGTTTTCACCATCGATGCGCGGACC
CAAATGGGGCATCTGCCGAACTCGATTGATGATTTGGTGGCAAGCTGTGCCCGCAACAAT
GACGTGCTGATCCCTTTTGGCAGTGTGGATCCTCGTACCGGCGAGGACGCGCTGGTGGAA
GCTCGCCGACAGGTGGAAGAACTCGGGGTGCGAGGCTTCAAATTCCATCCATCGGTTCAA
GGATTCGACCCATCCGCGCCAGAGTTCTACCCACTGTGGGAATTGCTCGAAAGTTTTGGA
TTGCCATGCGTGTTCCATACCGGACAAAACGGCATGGGTGCAGGTCTTCCAGGTGGTCGA
GGCATTAAGCTGCGCTTCTCCAACCCAATGTTGCTTGATGATGTTGCGGCGGACTTCCCG
AACCTGACCATCATCATGGCGCACCCTTCTGTTCCTTGGCAGGATGAGGCTAACTCGATT
GCCACCCACAAGGCCAATGTGTTCATTGATCTTTCCGGCTGGTCGCCGAAGTATTTCCCA
GAGTCTTTGGTCAGACAGTCCAATAACGTGCTATCCAAGAAGGTGCTGTTTGGCACGGAC
TTCCCGCTGATTACCCCAGAGAAATGGCTTGCGGCTTTCGCGAATCTGCCACTGAAGGAT
GAGGTTCGTCCGGGAATCCTCAAAGACAATGCGGTGAAGGTACTTGGCCTAGCCGCTAGC
ACTGAGCGCGGATCTCAAGCAGAAAAGGTCGTGCAACATGCG

>RXA01765-downstream
TGATCCCATTCAAGGTGCTGTTA

>RXA01767-upstream
ACACCAGCCCTCCACAAGAGCGTCGAAGCAATCTACGCTTCGACGCTCTTTTTTTCACTA
CCTACTCATCCCCCACATAAGAAAAAAAGACGACACCACC

>RXA01767
ATGATTGACCATAAACTGTGGTTTAACACAGTAACCAACAACGCCTCTGTCCGAGAAGCT
GCAGGAAAATGCGACATACCCATCAGAACGCTCAACGAGCAGCTTAACCGTCGAATACTC
CCTGAAAAGACCGTCATCGCTCTAGCACGCGCTTATGATCTCTCACCTGTTGATGCGCTC
GTTCGCACCGGACACCTCACCGAAGAAGAGGCTGGTAGTCGTGAAGAAGATGCCAGCCCA
GATTCAGCTGACGACTACCCTACCTGGGCACTGAACTCGCACCTTGACTATGGCATTCTC
GGAGCTTTTGGCGACATCGCTGAAGAAGTAAACAGC

>RXA01768-upstream
GACAACGAACACAACACCCAGATCCTGCACTGGTCCGGCGTTAATCGCTACCTCATGCAG
GCACTCTCCCGTACTCATTTCTAGAAAGGTTTTTCCCGTC

>RXA01768
ATGTCTGAATCTACTTCTTCTGCTAACTCCACCACCATCCTCAACGACACCTTCAACCCG
AAGCCTGGCGTACCTTATGCACGCGTCGATAATCTCGAATTTGCCACACGTGACGAATTC
CGCGCTTGGGCTACCGCAGAGATGGAGGCCGGTAACGTTATCTCTGCAACCATCGCCAAT
GCCCCACGCGAAGACCGCATCAAGTCTTTTGTCATGGATCTTGTTCGAGACGGTATTGAC
GACGCTGCTGAGGAAATCGTCTCACGCATTGATAGCGGTGACTTCACTATGAAGGAAGCT
CTCACCGCGATCGCGGCATCAATCAACGACCTCGATGCTGACGATGTAGTCAGCGACATC
GTTGAAAACCACTTCAAC

>RXA01768-downstream
TAGTCAACACACCAGCCCTCCAC

>RXA01769-upstream
CAGGACTAAAACACCTGCTGCTGTTGAGCGCTTCTCACACATCATCCTCACAACCCCGTT
GCAGCACCAGCATAAATCTATATTCGCTGTGACGGGGTTG

>RXA01769
TTGGGGCGCGCCCCACATTCACTCTTTTTCCCGATTGGTTTCTACTACACACCCATGACC
TCTATTACTACTACCGATACCCCGCTATATACAGCACTGCCCCATACCCGTATCTCTGAT
GCGGAATTGTTGACACCAACAACAACTGTGCACGAGATTCTCGTTTACGGACCGGCTGAG
TGCCCAGGGTGTACAGCAACGCTTGACTTCTTTGCACGCAAAAACATGCCGGCCACCAAA
GTCACTGTAGCTGCCGGTGATGTAGCACATACCTACATCACCCAAGACTTAGGTTATCTC
CAAGCACCGATTGTCACTGTCCGTATCAGTTCCTCTGCTTCTAACCACGACAACGAACAC
AACACCCAGATCCTGCACTGGTCCGGCGTTAATCGCTACCTCATGCAGGCACTCTCCCGT
ACTCATTTC

>RXA01769-downstream
TAGAAAGGTTTTTCCCGTCATGT

>RXA01770-upstream
TGCTCATGACAGGTAATTCAACGCGTTACCCTGCTGCAGCATAAAAGAACCTGCCTCAAC
ACACCTCCACTTTTTCTACTTTTAAGAAAGCCACATTCTC

>RXA01770
ATGCCAATTATCATTGATAACCTCAATTCTGACGACGACTCCACCATCGGCACTGCCACC
GAATACAACCCTGACACTGACGCCGATTTACTTGATGCTATTAACGCTGATGCTGACCTT
GATGGCGACGCCACCATCAGCACTAACGCGACAGAAGAAGGTGTAGACGCAGCAGCTGAA
AAACCTAAGAAAAAGCGTAAAGCCCCTGCTCTGAAGCCTAAAGGACTCACGGCAAAGTTC
TTCCACCGTGATCTTACTGGCGTAGGTGGTAGGACCGGTCGCCTCAACAAGAACGTACAC
CCGACCAACCCAGATCTGTCCTACCAGCCAGTCTCTGATGTCTACACCCCACAATCAGCA
GATCACAAGGGTATTAAGACCCGCTACATCCTTACCCATCCAACCCCCGCTGTTGTTCTC
AGTGAGTCCATCAGCAACGCGTTTCATGTCTCTACCCTGCGTCGCAACAATAATGTCAAC
AACTCTGATTCGGAATTGGCTGCCTGGCCGTACCTCTACCAACTCGATATTCCGCAGCTG
GACCAGATGATTAATGTCGCTGACATCTGTGATTACCATTTCCACGGATATAACCTGTGG
GTGGATTTTACCCCGCAGACTATCGCTCTACGATCCGGTAAGACGGTACTCGATGACGGT
ACCACCGCCTCTGATAACACCACTCATGTCTATTACCGCGTCACCGTTCACGTTATTGCC
GGTCAAGATCATGGATCTACTCTGCTTGATGACCAGGGCAACCAGGTGCTTGATAGGGAT
GATAATCCTATTTCTACCCCAAGTATCAAGCGTATTGGCGCTGTCACTGATCTTTTCGAT
CACAATCCTTTTGGCTTCGCTAGTGTAAACTCTTTCGCATTTGTCGATTTCTCATGGGAC
CCAGCCACCACCTTGGTCGATATGCTCAACAACCTTGATTCATATCTCTCTAATCACATC
AATATTGCCAGCTCCCCAACCCCCATTGCCCTCGATATGGTTGTGCTCAATGAATGGTCT
GAAAAGTCCTATCAGCTGTGCGAACGCGTTGTTGCACAGGCAAAGCTCATCAACAGCAAC
AAGATCACCGCACATGTGAGTGATGTCATCAAGCAAAATGCCCACAATATCTTGTGGTTT
ACCGAACAGATGAACCCTGGCACCACCAACCTCAGCGAGGTACCTATCTCCAAGAAGTCT
ATGCTGCCGATGTCTCGCCAGCTACGTATTTTGGAGCACTACGATGTACCACTGACCGCG
TACTCTGCTCTTTTCTGGACTGTCAGCGCCATTAAGAATGAATCTATGGTGCAGTACCTT
GTGCGACAGAATATGCAGCTCACCTTGAGCTCAAATCTGGATGCACTCAACTCCATTGTC
TCCCAGCTCCCTGTACCAGATAAGGACGTTGTGGCTGCTTCTGGCTACCAGATTCAGCCA
CACTTCTCCACGCAGCAGCGTGAAGCAATCACCACTGATAATCCTCTCGCGATTATTCAG
GCCGGTGCTGGTACCGGTAAATCCACCGTGATTCTGGAACGCATTGAGTACTTGTGCGCT
GCAGGCACCAACCCTGAAGAGATTGCTGTGCTGTCTTTTACTAATGCTGCCGCCGATAAC
ATCACAGCAAAAAATGACAAGGTGACCTCTATGACCATCTCCAAGATGGTTCATGAGATT
TACGCACACAATTTCCCTGATCATGAGATCTCCACCATCGACACCATTATCAATACGCTT
GATATTGAATACGGCGATCAAATGGTGACCTCCGATTACATGATTCAGCTCCGTGACCTG
CTCTATAAGGTCATGACGCAGGGTGGCAACGCCAACCTGACAGCGTTGAGCATCTTCATG
GAATCCCATATCGAGGCGTTCATCTCGGTGTTGGATCAGATCAAGCAGACTTCTCTTGAG
CTGGAAATCATCATCTGCTACCTGCTCTTGGATAAGCTGATCGAGCCTCATGCATCGCCG
AAGTACCTCATTATTGATGAGGTGCAGGACAACTCGGTCTTCGAGTTCGTCTTTGCACTT
CGTTTTGCGGCAAAGCACAATACGAGTCTGTACTTGGTGGGTGACTCGTCACAGACCTTG
TATGAGTTCCGTTCTGCTAACCCTAAGGCTCTGAACTCCCTGGAAGCATCTGGTGTTTTC
GGTACCTACCGTTTGACCACCAATTACCGTTCCAACCAGGAAATTCTTGACTTCGCTAAT
ATCCACCTCTCGGATATTGAAGCTAACCAGTTCGCAGGTATTCAGCTCTACGCCAACTCT

TTTGATGCACCTACTGCGGACAGCTTCAAAGAAAAGGTTGAACTGGACATGCACCATGTG
TCTAAGCAGTCTGAGTTTACCGACAGCATTCCTTATTTCATGGAGTCCAATAAAGCTCGC
TTTGATGCTGCGATCTTGAACAATGAGCAAACCATTGTGCTTGCTCATTCTGGTCGTGAA
ATTCGTGCAGCGCAGCAAGCGCTAGCCGAGATGTACCCCAGCATCACGGTGCGTAACTTG
CAGTCCGATAAGGGTTTCAACAACACGGTATTTTCGACCTTTATTAAGGATTTCTGGTTT
GAGGTCACCGCTGTAGACCCAGCTCATGCCGCATTTACCTTTACCAGCCAAGTCACCGCT
CATCTAGATAAGTTGGTACGCGGAAAGCGTGAGCAGATGGAGGATCGCGTTATCCGGTCT
ATGGCTGCATGGTGGCGTGAAAATGAGCGTGACATCCAGGGTTGGGTGCAGCAAACTCAG
TCCGGTGCGATCACCAACGAAGAGTTCTTCTACCGTCTTCGTCAGTGCATTCTTGACTAT
GAAATCAGGAATAACCGAGCACGTCAGTCCATGCTCAATGCGCGCAACAACGCTAACAAG
GAGGCTGTCGCACAGGAGAAACCACTGCTCATGGTCTCCACCATTCACAGTGCAAAGGGT
CTGGAATTCGATAATGTCATCGTGCTTCAAAAACCAAGCTCCGATGCAGAGATGACCGAA
GAAGGTAAGCGCGCAACCTATGTGGCGCTGACCCGTGCAAAAAAGCGTGAACTCATTATT
GCTGGTTCTACTCGCGCATACCCACGCATCGTCACCGATTATGAGCAAATCGTTGATCTT
CTTGAAAAGCGCGATGAGGAGCGCAAAATTAAGGAGGAAGAGGCTGCAGCACTCGCCACC
CTTGAAGCTGAACAGGAGACGCGCGCCCTTGCTGCTGCTGAGGCGCAGGCTCAGGCGTTG
TTGCTTGAGCACAACCCGTGGTTGCGTGATCTCAGCGATGAAGAAGTCACTGCTCTAACT
GAGCAAGAGATCATCAACAATGTTGAGCCAGCCCTACAGATTGAAGAAGAGGAGGAAGAG
GCTCGTGCACTCGCTGCAGCAGAGCCAGCAATTCAGCAGTACTTGTCTCAGTTTGCTTTC
GATGAGTTCCCGGACGACGACAATGTAGCCAACACTGTCGTACATGTAGCACCACAGCCT
ATTCTCCACCAGGCAGTGCCTGCAGATGTGACTGTACAATCAAGCACCGCCCCCGTAACA
CCTGTTGTTGCGGATCTTGAGGTAACCACTGTTGCAGCTGATCCAGTCGAACCGACTATC
GTTGCTGCACAGCCTGAGGTGGACGACAACCTTGTCTACAGCACGTCCACCCCTAATAGT
CACAGTGACGTTATTGCAGTGAACTCTGATACCTCAGAAAACGCTGCTGTTAATCCAGTT
CTGTCCGATATTGAGGCACTCCGAGCAATTTTCAACAACCAGGAC

>RXA01770-downstream
TAAAACACCTGCTGCTGTTGAGC

>RXA01771-upstream
TGCCCCGCTGTTGGTGGTTCCGGAGCGGCGATAATCGCTAAACGTTTGAGGTGATTGTAT
GGGTATTTTCAGGTCGCGGTCGCAGGATTTTGGGTGGAGC

>RXA01771
ATGCACCAGGCTGGCCAGCTCATCAATGATCCCAGTCAGGGTCTGTGGCGCACTTCTGCC
CTGCGCTCGCCGGTTGCTCGGGTTGGACATGCCGTGTTGCGCCAGCGTGCCGGTGAGATC
TCGCGCATGCAAGGTCGTGAGTTTTCTCGCCCTGGGGATCAGTTCCGACAGGTAGATTTG
CGCAGGCGACTGATTCAGGTCCATCCCCAATCAATTCCTACAGCGGATGCGATGGCCGTA
ACCATCACCATGGCGCTCACCGCTGCCACGATTGATCCGGTGAAGTTCGTCGCGGATTCA
CAGAACCCGGATGAAGAGATTTATTTGGCAGCTCAGATCGCATTGCGGGAAATGGTTATC
GCTATGCCTTTGGAGGATTTCATCGGGGTGCGCATTGATCTAGAGCCTGTTTTGGTGGCT
GCTCAAGCTGCTGCGAAGAATGTGGGCGTGGAAGTCTCGTCAATCTTGCTGAAGGATCTG
AATCTTCCCCAGGAGTACTCGGGAGCGTTGCAGGAATCGATCGTTGCGAAAATTCAAGCC
GAAACTGATCTGGAACGTGCACGAAATGAAGTGAAAACTACCCGTGCTCGACTTGCCAGC
GCGAAAGTGTTGGAGCAAAATCCGATTCTTGCCAAAATTCGGATGATTGAAGCGCTCCCA
CCGGGATCCACAATTGAGGTTCGGGAGGGTGACTCAAAGGCA

>RXA01771-downstream
TAAAGTTGCCCATTTCGGTGCCC
GTTTGTACTGTTCAATGAGCATTTTGTGGAACAACTTCGAGCACTG

>RXA01773-upstream
TTTCAGCGAGATGGCGTGCGCTTTGATCATACG

>RXA01773
ATGATCACCCACATTCAAGCCGGCCTGCATCTTGGTGGCTGCCGCGCAGCAGGTTTACTG
CCTATACCAGCACATATTGATCATATTGTGCGCCTGACAGCCGCAGATTTCTATGACACC
CAGTCAGCACCGCAGCTGCTCAGCAACACTGTGCTTGATGTATTGGACACCACCACTCAA
GACTTGAAGGCATTGTGGCCTGTTGCAGAACATATTGCTACAACCATTCCTGAATCTGAG

AACGTGCTTATCCACTGCCAGATGGGTATCAACCGCTCAGCTGCACTCATGACACGGGTG
TTGATGTTGCGCAACGATTGCACCGCCGATGAAGCAATTGCACTGCTGCGTGATCGACGC
TCACCGTTTGTACTGTTCAATGAGCATTTTGTGGAACAACTTCGAGCACTG

>RXA01773-downstream
TAAGCGCTCAAAGACCCATTACC

>RXA01774-upstream
CTGCGCAAGAAGAGAAAAAACAACGACAGCGAAGCTGCGTTCGGGCGAATCGGCGATAAT
CACACACCACTCTTCCTGAGAGAATCCTGAGGTCATCACC

>RXA01774
ATGTCACCGAACTTCCAAGCTCGCGGTACTACTGCGCCCACTGTTGCTTTGTCCATGCGC
CAGATCGCGCACATCCGTGAAGAAATTAAGAAATCACCACTCGCTGCTTCCGTTTTCATC
ACACCCACCACCAAACAAATGGTTGTCCGAGATCTAGAATCACTGTTCCAGCAGCTCTAC
CACACAGATCTACCTGAACCATCCATCAAAGACAGTGGTCTTATCAGTGCTATCGGCTCT
AGCGCCGGCAATACCAATAATCCAGCACTCGCCCTAGAAACTCAGATGGCTTACCACCTG
GTGCTTGCTATGCACCACACCGATGTTGCTACCTGGCACAAGGTGGTGACCAAAAACATC
ACCGAATCTGCTGCTGCACAAGATGCTGCGGTCGAGCACAGTGCTAAATACGATGCTGTG
TACGATGCCGCACAACTTATGGGCATCACTGTTGAGGAAGGTAATGTCGGTAGCATCGCT
ATTGCCTTTAGCACAGCACGTGCAGACGGTAAATCTGATTGGTGTGTTTCCGGCATCAGC
CGCTACATCGAGGTCACCGAAGCCTTGGATGCTGCGCGAGCTGTCACTAAAAATACTGAT
GCGCTCAATAAAACTGCTCTACCAGACGTGCAGCCGGCGCCGGTTGTGCATTCAGCACAG
TTCATGAACAAGTCCGCACACGATCATGGGGTTAATACTGCGGAAAAAGATCAACCAACC
TGTTTAAAGACTGTGCATTTACAACCACATCGTTACCCCCGAACAGGCTTTAAGGCTATT
CAA

>RXA01775-upstream
GTGGAAACCAAAGACGAGGAAAGTATGTCTATTTGTTTGTCCCCAGGTTGTCCACATTTG
TTTTATTCCCCGAGAATGTCCTAGAAAGGAACTCGACCCC

>RXA01775
ATGTCCTATTCACTCATTATTTCTAAAGCACCAACCCACTCCATGCCTTTTAATGAGGCT
GAACTCCTAGAGCTTGTCGATGAACTGCACTCCGACAACACCGTGAAAAAGCCGGTTATT
GTGCCACTCCCCGATGATTTCTCCTACACCGTAGATAGCGCCGTGCGACTACATGATTTG
GGTGTTGACCAGGAACTGACTGACTGGATTACTGCACAAGTTGCTGCAGCCTATCCAAAC
CAGATCGTCTCAGAGATTGCTGCTGCCCCTGATCCGCAAGCCAAGACCTTATTCTCCGCC
AATGCGTATAACACCAGGTCTTTTGGTACTTTTTGGACTGAGCACCCTATTACACAGCTC
CAATACAAGCGCTGCTACCAAATTGTCATCGAGAACGTTACGGGTGTCTATCATCCGTTA
CCTGTTGATAACTACCGCTACGTACCCCCTGTCACGCCCTCATTGCCACAGCCGGTCTAC
CACGAAGCTATCGCCTTAAATGAGTCTGATGTCGCTGATCACGGTACTCGTGCAGCCAAG
CACGCAATGATCAACCGCAACGTA

>RXA01775-downstream
TAACCACACACGCCACAGATACT

>RXA01776-upstream
CGTATAACCACACACGCCACAGATACTCAGCTATCTGTGGCGTGTTGTTTTACATCAACC
TCTCACCCATCCCCCATCACTATTAAAGAAAATCACCATC

>RXA01776
ATGACCCACACTGATACCCCAGCCCCTGCACACGGCGTAACACCGAGTGAATTCGCTGTT
ACCTCACACGAACTCACCACCTCACCAACACCTAGTCCGACACAGGTCGCTATTGCAGCC
CAGGAAAAAATTCGCCAGCGCAAGCTCGAAGAGCTTAAAGCAAAAAAGCGCACAGACACG
ACAGCTCAACCACTTCTACCTGCACCTGTGCTGCATACACGCCCACTCCCCTCACCGAAT
CCACCGCGACCATCTCCACCGGCACCTACCACTGGACACTGGGAACTTCTTATTGTCAGG
TCACAGCAGAAGAAAATGACCGCAGCCAATCCCTTTCTCAAATTCCTTCATCTCGGTAAA
GCCTTCAACGTGAAAGACCTAGGGCTCACCTGCGATCGCACCACTGATGTTGACCTCTCA

CGGCTTGGCAAGCTCAATCCGCCCAGCTCACTTATCCTTGAACTAGCAACGGCACTTGAC
CTGCATCCATTCCTCTCAGTCGCACTCTCTTCGCACAGTGCGGTCAACGCCCGTCGCAAC
CAACTTGAATTAACCCTGCACAACCATGACACTCAGGGCACAGCATTAGGTCACAGCGTT
ACTATGGTCCAGCTACCCGAGGTCATTAATCGAGCTGCTGTAGAGCCCTATATCAAACCC
AAGGGCTCGGGCAATGACCCGCTTGACCAAAGCCTGAACCACCGCGCACCCACCGTAAGT
GACGTGCAAAAAGCCCTTGTGCAGGAAAACACAGGCACGGCAACAGACAGCAACAACTAC
CTGCTTCCTTTTGATCCTGATTCTGGTGCACCAAAAACCACCGCGCTTAATGCGCCTAAT
AAGGATCTCCTACAGGCCAGGCATGAGCTTGCCTATATTCCCGAGATCCCCGCCATTGCA
TCGTGGCTCGATCACCTTGACCCCATCATGCGTGTGCACCGTAGTCTTGCGCTTTCAATT
TTCCCAGTGCAGCTTCTACGTGCTGCCGTTGAGAATCTCCCTCATAACGTAACCGATCTG
CATAATCACCTTGATCCTGAGGATCTGCTCCCTGAGGAACTCACCACCTGGCTCGATCAC
CTCTTCGATGCAGACTTAACCGCTCTCGCTTCATGCCCACAGCTTGCACCACCTATCGTG
CGCAGCCACAATCACGCCAAAGCGATCGCAGCTATCACCGTGACCTCTGTCATGGACGCT
CTCATCGCCAAAACTCTTGATGCGCATGACGATCCACTGCCCTCACTACCGGAGTTTGTA
GAACTACTGCGTGACGCTGTAGCCCAGCTCGCAGCGCATTTTAAGCAGCAGCGCGGCGAG
GTACTACCGCAGCCCAATGGCTTGCGATACGCCACCGACTTTGGCCTGCTCTCTTATATT
GCCGATGGCTTACATGAATATGCACTTGCCATCGACTTCGGGCTGATCTACCCGAATGAA
CTCATCACCGAG

>RXA01776-downstream
TAAACCCACTCCTAGAAAGGTCT

>RXA01777-upstream
CCGATGGCTTACATGAATATGCACTTGCCATCGACTTCGGGCTGATCTACCCGAATGAAC
TCATCACCGAGTAAACCCACTCCTAGAAAGGTCTTTACCC

>RXA01777
ATGTCTCGTATCATCACTGCTCCCGTCCACAAGCCTTATATTATTGCTCGTGAAGTCAAG
GGGGTCTCCCATGTCCACGACACTGTTGGCGGCAAGTGGCAGGCCACCTTGCACACACTT
AAACCGGGGCCCTCCTGGCCGAAACCGTCACAGTTCACTGCGCCTAAATCCACGTCCATC
TGGTTTATTGCGGTAGCAACCCACCCACGTAACCCACGGGCACGCAAAGGTACCCTACTT
GGTCGCGGTGGTCTTTACGAACTCAAAGACACTGATCTGAACTTTCTCACAGAGCGACAG
GATTTGCTCGCCACATCTACCTCTCGTGACCCAGAGGATTGCCGTTTACGCTTTAATTCG
CGTCACGATGCAGCAGCATTTTTACATGCTAACGCCCGCCACATCAACAAGCTTTTTCAT
CCAGCACTAGGTCATGCTCGCTACGATCTCATAGATGTG

>RXA01777-downstream
TAAGCACAACGCTTAGCTTATGA

>RXA01778-upstream
CTACTACCCCCTCCGGGTGTGGGGTAGCTGTAACAACTACCCCACAATCTTAGCCGGTCT
TCCATACATAACTGCGAAATTGGTTAGAGTCTTTTTCATG

>RXA01778
ATGCTCTACCAACACACCACACGCGGGCTGATCATTAGTGACGCGATCATCGCGAAAATC
AGCCAAGTCAACCAACTGCTGCTACTAAGACCCACGCTGTTGCAAGACAAAGATATGCAC
CATGCGACATTGAGTAGCGACACCCCATCAATTCGCAGTCGCCGTCGCTCCTATCGCGAG
AATAAAGCCGCCTATGCGACCACGAGCACCATCAGAAACCGTGAGACCTTTTTCAGCACA
TCTGATATTGATTTCGCCATACTCATGATTCAGGACGTACAAGAATCTCTCGTATCTTTT
GACCCCACCTTGGCTCAAGATATGAAGCCAAGAACCAACGCAGTCATTTCTGCACTCAAT
GAGCTACGCGAGCCACTGGATACCTTCTACCGTGCCCATGAATACGGTGACATCATCAGC
GATGGTGCTTATGAGTTCGATCATGCTGCCATTGATGCACAACACAGCCTTAGTGAACTC
GTTGCCGGTCTGCATAATTATGACAACCTCATGTTTCCCCAGGAAACCGCTCCGTTGATG
AGTGAATCCAATGGCATTCAGCTGGCTCAGTACTATAAGTCCACCAAACTCGATGAGTCA
CAATTGACGGTGGAACCTAATGAGCCTGGTATCAGCATTATGTGGCACGCCCATGATTTC
ACCTGGTCTTGCCTAGTGCGCTATGACGACATGAACCGTTACCCTGAGCATTTCAGCATT
TCTTTTAAAGACATGCTGATCCCTGAACAGATCTATACTTTCCACTTCACCCCACGTGAG
GCAATGCAACTGCGCAAGGGACTTTTTAATGCCATCGCTGCCTACAAGTCTCAGACATGG
GGTGATGAGAACACTGATCTCACCAAGGCTGAACTCGAATTTGGTGGCACCTCCATGACC

TTCCGCGCCGGCCTCTCACAGCTTAGCGTCACCGGACCTCCTGATCACCGCCAGGTGTTC
TGCTTGTCGTCTTCTGGTCGTGAGGATCACAACACCCCGCCAAACATGCGAGACGGACAT
GTCATTGATATTGCGGTTACTCAATTGTCCACCCTGCGTAACCTCATTCGGGTACTGTGC
ACCACTCACCCGGATCATTCACCAGCACTGCTACCTTATGGTCAGCAGTACACCATC

>RXA01778-downstream
TAACATGCTCTAACTCGACCCCG

>RXA01779-upstream
TTAGTATTTAGTCAATTAGCCAACTACGATAAAACTAGTGAATAAACATACTAGTTCACT
TTGTCGCGCTTAAAATACTAGAAAGTAATATAAAAAACTC

>RXA01779
ATGCGTTATACTCCCCGTACCCACCGCGCACTCGGACTTGCTGCACTTACCGCTACAGCT
CTCCTACTGAGCTCATGCTCGACCACCGCTGACCTTCTCGGCGCCGATTCTGTGGCGCAG
GCTGTCACCGATGGTGGCTCTGCCCTTGATCCCACTGCAGCTCATGTGCTCACCATCACC
AATGCCACTGCAATGACTCTTGCTGAGCTACCAGAAAACACCGACCCTGACGCAGCCAAT
AACACGGAGCCAACAATGGCCCAAAGCGCCCTCAAGCGTATTTACGGTCTCGAAATTGCC
GCCGATGGCACTCTGATTGCTGTCGCAGCGCCATTAACCTCGCGAAATAGTGGTTCTGAG
CAGCCTACTGTCGCAGCAATGGCTGATCCAGAAAACAATGCTGAACTCACCACAGCACAT
ATTCTTGAGATCGACCCAGCCACAGGAACTGCCACACCACGTCAAGATATTGCTCTGACT
GAAGATTTTCAGACCATGGCTAGCTCTTTTAGCCAGATCCGTAATGGCTGGGGTACTACC
CAACTCATCGGACAACACCCTGATGATCCCAAGCAACCTATTCGTTCAGCTGATACCTGG
ACTGTCACCGGCTCCACTCAGATCACCGGCTTTAACACCAACACCCCAACGGGAACCGAA
GATGCTGCCTACACCATGCCGGCGACTGAGCCAGCTGTGGGACTGTGCGCTCTAGAATCA
GGCTCCGATGCACCACTGGATGAACACCGTGAGCTCAGCACCAGTGCATTGCGTACCGCA
TCAGTATTGTCGAGCTCTGGATCTGCCACCCTCAAGCTGCATGATCCTATGGTCATGTCT
GCTACTGGCATTGTCCAAGCACGCGCCTATGTCGATGGCGAAGTCATTAACCAGCACGAG
ATTGGCGATCTCCGCGAGCAGCTCGGTATCACCATCGAAGAATCTGAGGCTGCTCAAGCA
GAATCGGATGCCCAAGCAGCCACCGATCACCCACTTGCAGCCCTGGGCTTAAGCAACCCC
ACCAGCTCAGCGTTGGTTCCAGGTCTTGCTGAGCTTGATTGTCTCAGTGCTGACCAGGCT
GCCACCTGGCATAACCGCGACACCAGCATTGGCACCGGTAAGCCCAGCGTGCTTGCTGTC
ATCAACGCGGAAATGGCCGATGACTTTACCCTGCAGCTGTTGAGCTCAGGTGCCACCACT
GCCGAAACGCAGCTTGCCCAGCTGCCGGATGAAACCGCGTTCGTGCTCATTGACCCATCA
TCTGGTGCTGTTACTGACCTGTTCTTTATCCAAAGTCTCAACACTGATCTGCCGGCACCA
ACAACCCAGATTAATTCTATTGCTGTTGATGAGCGCGACCCCAACATCATCTACGCCACT
TTTAGCGGCGATGACCACCTGTACCAAATGATGCTGGGT

>RXA01779-downstream
TAGTTACACAACTAACTAACCAG

>RXA01780-upstream
CCACTTTTAGCGGCGATGACCACCTGTACCAAATGATGCTGGGTTAGTTACACAACTAAC
TAACCAGGCACCAACATTTTCTTAAAGAAACACCCTTATC

>RXA01780
ATGACTTTTCTCCACCCCAAGGCTGCGTTCTACCCTCTCACCATGGATCATCTTACCGAT
CTCGGTCTTGATCCTGAGCAACTCATTAATGAGTTGCCGACGATTACCTACGACGTTCAA
CCACACAATGTCTTTGTTCTACAGTTCAGCACCGCCGATGTGCGCGTCTACCAGGAAGGT
AATACCCTTTTTATCCGCAGTGCTGAATTAATCAACCCTGAACTACGACAACGACAGCGC
ACACAGCTCAACGACGATCTCAACAACCCTGCTTCACTTCGCGTCTGTGATGAGATCAGT
GGCCGCAGCACCGTGTTCCTCAAAGACAAAAGTGTTGTCACTCACGATCACGGGACCAAT
TGCTGTGATTCCGCA

>RXA01780-downstream
TAATCCTGATGAAGCCAGCGCCA

>RXA01781-upstream

CGACAGCGCACACAGCTCAACGACGATCTCAACAACCCTGCTTCACTTCGCGTCTGTGAT
GAGATCAGTGGCCGCAGCACCGTGTTCCTCAAAGACAAAA

>RXA01781
GTGTTGTCACTCACGATCACGGGACCAATTGCTGTGATTCCGCATAATCCTGATGAAGCC
AGCGCCAAGGCTGTCGCTACCAAACATAAGCACACCTTGTCCGGCGCTACCTCTGATCAC
CCTTATGCCGGCATGACGCTTAAAGACATGATTGAACAGGGCTTTACGCTCACACCGCTG
GAATTCCCGCTCTGTGCTGTCGATGATCCAACAGATTCTGATCGCACCATGCACGTGATC
AATGTTCGCGAGCACAGTATG

>RXA01781-downstream
TAGATTCTAAAGTGCGGTACAAC

>RXA01782-upstream
ACGTGATCAATGTTCGCGAGCACAGTATGTAGATTCTAAAGTGCGGTACAACCTGTACCG
CCCACACAATTCCACCCTTTAAGAAAAGGACTTAGCCATC

>RXA01782
ATGACCACCTTCGCCCTTATTGCTAGCCCCAACAATGTTGATCCCACTGCTGAGTCCCCA
CTCGCCATTGAAATCCATACCGATGAGGACAGCAGCTATCCACTAGGGCTTATTGACTCA
GACCACCTGGTTCCTGCTGTGATTTACGGCGATATGGTGATCTACACCAAAACACTGCTC
GCACAGACCCCACCAGATGATGTGTCCACTGCTAGCGCCTTCTTCGACAAACTCACCGCA
CTTGACGCTCAGGGTCGCACCCGTGATCTGGTCTACAGCGCCACCTACAGCCAACTTGTT
ATTGCCGGCCACAACCGCACTGTATTAACTGACGACTCAGAGTTCTACGATGAGTTTTAC
CAGGTTATTGAGGCTGCTCCTGGGGTGATCTTGAAA

>RXA01782-downstream
TGATGTTTATCGGGCAACACCTC

>RXA01783-upstream
ACCAGGTTATTGAGGCTGCTCCTGGGGTGATCTTGAAATGATGTTTATCGGGCAACACCT
CACACTTAGGCTAGGTCTCTAACATGAAGCAGATAGCGCC

>RXA01783
ATGATCAATCTTTTTGCTGCAGCCCTGCCCGCATTCGAGCCTTTGAGTATTACCTCCATA
CTCGTGCTCGGTGCTGTGGCATTGATCTGTGGCCTCCCTGTTTTTCTCGCACTGGAAAAA
AGCGCTGAGCTCGATGATCTCTTCGCAGCACTCATCATCGCTGTACTTTTAGGTTTTGCT
GCTTATACGTTTGTGCTCCCCAAGCTCGTTGAATTGGGCTGTACTATTTGCCAGCTC

>RXA01783-downstream
TGACTAGCGACACTTACACTTTC

>RXA01785-upstream
GACCCTGGCCCAACTTTGCAACAGCACCATCCACAGTGATGGCACTACCAATACTGAGCC
TGACTACGCATCTAAGGCGGCGCACATTAGTGATGCAACT

>RXA01785
GTGGATCAGTTCGTTGAGTTCGGCGGTGGACAAGCAAACATTAACCCTGATGGATCAGCG
ACCGTTGATTGGGAGGGTTCTTTCAGCATCAACTTCTACGATGGTTTGGTGCCGTTTACC
ATCACGAATCCGCACCTCGAGGTTTCTGTAGCTGGTACTGGTGTTTTGACTGGTGACCTC
ACTAGCTATGCAGTGGAGATGTCGAACCCGAATGAGAAAACCCCGTTGACTGACTTGTAT
GAGGATGTCACGATCACAACGTTTGGGGGAGTGAACCTTGATCCTGAAGGTGTTGTGACA
AGCAATCCTGATTATGACGGAGTGATTGTTGATGTCCCACTGGATGCCACCTCTCAGGTT
ACTTCCGGTGCAGGTTGGGGAGCGTGGCCGCAGGGCTTCCTTGATTTCCACTTTGATACC
AACTTGCCTTCCTACTGGTATTCCTCAGATGGCGCAGGTGATCCTAAGAAGGCGCCTATG
AGCTTTAATGTTGATTTCACTAATGGTCCAGGTCTGGTGAACAGCCAATTGCTCCACAGG
CAAGTGATCTCAATGCCGGAAACCAAGGCAGTCTCG

>RXA01785-downstream
TAGTTCCATCGGAGGCAGAAGCT

>RXA01787
ACCGAGAAAATTGATAAAGCTCAACCACCTGTCGATCAACTCGGGAGTTTTCTCCATGGC
CTAGAGACCTCTGTCGCAGATTTGGGGGTTGGTGATCGCGTATTTTTGCCACGTTTTAGC
ACCTTTGATAAGAAACTCGGTCGCTACCGCATCCACACTGTTCTCGGATTCGCTGAGAAC
GATCCGTTTAACCCTATGACCAGCAGCGAGCGATTTAAAGGTAAGCCCTATGTCGATATG
TTCGACAATCAAGACAACGCCTTTAACCCAAATTCCTATATCACTACAGATACCGTGCGC
ATCGTTGTCGATCCTGTACCGGAAACTAATCCCGACGATGAGAAAGCAGGACGC

>RXA01787-downstream
TAGCCATGTCTCGCAGCTACCCC

>RXA01788-upstream
CCTTTAACCCAAATTCCTATATCACTACAGATACCGTGCGCATCGTTGTCGATCCTGTAC
CGGAAACTAATCCCGACGATGAGAAAGCAGGACGCTAGCC

>RXA01788
ATGTCTCGCAGCTACCCCATCTACATCATTTCTTTTGCCCCAGCGGATGATCTCCACGGC
GTTGGAGGATTCGAGTGGGTTCCAGCATCAACACCAGAAAACAAAGCTGCCGCCTTCACG
ACCTTTGATCGTCAATTCGATGATTCTCGTAACAATGGTGGCTCGCATATTGTGCGTCTA
CTCAATATCTCTGATCCCAATATCACAGCGGATATGACCCAAGACGATATTACCGCGTAC
CTCGACTCAAACATCGACCGCTGGGAATCCACGGAACATGCGCTCAAGCAGTTTGTCCCA
CTTAACGCGGGTGCTGATCGCGTACCTACCGGTGGTGCCGACGAGCACATTACCCACGCC
TGCCGCATAATAACTGTGCAGCGTAGCTGCACACGGATTCACCTGCGCTGTGGATGCATC
CCAACACCACAACACCGCCCC

>RXA01788-downstream
TAGTGCCATAAATGCTAGGGGTG

>RXA01789-upstream
TGCATCCCAACACCACAACACCGCCCCTAGTGCCATAAATGCTAGGGGTGTTTTTTTCAT
ACCCACAACACCGTTCTTCTCTAGAAAGAGACTCGATACT

>RXA01789
ATGCCTCATAACCCCATCGAACTTCACACTAATGATGTACTCGATGCTCTCGACATTGAC
GCCATCTGCGACGATGTGTTTCTCTACACCGACTTCGAGCACACCCCAGGTCAGCTTGAT
CGCTTCGAGCAACTCGCCTTCACAAAAATCTACGACATGCTGGAAACAGCTGCTGAAAAA
TTCCCAGATGTAGCAATTAATGACACTTTAAGCACTGGCAACCACGCTGCTGAACAGTAC
TTTCTTGCCAATCCCGGCAACATCATCGTGCTGACCAGCTTCGCGCTCAATCAGACCGAT
CTCCGCGACCTCATAATCTCACCGTGCATTAAGTACACAGCACATGCACGAGCACTCATG
CGTGCGGTGACACGAACATTGTGCACTGCAAACAACCCTGTAGAACGCGCGACTATCTTC
CCTGTGTCTGTCGCTAATGCCTTAAGCATCGAAGCGCTGTGTTCCGAATATCATGCGTTC
CGCACCAAGCAGGTGCTCAACACTGCTGCACTCATCAATCCTGATAACACTCTTATACCC
ATGTTGTTGAGCAAAGCGTATGAGGCATACGCCTGGCACAAGGGTGTCGAATCCGCGCAA
CGAGGTAGCAACCTAGCTCGTGAGTACTACGCAGGACTTATC

>RXA01789-downstream
TGAAAATTCACTACTCAACTCTG

>RXA01790-upstream
GAAAGGCTCGAACACCCATGATCGTTGAGGTAGCTCCGAGACCGAAGAGATCAGCCTCAT
TGATGATGATTCCCCTGATCTCGATGAGGACGATAACACC

>RXA01790
GTGCTCATCGCCGAAGACATCCGTGATATGGATGACTATGGCGAAGATCATCCTGATCTT

>RXA01790-downstream
TAAAGCTCACTGTTAAGCCCGCA

>RXA01791-upstream
CCGCCTGTGCAACTAACCCTGTTGTGCAGGCGGTTTTCTCTATCTACACCAACAACTCCA
CAACACTATCCGGTCCAAATCTAGAAAAGAGACAACCCCC

>RXA01791
ATGACCTCCCCCACCACGTTAAAGCCCTGGTCTATTCGCGGACCCATCGACGGTGAATAC
ACCATGCTTGAGGCATATCCGTTTCAGTATGTAGCAAATACTCGCCCGGCCATCATGCTC
TACGCACTCGATGAAAACGGTGTACCGGAACAATATGCCGACCTCACCATCAACCTTGCC
GATGTGGAGCTCAAGCAACTTAACCACGTCATCATTAACCCAGATCTGCACGCTGATGTT
ACCGAACTGTGCATTAGCGCCGGCCTGCTGCGACCTGGTGTTCTGGGCCAGCACCAAGTC
GGTAGCACCACCGCCAAGGTCTACCGACTCACTGAGCGTGCTGATGGCTGGCTACAGCTG
TTT

>RXA01791-downstream
TAGCAGCTACCTGCGCCTAATCC

>RXA01792-upstream
GACTCACTGAGCGTGCTGATGGCTGGCTACAGCTGTTTTAGCAGCTACCTGCGCCTAATC
CCCCCACCCATACTCACTCCAAAACAAGAAAGTAGTCATC

>RXA01792
ATGCCTCAGTACACCATCACAATCACCGACGAGCAGAAAGCTGTTCTACACAGCCTCACC
AACCCCCATATCGCCACTGCTGAACACGGCGCTATCACCGCAATCGAGATTCATGACGAC
CACGATGTTGTTGTCTATCACGTTCAACCAGACGGCACACTAACTTACGAGCGCCTTGTT
GAAGGCTTCCATTACGGCTGGACACGTTTTGACAGCGAAGGTTTTGAGATCGACTCCGAC
AATAACCGCGTTGTAGACGGACTCCGCGACGAA

>RXA01792-downstream
TAGTTAACAACAACGACCGCACA

>RXA01793-upstream
CCTTCTCTGCAGGCTACGCAGTGCTGCGCCTAGTTCGCAGCCTGCGCCGACTTTTGCAGC
GCCACTAAACACCCAAACACAACAAGAAAGAAACACCACT

>RXA01793
ATGGCACAATACCGCGTCAGTTTTATCGCGCTCGCCGAGTCAACCATCGAGGTCGAAGCA
GACAGTCCTGAAGAAGCACTCGACCTAGCCAATGCAGAATTTGACTACCCGGTCACCTTG
GCCGGCGATCCCTATGAGCTGCACGACTGGGAAGCACGCGCTGAAATTGAATGGCTCGAT
ACCAGCTCGACCCCGCAGCAACGCCTTGGAGAACATGTCGTCAAGATCGAAGAT

>RXA01793-downstream
TAAACTCGATCATTAAACACACT

>RXA01794-upstream
ATACCAGCTCGACCCCGCAGCAACGCCTTGGAGAACATGTCGTCAAGATCGAAGATTAAA
CTCGATCATTAAACACACTCTTAAGATAAGGACACTAATT

>RXA01794
ATGGCAACCCACCGCGTTCATTTTGTCGCAACCGCATCCGCCTACATCGACGTTGAGGCA
GATTCCCCCGAAGATGCTATAGAAAAAGCGTATGATCTCGCCGGTGATCTGCCCGGCCTC
ATCGCCGACAACGAATTTGATCTCGGTGAATGGGAGGTACAGGCCGATGTCCAGTGGCCT
GATAACTCTGTACCTCGCGAGCAACGCCTTGAAGAGGGCGTTGACCTGCTCGAT

>RXA01794-downstream
TAAACAGAATTAACTCAAACCCC

>RXA01796
TTTTACTGTCCGTCAGACCAAGATGCTTATGTTGACTTGACTTTGTTCGATCAGATGCGT
CAGTTCGGTGCAGAAAACGCCCCGCTTGCCCAGATGTACATCGTGGCGCACGAGTACGGC
CACCACGTCCAAAACCTCGAGGGCACACTCGGACTGTCCAATTACAACGATCCGGGCGCT
GATTCCAACGCCGTCAAGATCGAGTTGCAGGCCGATTGCTACGCAGGCATTTGGGCTAAT
CACTCCAGCGAAGGCCCGGATCCGCTACTCCAACCCATCACCGAATCTGAGCTAGATTCC
GCTCTCCTTGCTGCAAGCGCCGTGGGCGACGACAATATCCAGCAACGATCCGGTGGCGAT
GTCAATCCTGAAAGCTGGACTCACGGCTCATCGCAGCAGCGCAAAGACGCGTTCCTCGCC
GGCTACAACACCGGCCAGATGAGCGCCTGCGACTTCCTCGGCCGGGGCGTCTACAACGAC
GCT

>RXA01796-downstream
TAAAGCATTGCTTTTCGACGTCT

>RXA01799-upstream
TATTTTGGGCATGCACTCGTCATATCTTCACAGACGTATGGTTTTGTAACAACCTCCCCC
AAAATCCCCATAGTTTCCCCCGGTGCATATCCTTAAAGGT

>RXA01799
ATGGAAATTCCGCTGCCCACATCCCTTATCGATGTCATCACTGATGGTGCCCTCGGCCAA
ACCTGCATTGATCAGGCATTTGCTGCCCAATTGGGGCGAGTTACTGGAGTCGAATTCAAC
CTTTCTGACGATAAAACCGCGGCTGAAGTGAGGATCAATAAGGCGTCGGGGAGTCCTTTT
GATACCACCGGTGAAGTCATTGCGTGGATTAATAATCAGGAATTTGAGTGGGTCAGCACG
CGCGGTGAGGATTTGGGACTGCCTGAATTGCAGGGCATTCAGCCGCTCGACGATGATCTG
ATCACCGCCGCACGCACGCTGTATAGCAATGCGCCGGCGTTCATCGCCCCGTTGCGCGAT
GGTCGCAGGGCGTTGGTTGCGATCAATCACACGCCAAAACTGGTTGGTATCCGTCGCACG
CTCATCGAAGGCCTGCAGGCGCTGAAGCCTGGAACTGACCTCAAACGGGCATTGACTTCA
TTTGCTGCATTCTGCGAACTGGGCATCCGATTCGATGACAACCGCATCTCCTTCAGCGAT
GGCACCTCGCTGTTGCTTCGTGGCGGCAAAGTCATCGAAATCGCAGGCGGGCTGAGCTTG
CGCGACGTACGCGCGGATGCGGCGTTCATGTCCGCTGAGCATCAATTGCTTTTCGACGCC
ATCTCCTCGTCTCACAACGTCACCTTTGACCCACACACCAACGTGGCGACCGTGGCAAAC
GAACACCAAGTTCACGCCATCCCCCTTGCTGTTATCGACGGCACGCGTTGGGTATGGACA
TGGTCTTTAAAAGAACTCAATGGTCAAGCAACTGAAGGCCTTGCCCGCTTTGGTTTCGAT
AACGGCCTACTACTGCTCACCAATGCAGAGATCCTTGCTGAGGAAGCCACCGCATTCAAC
CTGATTGATGTGGCTAAACAGGTGCTCAACACTTGGACGCACACCATCGTGCAGCAACCT
GATGGCACCGGAATTGTCCTGCTGCTGGATCATCCTCGGCTGCAGCTTCCGCCAGCATCA
CATGCAGCTGTTGAGGCCACGCTGTATCACCAGCTACCAGGCGATATTGATGCCCGCCGC
GCGGTGGCGTCCTATGCAGCTCACCGACAGCTTCCTTTTGATGGCTACGCACTCACCGTT
GAGGGCCAACAAGTCGGCGTGACTTTTGACGGCGAGCATTTAACAAAGGTGGGC

>RXA01799-downstream
TAGTTTTCTAGCAAAACCCAACC

>RXA01800-upstream
CCAGCGCAGTTCATAAAACCGCCAAACTTTTGATAGCGTAGCAATGGCCCTTTCGGTGGA
TGGGGCCATGTTTGCACAATGCTTGAAGAAGGGTAGGGCA

>RXA01800
GTGAAGCCGCTGGGCAAGATCGCCGTTCCTTGGACTTGGTACCTGGGAATTGTTGGGGTC
ATCATATTTGATGTGGTGGCAGCAATAACGATGCTCACCCTCGTGCCCAACAAAATGCCC
GAAAGAGTCAACAGTGGGCTTGTCGCGCTGGGTGGATCGTATGCACCCCCGATGAGCCGG
GAAACACTCATTGCCAGAGTCATTGCCGGTGCAGTGCTGGTTCTGGTGATTTCTTTAGGT
ATTTCGCTGCTGATTTCCGCGCAGTCCAAGAACCTCGCGTCCGATCACCCGGATGCATCT
GCCATTCAGATTGCTCGGCGTTGGGCGTTTTTGAACAATATTCAAAGCTGTATCGGCTGG
TTTAGTTTCTTCCTCGCAGCGATTTTGAGCATCTCATCGCTAAGACTCAACGGCCCAGGT

GCCACCACGCATCTTGAGATGGCCGTTTACATCATCGCTGTGTCGGTGTTGGCTTGGGCG
TTGATGATTTCCTTGCGACGCGGCCAGGTGGCGATTGATCGTGCCATTCCAATTCGGGAA
GATGATTCCGAACTGAAATGGGGCATGATCTACCACGATGCTTCAGACAAACGAGTTTTC
GTGGAACTCGATGATGGCCACACGACCGTCATCAACATGGCGCGCGGGGGAGCGTGGCTG
CTCATCGCAGTGATGGTGCTGCCTGCGCTGGCCATCGTCGGTTGGGTTTTGCTAGAAAAC

>RXA01800-downstream
TAGCCCACCTTTGTTAAATGCTC

>RXA01803-upstream
CTAGCGGAAAGGCTTTAGCGACAAGGCTTTTTGCATGTTTTAATGCAGGGAATATTAACT
TTTTGTTAATCTCTGACCATTGACCTTGTACGCTTAAAAC

>RXA01803
ATGCGAAAGAAAAAAGACGGTCAAAATCTCCCAGACTTCCGGAAAAATCCGCCAAAGCTG
GATAAAAAAGGCTTATGAAAAAGAACTAAAAAGACTTCAAGCCGAACTCGTCGATTTGCAA
CAATGGGTTGTGGAAACCGGTGCGCGCGTGGTCATCGTCATGGAAGGCCGCGACGCCGCT
GGTAAAGGTTCTGCGATCAAGCGCATTACGCAGTACCTCAACCCCCGGTCCGCAAGGATC
GAAGCGCTGCCCACCCCAAACTCTCGGGAAAAAGGGCAGTGGTATTTCCAGCGCTACATC
GAAAAATTGCCGACTGCTGGTGAGATCGTTATCTTTGACCGCTCCTGGTACAACCGTGCA
GGAGTCGAGCGCGTCATGGGATTTTGCACCTCCCAGGAGTACCGCCGATTCCTTCACCAG
GCACCAATCTTTGAACGCCTGTTGGTGGAAGATGGCATTCACCTGCGTAAATACTGGTTC
TCTGTATCTGATGAAGAGCAGATTGAGCGTTTCGAAGACCGCCTGAGCGATCCGCTGCGC
CGGTGGAAGTTGTCGCCAATGGATTTACAATCGATCACCCGCTGGGAAGATTACTCACGC
GCAAAAGATGAGATGTTCATCCACACGGACATCCCGTCAGCACCGTGGTACACGGTGGAA
TCTGAGGACAAGAAGCGTTCCCGCATCAACGTCATTTCGCATCTGCTCTCGACGATTCCT
TATGAGAAGATCGATCGTCCATTGCCGGAAATCCCTCATCGCCCAGATTCTGAATCTGAT
TATGTACGTCCCCCTCGCGATGAGTTCCGTTATGTTCCAGATGTGGCAGCACACTTGGAA
GAAGAGCGCATCAAGAAAGAAGAAAAAGCCAAGAAGGCAAAGAAGCCAGCTAAGGCTGCA
GGAAAGAACTCGGATAAGCAGAAGTCTTCCGGAGGAAAAGGCAAGAAGAAGTCCAAGAAA

>RXA01803-downstream
TAGAACGCCTTTTAAGGGGTTGA

>RXA01804-upstream
AGTGGGACCGCATGGCAGAGTTCGCAGTCAACTAAAATATGACCTTTGCTGGTTGGCTAA
TTTTGGGTCAAAGTTTTGTGAAACGAAGTAAGCTTAAGTT

>RXA01804
ATGCATATCGTCAACATTCGCTTCAAGCCCAAGGCTAAGTACGTGGATACATTCCGCTAC
ACAGTCGACAAATTCACTGAGTCAACCAGGACAGAGGAAGGCTGTCTCTACTTTGATTGG
TTCCGCAACACCGATTACCCAGGCGAGTACCTTGTAATTGGTGTGTGGACGGATGAAGGT
GCGACGGAACATAAGAAGAGCGAGCACTTCTTGCGAGCTCAAGAAACACTTCCACCGTTG
CTGCAACAAACTCCAATGATTATTCAGAGTGAGTTTTCCAAGAAGAAGGGTTGGGAACGT
TTCAGCGATTTCACCGTCTAC

>RXA01804-downstream
TAAGGAGCCCGCAAAAGCTTTGT

>RXA01805-upstream
GGCATTGTCGAGCGAACTCATGGTTTAACTCCCTTCATGAAATGTGTGCGGGGTCACTGG
TTCCCAGCCTAGTCTGAACTGGCTAAACAAGATCGGTACA

>RXA01805
GTGGTGGTCGTGATTTTGATTAATGTGAAATTCAAGCCATTGCCAGAATATGTAGACACC
TTCCGCGAGCAGGTAGCGGAGTTTACAGAAAAGACCCGTGCGGAAGAAGGAAACATCTTC
TTCGATTGGTCAATTAACACCGACAACCCAAACGAGTTCATCCTCATCGAAGCATTCCAG
GACGACGCTGCCGAAGCTCACGTCAACAGCGACCACTTCAAGGCGGCCTGTGAGCTGTTC

CCAACCATCCTGTCTGAGACCCCAGAGATCATCAACACCCTTATCGAGGGCAAGACTGAG
TGGGACCGCATGGCAGAGTTCGCAGTCAAC

>RXA01805-downstream
TAAAATATGACCTTTGCTGGTTG

>RXA01806-upstream
AATCAAAATCACGACCACCACTGTACCGATCTTGTTTAGCCAGTTCAGACTAGGCTGGGA
ACCAGTGACCCCGCACACATTTCATGAAGGGAGTTAAACC

>RXA01806
ATGAGTTCGCTCGACAATGCCCCGCTGCTGGAATTGGATGTTCAGGAATGGGTAAACCAC
GAAGGCTTGAGCAATGAGGACCTGCGCGGCAAGGTTGTGGTGGTGGAGGTGTTTCAGATG
CTATGCCCTGGATGCGTGAATCACGGTGTCCCTCAGGCTCAAAAAATCCACCGCATGATT
GATGAATCCCAAGTGCAAGTCATCGGGCTGCACAGCGTGTTTGAGCACCATGATGTGATG
ACACCTGAGGCTTTGAAAGTGTTCATCGATGAGTTTGGGATCAAGTTCCCCGTGGCAGTG
GATATGCCGAGGGAAGGCCAGCGGATTCCTTCGACGATGAAAAAGTATCGTTTGGAAGGA
ACGCCCAGCATCATTTTGGCTGATCGAAAAGGACGGATTCGTCAGGTGCAGTTCGGGCAG
GTTGATGATTTCGTGCTGGGATTGCTGCTCGGCAGTTTGCTGTCAGAGACGGACGAAACC

>RXA01806-downstream
TAAAGCGCTTTGGTCTGCAGGCC

>RXA01809
CACATAAGGCATGAGCAGGCTATGCGAGATGGACACCAGGATCTCAGCGTCTTTGTCGGT
GCTGATGGGGCGATCATGCTGGAAGAACTTAAAAATCGTTACCAGCGCCCACCGGAGAAC
GAGCCCCATGATGATGATGTCACCGAAATGATAAAGACCACCGAGGAAACAGAGAAGGAG
AACGTAGAGATGGATCAGGATATAGCTGTAGTAGACAACGTTGATGAACAGGTTGTGGTG
ACACCTGCTCATGACGCTGACAGCGTAGCGGTTGTTGCTGAACAGGTCGTTGCGTCAGAA
CCAACGCCAGAGCCGGTACCCAAGGTTGAGCACGTAGAGATGAGTGTCGATCTAGCGGGT
GAGACTATTACACCGATTGATCAGGCAATTCGGTCTTTTATGCAGCTCAACGGTATTGAG
CACAGCGTGGTGTTGCGACGCTTGGGGCTGATGACTCAGGTGGCACATAATAAGGAACTT
GATGAGGTCTACGCTAAGGCACTTGCCGAGGGTGAATCCCATGCTCAGCAGCAGCATGAA
TTAGAAGCAGAAAATGAACGGCTTAAAAAAGAAGTTGATGCGCTCGCTGCAGAGCTTAGT
GCTGCGTTGATGGGCGAGGGTGGTGGTGATCATGAC

>RXA01809-downstream
TAAGGCCGTGACACCAATTGTGG

>RXA01812
AGCTTCAATGACGTTGACCCAGCGGTGACCCATCCGCATCTCACAGTGATCTACCCACCG
CTCACCCCTGCATCCGAAGAGAAATTCAACAAGATCACCTCAGTCGCTGCTGTGAGCAAG
CGCCCAACCACCCTGCCGTATTTCCGTGCAGATGGTTCACCTACTCGTGGCTTTGCTAAC
TTCTCCACAGGAGGTATTCACGGTGCGGAATACAACGAAGATCGTTTTGACCATGATCAA
GATCTACACACAGTGGCAACCCGTGAATTCTTCGCCATTCTTGATGCGACATTAGCGGCT
CTCTACGCAGCCCACCAAGCCGAACCTGAATCGGCGGACTACCAGATTGCACAAGACGCA
CTCGCCTGGGCAAAGAATGTACTTAGCGATCAAAAACTCATCGCTAAGTCGCCTCAGTTA
TACAACCCCGAAACCGGGGTCACCTATGAGTGGGAGTTTGTCGCTCAAGCAGCATGGTGG
ATTCGCAACAAACCGGTTGAGGTTATTTTACCAACAGGTGAATCAATGACCGTAAAACAC
AAATCTGTATTGGCATCTGCGTCCTACCCACTCCGAGACAACGTGGCGTACTGGCGTAGC
GAACCCAAAACACCACAGCTGTTTCCCGTAGCAAAATCTGGTGGTTCCTCGCTTGAGAAG
AAGTACAACTACACCTCTGTGGGTACTGCTATTCACGAGGACTTTAGCAGTTACTATCCG
CTCTTGCTCACCAATATGGCTGCATTTACCAATGCTGACTTAGGTATTGATGAGAAAACC
GGGCGCCCTCGTGACCGCTACCGTGAAATCTACGAACAAAAAGAGATCTATGGCGCACAG
CGCAAAGACCCCTCCATTGATGAAGAAACAAAGCAACGTCTAGGGATTTTGCGCGAAGGT
ACCAAGTTGATTCTTAACTCGGCCACCGGTGCTGCTGATGCTGGTCACGACACCCCGATC
CTCATGAACAATCGCGTTATTGCCATGAGGATTATTGGGCAGCTATTTTCTTGGAGAATT
GGGCAAGCTCAATCACTGGCTGGTGCAACGATTATTTCCACTAACACTGATGGCCTGTAT

TCCGTACTCGATATGGGGACTAACCAGCGCGTTCTTGATGAACACGCTACAGCCATCGGT
GTGCAAATTGAGCCTGAAGAACTGGATATTGTCTCCAAGGATTCCAACTCACGTGCCGAA
TTTCTCGGCAATGGCTACATCAATGCGGCC

>RXA01813-upstream
GCGAGAATTCAAGAAAACAAAACAGATCAAAGTAAGGCAACAAGTGAGCAACAAAGTTCA
GAATCCGAACCAAGGTGGAAGCAAGAACTTCCTCTGGGCA

>RXA01813
ATGGTGGCGATCGTCGTCGTTGCAATCGTCGTCGTCGGCTTCATCGTCATCCAAGGCCAG
GGCTCAAAAGCAGCCAAGCTTGGTGACCGCGACTACGAAGACACCTCTTTGGCAATGGAA
GTAGGCTCCGACTCCATCACGCTGACCTCCGCAAACACCTCCGCCGACGCAAAGTCCGTG
CAGCTTTTTGAAGACTTCTCCTGCTCTCACTGCTCCGAGCTCTCCCTCGCCACCGACGCT
GACATGAAGACTCAGATCGAAGACGGCAACCTGGTCGTCGAAATCAAGCCACTGAACTTC
CTTGACCGCGAAAACATCGACGGCCACTCCACCCACGCATTGGCAGCAGCCCTTGCAGTG
GCAGACTCCAACGACGCAACCCTCTACTGGAACTTCCGCGCATTCCTCATGGAAGATCAG
TCCGAGATCTACAACCAGTGGTCCGATGATGACTTCGCAGACGGCGTTGAAGCCCTTGGC
GCAGACTCCTCCGTAGTAGACGCAATCCGAACGGCGACAACATCCAGCGCGCATACGACC
TGGCAACCGCAAACGGTGAAGAACTCACTGAAGAAACCGGCAGCCTGTTCTTACCACGCG
TTCTTCAAGACGGCAAGGATGTTGAAGGCA

>RXA01815-upstream
GAATGAAAAGAAGTGGTGGCCGATGCTTGGCTATCTCAGCCTGACTTTTACACTTGGATA
TTCTGCTGTTTTTCTCGGGATGCGGCTCTAGAATTGTAGA

>RXA01815
ATGAATCGTTCAACAATTTCCCCAGTTGAAGCCCGCCAGCAATTCCGCGCAGGCCTTATC
CAACCCACCTCCGGCTGGTCCGCGGGTTTTGCCCAAGCCAACCTCATTTCCATGCCCCAG
GATCTGGCTTATGATTTCCTGCTTTTTGCTCAACGCAACCCCAAGCCCTGCCCCATCTTG
GAAGTATTAAATGCTGGCGAAACCTTCGGCGGAATTTTCGGCTCAAACGCCACCGAAGCA
GACATCCGCACCGACGCGCCCCAATACCGCATTTACGCACACGGCGAACTTATCGATTCC
CCCGCCAGCGCCGTCGATTATTGGCGCGACGACCTCGTCAGTTTCATCATCGGCTGCTCC
TTTACTTTTGAACATCCCATGGTCCAAGCAGGCGTTCCCGTCCGCCACCTCGAGGCCGGC
CGCAACGTCCCCATGTATGAAACCTCACTTGCCTGCCGACCAGCCGGTTCCCTATCAGGA
AACCTCGTGGTGTCACTGCGCATGATCCCCGCATCCCAAGTCGCGGATGCCGTCCGCATT
ACCTCCCGCTACCCCGCGGTTCACGGAGCACCAGTCCACATCGGCGATCCTTCACTGATC
GGAATCGATGACATCAACAACCCTGATTTCGGCGATGCCCCGCTGTCCGAACCAAGCGAC
GTCCCCGTGTTTTGGGCCTGCGGAGTTACCCCTCAAGCAATGGTCATGTCCTCCAAGCCA
CCGCTGGCGATCACTCACGCACCCGGACACATGCTGATCACCGACGCCCCAGATCTGGGA
TTCCAGGTTCCT

>RXA01815-downstream
TAAACCTGGATCCACCGATGTGA

>RXA01816-upstream
TTGGGTGTAACGGCGTGGGAAAATAGGAAATGCCCTCCTGAACAGGAAGAATCAAGCTTA
GTTAGAGTCCTTCTTCCCCTGCCAGAAAGGCACCTCACAG

>RXA01816
GTGCAATTATTACACACCCCCGCAGCCATATCCATTTCCTTCGACGACCCCAACCTCATC
TCTACCGCAGGGCTGGTCCCGACCATGGCCCTGGCCGAGGACCGGTTAACAGTACCAACC
GACAAAGGTGCTAACCCAGGTGCCAAAATCACGACCCTCATTGCGGGGATGGTCGCCGGT
GCCGACTCCATCGACGATATCGATGCACTCCGCCACGGCGGTATGCACCGACTCTTTGAC
TGGATCTACGCCCCCTCCACGTTGGGGTCGTTCCTCCGGGCCTTTACCTTCGGGCATGTC
CGCCAACTCGACGCTGTGGCCTCCCGGTTCCTGGTGGGTCTGGCAACACAGGCCCCGGCC
CTGGTCCCGGTTGATGCTTCTACCAGTGATTACGTCTTCATCGATGTTGATGACACCATC
ATTAAGGTCCACGGACATCAGAAACAAGGCGCTGGTTTTGGTTACTCCGGTATCCGTGGA
CTCAACGCCCTGCTGGCCACAGTGACCACACCAGAGTCAGCACCAGTGGTCGTGGCCCAA

CGATTACGGAAAGGATCGTGCGGTTCCCCGCGGGGTGCAGGCCGGTTGATTGCTGATGCG
GTGGCTACCACCCGGCGTTTGCCGGGGATGGAGGATGAGAAGATCCTTTTACGCGCGGAT
TCTGCCTTTTATGGCCATCCCAGTATCAGTGCTGCGATCAAGGCAGGGGCGGATGTGTCT
TCACGGTGCGGA

>RXA01816-downstream
TGACCCCCAATGTCAAGAAAGCG

>RXA01817-upstream
AGGATGAGAAGATCCTTTTACGCGCGGATTCTGCCTTTTATGGCCATCCCAGTATCAGTG
CTGCGATCAAGGCAGGGGCGGATGTGTCTTCACGGTGCGG

>RXA01817
ATGACCCCCAATGTCAAGAAAGCGATCGCCCAGGTTCCTGATGATGCGTGGCAGACAATT
AAGTACACCAACGCGATCTTCGACGAGGACACCGGGCGCTGGATCTCGGTGGCCGAGGTC
GCCGAGATACCGTTCACCGCATTTACCTCCCGGAAGAAAACCGACCACATCCCCGGACTG
CTGGTGGTACGCCGGATACCGGAGCTGAATAACAAGGATGTGGATCAGCCGGGGTTGTTT
GATCTACACCGCTTCCATGCGGTGTTCACCACCGCCGACCCAGGCATCCTCGATACTGTT
GCTGCGGATAAAACCCACCGTCAACACGCAATCATCGAACAAGTCAACGCGGACGTAAAG
GCCAGTGCGTTGGCGCATATGCCATCAGGTGTATTCACCGCCAACAGCGCCTGGTTGGTG
TGTGCGGTCATGGCGTTCAACCTCACCCGCACAGCCGGTGTGATCGCTGCAGGCGCGATG
GCCAGGGCCACCACCGCAACGATCCGGCGGAAACTTGTGGCCGTTCCGGCCAGGATTGCA
CGCAGCGCCCGGAGATTGATTCTTCACTTGCCACGGAACTGGCGGTGGGAAACCCAGTGG
TCAAGATTGTGTGATCACGGCCGTTTACCACCG

>RXA01817-downstream
TAACCGGTAGCTCCCTGACTACC

>RXA01820-upstream
AAATGCCCTCCTGAACTGGAAGAATCAAGCTTGCTTAGAGTCCTGATTCACCTGCCAGAA
AGGCACCTCACAGGTGCAATTATTACACAACCCCACAGCG

>RXA01820
ATGTCCGCATCCTTTGATGACCCCAACCTCATCTCGCTTGCTGGACTGGTTCCAACCATG
CACTTAGCCGATGCTGCCAGCCTGTCCACCTTGGCCCAGGACCGGTTGAGCATCACCGGT
GATAAAGGTGCCAATGCTGGTGCGAAGATCGCCTCCCTAGTCGCGGGCATGGTCGCCGGT
GCTGATTCCATCGATGACATGGATGTACTCCGCCACGGAGGTATGCGCCGACTTTTCGAC
CGGATCTACGCCCCATCCACATTGGGGTCTTTTCTGCGGGCCTTCACTTTCGGCCACGTA
CGCCAACTCGATGCTGTGGCCTCCCGATTCCTGGTCAACCTGGCCAGGCAGGCACCACAC
CTGGTGCCACCACCACCGGCAGGCAGTGGCGGTAACGGGTATGTGTTCGTTGATGTTGAT
GACACCATCATTGAAGTCCACGGCCACACCAAACAAGGTGCCGGCTTTGGTTACTCCGGT
ATCCGTGGACTCAACGCCTTGCTGGCCACGGTCACCACCGCACAGTCCGCCCCCATCATT
GTGGGCCAACGATTGCGGAAAGGATCGTGTGGTTCCCCACGAGGGGCCCACCGCCTGATC
GCCGATGCGATGACCACCACCAGGCGCCTGCCCGGGATGGAGGATAAGAAAATCCTCGTC
CGGGCAGATTCGGCGTATTATGGTCATCCCAGTGTCAGTGTGGCCCTAAGGTCCGGTGCG
GATGTGTCCGTCACGGTGCGGATGACCCCGAACGTCAAGAAAGCGATCGTCGCGATCCCG
GAAGATGCGTGGCAGACGATTCAGTACACCGATGCGATCTTCGATGAGGCATCACAATCG
TGGATCTCCTTAGCCCAGGTCGCCGAAGTGCCTTTCACCGCGTTTACCTCCCGGAAGAAG
GCCGACCATGTTCCCGGACGCTTGGTGGTACGCCGGATTCCTGAGCTGAATAAGAAGGAT
GTGTATCAGCCGGGCTTGTTTGATCTTCACCGCTTCCATGCGGTCTTCACCACCGCCGAC
CCAGGCGTGCTGGATACTGTTGCTGCGGATAAAACCCACCGTCAGCACGCGATCATTGAA
CAGGTCAACGCAGACTTGAAGGCAAGCGCGTTGGCGCATCTGCCGTCGGGGACGTTCACC
GCCAACAGTGCCTGGCTCGTATGCGCGGTCATGGCGTTTAATCTCACCCGTGCCACCGGG
GTTATCGCTGCAGGCGGGATGGCCAAGGCCACCACCGCGACGATCCGGCGGACACTGATG
GCCGTTCCAGCCCGGGTCGCCCGCAGGTCCCGCCGACTGGTGCTCCACCTTCCCGAGGGG
TGGACGTGGCAACCACAGTGGCAGAAACTGTTTGATCACGGCCATTCACCACCG

>RXA01820-downstream
TAACCGGTAGCTCCCTGACCACC

>RXA01825-upstream
GTCAAGGTAGCTGGCCCGGCAACTGATACGTTAAGCTCAAACAAGATAAGTACCAGTTGC
TGGGGTTTTTCCAAGACAATAAATTATGAAGGTGTGAACA

>RXA01825
ATGCCAAAGGCAAGAGTAACTAAAAACGAGACCGCACCGGTTTCAAGCAACCCAAGCGCA
AACCGCACCCCGGTTAAGATCAATTCCGCCGGAACCCCAATGTGGTACAAGGTCATCATG
TTTGCCTTCATGATCGTCGGCCTAGCCTGGTTGATCATTAACTACCTCGTGGGCCCACAG
ATCCCATTCATGGCTGATCTTGGTGCATGGAACTATGGCATCGGCTTCGGTCTGATGATC
ATCGGCCTACTCATGACCATGGGTTGGCGT

>RXA01825-downstream
TAATCCTTCAAAAAAGTGACTGC

>RXA01831-upstream
CCTGTGGATAATTGGTTGTTGGCTGATGGTGATGTCATTACGGTGGGTCATTCCAATATC
GAAGTTCGTATTGTTAGTCCCTAGAGGGAGAGGTTGATCA

>RXA01831
ATGGATTCTCTGGTCCTTCTTGGGCTTCGCATCGCTTTGCTTGTGGTGTTGTGGTTTTTC
GTCTTGATGGCGCTGCGCGCTATGAGGGCAGATTTGAAAGTGACGGGTCAAGCGTCGACA
AGCAGCTCCTCCGTCGCGGCACCGCAGGGCCTTGCCCGGGCTTTTAATCGCTCCAGCCCG
CCTCGTCTTTTGACGGTGGTCGAGGGCCCGTTGGCGGGCTCCTCGATTGAGGTGTCGGAG
GATATGACGATGGGCCGTAGCCCTGAGTGCACGTTTGTGGTGGGCGATGATTACGCCTCC
GGCATGCATGCGCGGGTGTTTAAGCGTGGTTCGGAGTGGTTTGTGGAGGATCTGGATTCG
CGCAACGGCACTTTTGTCGGTGGTACGCGCATTGATCAGCCTGAGCAGATTGCGGTGGGC
ACGGATATCCGTATTGGTCGTACAGCAGTGAGGCTTGTTCCC

>RXA01831-downstream
TGATGTTGAAACTTAAATATGCG

>RXA01834-upstream
ACTAAGAACGTGAGCTTGGTTTCATAATACCCCCCAGGGTATTGTTAGCCAGGTGATTCT
AGCCCTTCTTGGCGGCCTAATAATAGGCCTACTTCTTGGC

>RXA01834
ATGCTCGGTGGTGGCGGTGCCATCCTTGCCATTCCGCTGCTTATTTATGGATTTTCTTTT
AGCGCCACGCAAGCTACTGCAGCTTCATTAATCATCATCGGACTTGGCGCCCTCATTGGA
CTGATCAGCCAATACGCTGCCGGGCACGTCCGCCTTAAAGAGGGTCTAAGCTTTGGCCTT
TTAGGGTTGGTCGGCTCATTTGTGGGCAGTCACCTTGCTAGCAATATCCCCGATTCCCTA
CTCCTGAGCGGCTTTGCCATCCTCACGCTCGTGGTGGCGTTGACCATGATTTCTAAATTA
AGAAGCACCCGAGAATACATAACCAGAAGGCCAAGCATCCTTGCCATTGCTCTTAGTGCC
ACCGGCGTGGGATTTTTGACGGGATTTTTTGGTGTGGGTGGCGGTTTTGCCATTGTGCCA
GCCTTGATTTTTGCGCTCGGTTTTTCCATGCGGCAGGCTAGCGCCACTTCCCTAGTGGTG
ATCGCCGTTAACAGCGCTATTGCCATGGGATTTAGATATTCCGATTTGGCAAGTATTGAC
TGGTCAGTGATCTCGCCAATTATCATCACCACCGTATTGGGCGCTTTTAGTGGCGTAAAA
CTAGCCAAAAAGGTCAAAGCATCATCACTGCAACTAGGTTTTGCTGGCTTCTTGATCTTC
ATTTCGATCTATATGGGATTTCAGAATTTCCCGGACCTTTTT

>RXA01834-downstream
TAAAACTTCAAAATATACCCCCC

>RXA01842-upstream
CACGTCATGGTCTCGCGGTGATCATCTTCCTACCGTGACAGGCAAGGCCGCAAACGGCCG
TGACCACAGGAAAGAAATTCACGAGGAGAGGAAGCACACG

>RXA01842
ATGTCGAAGGTATACGTGTCCAACGAGTACGGCGGCCCGGAAAACCAGGAACTGATCACC
CGCAACACCCCCCAGCCAGGCCCGGGAGAACTCGGGGTCAAGGTCCACGCGGCCGGGGTC
AACCCGCTTGATTGGAAGGTCCGTTCCGGGGTTGCCGGAACCCCGCGAGAGCTTCCGGCA
CCCCTGGGCGAGGAGGCCTCCGGGATCGTCACCGCCGTTGGAGACGGTGTGGAGGGCTTC
GCGGTCGGCGATCCGGTGCTCGGCCTGGTGGCCCCCGGCGTCGGCGGATATGCCGAGGAC
ACCCTGCTGGTGGCAGAGAGTACCGTGCTAAAGCCGGAGGAGATCTCGTTCACCGACGCC
GCCGCGATCCCGGTCGCTGGGGCGAGCGCCTACGCCGGCACTCACCAGGTCGAGCTTGAA
CCAGGCCAGTCGTTGCTGATCAATGGGGCCGGTGGTGGGGTCGGGCTGATGGCCGCGCAG
ATCGGACGGGTCCACAAGTTCCAGGTCGTCGGCGTTGACCACGAGGACAAGCGCGAGCTC
ATCGAATCCACCGGTGCTATCTTCGTCGCCACCGGCGACGCCGTCGCGGAGCAGGTGCGT
GCGCTGCTCCCTGACGGTGTGGACGTAGTCTTCGACCTAGTCGGCGGGGAGGCGTTGCGG
GTGGTTGCTCCCTTAGCGAAGAATCCGGCGCACGTGATCTCGGCGGCTGATGCTGCCACC
GTGGGAGAACTCGGTGGACAGGTGCTGCGCCGCACCCCGGAAATGGTCGGACAGATCACC
GGGGTGGTCCAGTACGGGCTGGTCGACCCGAAGGTCGATACGACCTACCCGCTGGAACAG
GCCGGTAAGGCCCTGGCCCACGTTGAGCAGGGCCACGCCCGCGGCAAGATCGTCCTCGAG
CTCATCACCTCCCAGGAC

>RXA01842-downstream
TAACCAGACAACGCGGTGACCTC

>RXA01844-upstream
GACCAATTGGTCCTGCTGCATCCGCATGATCGCCAACGCCAGTTGCGGGTAGGCGTCCAC
GACCTCGGCCAGGGCCTCGACGGGCAGGTAGAGCGCGCAG

>RXA01844
GTGGTCTCAATCGCCCAGGAGTTGGAGATCATTGAGGACGGCACGGGTGCGGTGCTCGTC
TCGGAGCAGGCAACCACCTTCGACAACGGGTTCATCGGCTACTCCTACTTCACCACCGGT
ACGGACGGAGCCACCTGCATCACCGACCTTCGCCTCAGGGCCTCCCCACTGCCGCAGGTT

>RXA01844-downstream
TAACCGGTACTAGCCGGTTTTTC

>RXA01845-upstream
GGCTCCGTCCGTACCGGTGGTGAAGTAGGAGTAGCCGATGAACCCGTTGTCGAAGGTGGT
TGCCTGCTCCGAGACGAGCACCGCACCCGTGCCGTCCTCA

>RXA01845
ATGATCTCCAACTCCTGGGCGATTGAGACCACCTGCGCGCTCTACCTGCCCGTCGAGGCC
CTGGCCGAGGTCGTGGACGCCTACCCGCAACTGGCGTTGGCGATCATGCGGATGCAGCAG
GACCAATTGGTCCGGTCCCGGGAACGCGAGACCGCACAGACCACCTCGACTGTCGAGCAG
CGCGTGGCCGCCGCCCTCCAACACCTGGACGCCAAGCTCGGGCAAATCCGACAAGACGGA
TCCAGCCTGCTGCAGGTCCGCCTGCGCCGCGACGACGTGGCCGGCACCACCGTCGAGTCC
GCCTCCCGGGCAATGGCGCGGATGAAGAAAACCGGTGTCATCGACTCCGGCCGCGAATGG
ATCGCCATTACCAACCACCAGGCCCTGGCCGACCTGGTCGCCGGCCTC

>RXA01845-downstream
TAAACGCCCACATCCCTCTCTCT

>RXA01846-upstream
GTATTTAGGAATTGAAACCCACTAAAAAACAGACTAAGTTACTAGGTGATAACAAAAGTT
GTTTATTACTTATGGGAATAGTGTGGAAAGTAGGGTGAAT

>RXA01846
ATGTCAATTCCTGGAAATGTTAGTTATGTTGCACAGGGTGGCACCGGTTGGGATGGTGCT
GATCAGTACACCACGGGTGAGAGTTGGGATCTACAGTCGTTCCTTGAAAACTCGACTGAC
TACCTCATGATTATTGGTGGTTCGCTGCTGGCACTTGTTGGTGGTGCTGCTGTGATTTGG
GGCTTTGTCAACGTGATGCGCAAGCTCTTCGGTGGTCAGAGTGGTCAGCAGATTCAGTGG

TTCACCACTATTTTGCTC

>RXA01847-upstream
GCCCTGCCCCCTCGATTTAAGAGGCAAGGCTTTTACAGTATCCTCTCATGC

>RXA01847
ATGCTTATTGTGTTGCCTCCCTCAGAAACTAAGACCCACGGCGGTTCAGGAAAACCTCTG
GATTTTCACCATTTGAGTTTCCCGTCGCTCACCAAGGCACGCCAAACAATACTCGCTGAC
CTGCAAGCTTTGGAGGTAGATGAGGCGCTGAAAGTTTTGGGCATTTCTGAAAAGCTCCGC
CCTGAGGCCGAATCCAATCGCGCGCTGGAGACCAGCCCTACGATGCCTGCGATTTTTCGG
TATTCCGGAGTGCTTTATGATGCGCTCGACGCTGCAACGCTGCCGGAGAAAGCACTGGAA
CGCCTCGCCATCGGCTCGGCACTTTTCGGCGTCATCCACGCCACCGATCCGATCCCGCAT
TACCGCCTGTCCGGCGGCACAAAACTGCCCACCAAAAGCGGCGAGCTGCCCACCATGAAG
GCGCGTTGGGGCACAAGCATCAGCGAAGCGCTTATCGACGTCAACCAGCTGGTGATTGAT
CTTCGCAGCGGGACCTACCAACAGTTGGGTCGCGTAAAAGACGCCGTCACGGTACGCGTG
GAATCAGTCATGGAGGATGGCTCCCGCAAAGTAGTCAGCCACTTTAACAAACACTACAAA
GGTGAACTCGCCCGCGTGCTCGCGCTCTCTGAAAAAGAAGCACACACCGCAGAGGACGTA
ATGAGCATTGCGCAGGCTGCGGGCCTTGTGGTGGAGGAAAACCCCAACCACAAGGAAACC
CTCACTCTGGTTGTC

>RXA01847-downstream
TAGGCGTTAATCACCATTTTGAT

>RXA01856-upstream
CACTCTCCAGCGTTCGCGCCAGATATGCAGCCAACTCTTGATCGTGGTGTGGAAGCGCTG
GTTGTAGCTGCTTCTGCGTGGCTAGTAAAATAATTGGCTA

>RXA01856
ATGAATCCTTTTCTTTCGGACACGTTGATTGTCCAGCAGACCTCTTCCTTCCTGTCTAAC
AACTTTGAGATCTACAATCCAGACGGCGAAGTTGTTATCAGAATCAAAACTGAAGGGTCG
TTGGGCTCTCGGCTGGTCAAGGGCGACCGCAGATTCACACTGGAAGACGCCTTCGGCACC
CCATTGATGCAGGTGCGCGATCCCATGAACTTTGTTCGCGACACCTATGAAATTGATGAT
CCAAATGGCAATCCCATTGCTCATGTGCGGAAGCGTTTCACCTTCTTCAACAAGCGGATG
GACATCGAACTACCAGGTGACCGCGTTATTGAAATGCACGGTAACTTCCTTGGATTTGAA
TTTGAGTTCCGCATGGGCGATCGGATTCCTGCGAAAGTAACCCGAAAATGGTCCGGCGCT
GGCAACGGATACCTAGGCCGAAGCACCTACGCCCTTATTTTCGATGAAGAAGCCCCTGAT
GAAATCAGAAAAGTCATCATTGGAGGCATGGTCGCGCTAGATCTGATCCGGGAGAAGGAA
CGTAAT

>RXA01856-downstream
TAAGCCACCCCCGTTTCATGTCT

>RXA01857-upstream
TTAAGGGACTTCGCAGCCTACTTGAGAGATTTTGACAGATAACTAATAACCTCCACTTGG
TCGTACTAATCTAACTTAATCTCTCCCTAGGAGTTCTCCC

>RXA01857
ATGGCTTCACGCCGTTTCCGTATGATGCTCACCGCAAGCATCACCGCAGCTTCCCTTGGT
TTTTCCCTCACCCCAGCAATCGCCGATGAAGCTGTAACCGTTGCTACGGCACCCTCCGTC
GGATTCGATTCCGGCGTCGAACGCGATGCACCATTCACCGCAGTTCCACACGACGTAGTT
CTCGGCGTTGGAGCGACCCAGTCCGAGCTCATTTTCAACTGGATCACCGCGCAGGGCCTA
ACCGGCCAGGTTGCACAGATCTCCCTGGACGATACCTTCGCATCCCCAATCACCGTTGAT
GCAGTTTCTGAAAACGTCAGCATCGTGAACACCGAAGGCGATTCCCGCGACCGAGCTGAA
GGTGAATACGTTGAATACCGCGATGGCGCAGTCAACCGCGCAACCGTAGATAGCCTCGCA
GAAAACACCACCTACTCCTACCGCGTCGGCTCCGAAGCTGACGGCTGGTCCGAAGTGCAA
ACCTTCAACACCGGCACCTACGGTGACAACTGGAACTTCCTCTTCTTCGGCGACACCCAG
CTGTACAACACCCACTCCAACCGTGCAGAAGAAGTCCAGAACTGGGCAAACAACCTGGAA
CGGCGGCCCACCAATCGAAAACCCAGGAACCTCCTTCATCCTCTCCGCGGG

>RXA01857-downstream
TGATCAGGCAAACCACTCCAGCT

>RXA01858-upstream
CGTGTGTTTGTTTTGACTGGAACAGCGTCGGCTTTTCGGCCACGCGGCCTGCGGACAGTA
GCGGAATCACGCGGGACATTGATCCCCGGACGTAAAGCCG

>RXA01858
ATGTTTATGACACCGCGGGCGTTGACCGAAGATAATGAGTTGACCCTGGCTTTGAAATCA
CTCGGAGGGCTTATGGTGTCACCCAATGAGTGCTCAGTAGTGACAGAAGTGATGCCGACT
TGGAGAGAATTATGGCATCAAAGGCTTCGATGGCAACGCGGTGCGCTGGAAAACCTCGGT
GCTTATGGCATCACACCACAAACGACACGGTATTGGTTCCAGCAGCTGGGAATCGGTTAC
GGCGCATTAGCCTTGGTCGCCTATTTCGCAGTCATTATCATTACGTTTCTCGCCCGCGAT
CAATGGATCTGGTATCCATTCTGGATGCTGCTGGGACTGTTGTTCATGATTGAACGCGTG
CTAACGGTGTGGAGATCCACATGGTTTGCCAGGTTTGTTGCTGCGTTATTAATCCCAGAG
CTCATCTACGCCAGCTATCTCAACCTGGTATTTCTCAAAGGCGTTGTGGATATTCTATTG
GCCAAGCAAGCTCACTGGGGTGAGCATGGTGACAAGACAATGCAGGTAGCCGATGCAGCT
GCCGAAATTAACGATGAAGGGGAGGAACGCCGA

>RXA01870-upstream
GGATCATGTCCACCCCAGAAGGTAGCCTGTCAGTGTGAGCGTAATCGAGGGCAAGTACCA
GCTGAAACCTCAAGGCCGAGGTGGCCTGTGGTGGTCAATC

>RXA01870
GTGGGTGTGGCAGTTGTTTTGTTGCTGCTTCCAACGTTGATCAACCTGGTGGTTCCGGAT
AAAGCCAATGACTACAAGCAGCTAGAAATCGATCTTCTGGGTGTGGATTGGTCAGTGCCA
ATCACCACGGAGGAATCCGCTGCGGTGCTGTGTGAGGAAACATCTGATGAAATCACACAG
AAGTATTGGGACTGCAACGGGGACACCACGGTGGTGACCATGATCGTCGAGGGCGTGAAA
GATCCGTCCAATACGTTGCGTCGCATGGTGGGTTCATCGCTGATAACCAGTGTGGATGAC
AGCCTAGAGGCAGTATCTAGCGAAGATGGCCGTGCGCATGCGTTGTATGTGCCAGGTCAG
CAAGAAGGATCTTTGTGGACGCTGCCTATCGTGGCACTGAGCGTGCAGGGTTCGGGTGAT
TATGAAGACCTCACAGCGATCGCAATTATCAACGGCACCTCGTTGGATTATTACAGCACC
CACATTTGGTCCAGCATGGCCGCTGACCGCGGGTTGCCGTACCAGCAGGACTTCCCCCTG
ATGCTGGAAGAGGAGCCATGGCAAGACACCCCCGGCGGGGATCGTCCCTTCGAGCTGCCC
AATGATTTCTTTGATCAGTACCCCGATCTTTTTGGCCCAGGCTCCGTCATTCCCAACCTT
GAAGGAGAATCCCTA

>RXA01870-downstream
TGAGTCGCATGTTTAGCATCACC

>RXA01871-upstream
GCGGGGATCGTCCCTTCGAGCTGCCCAATGATTTCTTTGATCAGTACCCCGATCTTTTTG
GCCCAGGCTCCGTCATTCCCAACCTTGAAGGAGAATCCCT

>RXA01871
ATGAGTCGCATGTTTAGCATCACCTTGTGGGTTGCCATCCTCCTCTCAACCCCGGCGCTG
TTTTTGAGCTTGGCCACGTTCATCTTCGTGGATGGCATCTCTGTCCTCGTGAATATAGTG
TTCGCGGTGCTCTACTTGGTAGTCATTGTTTTCCTGTTAAGTCGCACCCCGCTGTGGCCA
CGTTTTAAAGGCTCCGGCAGCAAGAAGGGAGGCGGATTCGCGTGGGCGGCGTCATCATTG
TTGTGGGGCGCGTTCGTTGGTTTCGGCATCGTCATGTTGTTTGCCGGTCCGGTCATGGAT
CTCACGGACAAACTCGGCTGGGATTTCGTTGCCATGAGTTTCACCGGAGCGTATCCAGAA
GAAATCGCCAAAGCGTTAGGCGTTGCCATCATCTTGTTGAGCTTCCGCCAACTCAACCGT
CCGTGGCATGGATTTATCACCGGCGCGCTAGTGGGCTTAGGTTTTGAGGTCAACGAAAAC
CTCCTCTATGGCGCCACCGGTGCAATCATGGACCCCAACGCTGACCTCGACGGCGTCCTT
ATGATGTGGCAATACCGCACCATGTTGGGCCCACTCATCCATACGTTGCTCACCGGATTC
GCAGGTTACGGCATCGCGTTGGCATTCTTCCGCGCACGAAAAACAGTCGCCTGGCGCTGG
GGCGTGGCGATCGGTTGGACTCTCATCGCCTTCGCACTGCATTTTTCATGGAACCTGATG

TGGGAAAACGTAATCGGTTCCTATGTCACCATCATCGTGGTCAGCGTTGTCATGTACGGT
CTGGCTATCTACATCCTCTGGAGTAATTGGGCCGAAGCCCGCAACGACTCCAGCTACGCT
TTCGTCCCGGGAATCATCACAAACACCAAAGATTTATCGCTTCTTGACGCCCCCATTCCA
GTAGGCGCTGAGGTTCCCGAGTCGCGCATTCCCCAACAGATAGAGGAACCCAAGGCGGAG
AAC

>RXA01871-downstream
TAGCTTTCACTCGCTCTCCATCC

>RXA01874-upstream
AGTGTCGGCGCGACGATTGTGGGCGGTGCTTTGGCGTGGCACGCAGCAGTTTGGCATCAC
AGTTCCGGAGCGCAAAACGCGGTCAGCCTTTCGCGTCGCA

>RXA01874
GTGATCGCGTATGTTGCCAGCGCGTGCTGCCTGCCGTTTGGCGCATTTGCCGGAGCGTTG
TTGTCCAAGGAGCTGTCGGGACATCTCCAGGAACGAGTCCTTCTCACCCACACGGTGATT
AATTTTCTAGGTTTCGTGGGATTTGCTGCGCTCGGTTCGCTGTCGGTGCTGTTCGCCGCG
ATTTGGCGCACCAAAATTCGCCACAATTTCACCCCGTGGTCTGTGGGGATCATGGCGGTG
AGCCTGCCGATCATCGTCACGGGCATCCTGCTCAACAACGGCTATGTCGCCGCACAGGCC
TGGCCGCGTACGTGGCAGCATGGTTGCTGGCCATGGTGGGGTGGGGGA

>RXA01875-upstream
CTWKCKTSRSWTGTGTRSYWGAWWMMCWYWCSCAGCATSRWGCWRGWWWYRMGKWKTSCA
SYAAACWGGRGTCARTCSCGGATCTTTGGGTGGACATGTT

>RXA01875
GTGGATAGTCTTCTAAACAAGGGCGTCGCAGCATCAGACATCGTTGCCATTGTTCGAAAT
GAAGAAAAGGCAGCAGACCTCAAAGCCCGTGGAATCGCTCTTGGTGTGGCTACTTTTGAA
GACGAAGCGGCACTGACTGCAGCTCTTGAAGGTGTGGATCGCCTTGTGTTTATCTCTGGC
AGCGAAGTGGGGCAGCGCGTTGCGCAGCACACCAATGTCATCAATGCCGCTAAAGCAGCT
GGCGTGACATTCATTGCATACACCAGCTTGCTCAACCTTGGTACCTCAAAGCTTGCACTT
GCTCCAGAGCACATTGCAACGGAAAAGCTCCTGGCAGAAAGCGGCATTGACCACGCGCTG
CTGCGCAATGGTTGGTACTGGGAGAACTACGAATCTTCAATTGGCGCAGCGAAGGCCACC
GGGAAGGTATTCGGCGCAGCTGAAGGCGCACGCGTTTCCGCAGCCGCACGTAAGGACTAC
GCAGAGGCAGCTGCTGTTGTCATCACCAGCGACAACCAGGCAGGCAAGGTCTATGAGCTC
GCAGGCGCACCAGCTTTGACCTACCCAGAGATCGCAGCTGGCATTGGTGAGGTCATTGGT
TCTGAGGCAGAATACGTCAACCTCTCCGTGGAGGAGTACCAAAATGCGCTGGAGCAGGCT
GGCGTTCCAGCTGAATTTGCAGCACTTCTCGCAGGCATGGATCCCATCATTGCAGAGGGC
GCGCTGTACTCCGACAGCACCGACCTACAGGATCTCATCGGACGCCCGAGCACCTCAATC
GTTGAGGCCCTGAGCTCA

>RXA01875-downstream
TAACCTGCTACTCACCTAAAATG

>RXA01877-upstream
GTATTGTACTAATTGTAATTCCCCGGAGAGGGAAGAAGTTTACATGGCGCCCCATCAGAA
GTCAGGGATCAACCGGATCAACAGCACCCGCTCGGTGCCG

>RXA01877
TTGCGTTTGGCTACCGGTGGCGTGCTCGCCACCTTGCTTATCGGCGGAGTCACCGCTGCA
GCTACCAAAAAGGACATCATTGTTGATGTCAACGGCGAGCAGATGTCCCTAGTGACTATG
TCCGGCACTGTTGAAGGTGTGCTGGCGCAAGCTGGTGTGGAACTTGGTGACCAGGACATT
GTTTCCCCTTCACTGGATTCATCCATCAGTGATGAAGACACTGTGACTGTTCGTACTGCC
AAGCAGGTGGCGCTCGTGGTGGAAGGTCAAATCCAAAACGTGACCACCACTGCGGTTTCC
GTGGAGGACCTCCTGCAGGAAGTCGGTGGCATTACCGGTGCTGATGCGGTGGACGCTGAT
CTTTCAGAGACCATCCCAGAATCTGGTTTGAAGGTGAGTGTTACCAAGCCGAAGATTATT
TCCATCAATGATGGTGGCAAGGTCACTTACGTTTCTTTGGCAGCTCAGAACGTACAGGAA
GCCCTAGAGCTGCGGGATATTGAGCTGGGTGCTCAGGACCGCATTAATGTGCCTCTGGAT

CAGCAGCTGAAGAACAACGCTGCGATCCAGATCGACCGCGTTGACAACACCGAAATCACT
GAAACTGTGTCTTTCGATGCTGAGCCAACCTACGTGGATGATCCAGAAGCTCCAGCTGGC
GATGAAACTGTGGTCGAAGAAGGCGCTCCTGGAACCAAGGAAGTTACTCGCACCGTAACA
ACCGTTAATGGTCAGGAAGAATCTTCCACGGTGATCAATGAAGTTGAAATCACCGCAGCA
AAGCCAGCAACCATTAGCCGTGGCACCAAAACTGTCGCTGCAAACTCCGTGTGGGATCAG
CTGGCACAGTGTGAATCCGGCGGAAACTGGGCAATCAACACAGGTAATGGCTTCTCCGGC
GGCCTACAGTTCCACCCACAGACCTGGCTCGCATACGGTGGTGGAGCTTTCTCCGGTGAC
GCTTCCGGTGCAAGCCGTGAACAGCAAATCTCCATCGCAGAAAAGGTTCAGGCTGCACAA
GGTTGGGGAGCATGGCCTGCTTGCACCGCAAGCTTGGGCATCCGA

>RXA01877-downstream
TAGTAGAAATCTGGCATCCAATA

>RXA01879-upstream
CTTTGCGGGCCGCTGATATTGATCCAACGCTTCGTGGCGAAAAGCTTGATGTCACTGACT
ATGTGCGCCTAGCTGGGGTGTTGCAGCAAAAGGATGAGAA

>RXA01879
GTGAAAATTACCGCTAAGGCGTGGGCGAAAACCAACCTGCATTTAGGTGTGGGACCGGCT
CACGACGATGGATTTCACGAGCTCATGACGGTGTTTCAAACCATTGATCTGTTTGACACC
GTCACCTTAACCACCCTCGATGAGGAGTTGGTGGAGGAGGGGAGCGTCGTCAAGCAATTA
TCTGTGACCGGTGCCCGTGGCGTGCCTGAGGACGCCAGCAATCTTGCGTGGCGCGCTGTG
GATGCGTTGGTTAAGCGGCGCGCGGAAAAGACGCCGCTGTCTGCAGTTTCGCTGCATATT
TCCAAGGGGATTCCGGTGGCTGGCGGCATGGCTGGCGGCTCTGCGGATGCGGCTGCGACA
CTGCGCGCAGTGGATGCCTGGATTGGGCCTTTCGGCGAGGACACATTGCTGGAGGTTGCC
GCGGAGCTCGGCTCAGATGTGCCGTTTTGCCTGCTTGGTGGCACCATGCGCGGTACCGGT
CGCGGCGAGCAGCTGGTAGATATGTTGACGCGCGGCAAGCTACATTGGGTGGTGGCCGCG
ATGGCGCATGGCCTGTCCACCCTGAGGTATTCAAAAAGCATGATGAGC

>RXA01879-downstream
TGAATCCGGAATCGCATATGGAT

>RXA01880-upstream
AGCTCGGCTCAGATGTGCCGTTTTGCCTGCTTGGTGGCACCATGCGCGGTACCGGTCGCG
GCGAGCAGCTGGTAGATATGTTGACGCGCGGCAAGCTACA

>RXA01880
TTGGGTGGTGGCCGCGATGGCGCATGGCCTGTCCACCCTGAGGTATTCAAAAAGCATGAT
GAGCTGAATCCGGAATCGCATATGGATATCAGCGACCTCAGCGCCGCACTTCTCACCGGC
AACACCGCCGAGGTGGGGCAGTGGCTGCACAATGATCTGACCAGCGCCGCACTCAGTTTG
CGCCCTGAACTGCGCAGCGTCCTCCAAGAAGGCATCCGCTCCGGCGCGCATGCAGGAATT
GTCTCCGGCTCCGGCCCGACCACGGTATTCTTGTGCGAATCGGAGCACAAAGCGCAAGAC
GTTAAAGAGGCGCTAATCGACGCCGGCCAGGTGTACGCTGCTTACACCGCCACCGGCCCT
GCGGCCTCAACCGCCGACCAGCGCGGCGCACACATTTTGACTGTTTCA

>RXA01880-downstream
TAATAAAGACAAACTTAAGTATC

>RXA01896
GCCCGCGCCGCCCTGCACGCCTGGTCGCCGACCGTGGGCGTCGACACGGATGTTGAGCGC
TGGATTGAGCTGGATAAGTGGGGTTTTGCCCGTTTTGAGCGCGGCGAAACCACGCATTTA
GGTCAGCGGCGCGACCGCATCAGGGCGTACCTCAACAGAGAGCTTGACGACGCCACCTGC
GATGATATTTACTCCGGCTACCTTAAAGCATATGAGCAAAACTGGACTGCCTACCCCGAT
GCCAAGGGCGTTCTCGATCGCGCGGTAGCCACCGGTGCCCCTGTGGGAATCCTGACCAAT
GGCGCAGCCCCCATGCAGCAAGACAAGCTTGATCGCACCGGCCTTGGCCTGCCAGAACTC
GTCATGTTGGCGGCGTCCACTCTGGATTCTGCGAAGCCTCGCCCCGAAATGTATGCCCGA
GCGCTCACCCATTTGGGTGCCCGAACCGCAACAATTATCGGCGATGATTGGACCAACGAT
GTCGCAGCTCCCCGCGAACTTGGCTGGAATGCTCTCTATTTAGATCGTTCCGGAACCGAT

CCACGCGCCGATATCCACTCCCTGGATGAACTCTTTCAC

>RXA01896-downstream
TAGGCTGGCCTTTATTGTTTCCG

>RXA01899-upstream
CCTCGCAGCACTTCGCGCAGGCGAATCCACAGTGGCCGCAACCTTGATCAAAGAACACAT
CGAAGGCTACTACGAAGAAACCGCTGCCGCCGAGGCCTAA

>RXA01899
ATGTCCCGCACTCTGTGGGCGGTTTCAGATCTACACGTCACCTTCGCCCAAAACCAAAAC
ACCGTTGATGCCCTCATGCCGCAGGACCCCGGCGACTGGCTGATCGTCGCTGGCGATGTA
GCAGAGAAAATCCCCGATGTGGTACGTACCTTATCCGCGCTGGTCAAACGCTTTGACACC
GTGATTTGGGTGCCGGGCAACCACGAACTCTTCAACCGGAAAACAGACCGCGTCAACGGC
AAAGCCCGCTACCGAGCATTAGTCGGACAACTCCGAGCCATCGGCGTGATCACCCCCGAA
GATCCCTATCCGATCTTTGGTGGCGTCACCATCTGCCCACTTTTCACACTTTACGATTAC
TCTTTCCGTCCCCTCGGCCTCACCGCGAAACAAGCCCTCGCCCAAGCAAAAATAAAGCTA
GACGACGAACTAGCCATCGCCCCCTACGTAGACATCCCCGCCTGGTGCGCCGAACGAGTC
ACCTACACAGAAGACCGCCTAAAAGCCACCAAAGGCCCAAAAGTCCTGGTCAATCACTGG
CCGCTGGTCATTGAGCCCACCCACCGGCTCTTCCAAAAAGACATCGCGCTGTGGTGTGGA
ACCACCGCCACCAGGGATTGGGCCGTACGATTCAACGCTCTCATGGCCATTCACGGTCAC
CTACATATTCCTGCCGAAACCCGCGTTGATGGGGTAAGCCACGTGGAGGTTTCTTTGGGT
TACCCCTTTGAAAAACACCCACCTCACATGAAGCGTCCGTGGCCGTTTCCGGTCATGCAG
ATTAAC

>RXA01899-downstream
TAACTCTGTTGCTTAAATGGGGG

>RXA01902
AACTACGACGCCTACAACGCGATGTACCCACGCCCTAACCAGGTCGATGAGAACTACTTC
TTCGAGTACAACAATGCACTCTTCCTGTCCCTGGACTCCAACGACTACTTGGACATCGAC
GACGACATCGCATTCCTTCGCGACACCGTCGCAGCACACGGTGACGACAAGGACTGGATC
GTCCTGACCTACCACCATTCCACTTTCTCCCAGGCCTACCACATGGATGACGCTCGCATT
AAGTACCAGCGCGAACGCCTCACCCCAGTGATCTCTGAACTGAACGTTGACTTGGTTCTC
GGTGGACACGACCACATCTACACCCGCTCCCACCTGATGAACGGCTTCACCCCAGTCGAT
GCAGGCCGCGAAGCAGTTGTCGGTGAAACTCTGAACCCTAAGGCCGGCGAAGTTGTTTAC
CTTGCAACCAACTCTTCCTCAGGCTCCAAGTTCTACGACTTCTACGACTTCCAGCTCGGC
CAGCGTTACGACACCGGACTGGATTTCCAGGAAACCGTCGATCAGAAGAAGATCCGCACC
TACACCGCAGTCTGGAACCAGGACCAGGTTCAGGACTACACCAACGTTGAACTGACCCCA
GAAGGCCTGACTGTGACCACTAAGGACGCAGTCTCCGGCGAGCTGGTTGACCAGTTCACC
CTGAGCAAGCAGGACCGCGACGAAGAATCTGAAGTCCCAGTTGAAGATGACAAGGACGGA
GACAACGCGACCGGCTCCTCCAACCTTGGTCTAGCTGCTATCTTGGCTCCAGTTCTGGCC
ATCTTCGGTTTCGTCGGTGGACTCTTTGTTGGCGGCGGCTCCCTCGCTGAGTTCTTTGCC
AACCTCGGCGTGAAGATGCCTTTC

>RXA01902-downstream
TAATACTGTCTGAGATTCAAGCA

>RXA01903
GCTCACCTTGATGACCGTGGCATCTATATCATCCCAGCTCAATATCCTTGGGGATACGAG
GAAATCATTAACCTACCGGCACGCGCTACCTCTACACCTGCTGTTGCTCCTCGCACTGAG
GCTGCTCCAGCTACAGTATCTGATGCTGAGGTCCAGAGCCTGCTTGAGTACTTGCGTACT
AATGCTTTCGTAAGTCGTCACGACGGCGACACCACGAAGGCCGACATCTTCAACAAGCAC
GCGGATACTGTCAACAAGCTTGCAGCACTACGTGCACCC

>RXA01903-downstream
TAAACCCACACCGCATAACCCCC

>RXA01904-upstream
ATTAGTTTTTATTCGCAAGGGTGGTCTAAATTTTTTACTACTGCGTCGTGTCCACCGGAT
ACACTTGAGGTAATACAGTTACGAGGCTAAGGAGTATGTA

>RXA01904
ATGAGCATTTCGCCGAAGAATTCCGGTACACCAAACGAGAACGCCGCAGCAGCGCAGGTG
GCAGCAAATCTGGCTAATTTAACGTCGCAGGCTACAGGGTCCATGGACGAAACTAATGAG
CAAGTCATTAAAAGTAACGAGCATGGCTCTGATGCTTATTTGGCGGATATTAAAGCCAGT
CGAGAGATGTGGGCAAAAATTGCGCTCGATCCGAATCAATCTGAAGAAACTAGGAAAGAA
GCTCGGGAGAATATGGCGCGGATAGATGAGTACGCTCGTGAGCACGATAAAGACAACAAG
GGTTTGTTGCAGAAGTTAGCGAAAAACAAAGCAGAGCTCATCGGGACTGTTGCGGTTGCA
ACCTTAGGTGTAGTGGCAGCCATTGCTAACAATGGCAAGATACCGATGATTCAGTTGAAA
AAA

>RXA01904-downstream
TAACCCCCGCACAGGCTGGACAT

>RXA01905-upstream
AAATGAAAGTCACAAACTTTGTTGGGGTTTCTTTAAAGTAAAATACAGAAGTTTCTCTGG
CAAAAAACCTCACTACTTTCTACAGAAAGGCGTCTTCCTC

>RXA01905
ATGAAGGCTTCTCAGACCCTCACCCGCAACACTCGTGCACGCAAGCTCGGCATGGGTATT
CTCGCAGCAACTATTATGGCTACCGGTGCACTTGCTGGCACTGCTCCACAGGCGACAGCA
GCAGTAGATACCACTGCGCCATACGTGTCCTATGTCGTTGACATTCCTGGCAAGGTTGGT
GAACCAATCAAGCCTCAGTACCTCACCATCTCCGATCAGTCCGCCTACACCGTGACCTTC
AAGTACATGCCATCCTGGTTGAAGTACGACGCAAACAAGAAGATGCTGTACGGTACCCCA
ACCGAGGTTGATGTCTGGACTCCTGAGGTACATGTTGTTGATGCTCATGGCAACAAGACT
GTCCGTTACTTCACCGTTGTAGCAGTCCCAGCAAACACTGGACCAACCACCACCACGCCA
TCTACTTCAAAGCCATCTACCCCGCAGGTGACCACCCCAACTACTCCGAAGGCGCCTACC
TTGCCAAAGTCCACCTTCGACTGGACCTTGTGGGGCTCCATCTTTGGTTTC

>RXA01905-downstream
TAGTTCTCACTAGCACCTCAAAA

>RXA01906-upstream
GCGTTCGGGTAAACCCGTGACAATCGCACGGGGCTTGTTTACCTGACACTCAAGCCCCGT
GCACCACAACAACCCACCTTAAAGAAAGGTTTTTCCACCC

>RXA01906
ATGTCCGAATTCCCTACACCTACGACTTTTCACGTCGAACCAGAAACGCTTAGCTCCGCC
ACCGATCTCACTGTTGATGCACATAAAATCGCAGAACTGCTGCTCAGCACCACTGATTAC
CGTGTGTTCTACATGCCGCGTCTCGCCGGTGTGACTCCTATCGTGTCCTACCTCTATGTC
TACGATGGTGAAAACTTCCTCATTGTTGGTCGCTCCACTCATGTGCCGTGGGAGTACTAC
GTTCACTACCCCATCAAGCCATCACGTGAATTTGGCTCTGCTATTGCTGTGCCTCTCGAT
GATTCTGATGACCCTTATGATGCAGCAGAAGTTGTTGCTCTAGTAAAGCAGTACATGACG
CCCACGCTCACTCCTGGTGAGGGTTATATGCAGGGCTTTTACAAGGGTCTCACCTTCACC
AACCACCTCGATATACATCGACCACTGACCCAGATTATCTCAGAC

>RXA01906-downstream
TAACAGCTATATTCACCCACCTA

>RXA01907-upstream
TTCGTTTTACCCACACCAGCACGTCACCCTCTTGCATCACGCCGAGAGGGTGACGTGCTT
TTTTCCTACTTTTCCTCATAACTACAGAAGGGACGCCCTC

>RXA01907

ATGTCTGCTTTTGATGAACTCCGCAAGAACTACCGCTACAAGTTCACTGACACCTGGCCG
GCCAACGCTGTTACCGGCACCGGCTACTACGCCAACCCAGCTTTTATCATCATCTCCGCT
GATGCCATGACGCAGAACACCCATGCCGATTCCAATCTCATCACGGTTAAAGAGCACCTT
AACACCCTGTTTCCGTACAGCGTACAACGCAAGGATCGTGCCTTTGTCTCTGAGATCTAC
ACCCCTATTAACCTGCTCGAAGATAATCCAGAACTAGCTCAAGAAATACTCGATGTGCTC
GACACCCTGAGCAACAACGCTGTTTTTAACGATGCGCACTACAGCGAGCTTGAACTAGAG
CGCCTCAATGAATATGTCATCGACACCTTGGCCTATGACATGAAGTCCGACATGATGCGC
GCCCTCGTTAAGGCCCGACCAGAGGCCGATCTTGAGGCGATGGAAGAACTCGACATTGCC
AATATCCAGAGCTGGATTAATCTCCACTCCTCCACTGTGAGCGAACACAACGATGGCAGC
GTTGATGATGCACCGTTTAATTCTCTCGCATTAGCTGAGATTTATTTGCAACAGCTTGCA
GACCACACTGTC

>RXA01907-downstream
TAAGCACGCTGTGTAACTACCAC

>RXA01908-upstream
TCCACGACATCTGACACAGAAAGAAGATTCACCATGTCTAAGAACAACGCAGCTCACCCG
CAGTCTGTCTTCCATATTTCATATCCCAGCACATACCACT

>RXA01908
ATGCACTCTGACCGCTTTGAGCACCCAGACAACGGCTATGGCTACACCATTCGTCAGGAC
ACTGATGCAGAGAACCCGATGACCCATCACGATACGAAAGATGCAGCTCTCTGGGTTCAC
AACCGACCACGACGCGGAGATACCGTCGCCGATAAGCCAGAAGGCAATGAGATTCTCGAC
ATCTTTGCCAAGTTCATCTGCGGCCAGCACGATAATGATGACAACCCGTTCGAAGTCTGG
TCCGACGGTGACTCGGATGCATCACTCATCCGCACCAAGGCGTATGTTGCCGAGCACCAC
CCCGAACTTATATTCGACATCTCTGCGAAAACCATCACGGGTTATTCCCAAGGCGATTGG
CTCGATGTGGTCTGTGTTACTACTGCCGCCACTTGCGACGAACTTATCCCTGCTGACAGT
CTTATTGACATCTACCGCCAGTGGGCTTTTGGTGATGTGTGGACAGTGATTCCTGATTCT
CAG

>RXA01909-upstream
TTGTTCTGGGAAGTAATATAAAAAGTCCCGAACAAATTAGTGTGAAAGGGTTTGTATC

>RXA01909
ATGGCTAATTTTCGAAGCAAGGATAAAGATGGCAATGTCATCAATCCGAACGCGTCTACT
AAAGGTGTAGATCTTGTTGTCAACGTCTACGACAGCGCCAAGCATGTGACCGAAAAGGGT
AACACTGTCCACTTTGTGGATGTTCAGGTAGCGCAAATTCCGATTGACGCTGACGGCACT
CGTGCGAATGCGAATCTTGCACCACAGACTATGCCTCATCTGCATCTTGACACTAAGGAC
GGTCAGCGCAACACAGGTGTTGCGTATTCTGATGCGCAGATTCAAGCGATGCAGACGGTG
GCAGCACAGGGGCGCAACCATATGACCCCGCTCTTGAGCAAAGACGGTGAGACAGTTGGT
TACTCCATGTTGGTCAAGGCTGATGTCATGTTCCCGAAGACCAAGGACGGCAAGTCTCTC
CCTGCGGTCATGAACACTAAGTCTCTGCAGCCATCTGGGGTTCCTATTTCGGACGCGATG
AATATTCAGCAGCAGCAGTTTATGGCTGTGGCAATGAATCGCCAAGCAGCAGAAGCGCAG
AAGGCTGCACAAGCCCAAGCGACCCAGGCTCAAGCACCACAGGTGGCACCGCAGCCAGTT
ATGCAGAATCAGCAATTCCAGGCACCAGTGCCACAGGGCCAGCAGCCAGCATATGCAGGA
GCCCCTGTCTATGCAGACGCGGTAGCTCATGCAACCGCGCAGCAGCAGGCAGCAGCAGCT
CAGGCACCGCAGGCACCTGCTGGGAATCCGTTTAACCAGCCGCCAGCAGTAGCAGCAGCT
CTGGCACCGCAGACGCAGCCGCCAGCAGTAGCAGCAGCTCTGGCACCGCAGACGCAGCAG
CCGGCAGCACAACCTCAGATGGATAACGAGCCACCGTTT

>RXA01909-downstream
TAAAGGCGCAATACACCACACCC

>RXA01910-upstream
CACCGTTTTAAAGGCGCAATACACCACACCCCAACAAACTTTTTGATTGTTGGGGTGTTT
GTCTCAGATCATGAACAGCACAATGTAGGAGAAGATTGAT

>RXA01910

ATGGCATTTCCGCTTCTAGCGGTTGCTGGCACAGTTGCCCCCGTTGCAGCAGGATGGGCA
AAAGATAAGTTTCTCAGCAACTCTCAGAATAATCAGCAGGCCCAGAATCAGCAGATGAGT
TTTGGACAGGTCAACAACAGCGCACAGAATTCTGGATCAGAAAACAGCGGTTTCATGGGT
CAATACGGCAATCTGGGTGCAGGTTTGGCAGGTGCTGCTACAGGCGCAGGGCTTGCGTAT
AGCGATTTTGAAGATGGTCAAAGTTTGTCCTCGAAGGCCCGCAACATGGTCGGCAAAGGG
CTCGCTGGTGCCGGAGCTGGTGTGTTCACCAAGCTTGCCAATGATGCAATTCAGGCCGAG
GGTGGCTCGATGAAGGCTAGTGCTTATTCTGCCATTGCAAGCGGCTTGGGATCGTATCTC
AAAAACGGCGGTCCGGGTGTGATTAAATCCGCGATGGCCAGCGGTGCAGCCGGTTTTGGT
GCGGATAAAGTGCACGATAAATTAGCTGAGTCTGGTCATGAGGGGTTGGCTGATTCCTTG
TCGGGCGCTATTCAAGGAGGTGGTCTTGGTTACTCCACGCTTGGCGGTGTCACTGGTGCT
GGTATTGGCGGTGCGACGGGCGGTCTCGCAGGACTAGCACAAAACTACTTTGGTGGTGGC
GATGACTACAGCAACGCTGGGGCATCTGCATCGGGGTTTAGTGCCAACCAGGTTAATAGT
GAGATCAGCACCGAGATTCCGCAGTTTGCGAATCTTGGTCAACCACAGCGATCCGAGCTT
GAACAATTAGCGCTACCTCAAGAATCACGGTCTGTAGATAAGAGCTACGACCAAGGCTAC
GAAGCG

>RXA01910-downstream
TAAGCGCTTTATAACAACCCCGT

>RXA01911-upstream
AGATGCCGCAGATCACCGAGTGAGCGTTACTGAGATCACTGAGTCTCGATGGGTAATCCA
TATAATTGTGAGCGGGATTCTTAGTGCGCTCGCGGTTCTG

>RXA01911
GTGTTTATTATTGGCGCCGGCTTGCCACTGTTGTACGTGCCGATTTTTGTGACTGTCATC
GTCATGGTGGTGTATGCGCTATTGCGCTATGAGCAGCGCATGTCAGGCACAGTCTACGAG
GAAGCAGATCCTGTCGAAATGGATTCAGTGATCTGGGAGGGCATCAAGTGCGATATTGCC
TCGGATATTGCAGCCCGAGCAGAAGCGAAAAAAGCGAAAAAGCCAGTTGCGTCAGATGCT
GTTGCTGTTGGTAACTATATCGCGTCCTTGCGTCAGCATATGTTGGTAGAAACCCAGCGA
CGTTATCACCACAAGCTTGGTCGTGAGCTGCATAATGATCCAGCGCAACTAGAGGATTAT
GGCTCTGGTCTGCGTGACTGTGAGTGTCGGGCATGTGTGGTGGCTCAGAAATTGGGTGTC
ACGGTGCACGCTCATGGTGTGGTGCAGGCGAGCGCACGTAAAAAAGATCGCGTCATTATT
GGGCGAGCCGATGGTATTGATGTGGCCGGCTGGTGGAACCACCGCCAAGAAGCTCGACGT
AAAACGAGCGCGGCTAAGCAGTTGGAGCGCGATGCACAACGCAAGCGAACCCAAGCTGAG
CGCGATAAAGAGATTGAGCGTAAGCGTAAGGCTCAAGAATTTGTAGCGGAGCAGTCAGGG
AAAGCTGCTGCAGCACAACGGCGGGCCGAGAAAAAGGCTGCGAAGCAAGCGCGTGTAGAT
GAACTGGTGGCGCAGAAACAGGCTGCTCAGGAGCAGAAAACTCACTGTAAGCGGGACAAG
CAGCGTGCGAAGAAAGCACAAGGGCGCAAAGTTGGTGCCGTTGATAATTCCGCTGTGGAC
GATGTG

>RXA01921
CACATTGATATTCAACGCCTCAATGAAAAACAGCTCTTTGTTGGACTCAAGCGCCTGCTT
GGTCTCCTCGGTCACCAGATTCTCGAATCTGATCGTCTCTCTGGTGATGATGCCCATGTT
GATACTAACGAGGATGTACTTGATCTCATTGCCTACAACGTCTCAGACGTGGTGGGCACC
AGACTGCTCGCTGAGGACCCGGTGTACTCCGGCTCTTTCGATCTGCGGGCAGGTCTACTG
AGCACCTACCCAGAGACTGTTTTTGATCATGATGGTACTTTCCGTCAGCCATCCACGCAG
ATGCGTAAAGATCGCCTAACGATTAATACCTCATCAGCTCAGTTCGCAGCGCGTATTTTG
GCGCCATATCGCCCACTCCGCGATGTCCCTGATGCGATTGGCGACATGCCGGTGGTGTCT
TACTTGTACCCGGATGCAGCAGTCGCCGAAGCAACAGGTCAAAAACAAGTCAACGTGCTT
GATGAGTCAAAGAAGTTCTTCTATGACAACATCACCGACCCGGAAGCACGTGCTGCCTTT
GATGAGGTCTTTGCTTTTTACGCTGATATTGAGGGTCGCAACTTCAACAGTCACAATGAG
GCTATTGATACCCAGATTAACCAATTACGTGCTTATCTCAACCAGGTTGTCGCATTCGAT
GCAGCTGGGTATGCGCTCTATGATGTACGTACACGTTTTGAGCAGATCTTCCCCAAGGAT
CGCAGCTACATCAACGATGCTACGGATATGACCCCTCGCGCAGTATCGAGCTTTGACGAT
CTGGTTGCACTCTGTGATGATATTCGCGGTGTACTTGATCGAGGTTTAGAGATCTCATCT
CCGAATCATCATGAGATGGTGGATGCTATGCGCAAGCAGCTGCACTATATTCAGGCATTT
ACCGTGCCTGGGACCCATCAACGCCGCTTCAATGACGCT

>RXA01923-upstream
CCAAAGTGAATACCCCGACTGCAGCAGCGCAAAAGTTCAAGTACTTTGGGATGCAAATCT
AGTAGCACGTCCCATGTTTCTCACACTCTCAGGAGCTGAC

>RXA01923
ATGTCTGCACTTATTAAAGGTTCAGGACCTCATCATGTGGTTGTCTTAAATGGTTGGTTT
GGTCATGCTGCGGGCTGGGGAGCTTTCGCTGACTATCTTGACCTCGGCAACTACACCTGG
CACTTTTGGGATTACCGAGGTTACGGCAACAGAAAAGACGACGCAGGAGAATTTACTCTG
GAGGAAATTTCAGCGGATATCGTTGCATACATCGACTCGATTGAGGCAGAAAAGGTTTCC
ATCCTGGGCCATTCCATGGGTGGAGTGTTCATGCAGAAAGTCCTTGCAGACAGCGCCACC
CCCATCGCTTCACTGGTTGGAATTTCTGCCGTTGCTGCAGCTGGAACACCATTCGATGAG
GATTCTCGGAAGCTTTTCACCTCAGCAGGGCACAACCCGGACTCGAGGCGAGCCATCATC
GATTTCACC

>RXA01930-upstream
CGAAAGAAGCCATAATTTAGAGAGGACAATTCTCTACTATTGGTCAAGGCTCCCACCCGG
TGTCATTCGACATTATTACCGCTCACTCACAATCGATGAA

>RXA01930
GTGATTTCAACAAATGAGATTGAAAATATTCACTCAACTCGTCGGGATATTGAAATAGCG
CTTGATGAATCTTCCACTAGTGAGCCAAAGAGATTTTCGGAAATTTCACACCTTTACCTC
GCACTTGCCGAAGGTAAAATATCCTTTCCGGAAAGCCCAAGTGAACTTCGAGAACTCTAT
GACCATTTAATGCACGGCGAGCTAGGTAAAGAAAATGAATTAGATGGTGAGATTTTCCGC
CAAGGACCCGTGGAAATCCGCGATAGTCGGCAAAAAGTGATTCATTCAGGTTTTTCTCCA
GAATCACAGATCATCGAAGGAATCAACGCAATTATTAAGCTGGCGCACTCAGAAGAGGAA
TCCAACCTTGTTGGCATCATGATGTCACACTTCATGTTTGAATCAATTCACCCGTTTTAT
GATGGAAACGGAAGAACTGGGCGCTACCTTCTCGGGATACAATTAAGCAAAATTCTCTCC
CCTGCTACAGCACTGACAATGTCTTCGGCAATTAATCAATTTCGAAACAAGTACTACAAA
GCGTTTCATGCCGTAGAACACCGATTAAATCGCGGAGACGGAACACCGTTTGTTATTTCC
ATGCTTGAGCTGTTAATTGCAGCGCAAGAAGGTCTCATTGAGAATATAAAACAAAGAATC
GACTTTTTGGCAAGCCTTGAGGACGCCATTAAAACGCTTCGGGGTACCAATTCCTTTAAG
AACCATCAGATCAATCTGTTGTACATTCTCGGCCAGATTCAGCTTTTCGGTAAGGACGAA
ACACTTTCACTTGAATCGGCAGCAAAGTTTCTTAAAGTTTCTAAGGCAACTGCAACGAGG
TATTTTAGAACTCTCCGAGAAATGGAATTAGTTCACGAGGTCAGCAAACGCCCTTTGCGG
TTTGCGCTCACGGATAAAGGTCGTGAGATAGTAGGTCTTGAGGTAAAAATT

>RXA01930-downstream
TGACTCCATAACGAGAACTTAAT

>RXA01931-upstream
TCGATAGGCATGGCGCCGATTCTAGGTCGAACTGATCTAAAGTCCCACCACGCAAAAGTA
ACCAAGGCGTACATCTACCCGGCACTTTAAGATCAGTGGC

>RXA01931
ATGAGCACTTCTTTTGAGTCCATTCCCGGAGTTACTATCTCCGCTCGAAAAGCCTTGAGC
ACTGCGGGGTTTAAAGATCTGGAATCGCTTGCAGGTACCAATTACGAAGAAGTGGCTGGT
CTGTCAGGAATTGGCGCACGTACTTTGGAGCGATTGCAAGCAGCGCTGGTGGAGAAGAGA
ATGAGCTTTGGCGGTAAAGTGCCAGAGGCAGAACAGCGCACCGCGACGTGGACAACGCTA
GATTCTGCAGCACCAGAGGCAACAGAAACCTCAGAATCCCCAGAGTACTTCATTCAAAAC
CTAGACATTCCTCGCAGAATTACCCACGGCCGGTTGTTGTTGGAAATTTTCAACAGAGCG
ACAGGCCAGAAACCTTATGTAGCAGGGTCTTCGATTGTTGGTTATGGGCGAGTTCATTAT
CGCTATGCCACGGGTAGGGAAGGGATCACTATTCGTGTGGGTTTCAGTCCGCGAAAGGCA
AAGATTTCACTTTATGGACTAACCAGTGCGCCTGCGTCTCGAGAACTTCTGAAGAAATTG
GGTAAGCATTCTGTTGGTGTGTCCTGCCTATATATCAACAAACCAGAGGATGTTGATCTT
GAGGTGCTTGAGGAAATGATCCGTATTTCTTGGGAAGCGGAACCTGGCGAATGT

>RXA01931-downstream
TAAATCTCAACCTTTAACAAAGT

>RXA01941-upstream
CCGGACTTGCCGCTGGTTTAGTCACTTTTTGCTCACGACGGTATTTATTGGTCGATTTCA
CCAGCGCAGCGTTGAAAAACGTTGGGCGCCAGTCACCCAC

>RXA01941
ATGGCCTTGACTTCACTTTTGCACCAGCTTGCAGATAAAAAACACAGTGACCTCAGCCGG
GAAGACATCGTACCGCGGGCCTTTACTGTCCCGACCTCTACTGACGCCCACGCTATTCAT
CAAGACTTGGAAAAACTCCGAAACTCCGTACTCAAAGAGCAAAATCACCTAACCACTGTG
TTGGGAACTTGGTCAGAATTCCTCACCTCCAACAGCGATAACTCCGACATTTTGCGTTCC
TCCGCTGAACTTGGGCTCCAATTGGAGCAGGTCCGCGATAAAGCACTCGAAGTGGAACAG
CGTATCAAAGCCTCTGCTCAGGTGGATCTTACGGACCTGGCTCATGAGATTGAGATCTGC
AATCAACACCACGCAACCCTCATCAGTGCGATTCAGGTAAGACTGCAATCGCATACTGCT
GAGCTTCGGGCTGGG

>RXA01941-downstream
TGATTTCTTAAGACTGACCTAGT

>RXA01942-upstream
GCCGCGAAATTCGGTGAAATTGAAGGTATTCCTGCAGATCAGGCAAATTCTTCCACGACT
GTGATCAAGGTCAACGGCAAGAACGAGTAACCTGGGATCC

>RXA01942
ATGTTGCGCATTGGACTAACAGGAGGGATCGGCAGCGGTAAATCTACCGTTGCCGATCTT
TTGTCATCTGAAGGATTTCTCATCGTCGACGCGGACCAAGTTGCCCGCGATATCGTCGAA
CCCGGACAACCGGCATTAGCAGAGCTAGCTGAAGCTTTTGGCCAAGACATCTTAAAACCC
GACGGCACTCTAGACCGCGCGGGATTAGCAGCCAAAGCATTTGTCAGCGAAGAACAAACA
GCGCTGCTCAATGCCATTACCCACCCTCGTATCGCCGAAGAGTCAGCTCGTCGATTCAAC
GAAGCCGAAGATCAAGGCGCCAAAGTTGCGGTTTATGACATGCCTTTGCTTGTAGAAAAA
GGCCTTGACCGCAAGATGGACCTTGTCGTCGTAGTTGATGTTGACGTAGAGGAACGCGTC
CGCAGACTTGTGGAAAAACGTGGCCTCACAGAGGACGACGTGCGGCGTCGAATCGCTTCT
CAAGTGCCCGACGACGTCAGACTTAAAGCCGCTGACATCGTTGTGGACAATAACGGCACG
CTAGAGGACCTTCATGCTGAAGCAAGCAAGCTGATTGCTGAGATTCTTAGTCGCGTGAAT

>RXA01942-downstream
TAGCACTAAAACATCGTCAAAGT

>RXA01944
ATCAGAAACCTTCGACTAATTCTGCCTGATGGCCGGACCCTCACCCCTGCCGGAATTTCC
GATTCTAATGCGTGGCTCAACATGGGAGACAGCGCTGGAAAACTCGATTTCTTCGATGCC
ACCTTCGCCCTCCCTGAGGATGCTTTCACCGGTGTGGCACACGCATGGGATACCACCCAA
AGCACAGATGGAGAACACCACATCACCATTTCCCGCGAAGACGGCGGGGAAATCAGCCGC
ACCATCCGGGTTGATAATACTGCCCCAGAACTCACCGTTTCTGGAGTTGAAGAAGGACAA
GAACTGCGCGGCACCGTAGAAATTGATGCCCAGGCAACCGATGCGGGTGCGGGCGTGAAG
AGCGTCGAGACGCTTCTCGACGGC

>RXA01944-downstream
TAACGCGTGCAACTTCCACTAAC

>RXA01945-upstream
AGAAGGACAAGAACTGCGCGGCACCGTAGAAATTGATGCCCAGGCAACCGATGCGGGTGC
GGGCGTGAAGAGCGTCGAGACGCTTCTCGACGGCTAACGC

>RXA01945
GTGCAACTTCCACTAACCACCGGTTCCATCGCTTTGGATAAAGGTGAACACACCTTGGTT
ATCCGTGCAGAAGATGAAGTAGGAAACCGCACCGAGAAAACCATCACGTTTAGCACTCCG
GATGAAAACCCCATCAGTGGTGACTACGCTCCAAGCAATGGGGCCACCGTGGGCGTCGGT
GACGTTAAGTTATCTGCACGAGCAAGTGATCCAAGTGGCGATACTGTCAAGATGACGTTC

CTGGAAGCCGATTCACCAAAATTAGATAGTGGTCGCGTCCGAATGTCATCAGGAACGGTA
GAAGATGCCGGAAGTGTCTCGCGCGCCGAGGCGAAAATGTTGGAGAGGGGAGACGTCGAG
AAGCTATCCAGCCTGGATGGGCTGGGCATGGAAGTTACCTCCGACGCCGCACTGCCGTAC
CAGCTTTTTGAAGTCGATGCGGCGGATGCACTCGCGGCCGACACTGAAGTGCGCCTGAAT
TGGGCGGGATCCGCCGATGGTCGCGCGCAGGTGATCATGTATGTTTTCGATGGCGAGGCG
TGGGTTGAGGTGGATCGTCACTTGACCGGCGATGAGCTGGAAGAGTTTACGCTGCAGGGC
GTCGTCAATGCGGAAAAATTTGCAATCGGCGGCACTGTCACCGTATTGATTCAGCACTCC
GAAGGCTTCGCCGGTGCGGATCATTCAACTAGAAATTCCGACGTGACCGCAGCGCACCCG
GATGATGTGGCTCGCTCTGAGTACGATTTCACCCTCGCGTGGGAATCTGACACCCAGTAC
TACAACGAGGAATTCCACGAGCACCAAACCAACATCCATGACTACGTGCTCGCCGAACGG
GAGAACAAGAATATTCAGTTCATGTTCCACACTGGCGATGTTGTCGACGACTGGGATCAG
CCCGCGCAGTGGGCCACAGCCAACCCCGAATACCAGCGCCTCGACGACGCCGGCCTGCCA
TATTCTGTCCTTGCCGGAAACCACGATGTTGGCCACACCAGCAATGACTACACCGAATTC
AGCCGACACTTCGGCGAACAGCGCTACGTAGACAACCCGTGGTACGGCGAATCCTACCAA
GACAACCGAGGGCACTACGATCTATTTTCTGCCGGCGGAATTGACTTCATTAACGTAGCG
ATGGGCTGGGGTCCAGACGACGAAGAAATCGCGTGGATGAACGAGGTCCTGGCCAAGCAT
CCCGAGCGTGTGGCGATCCTCAACCTCCACGAATTCATGCTC

>RXA01957-upstream
ACCTCAACTCCACAGAGCGTTGTTATCAGATGCTGATATGGCTCGCCTTGCAGCACAACT
GACCGACAAACACTAAAACCTCCACAACAAGGACATCATC

>RXA01957
ATGACTACTCGCACCGTATCTACTTCTGCACCCCATGTCACTGTCAACATCAATACCGCG
CACAACAAAACACGCACTGTTACCAATGGCGCCAGAAAAACTAATGCAGAGCGTGGCAAG
AGCTGCATCTCATTTCGTGTAGGGCCAGAATTGTTTGATGAATTCAAAGCGACCTGCATC
GACAACGATATTTCCATGACCAAGGCGTTTGAGAAAGAGCTTCGCACCTGGGTTGATGAG
CACAACGCTGGTGCAACAAAGAAAAGAAACACCCATCGCACCTACGTACAAGCACCCGTT
GGTACTGTCGCCACCAGCTCTATTCCAGGTCTTGGGTTATTTACTGTGTTCAAGAAGAGC
TCTGATCAGATGTGGTACGACCTGGAAAGCAGCCCGCTGATCGCACAAGAGCCCATGTCG
AATATGGACATGCATCGTAACGGCTCTTTTGAGCTGCACCTG

>RXA01957-downstream
TAGATCTCTCTCTCGACCACACA

>RXA01958-upstream
ATATGGACATGCATCGTAACGGCTCTTTTGAGCTGCACCTGTAGATCTCTCTCTCGACCA
CACACAGCTCTCACCACCTCCTAGAAAGGACGGTTTCACC

>RXA01958
ATGTCTAAAAAACGCGACCACCTCACCGTCATTCCTGACCTTGAGTCACGCACCCATCAC
AGCCGCAGTACACAACCGCCAACTACGCTGCCCGCACCACAGCTGACTATTATCACCGCA
CCAGACAAGCATCAACCACAGCTTCGGGTTGTTAAAAACACCACCACCCCATCTTCTGTG
CAGCCCTCGCCGATCAACTACAGCTTTACTGATCCTGTACTTCGCGAGGCTCACTATGCA
TTCCAGCACAGCGAACTTGCCAGGCCAACAGTCCTGGACTCACACTGGGTTCGTCGCGCA
CAAGAAGAATTCGACACTGAGCATAATGCTGCCTATGTCCGTGCCGCTGACCAGCTCTTA
TCCCCTTTTGATGCCTACATCCTCGACAACGGCGATGTTTACACCAAGACCCCACGTGCC
ATCAGTGCTGCTGAACAAGAAGAAATACTTGAGCACTTGCACGAACACCATATCTGCTGG
GACGAAGAAGCTGAATTCCTGCTGCGC

>RXA01958-downstream
TAAAGGTTGCCACTGGTTTCAGG

>RXA01959-upstream
CCCAACTACTATGCACAGCCCGTAACCATCGAGCCGGCTAAAATCTATCAACAGAAAAAC
CACTGCCTATTTGACCATTCTTGTGCAAGAAAGTACACCT

>RXA01959
ATGCCCCACGACGTTTACGATGTCGAACACATCATTTCCAAGCAACCTTTCTGCTCCATC

TTTTTCCAGCTCCCCGCTGCAGCGCTGAAACCTACTATTCAAAAAGCTGCCACCAACCGC
GACCTTACTAAGCTCAACACCGAACAGATCGCTGAGAACCTACAGCGCTACCTCGACACC
TACAGTGTCATGTCTCACCAGCGTGTCACCATTGAAGAGGTCACTCATGTGCGCAACCCT
CATGAGCCTGATTATGAGTTTTCACCACAGTACGGTGCACATATCTCGCTCATCGGTGAG
TCTTATGCTGTGAACACGGCCACCAACGAGCCTTATGCCACCGACTCCGAGGGCCATCCT
CTCGCACTGTATTTTGAAATG

>RXA01960-upstream
TCCAGATTGATCGTGCCAACAAAGACTAAGCCACTCTAGCTAAACCAACTTACCCCACCC
CAACACCCCATGAGGCATCTGCTTCATGGGGTGTTTTGCT

>RXA01960
ATGCCGCAACACTTTTCTCAAGAAAACTACAGAAAGGCCCCCGTCATTATGTCTGCACCG
CTCACCATTCATGATCTGCTGTCCACCAATTCGAAGCTTAACCTCAAGTGGCTGACCTGC
ACTGTCTTGAACAGCCCAAATCTCCCCGAACCCTGCATCACGGTTTCTGTGAACCACACC
GAAGGCATGTCCCTGGTCTCTTTCGAAGGTGGTCACGGGCTCACCGAGATTGCCAACACC
CAGCTAGTGCCTGTGCTTGAGCTACCAAAGTTCAATCCTTTTGAGGCACTTGCTATCCAC
CTTGAAGCCGCCAACAAC

>RXA01960-downstream
TAAGAAAGCATCCTTCATGACTG

>RXA01961-upstream
AACACCCAGCTAGTGCCTGTGCTTGAGCTACCAAAGTTCAATCCTTTTGAGGCACTTGCT
ATCCACCTTGAAGCCGCCAACAACTAAGAAAGCATCCTTC

>RXA01961
ATGACTGACAACGCTGACAACACCACAGATAACGTAACCAATAACTCAGACACCAATCTC
GATTACAGCTTCGACCCGCTCCCTGACGAGCCCTATGCCTACGGCTTTGAACTGGTCGCT
GCTGATGCACACTCTGACTCAACAACAACCAGCACCGATACCCCAGAGACTGTCGCTGTG
GCACTTAAAACCCGCGAGGACACTATCAACTGGGTCAACACCCAGCGTGCCGAAGGTAAA
CCCGATGAAATTCGTATCAATAACCCAATTCGATCAGAGCGTATTGCTGAGTTTGTCCAC
GAAATGATCATGCATCACGGCCTCGTAGCCTGCATGGAAGATCTCGCAATACTTATCAAG
CGCGACAAGCTCACCCAGCTGGAAGCCGAAAACGCTATCACAGCCTGGCACAACCTCACC
AAAGAATCCCTTGGTCAGATCATGGGGCTCTTCTATCAGTACGTCGAAAACAACACAAAA

>RXA01961-downstream
TAGGAAAGAAGAAACACCATCAT

>RXA01962-upstream
AGCCTGGCACAACCTCACCAAAGAATCCCTTGGTCAGATCATGGGGCTCTTCTATCAGTA
CGTCGAAAACAACACAAAATAGGAAAGAAGAAACACCATC

>RXA01962
ATGTCTGACAACACTCAGGACAACCCTTTCTCCATCCGCTACGCACACCCTGACCACCAG
CTCGCTCTTAATGAGCTTGTTGATACTGCCGATCTACCTGCACCAACAAGCTATATGAAA
AATCCCTGGTCCGGGGACAACACGCCTATCGCCGAGTGGCGACGCGAGCGCATCACCCAG
TGGCAGCGCACCGAGATCATTGTCAATCAACGCGATGATGACGATCTCATTCACGTCAGC
TTCCCGAAGCTCGGCCAGCACATTCAGCTCAACACCGACGATATTCTCGCATTGGTCGCA
GCCTGCGTCACACCCACTGCTAACGACATTGAGGCAACTATCGAAGAAAATCTCCACTCA
TATCCGCACGATACGGTCATCATGTTTAACGCAGATGATCTAGATGATGCCCTTGGTCTC
GTTGTTGCCGTCAAAGACGCGAGCGGGGAACACTCACCGCGCGCTGTCTGGCGCACCAAC
ACCGATCATGGAGCTCTTGACGAGACTGAACTCGCGCGGCTCATTCTCAAATTCGGTGGC
AGCTTCGATGACTACGGCGTGCTGCAACAT

>RXA01962-downstream
TAAACCGACTCACTAAGCACCGC

>RXA01963-upstream
CAGATTTTCTCTGTGTGAGCTGGGGTTTTCTGCATTTCCCACTTGTTTTTCTCCAACACT
CCACACACACACCTTCAAAGAAGAAAGTTCGAAAGATTCT

>RXA01963
ATGAAAAACCGTAAAAAAATCATGTCTACCCTCACCACTGTCTGCGCCGTACTGGGTATA
GTTGCAGCTCATCCATTCCACGCCTCTGCTGTCATCGGCGGCTCTGTCCCATCAACTGAT
TCCGTTGCCAACGCTGTCGCAAAAATCGGACCAGGCGCATTGAACTGCAGCGGTGTCATG
ATCTCACCATCGTGGGCACTCACCGCACGCCACTGTGTCGATGACATCAACATACTCGGC
GACATCGACACCATCACGCCTATTACTCCAGGTATTCATCGCAATGAAGGTAACTATATG
GGTGAGGTTTACCGCGCACCGTCCGGTGATCTAGCGCTCATTAATATCAACGGCGTGCAC
AAGGGCACCATTGCGCAGCTCCCCACACAAGAATATCCACTGGGAACCGCTGCACAGTCA
GTCGGTTTTGGTGGCGGTGGTGTCAATATCCGCACCGCTGAATCGGTCAACATGATTCTC
ACCGACATATATAGCGTGAGGTCAGGGAAATTCCATCACGGTGTCGGTCGATCACACTAT
CTCCTCTTTGATTATGACAGTGCTGAAACTGGTCGAATCCACAAAGGTGATTCTGGGGGC
CCCATCTTCATTGGTGACGAGGTTGTGGGCATTATGTCTCACGGCACAATAAATAAGAAC
GACGGGTCTTTTGATGACGAATCC

>RXA01964-upstream
AGAGCCAGATGATGGCTTTGATATGGATGATGTCATGGGCCAAGCGTTCGGTCGCTAGCT
CATACCTTGTTACAACGACACTTTTTAAGGGAAGAAGATT

>RXA01964
ATGACCAGCGCTGTGAATGTGCAGAAGAAGACCACACAGAAAGTACTTAAGCCCATTAAT
ACGAAGAATTACTCTGCGACAGATGCAGTACAGACAGGCCAGCACGGATCTGCTTTAGGC
TCGAATATCGGTGTCTACACCTATACCGCTGGACTCGATATTGGAAACGGTTATGTCAAG
GGCATTATCGAGGCAACCGGTGATACGACTGGCACGTCTGTTGATGTTATTGATATGCCC
TCTGCAGCAACGCGCATGAGCCGGCCAACGGAAGTTCCCGAACCAGATGACACCGCTGTT
GCTGTCACCGGTGCGGATTTCTTCAACCACATTGATACCAATTTCAATTCGCCTATGGTG
AAAGGTAATTATCGTTACCTTTGTGGCACGCGCAGCTTGTCTGCACGAGGTAGCTTGGAG
GAATTTGATCTGGTGGGTAACCGCTCCAAGGCGGAACAAGAACTGAGCAAGGTGCTGGTC
ATGGCAGTACTTGCGGCCAAGGCTGTGAAAGACTTTGTGGCAGCACATGGTCGAATCCCA
CAGGTTGCTGTTGAGGGTGATCCCGGTGTGCTGCGTGTGCATACGTATCTTGCACTTGCG
TTACCGATTAATGAATATGTGGGTCACCGTCATGGGTATAAGGCACAGTTTATGGGTGAT
GGGGCAGCGAACCCGGCTGTGCATGTGGTGACGGTTAACAACTTTGAAACCCCAGCAACG
GTGCAGCTCATCTTTGAGCGTGTCGAGGTCATTGCCGAGGGCGCATCGGCACAGTATGCC
ATTACCGCAGGTGGCGAAGTACTTATGAACGGAATGCTCGCCGATGTACGCTCCAAAGGG
CTTGCTCTAGAGGGCGTGACAGCAGGTGATGTGCTACAAGCTCGCCACACAATCGGTGTG
GATGTGGGTGAAGGTACTGTGAATTTCCCAGTCTTTACGGATGGGCGGTTTAATCATGAT
GCTTCACGCGCCTATGACAAGGGTTATGGCACCGTCTTGGAGTCGGCGATTCAGGCTATG
GACGATGCTGGGTTGGCACACAACTTTAACTCGCGTAAGCAGTTGGCTGATTATTTGCAG
CGACCACCGAGTGCACTCAAGCGGAATTTCTATACCCGCGTGGAACAGCATGTTGATCAG
GAGGCAGTGTTCTTTGTTCAGGATGTGGCTGCAGAGTTCGCACGAGTGTTGAGCGACGTG
GGTGCTCTTACCGAAGTAGCCTTTGTCTACGGCGGTGGTTCCGGCCCGCTGCGTGATCGA
CTGCATGAAGCGTTGCTGATTAAGGCAGCGGAGATGGGTTCGGAAGATACGTTCCCGGTG
CTGTAT

>RXA01965-upstream
ACTTCTATGTTACTATTAAATTAGTCAATAACGTTAGTCATAAACAATGCAGTTATTGAA
GAGAAACTTCCCGACACAATGTACGAAATGGGGGTCACAC

>RXA01965
ATGGCTCAAAAACAGGACACGACACATGTATCAGAGGACGATGCCCCGTGGCGTAATGTG
CGTATGCGCTTCCCAGAAACAGACGCTATCGTTGAGCGGTTTTTGGAAACACAGGGTGCT
CGTGGCATCTCGCTTGCGATGCGACAGCTGATCTATTTGTTTGTCGCTGAATACGGTGAT
GTAGAGGTTGCTACCGTTATTGGCCTCAAGCTGGTGGAAAGCCTGCAGGCAGGGGCTGAG
GGTAGTGATCTTTTTGCTCAGCTCGCGGCCGGGGTTGCTGACGTAGACGCTGTGACTACA
CGCAAGAAGGCACCGCAGCAGATAGCACCGCCATCGACCACAACCCGTGCACCTGATCAG

GTAAATGAGTTTGTTGCCGAGGCGGAGAGTCAGCCGGTTGAGGAGTCAGTTGTTGAGGCC
AAAGTACCCAAGCAGCAGGTAGCACCACAGCCGGCACAGAAGCCGGAGCAAAAACCAGAA
CAAAAGTCGGCGCAACCAGCACAGTCAGAGCCAGATGATGGCTTTGATATGGATGATGTC
ATGGGCCAAGCGTTCGGTCGC

>RXA01965-downstream
TAGCTCATACCTTGTTACAACGA

>RXA01966-upstream
CCCTGTTATGGGCTGGGTTTATAAGAAGATGGGTTAGTTTTTAAAA

>RXA01966
GTGTCTGAATCTGAAAACAACACAACACCAGCAGTCGCAGCTCGCGATGACCGTCTGGTC
TGGGTCGATCTGGAAATGACTGGTCTAGATTTGAAGCGCCACGTGATCGTGGAGGTTGCG
GCGTTGGTCACTGACGCTAACCTCAACGTTTTGGGCGAGGGCGTGGACTTGGTTGTTCAC
GCAACTGAAGAAGAGCTCGCGCAGATGGATGATTTTGTCACCAACATGCACGAATCCTCT
GGGCTGACTGAGCAGATCCGGGAATCCGCGGTCACGTTGAAGGAAGCCGAAGATGCTGTG
CTCGCATTGATTGAAAAGCACTGCGATCCAGCCCATCCTGCACCGCTAGCTGGTAACTCC
ATTGCCACTGACCGCGCGTTTATCCGCGAACATATGCCACGTCTTGATGAGGCCCTGCAT
TACCGCATGGTGGATGTGTCCTCGGTGAAGGAATTGGCGCGTCGCTGGTACCCACGCGTG
TACTACAAGCAGCCGGAGAAGGGTTTGGCGCACCGCGCGTTGGCGGACATTGTGGAGTCG
ATTCGGGAGTTGGATTACTACCGTCGCTCATTTTTTGTTGCAGAGCCTGGTCCTACCTCT
GAGCAGTGCGCAGATGATGCGCAGGCAGCGGTGGACCGTTTTGCACCCTACTTTGAT

>RXA01966-downstream
TAGAGGGTTTTAAGCAGCCTGGT

>RXA01968-upstream
GAACTGGCGCTTTTTAAGTTGTGGCAATTTTGCCAGAAGGGCGTAACAGGTGCGGGTTTT
TCGTGGTAGGCGCGGAGCAGTAGCAGGATCTTTTCTTGCA

>RXA01968
GTGCTGGCAATTGGTTCACTGGCGCTTACGGGTTGCACAATTGAACGAAGCGATGCGCAG
GAGCAATCCTCGCAGCAAAGTACAGAAGTTGAAGCTGAAGAAGCTCAAGCTCCTGTGATT
TCTGTTGATGATGGTGATGAGGATGTGGACCCTTCGGAATCTGTCATCGTAAAGTCGATG
GGTGACGGTCTGAGCAAGGTCACCATGACTAATGAAGAAGGCTATGAGGTTGAGTCAGAG
CTTTCTGACGATGGCCGTAGCTGGACCACTGCGGAAACCCTTGGCTACAACCGCACGTAC
ACCATTAAGGCAACCGATAAGAACGGCGAGACCGCTACTGCGTCTTTTAGTACTGCAACC
CCTGCAGCTACCACAAACGTGGCGCTTTCTCCGCTGGCTGATTCTGTCGTTGGTGTTGGC
CAGACTATCGGTTTCCGTTTTGGTTCCCCTGTGAAGGATCGCAAGGCGGCTCAGGATGCT
ATTACTGTGACAACTTCACCAAAGGTGGAGGGTGGCTTTTACTGGTTGAACAACAGTGAG
TTGCGCTGGCGTCCAGCGGAGTACTGGGAGCCAGGTACTGAAGTTACGGTCGAGGCTGAC
ATTTACGGCAAGGATCTCGGCGGCGGTGTCTGGGGCGAAACTGATAACGCCACCAACTTC
ACCATTGGTGACAAGGTTGAGGCTGTGGCAGATGATGCCACCAAGACCATGAGTGTGTAC
AAGAACGGTGAGTTGCTGCGCACTATGCCGGTATCCTTTGGTCGTGACACCTCTGAGTGG
GCAACGCCAAACGGTACCTACATCATTGGTGATCGCAATGAGTCGATGATCATGGACTCC
ACCACCTTCGGTCTGGGATATGAGGAGGGTGGCTACCGCACTCCGGTGAAGTACGCGACC
CAGATGTCCTATTCTGGAATTTACGTGCACGCAGCACCGTGGTCTGTAGGTGCGCAAGGT
AGCTACAACACCTCACATGGTTGCATCAATGTATCCACCGAAAATGCTCAGTGGTTCCAG
GAGGCCGTGAAGCGCGGTGACATTGTGACCGTGAAAAACACCATCGGTGAGACTTTGAGT
GGCTACGACGGACTGGGGGACTGGAACATTCCATGGTCTGAATGGAGCAAGGGGAACGCG
GATCAAACTTCGGCGTGG

>RXA01968-downstream
TAACTGCGGAAGTCGCAGGTAAA

>RXA01969
AAATGCCAGCGTCGTGGTTTAAGCCAGGATCCGTTGTATAAAAACCGGAATTCCTTGTTG

ACCACGCAGAAGTGGTTTAGTCCTCGTCAGCAAGAAAGCTTGGAGCAGTTGTGGGCGTAT
GACAAAGCCTACGGGGCGTTAAAGCTTGCGTGGCTTGCGTATCAGGCGATTATTGATTGT
TATCAGATGGGTAATAAGCGTGAAGCGAAGAAGAAAATGCGGACCATTATTGATCAGCTT
CGGGTGTTGAAGGGGCCGAATAAGGAACTCGCGCAGTTGGGTCGTAGTTTGTTTAAACGA
CTTGGTGATGTGTTGGCGTATTTCGATGTTGGTGTCTCCAACGGTCCGGTCGAAGCGATC
AACGGACGGTTGGAGCATTTGCGTGGGATTGCTCTAGGTTTCCGTAATTTGAACCACTAC
ATTCTGCGGTGCCTTATCCATTCAGGGCAGTTGGTCCATAAGATCAATGCACTC

>RXA01969-downstream
TAAAACAGGAAGAGCCACTTAAG

>RXA01973
TCCGCGATGTCTAAATCGCAGGATGATCGAAAAATTGCAGAGCTTGAAGCACAGTTTCAT
AGTCTTGGTCTTAACAACACTGAACTAGTTACCCTTGATGATGCAGCGTCGCTATTGGGT
GTGCCGGCAGGTATTCATCAGATTGAGGCCGAGGTGATGTTGGTGAATTTCGGTGATGGT
GCAGATGGCATGGGCGGTGACACGACGAAGTTTTTGCATTATCAGCCAGATGAGTCGCAG
CCTTACGTCTGGGTGATGAAGCGGGTGTATTCCTTTGAGGCGATGAAAAAGCTCATGGTC
GGGTTGTTTATTGGCTTGTGCATACTCATCGTGGGTGGGCCAGCTTTAGGGCTTATGCTC
GGTGGTTTTATCGGTGTGCTTATTGGTCTATGTCTAGGTACTTCCGCAGCCATGATTGTT
GGCCCTTTTGGGCTTATGCGGATGAAGGCGTATCCACCATGTATGGACAGTCCATGGGTG
TATATGTCACAAGAGCAGTGGCGCACCGCTATGGGTGCGGCACAGCAGACCGAGGTGTCT
TTTGTTGAGCACTGGGACAATATTTACGGGGATAATCTGCAT

>RXA01973-downstream
TAACAAATTAGTTAATAAAGTGT

>RXA01974-upstream
ACAATATTTACGGGGATAATCTGCATTAACAAATTAGTTAATAAAGTGTAGTATTTAATT
AATTATTAAATTCAATTAACTTTTTTGTAAAGGTGGGAAG

>RXA01974
ATGACCCAGGTTGTGGCGGGTACGTTGGTGGGAGAGTCGATTAATCGTGAGATTGATGAA
GACAAGTACCCTTATTTGAGCTCGTATGCAGCGCCTGTTGCTGTACCGGTGCGTGAGATT
ATTGGGCGCGAAGAAGAAGTCAATAAGATTATGGCCGCGCTGATGCGTCCAGAGATTTCT
AATGTCATGCTTGTGGGTCCTGCTGGTTCGGGTAAAACTACGTTGGTACAGCAAGCACTG
GTGAAAGATCCAGAGCGTAACTACATCGAGGTCGATGTAGCGAAAATGGTTGCGGATTTG
AGCACCCCGGCGCAAATGGCTGCGCGTATTAAAGGTGTGTTTGAGGACGCCATTGCCTAT
CGCAAGCACGAAGGTCATGAATTGGTGCTGTTCGTTGATGAGTTTCACCAAATTGTGCAG
CTGTCTAATGCTGCGGTAGAGGCAATCAAGCCGATTTTGGCGATGTCTGGTGTCCTTGGT
GTGCGCGTTATCGCTGCGACAACTCTCGAAGAATTTCACGAACACATCAGGCCGAACCAA
GCATTGACGGAGCGTTTGCAGGAAATTCGACTAACGCCGACCGATCAGAAGACCACTGTG
GCGATTTTGCGTGGTATGGCAGATCGTTATGGCGTAAGTGATCAGTTCTATGACGACCAC
GTTTTTGAGCAGATTTACTCCACCACTGAGCGTTTTATGCCGAGTTCTGTCCAGCCTCGT
AAATCCATTCGTGTCCTTGATGCGATGGTTGGTTGGCATCGACTTTCCGGCAAGCCGATG
GATATGGATCTGCTCGGTGATGTGCTCCACGATGCTATTGGTGTCGATATTGCATTCAAG
GTCGATGGTACGAGCATTAAAGACAAGCTTGATGAGAAGGTAATGGCGCAAAGTCTTGCC
ACCACTGTGGTAGCACGTCGTTTGCAGCTGGTGGTGGCGGATCTTCATGATAAATCACGG
CCACTGTCGAACTTCTTGTTCACCGGGCCTACTGGTGTCGGTAAAACAGAGCTGGTCAAG
CAACTAGCACGGGTGCTCTTTGGTGATGACACTGGGCGATTGATTCGTTTTGACATGTCA
GAGTTCGCCTTAGAATCAAGTCTTGACCTTTTCAGGTCTGAGCTCACTCGTCGTGTCGCT
GACCAGGGTAACGCTATTGTCCTGCTCGATGAGGTTGAGAAAGCTGATCGAGCTATTGCG
CGGTTGTTACTGCAGGTACTTGATGATGGCCGACTATCTGACGATTACAACCGTGAGGTG
AGTTTTCTTAATACCTATATCGTCATGACAACTAACGCTGGTTCTGAGATTTTCGAGACA
ATTTCGAACTATGCCACTGATGACACGGGCGATGGTCGGGCGATCAAAGACTTTGTGAAA
AACATTCACACGTCGATCAAGAATAAGGGTTTTCCACCTGAGCTTCTTGGTCGTGTAGAT
GAAATTGTGCCT

>RXA01976-upstream

GTGATTCCGGGCGTCTTCGCTTAGAGTAAATTAAACCGTAAAAATAAACTCAATTAAGTT
AGTATATTAATTACTTGATTTAATTGAAGGGGTTTATAGT

>RXA01976
ATGACGCAAACACTTGCTGGCGAGCGCAGAATCGTCACCACGGCAGAGCTTAAAGCGATG
CTGGCACGAGGGGATAAGGTGTTTCTGCCTGGTGTCGCAGCGCGGGCGCCAGAGATCCTC
GACAACTTCGATCCAGCAGATCGGGCACGTCTCGACGTGCCCGCAGCAGACAATGAAATC
GTCTCTGTAGAATTCTCCCGCCGCGATACCGTGCAATGCATCAGCATTGCCGACCGTGAC
CATCTCTACATCACTGACGATATGATCCCGACCCACAACACGTCCAACATTATCTTCTTG
AAATCCACAGACGAAACAATGATTAAGACGTTGGTGGATTGGTCAGGTGAGCGACATGTT
GTACGCAGAAATTCAAAGACCGTAACCCGTGACTTGGCACAGTTAGTTATGCGCACCGAG
GGTAAAGTGTCGTACACGTCTGCAACTGAAAAAGAGCCGGTGGTGTCTTATAATGACCTA
AATACTCTGCCATCGCAGAACGCCATCGTCTTCCGTGCGGGTCAGTATCCGGTGTGGTCA
CGCAATGAAACGATTTGGCCGATGTCGTTCATGTTGTTTGCTAACCAGATTATCCAACCG
GGTCGCGAATACTCGTTGCAGACTATTCCAACACTGTCGAGCGCTAATGAATTCGATGTG
AATCAAAATGCACCGGACTTTATGGCGATGCTGGAAAAGCGCATGGCGCAGTCGATTCGT
ACTCAGCGTGCCGTCGATATTTATAAAAAGGCGACTGGGCTCGATGACTCTGATATTGCA
CGCCTGGATATGGATGTGTATTCAGCAGAAATCATGGACATCGTGGACACGATGATCGCG
AAAGATGAGTACGATGACACGCCGGATTATGACGAGGGGGATGAGTCTGTCATGAATGCT
CGTGATTTCATGGAGTCTGAATATGACGTTTTTGATGATGAGTTCGAAGACAGTGCTCAG
GGCTTCCCCGTGGCTACTGGTACGAAGGTGAAAAAGAAATCTCTGTCTGAAGAAGCAGAG
GTCAATGATGAATTCATTCACGATCAGGAGAATGCAGAACATAAGCTCGCTGACATGCGG
TTGAAGCGTTATGCCGAAGGCAAGGTGTCACGAGATATGCTGGCTGATCAATTCGGCCAC
ATCCTGCAGGACTCACTCGAAGATGAGCTCACTGCAGCCTATGATGAGAGCCTGCACGCT
TTTGCTCAAGATCCGAATTTCCGGGTGACTGCTAACAACGGCTTGGTTAATGCTGTCGAT
GGCACTGTGTTGATTGAGGCGTTGTCGCAGGAAGATATTGCACTTATGCGCGCGCAAGCA
GGAGTGGAGCAGTCGCGTGTCTACTCTGAGGGTGAAGAAGCTCTATCTGGCACAGAGGAT
GATCCGCTGTCTGCTATGGGTAAATATAAGACCACCCGAGCATTCCGCATCATGCTGGTG
GAGCTTCCGCATTGGCGTGATCTCGCCCAGGGTCACTTTGATAAAGAAGTCGCGCGAGCC
TTTAGGCGTATTGAAGATGCT

>RXA01976-downstream
TAAGTGTCGTGAGCGATAAAAAA

>RXA01977-upstream
AAGTCCAGTGACTAATACCAATAGAATTGAAGACCACTACCTCAAGGGCGGACGTGGCAG
GGGCACAGACGATCCTAGCAATATGCAAATTGCAGGAAGT

>RXA01977
ATGTTGCGCACATTATTCGTCCGCAAGATTAGAGCGCTGCTGCTGGTTTTGATGATTGCG
CCAACTCCATTGGTCGAAGGGCTAACTTCGACTGCAATGATTGTATCCGTAGTAATCCTG
GCGATCTACATGGCGATAACAATGTATAGAGTAGTGCACGGTCGCCATGAGTTCGCGCAT
ATCGCACGTCGCATGGCGCTTTACGTCAACAAGACTTCTTCTAGGTTCAGTGTTGTTATT
GCTTATGTAGTATTAATTGCTATTTATGCGCTACTAATTCCCGGACTTGTCTACTCTGTT
ACATTTGGATTCATCGTCCCAAGCACACCTAATACGTTTAGTGATGCACCTGCATGGATT
ATGTGCGTATCGCTGCTGCTCATTGCAGTCGCCAGTTTCATCACATCAATCATGGATGAC
TTTATTGATGGCATACTCACTGATTTTTATGACGAAGATAATGCTGATAGCCCCGATAGT
CCTGCCGAGGATATAGCCACCCGTCCTGTCGAGAGCGCAACAACAAGTGCTCTTGCTGGA
TTTGCTGTTGGTTATATTTGTGGGCGCTTTAATCGC

>RXA01977-downstream
TAACACTTAAAACACTTCTCAAC

>RXA01982-upstream
TGCCGCCGACCATGAGATGATCAAGCGCTTTTTCACCCTGCACCTTCGCTAAGACTCTAC
CTTCACCCAACTCATCATCTACTGAAAGAAGGCTTCTGCT

>RXA01982
ATGGCTACCACCAGCCTCCCCACGACGATTACACCGGATTCCGAGGAGACCGTAGAAAAG
CGTCACTCCCTGACCCCGATCCTGGATTCACTTCCCTGCGAGTCAGTTCCCTATGCTCTG

GCTGCAGGTGAGGGACAACAACACCAGCTTGGCCCCTACCATCTCACAGTTATGTCCCGT
CCCGAAGACAACGGTGGAATATTTTCGCTGGCTCGTGTGAGCGCAGGCAAGACTCCCGCC
ACCCGGTTCTTCTCTGTCGCAGGACCGACGTTCCTCTACATGATGGAGGGGCGGTTGACT
CTCTGGTTCGCTGATGGACGTCAAGAGATCATCGCTGGCGGCAGTGCCACCATTCCTACG
AATACGCCCTGGTCCTTCGCCTGTGAGGGCCTAGTAAATTCAGCTCTAGTGTACTACTCA
TCCTCGAATGCATTCCTACACGCGGCAGAGAAACTTGGCACGTCCTCGTTCTCCCACACC
TTCCGCGTCAGTGGCGAGGTCACAGGGATTCCCTACGAGGAACTGGAGGATTGCGGATTC
ACATTCTATGAGCGGGACCACCTTGCCGAGCTCGGGCCGCATTTCGATCGCCTCCCAGAA
GATATGAAGGCGTTTGCCCTGAACGATGGTGAGGGGGACCGGCTTGAGCAGTTCGAGCAG
ATCAACAGCTTCGTCTGCCGTCCGAGACACACCGGAAATCAGTTCCTCGCTATGCAGACC
AAGGGTGCCAAGACGCCTTATATACCTCGTCATTTCCACCGCCTTCACACCGAAAACTTC
ATCTGTCTGGACGGGCGCGTCAAACTGCACGTCAACGGTCAAGAGATCATCCTCTCCCGT
GGGGATTACGTTCATGCCCCAGCCGGAACCATCCACTCTTTCGCCTTCGCAGGGCACAAT
ACCCAGATGCTGGGAGTGCTCACCACAGAGGTATTCGAGAAGTTCTTTGACTACATAAAC
ACTCCGACTAATGCTCGAGTTCAGCTGGAGGACGGGGGGAAGCCATTTTTTCCTGCTGAA
GCATTCGCGAAAGTCCAAGCTGAACTCGATGTCGTGGTGGTCGGCCCCCCACGAATTAGT
ACCCTGGATGTTGTTACAAACTCGCGTTTCGAACCAATTAACAGAACTATCACCTATCGT
GCGCTGGACGCTAACCAA

>RXA01982-downstream
TAGTGAGTGAGCCGAAATCCCTG

>RXA01987-upstream
GGGTTAGGAGAGGGGAAATCCCCGATGTGCTCTAGGTTCTTATTGGCGATGATTGAAGAA
GAAAGAAAAACTCAATCAGCCATAAAGGAGCTTGATCCCG

>RXA01987
ATGACTTTCCCAGCACAATCTCGACGACTCGCCCGAAGCACCACCGACAAATGGATCGGC
GGCGTCGCTGGTGGCCTCGCAGAGACCTACGGTTGGAATCCGGCCTATGTGCGTCTCGCG
TTCGTGGCGTCGGTTCTGTTTCCACTGCCAGGTTCACAGATCCTGTTCTACGCCCTAGCG
TGGCTGATCATCCCATCCCGAGAAAATCGCTTC

>RXA01987-downstream
TAACGTGCGTTGCATAACGCAGA

>RXA01988
ATGATCGACCCACTAACTCCAGTCGTTCCCATCACCACGGGCACCTCAGTTGCCGAGCTT
TATGCTGACGCCCGCGAGCACCTCGACAATGGTGCAACCCAGGTGATGATCCCCGTCATT
TCACCTTCCAACCTGACCTTGTCAGTAGTTGCCCTGGGCAATCAAGAGGTTGACGCACTG
GGCCATTCCGAAGGACAAGCAGTTCACTCCCTTCTGGAAATTCATACCCCGAAGCGCAGC
TGGCCTCTTTCCGAGCTTTATATTGATGACAATGAGGGTTTGGCTCAGGTGTCGCGCTGC
TTCGCCCGCCTTGTTGGC

>RXA01988-downstream
TAGTCCCACCCCACCAATTGCAT

>RXA01990
ACATCTGATCATGTGGCACAGTTTGGTATGGCAACTGCGTCTGCTGCGACGTTGCCGGAC
AGTATTGTGACCAGTGTTTCTTATACGTTGAACGGGCTGTCATTTTCTGACCCGGTTGAG
CTGGGTATCAGTGACAACGACAAGCGTGAAGAGCTTCTAGGAGACATCACCAAGGGTGAA
CTGCGATTGCAGATGGAGTTTTCGATCCCGGATTCAGCAACTGCCGAGGATGAGTACGTC
TTTAATCTCACCGGCGATGGACTTCGGTTTTTCAATTCAAACGATCGCACCGTCCCTGTA
CGCAATGATGCAGGTATTCGTGTCGCAGATCTTTTGGTGAGCAACGGTGGTACGCGCGGT
ACGTTGACAAACTTTAGTTCGGATGCTGGCACTACTTCTCGCACCGCAGCTCTTGATATG
GAACTGTACGGGTGGGTGAGTAGCGCCCAGCAGACGGGTGAGCGACCAATTCAAGACTGG
ACTGTGGGTAAGACTGAGGGTCAGGTTGAGAACAAGGTAGTCCGCTACGGCGTTGCTGGA
CACCCGTGGATTATCAGTACTGTCCAGCACACGTGGGTTAAGTCTACGCAGACCGTGTCG
CATTTCCGAAGTGAACAAGACTGGAAGATTAATCAACCACCAGCTGTTGATATGGGCGCA

TTAGCATACGCAGCTCCACTTGGCGTCGTGGTCGGGCACGCCAATGTTGTCATTAGCAAT
AACAACGGTGCTGGATTCCGGGGTGCGCTTGTCAATACCACACCCACCACACGCGACGTG
ATACTTAATTTCACAGCCGCAGACGGAGCCACTTTACGCGAACGTTCCGGAGGTGGATTT
GAGGATTTCGACGTTTTCTCGGAAGTTCCTCGGGTAGAGGAAACATCGACGAGGATCAGC
TATTCTTACAAAAATTCATTTGAATATGACGAATTTGTTGCCGCATTTCCCGAGTACCGA
CGTAGCTGCGTGGGAACCAACCGTTGTGTATTCAGCGGA

>RXA01990-downstream
TAAGACCACAGCAACAGCGACGT

>RXA01991-upstream
TCCGGAGGTGGATTTGAGGATTTCGACGTTTTCTCGGAAGTTCCTCGGGTAGAGGAAACA
TCGACGAGGATCAGCTATTCTTACAAAAATTCATTTGAAT

>RXA01991
ATGACGAATTTGTTGCCGCATTTCCCGAGTACCGACGTAGCTGCGTGGGAACCAACCGTT
GTGTATTCAGCGGATAAGACCACAGCAACAGCGACGTTTAAGAATATTCCTTCGGATATT
TCCTTTAGTTGGACTGGTATTGAAGCACTAGAGCCATTTAGCCCTGGTAAAACCTTCGAA
CATAAGGTGCAAGGTTCTGTTGGTGAACCAGCGGGGGCGTTCACTAGGGATAACTATTTC
ACTGAGGGTGAGCTCTACAAACATCGCCACGCAGACGATCTGCTTTCCGGTGATGGCTTG
TTTGGCCCCAACATCACCGATGGCGATGGCAACCTCCCCTCTGTTGATGACGGCAAGGAC
GGTGACGATGGGTCTGATGGCTCAGACGGCCGAGACGGTGTTGTCGCCATTGATGTTGTT
GACAATGCTGACGGCACGGTGACTGTCACCTTGTCCGATGGCACTACGTTTACTCTTGAT
GCTGGTCAAGACGGCAAAGATGGTCTTGACGGGCTTGATGGTACTGGCCTAACGCTGGAA
TCTGCTACCCCTGATGAGGACGGCAACATCACCTATGTTCTTTCTGACGGTACTGAGTTC
ACTGTGCGCAACGGTGTTGATGGGTCAGACGGTAAGGACGGCAAAGATGGAGTCAATGGC
ACAGATGGCGTAGACGGGTCAGACGGTAAAGGTCTGGTAGAGGTGTCCCGAGTTACCAAC
GACAACGGCTCAGTGACCATTACCTACGAGGACGGTTCACAGATCACCACGAAGCCAACG
CCGACAAACTGGCTG

>RXA01992-upstream
ATAGATCAATGCTGGCATAAACTAAAGGCACAACAGCCGATTCACTTATTTTTAGGCGAA
TGCTTGAAGTCGAAGTAAGTGAGGGGGAGAGGATCCGTTA

>RXA01992
GTGTACTGCCCATTTTGCCAACATGATCATTCAAAAGTCATTGACTCCCGCGTCATTGAC
GCCGGAAGCGCCATTCGCAGGCGCCGCGAGTGCAGCAAATGCGAAGGCCGTTTCACCACC
ATCGAAAAAGCTGTTCTCCTCGTTGTTAAAAGAAACGGCGTCACTGAACCGTTCAGTCGA
GAAAAAGTAGTCACCGGTGTCCGTCGTGCATGCCAAGGCCGCGACGTATCAGATGACGCG
TTGAAACGCCTAGCTCAGCAAGTGGAAGAAACAGTCCGCAGCAACGGAAGCTCTCAAGTA
CGCGCTAACGATATTGGTTTAGCCATTCTCGATCCACTGAGAGAACTCGACGAGGTAGCG
TACCTACGCTTTGCCTCTGTGTATAAGTCTTTTGACAGTGCTGACGACTTTGAAAAAGAA
ATCCGCCTCATGCGCAGACGCGGAAGGGAC

>RXA01992-downstream
TAGCAGACACAAAGTCTTAACTA

>RXA01996-upstream
GAACACGGCAGCGACACAAACTGCACAGATGCAAGAGTGTCGGTACCGTTAAAAACGAAA
CACACTTTCACCGAAAAGGACTTCCCA

>RXA01996
ATGAGCAAGTTGACTGGCACCTGGACCCTCGACCCTGCACACACCGAAATCAAGTTCGTG
GCTCGCCACGCAATGGTTACCAAGGTTCGCGGTGAATTCACCGAGTACACCGACTCCATT
GTCGTAGATGCTGAAAACCCAGAGAACTCCTCTGCAAAGGTTGTTATCAAGACCGCTTCC
GTTACCACCGGCAACGCAGACCGCGATGCACACGTTAAGGGCGACGACTTCTTCGCAGTA
GACAAGTTCCCTGAAATGACTTTCGAAGCTACTTCCTTTGTTATCAAGAACGAAAACGAA
GGCACCGTTACCGGCGACCTCACAATTCGTGACACCACCAAGTCCGTCACCCTGGACGTT

GAGGTTGGTGGCGTTGCTGAGGATCCATTCGGCAACACCCGCCTTGGCTTCGAAGCCTCC
ACCGAAATCAACCGCAAGGACTTCGGCGTAGATTTCCAGGCTCCACTCTCCACCGGTGGC
GTTCTGGTTTCTGAGAAGATCAAGATCGAGATCGACGGCTCCGCAATCAAGGCTGCT

>RXA01996-downstream
TAAGCGCCCACAAACAAAAAGCC

>RXA01999-upstream
GGGTATGTAGTTAGAGACGACAGACACAGAAATCTTCAGCCTCGCGAACCGAGTGATAGC
ATACTTGACCATATCGAATTCTCTACCAGCTCGAGGCATC

>RXA01999
ATGACTCTCCCCACCCCTACACATTCCACCAAAGGCAGTTCAGGCCGCATGAAACGAATG
GCCCTTATCGGCTCCTCGCTCATTATTTCCATGGGACTTATTACTGCGTGCGGTTCGGCC
GCTGCAGAACCCGAAGCCCCTGCACCAACAGTTACCGAAACTGTAACAGCCACGGTGACA
ACCACAGCTAAAGCCAGCACGATCACCTCGACAGTGACGGAAACTACCTCCGCGGAAGAT
CTTGCCCAAGAAATTGTGAAGCCAGCGGCCGTGGAGGAATATTCAGAGCCTCAGGTAAAT
ACGCCACAGCAGTTTGCGGCCATCCCGGAACCTGCACCGGCGGTTGCACCAGCTCAAACG
TATTACGCCAACTGCGCGGCAGTTCGTGCGGCGGGTGCAGCTCCCCTTTATGCGGGATCA
CCTGGATATAGTTCCAAGCTTGATCGCGATGGCGACGGAATTGCCTGCGAA

>RXA01999-downstream
TAAATAGGAATAGTTAAAAACAC

>RXA02001
ACCCGCGACCCCATCGTCGCAGCCGTCGGAATTGTCCAAGCGTTTCAAACGATAGTCAGC
CGGAATCACAATCCGGTCGAGGACCTTGTCGTGTCGGTCACGCAAATCCACACCGGCAGC
GCCGATAATATCATCCCCGAAACCGCCTATATCAACGGCACTGTCCGCACCTTCAACAAA
GACGTGCAGGCCATGGTCATCACGCGGATGGAAGAAATCGTCGCGGGCCAAGCTGCAGCC
TATGGGGTCGAGGCGACGCTGACCTACAACCGCAACTATCCCGCCACCATTAACGACGCC
GCCAAAGCCGCCATCGCTGCCGAAGTCGCGGGCGAGGTCGGCCTCGGGGTCAACCCGAAC
GGCTCGCGCGGGATGGGGGCCGAGGATTTCTCGTATTTCCTCGAAAAGCGCCCGGGTGCC
TACCTGTTCGTCGGTAATGGCGACAGCGCGGGCCTTCACAACCCCGCCTATAATTTCAAC
GACGAGGCCGCGCCCTACGGCGCATCGTTCTTGGCCCGCATGGCAGAACGCCCCTTGCCG
TTAAAGGGC

>RXA02001-downstream
TGATCCATGGCGCTCGAAGATGC

>RXA02004
CGCGTCGGCCGTCTGATGCGTCAGAACGGCATTCTCATCATCCGCAGCCGGAAGTTCAAG
CGCACGACCGGCAGCGATCATACCTTCAACATCGCACCGAACTTTCTGCAGCAGGACTTT
ATGGCGAGCAGGCCGAACCAGAAGTGGGCGGGCGACATCACCTATGTCTGGACGCGCGAG
GGCCTGGGTCTATCTGGCCGACATTCT

>RXA02004-downstream
TGACCTTTATCCCCGCCGGGTGA

>RXA02006-upstream
ATCATCCATACATGCAGAGCACAGCTTTCACACATAGACATCACTGCACATTTATCTAAT
GGGAGACTCA

>RXA02006
ATGACAGTTGCACACAAACGAAGTCTGACATGGATCAAGAGACTATCTGCGACTACATTT
GCAGCTTTTCTTGGCATTCAGCTTGTGACCCCCGCTCACTCAATTGAAAACACGACGCAG
ATTCCAGAAAGCGAATTGCACAACCTCGGGCTCACAGACGAAGAAATTCAAGAATTCAAT
CAATATCTCATTGACGAGTCACTCTTTCAAGAGACTGTAGAAACCTCTCCGATCGTAGTC
AGCGACAATGAAGATGCAGCCCAAGATCCCGGTTTCGGCCTTTTCACCACAAATCCTGTG
AAACACACAGATGAGCACATTGGCGCTCTATACTTCTCCGACCTACCAGGTATTTCCAAT

CTTACGTGCACTGCCAACTACATCGGTGGAAAATTCTGGACCACAGCACATCATTGTGTT
GAAGGCCGCAGTCGCTTCGTCGGCTTCATCGAGCAGTCGGACGGACAATATGCAGGCATT
GAGCATGTTTACACA

>RXA02007
GGCATCACCGCAAACTACGCCTTCAAGGGCAAAAAGGTTGTGGCTTGGAAAGACCTCGCA
GGAATCGGATTCAAGGGTGCCCGCACTTTCGCTCGCCCCACCTCCGATGCAGAAGTCACC
CTCCCGGGCGTCACCTTCAACTCCCTTCCCCGCCTTGAAGCTGCTTCCCACGGCCGCATC
CCCGATGCGATCACCGCAAGCAAGGAAGCAGCCGACGGCAAGGTTGTAGTCGTTCAAGAA
GACGGCTACTCCGTGATGATGTCCAAGGAAGAGTACTTGGAGCGCCAAAAGGCACTGGGC
AAGCCAGTTCAGTTGAACTTCGATGACGACACCGATGGGAATACAACACAAACAGAAAGC
GTTGAATCCCAAGAGACCGGACAAGCCGCGTCTGAAACCTCACATCGTGATAACCCTGCG
TCACAGCAC

>RXA02007-downstream
TAGAGTGTAATAAGCCGTCCGAA

>RXA02009-upstream
AACTGCATCATTGTCGTTCCTGAACAAGCGCCGTGGTTTAAGCCAGCCATCATCAAACAG
GCTTAAAAATACTCAATCGTCCCATTCAAGAAAAGAGCAC

>RXA02009
ATGACCATGTACAACGCCGCAAAGACCCTTGTTCCCCAGATTGTTGCTTTCGATGACACA
GCAATCATCGCACTCGACCAAGCCGCGGAAGATGAATTCCGCAAGGCTAACTACCCCGAG
GTT

>RXA02011-upstream
TGAATTCCGTTTCTAGATTTTTTTTATTGATTGTGAGAGTGCATT

>RXA02011
GTGGCTAATGATTTTATAGAACCAAATGATGCCCCCGATGCACCTGATAATGGTGACTCG
GGAAGCTCGGGGTTTGTTGATGAAGCAAAAGATAAGACCCGCTCAGCTGCACAAGGCTTA
GGTTATGGCGCACTACGTGTAGGTTTTGGTACTGCAGCACTTGCAGCCAATGGTGCTCGC
TCTATGGGTAATTTGGCTAAAAACCTGTGGACACCAATGATGGGGCTTGCCCTGTCTGCC
GGTACTGGTATCTCTGCTGCCACAGGTGGCATGATCACTGCACGTGTAGGCGCAATGCTG
GCAGGTACAGGCTCGGCG

>RXA02013-upstream
ATCACCGCGCTGGCGACAATTTCAGAAAACTCCCACAAAGCACTGCTTGGCCTTTATTTG
TCCGGTCTTAAACACGGCATGATGGCTAACATCGGAGAAC

>RXA02013
ATGACGGAAAGTCCTGATCTAGCAGTTTCCTTTTTAGCCGCCTTCAATGACATCGAAGCG
CACCTTCGAACCCAGCTCCGCGCTAAACGCTCCGACAGTTTCAGATGGATGGTACGTATC
GCCGAGAAACAGCATCTGATTTCCAAAGAACAAGCAGAAACCCTTGATGCTTTTGCGGAG
CTGCGCAACGCAATTAGCCACGGCCAATACAACGATCTACGCCCGATTGCCGATCCCCGC
CCCGACACCGTGGACACCATTGAGAAGATTCGCTCCCTCCTTCTCAATCCTCCAATTGCG
TTAAACGTCCTCCCGGAGCAAAAGGTCCGCTCCTACTCACTTGAAGATCCAGTGAGTAGG
GCCTTAGAAGTTGTGCACACCACGGAGATCTCCCAATTCCCCATATATAAGGGAACGGAA
TACGTGGCACTGCTAACTACCAACACAATCGCTCGCTGGGTTGCCTCCGATTTACATGAC
AATGCCCAGCTGGATGCACGTTCTATCAAAGAGGTTCTGGATTATGCAGAATCCTCTGAC
ACTGCAGTT

>RXA02014
ATCTCCCTCCAACTCCAAGCCATCAGCACCTTCCCCACCGACCCAGAAGGCGTGTGGACC
TCCTTCAACCAACTACTTTTCGACCGCGGCCTAGGCTCCCTCGTCCCAGCACTTGCCCCA

GAATCCTTAGACGACCTCCCCGACGAGGTCTCCGCCCTGCGTCGCACCACAGAGAAAAAC
ACCACAACACTCATCAACCTAGCCAAGCAGCACGGACTCGTACACCACGACATCGCGCCG
GGCACCTACATCGTCGGTTTGATCACCATTTCCCGCCCACCTATCACCGCGCTGGCGACA
ATTTCAGAAAACTCCCACAAAGCACTGCTTGGCCTTTATTTGTCCGGTCTTAAACACGGC
ATGATGGCTAACATCGGAGAACATGACGGAAAGTCC

>RXA02014-downstream
TGATCTAGCAGTTTCCTTTTTAG

>RXA02019
GCTGGCACCAAGGTTGAGGCCTCTGACCTTGGACTTCAGGCAATCCCTACTTCCCTACTG
CCCAGCACCTCCTACGATTCGATTGACGATGTAGTTGGGCTCGTTGCGGCCTCCACATTA
AGTTCCGGGGAAATAGCCACAAAGCCTCGATTCGTGGGCACCGAATTGATAAACTCCATT
GCGACAAACGTCACTGATAGCTCTTTGGTGGAAGAAATTAACATGGTTCCACTCAGTTTG
GCTGAACCTTCCGTCATCCCCCTACTGCAGCATGGGGACACCATTTCGGTTGTTTCCCAA
GACCCAGACACCGGTCTCCCAGAGAACATTGCTGCAGGTGGAACAGTAATTCTGGCGGGT
GGTACAGACCCCTCAACCATCTTGATTGCGCTTCCACAATCAATCGCTGAAAAGGTTGCA
GCACAATCGCTCAATACCCCTCTGGCGGTAGTCCTGACCGGAGACAGAGCAAATAATTAC
ACAACCGAAGAA

>RXA02019-downstream
TAGTTCCCTATTCAAAAAAAAGG

>RXA02021-upstream
TTGGGTCGCCGAGGAGATCTAATCCTGGTTTGAGTTCAGAGTTCACAGGTTTAAGCCTAC
AAACCTTAGTTAAAACATGATGGAAGCGGTCGATTAAAAA

>RXA02021
ATGAGTGAAAACATTCGCGGAGCCCAAGCAGTTGGAATCGCAAATATCGCCATGGACGGG
ACCATCCTGGACACGTGGTACCCAGAACCCCAAATTTTCAACCCGGATCAGTGGGCTGAA
CGCTACCCATTGGAAGTGGGCACCACACGCCTCGGAGCAAACGAACTCACCCCACGGATG
CTGCAGTTGGTAAAACTGGACCAAGATCGCCTCGTCGAACAGGTAGCAGTCCGCACCGTT
ATCCCCGATCTGTCTCAACCTCCAGTAGACGCGCACGATGTTTACCTGCGCCTCCACCTG
CTTTCCCACCGGCTGGTCCGCCCCCACGAAATGCACATGCAAAACACCTTGGAGCTGCTG
TCCGACGTGGTGTGGACAAACAAGGGCCCTTGCCTTCCTGAAAACTTTGAGTGGGTGCGT
GGTGCTCTGCGGTCCCGCGGACTCATCCACGTCTACTGTGTGGACCGTCTTCCCCGCATG
GTCGACTATGTGGTTCCCCCTGGAGTCCGCATCTCCGAAGCAGAACGCGTGCGCCTAGGT
GCATACCTTGCTCCGGGTACCTCTGTGCTGCGTGAAGGTTTCGTGTCTTTCAACTCCGGC
ACCTTGGGTGCCGCAAAGGTGGAAGGCCGCCTGAGTTCCGGTGTGGTCATCGGTGAAGGT
TCCGAGATTGGACTGTCTTCTACTATTCAGTCCCCGAGAGATGAACAGCGCCGCCGTTTG
CCGTTGAGCATCGGCCAAAACTGCAACTTTGGTGTCAGCTCCGGAATCATCGGAGTCAGT
CTGGGAGACAATTGCGACATCGGAAATAACATTGTCTTGGATGGAGATACCCCCATTTGG
TTCGCAGCCGATGAGGAGTTACGCACTATCGACTCCATCGAAGGCCAAGCAAATTGGTCA
ATCAAGCGTGAATCCGGCTTCCATGAGCCAGTTGCCCGCCTCAAAGCT

>RXA02021-downstream
TGACCCATTTTCATAACCAGTGC

>RXA02023-upstream
GATGTGGCAGCAATTTTGAAGCAGTACCTGAGCGAGTAACCGCATTCGGGGTTATCGTGG
GACTTCCGAAATGTAACTAGAGACTAGAGGAGGAAACACG

>RXA02023
ATGGCTCCTAAACAAACTCCCAGCCCAGAGAAGAATCGAAACCTGGTGGGACCAGTTCTG
CAACGTCGGCAGACAGAGGGTACTTTTGATCAACGCTTGCTAGAAATGCGCGCTGATCAC
AATTGGAAGCACGCCGATCCATGGCGTGTACTGCGTATTCAGTCTGAGTTTGTGGCGGGT
TTTGATGCCCTCCACGAGATGCCAAAGGCCGTAACCGTCTTTGGTTCCGCACGCATTAAA
GAGGATCACCCGTACTACAAGGCGGGTGTAGAACTTGGTGAAAAGCTCGTTGCTGCTGAC

TACGCAGTTGTCACCGGTGGCGGTCCAGGTCTGATGGAAGCCCCCAATAAGGGGGCAAGC
GAGGCCAATGGTTTATCAGTTGGTCTGGGCATTGAGTTGCCACATGAACAGCACCTGAAC
CCTTATGTGGATTTGGGTCTGAACTTCCGGTACTTCTTCGCACGCAAGACCATGTTCCTG
AAATACTCCCAGGCTTTTGTGTGTCTGCCTGGCGGTTTCGGCACGCTCGATGAGCTTTTC
GAGGTCCTCTGCATGGTACAAACCGGCAAGGTAACCAACTTTCCCATCGTGCTGATCGGC
ACTGAGTTCTGGGCAGGTTTGGTGGATTGGATCCGTCACCGCCTGGTAGAGGAAGGCATG
ATCGATGAGAAGGATGTTGACCGGATGTTGGTCACTGATGACCTGGATCAGGCCGTCAAA
TTCATCGTCGATGCACACGCTGGATTGGACGTAGCGCGTCTCCACAAT

>RXA02023-downstream
TAAGCAGTGGCTACATTAGGTGT

>RXA02032-upstream
CTTAAAAAGGGGCTTTATCGGTTCAGGCGAGCGAGACCTTCGGCGTTCACACTTCGCCGG
GGTCTATTTTTTATGCCCAGGCACGGCTCATAGGAGAACC

>RXA02032
ATGCCCTTTCTACAAATCTCTCTGCTTTCCATCGGTGTCGCCGCCGATGCGTTTGCTTGT
TCCGTTGTCCGCGGCACCGCCATTCAAGTCAACCTTTTCAAACGCGCACTTGTTCTCGCG
GGCATCTTTGGTGTCTTCCAAGCGGCAATGCCTTTAATCGGCTGGTTCATTGGCCGTTTC
TTTGCTGGAATCACCTTCATCGCTGAAATTGATCACTGGATCGCTTTTGCACTATTGGGT
ATTGTCGGCACCAAAATGATCTGGGATGCCTTCCAACCTGAAGATGATGAAACCATTGTC
GATGACGGCCGCGTTCAATTTAGACCAGCAATTATCCTGGGGCTAGCCACCAGCATTGAC
GCATTAGCCGTAGGCATGGGCCTGGCATTCGTGGAAGTTTCCATCCTCAAAGTGGCACTG
TCCATGGGCAGCATCACCTTCGCACTTTCGCTTGCTGGCGCCTGGATCGGACACCATGGT
GGAGGAAAGTTTGGCAAGTGGGCTACGATTCTTGGCGGAATAATCTTGATCGGAATCGGC
GCAAACATCGTCTACGAACACCTCAGCGCG

>RXA02032-downstream
TAACCCTCGGCGCATTATCCTCA

>RXA02036-upstream
CTAAAATGGAAGGCAATGGATACCCGCCGCATGAACCTCCGCCAATGGAAAATCCTCGTT
GCCCTCATCTCTGCTGCAGTGGCGGCTCTCGGAGGGTGGT

>RXA02036
GTGCATATTCCTTTTGGGCACCTCGCCGACACCGTCTCCTGGGACTGCGGGGGAGGCAGC
TGCGCCACCAACGATTTGGTATCCCTGTTCATGCCGGCCGCCTTCATGAGTACCCTCGCC
GCCTGCGTATTTGGCGCGTGGGCCATAGGTTTGATCGCTCCCGCACTATTCATCGCGGTG
ACTGCCTGGGCATTTCGCTCCGGCGTGCAGGCTGCGATTGCCGACGGCTACACGTCCGCG
ACTTCCGTCGGCTTCGAAATGACTGTCTCGCTCATTCTTTTCATCATCGCAGGTCTGTGC
TTTCTGGGCTGGATCCCCATGTTCATCAACAACCGCCAAGTCGCGCGCAAGGTCCGCGAG
AGGGCTGCGGGCTTGAGCAAT

>RXA02036-downstream
TAGGCTCTCGCTTTTCGACGTTT

>RXA02039
ACGTCCACCTCCACCACCGCACCCCTTTGGCTCGTGGGCACGCTTGTGTGGCTGGCGGTG
CAGGCGGTGATGCATGACGGCGAGCTTTACCATGTGGAAGTTCCCACGATTGCGCTGGTC
ATCGGCTTTGGCGCGCAGCTTCTGATCGGTGTGATGAGTTATCTACTGCCGTCGACGATG
GGTGGCGGCGCGAGCGCGGTGCGGACTGGAACGCACATTTTAAACACTGCGGGGCTGTTT
AGGTGGACGCTGATCAACGGTGGCCTGGCGATTTGGCTGCTCACCGACAATTCGTGGCTG
CGCGTCGTGGTGTCTCTGCTGAGTATCGGAGCGTTGGCAGTTTTTGTCATTCTGCTGCCC
AAGGCTGTGCGGGCGCAGCGCGGAGTGATCACCAAAAAGCGCGAACCAATTACTCCGCCG
GAGGAGCCTCGACTCAATCAAATTACCGCGGGAATCTCTGTGCTTGCCCTGATTTTGGCA
GCATTCGGTGGGCTCAACCCCGGTGTTGCGCCGGTGGCAAGCTCAAATGAAGACGTCTAT
GCTGTGACCATTACCGCAGGTGACATGGTGTTTATCCCTGATGTGATTGAAGTGCCTGCT

GGTAAATCACTCGAAGTCACGATGCTCAACGAAGACGACATGGTGCACGATCTGAAATTT
GCCAACGGTGTGCAAACCGGACGTGTGGCGCCAGGTGATGAAATTACGGTGACCGTCGGC
GATATTTCCGAAGACATGGACGGCTGGTGCACCATCGCTGGGCACCGCGCGCAAGGAATG
GATCTGGAAGTAAAGGTTGCGGCTCCGAAT

>RXA02039-downstream
TAACCAAGGGCTGCTGAAAAACT

>RXA02040
TACATACCTTTTGTCATTTGGTCCGATCTCGGTGAGGCTGCCGAAGGTGAGAACTTTGCT
CGCTTCTGGTCCTGGCTGAAATCGCGCCGGGACAAAGCTCGCCAGCAGGGACAAACCTTC
GGTGTGTTCTGCTATGCCAGCAACGGCGAAAACCACTGGATGCTCTCCACTGCTCGCAGA
TTCTTCGGCAAAGTCAAAGGTGTGCCCGACGAGCAAGAAATCCGCAGCTTCATTAGCTCT
GACCAATGGAATGACATGTTTGCTGTCGCGCGCTCCCAACTTGTTGGCCCCGGTGGTTTA
GGTCTGAAACAACTCGCGCCGGCAGCTGGATTCCATTGGGAGGAAGAAGACTTCGCAGGT
GAAGATAGCCTCCACGCATATCTCATTGCTTCCACGGCTGCCGAACCAGAAGCTGAGGCC
GCTCGTGCTCAATTGCTCAGCTACAACGGCGATGATTGCAGGGCCACCGCAGCGGTTCGC
CATTGGCTTCGACAAGGTGCGCGCACGGCACCTGTGCTGGGGAATATT

>RXA02040-downstream
TAAACCAAGGAAGGATTCTCCAG

>RXA02045-upstream
CACCTTCCGCCCCGGCTGCTTCTGAGATTACAGAAGCTCCTGCCGCTCCAGCCGCTCAAG
CCGTTCAAGATCTCAACAACGAGAATGAGGTAACCAAGTA

>RXA02045
ATGAACTTCGCTACTATTTTCGGAAGCATCTTTGAGGTCACCCTCGTGGGCATTTTGCTC
GGCGCAGGCCTTCCAGCCCTTTTTGCATTAGGAATCCGCTTTGCTCACAGCCCTTCTTCC
AACGGCACCAACGCTCTTGGAAAAATTGCTTCAACCATCTGCTTTGCCATCATTGCGGTT
GCTATCATCGCTGGCATTCTCTGGGTCACCAAAGCAACGATCTACCAGTACTCTGGTTTC
GACATTTTCGGCACTGAAGGC

>RXA02045-downstream
TAAAAGCACCAGCTGCGAATAAC

>RXA02046-upstream
TCCGTGCCATCACCACCGGCGAGATCACTGGCATCGTGGACGCAAAACAAACAGCAACAG
AAATTATTAACATCCGACGCAACGCTTCAGGAGAGTCCTC

>RXA02046
ATGAAAGAGACACTGACCACCGGTTTAACCCACCAAATGACCTACATAGTGCCAGCAAAC
CGCACAGTTCCGCATCTGCTTCCCGAAGCAGCAGAATTTGAAACCATGCCAGATGTCCTG
GCCACTGGATATATGGTCGGCATCATCGAGTGGGCCTGCATGGAACTTCTGCGTCCCCAT
TTGGACGACGGTGAAATCTCGCTGGGCACTCATGTGAACTTCTCCCACGCAGCTCCAACG
GTTCCTGGATCCACGGTCACCATC

>RXA02049-upstream
TCTACGCAGTCTCCACAGACCACGCAGCTTTAGATGCAGTGTGGCAGTCCTGGCTTCGCG
ATCTGGAGTTGCCGGAGTTTCCTTCTGGTGGTTTGGACTA

>RXA02049
GTGCGCTATCTGACGCTGGCCACAATCATCGCAGGTCTCTCCGGGTTCGTCGTCATCATC
ATCGCTGCCTGGGCCCTTGGTGATTCCAGCCAACTTTCCGAAGAATTCACCGCCTACTGG
GGTCTGTTCTTTGCAGGAACCGGAGTGCTGACTGGGTTGACGCAGGAGACGACCCGCGCG
GTGACGGCCGGTTCTCGTGGTGGTTCTCGTGGTGGGCGTGCTGGTTCTGTTGTTGGATTT
AGGCCGTTTTTGTTTAGCTTCGTGGTTGCGGCGATAGTGCTCGTGGTGCTTGGCGCTTCG

GCGCCGCTGTGGATCGGCCAGCTTTTAAGTAATTTGCAAGGTGTTGGTGTTGGGCTACTT
GCTGTAGGTCTTGCTAGCTACGCGATCCAAGCGACAATCTCCGGCATTTTTGTCCGGCTG
CCAATTGTGGAAAAGAGTATGCCTCGC

>RXA02049-downstream
TGATTTCTTTGGACACCGGCGTG

>RXA02050-upstream
CGCGCTCCCCTGCTGGTTCCGCTGCAGCAATTCCAATCGGCGATCATCGTTCGTTTTGTC
AAAGGTACCGTCCGGTCCATTGAAAACTTTGGCGGGTCCG

>RXA02050
TTGGCAATTGTGTGGGCAGTCGGACTTGTTGGAGCTGGTCTTGCATGGTTAGTTGGCCCA
TGGATCCTGGACGTTGTACTCCAAAAGGAACTCTTCGCGGTCCCTGGCTGGCTACTCGCG
ATGCTCACCTTAGGCGCCACCACCACCGCTTCATTGATGGTGTCCGGCTGCGCGGCGATC
GCCTTTGAACGTCACGGGATCTATCTCACCGGATGGGTTGTTGCCACTGTTGTTGCCGTC
GGATTCTTGCTGGGACCTTTTGATTTGGGCGTCGCTGCTGGCCTTGCGCTCATTGTTGGC
CCACTCTGCGGTTTGCTGGTACACATGGGAGCGTTTGTTGGTGGGGATCGGAATCGGGTT
TTGACTGCGGGA

>RXA02050-downstream
TAGTTTGGTTTGATTGGGGGATT

>RXA02051-upstream
CGCACTGATCGGTGTAGTAACTGGCGGTATTTTGCTGCTAATTAACTCGCAAAACGGTGA
GCAGACATCATCTTCAACTCGCACAACAGTCAATGACTCC

>RXA02051
ATGGTCATCAGAGCTCTCCAGCGCGAAGAAGAAATCGTCCTTCTCAGCGCCGGAGCACTT
GGAATCCATGAGAAAACCGTTGAACGTACAATTCGTGGAAAACGTATTCCTGGCACGCAA
AAGACCGTGCACGTCCAATACAGCTACACCGGAAAACTCGGAATCGATGCCTCAGATGTT
GAAATCAAATCCGCAGGTGACAATAAGCTTTCCATCACTATCCCTGAGTTCATCTTCATC
GGATACGACGATCTAAAGTTTAAGACCATAGCCGAAGATGACGGTTGGATCAGTTTCAGC
ACTGACGATATCGATACTGCAGAAGTAGTTTCTGAGATCATGAGCCAAGAGAACTTCGTC
GAGCAAGTAACCACTAACCGGGAAATGTTGGAAGATCAAGCGGTTGATTTCTACAACGAC
CTGCTCCACGAATTCACCGAGAAACTCGATACAGATCGATACGAAGACACCAAGATTGAG
CTCGAATTCGAGTTTGAG

>RXA02051-downstream
TAGATAGTGCTTCGAAGACAGTT

>RXA02053-upstream
AACCAGCCAGAAACTATCTCCAAAAGCTAATAAAACCCTTGCACTGACAAATAAGGCGAC
CTACCATGACTCTGTTTCCAACACATAAAAAGGATAAAAA

>RXA02053
ATGTCACTTTCAGTCGTCGAGGCGATTACCAACCGCCGCGCCACCCGCAAATACACCGAT
GAAGCTCCTACCCCTGAGCTGATCGACAAAATCGTTGACCTTGCCCTGGAGGCACCCAGT
GCGTTCAATGCGCAGCAACGTGAAATTGTTGTGATTACTGATCCCGCACAGAAGCAGAAG
CTTTACGAGGCCTCCCATCAGAAACAATTCCTCACCGCACCTGTAACTTTCATTGCGGTT
GCCCGCGTGGAAAACGAGCCTGAGGATTTGGAAGAGATTCTTGGTACGGAAAGGGCTGAA
CGTGTCGCGGGATTCATCAACGGTCGCAGCATTCAGCAGGCACGCGAAGCAACGTTGAGG
GATGCCAGCCTCGCGGCGGCTTTTCTAATTCTGGCTGCCCAGGCGGAGGGTTTGAGTACC
AGCCCGACTACTGGTTGGGATGAGGAAAAAGTGAAGGAAGCAATCGGTCTCGGCGGGCGT
GAGGATCGTGCAATCGCCCTTGTTATTGCTACCGGATTCCCTAATGAACAGCCGGAGCAC
CCTGGTCGTTTGCAGAATAGGCGCATCGACAACAGCTAC

>RXA02053-downstream

TAACTCTGCCAGCTCGCCCGGAC

>RXA02057-upstream
AAGTCTTTATAGTCCTGCACTAGCCTAGAAGGGCCTTATGCCGTGTGAATCACACAGCAT
ACGGCCCTTTTTGCTGCCGTGGTTGCCTAAGGTGGAAGGT

>RXA02057
ATGAAACGAATCTGTGCGGTCGCGATCTCTTCAGTACTTTTGTTAAGTGGCTGCTCCTCC
ACTTCCACAACGCAGCTCGAGGGATTCGATGGACGCTCAGCGCAGGAGATCATCACAGAA
CTTGATCAAACCCCAGTCGCAGACAGAGCAACTAACCTCATGGCCTCCATTCGGGCAGAT
GAGTTAATTCTGTCGGATCAAAGCGGACAGCTCAGCATTGACATGCCTGCAGATGAGTTC
TATATCTCCGCAGCCCCGTACACCACCACAACCCACGAGTGCTTCTATCACAGCCTCACC
ACATGTACTGGTGAACTCGCCAACACCCCAGTGAAAGTAACGGTGGTGGCAGATAATGGA
GAAACCATCCTCGAAGAGGACACCATCACCTACGATAATGGATTTGTTGGGATGTGGCTC
CCCCGCAACATTGATGCCACACTCACCATCGAACATGACGGCCTGAAATCCACCCAGCCG
ATCTCTACGGGTGATGACGCCCCCACGTGCATCACCACGGCTGAACTAGCG

>RXA02057-downstream
TGAAAATCCTTTAGACAATAAGA

>RXA02058-upstream
GAAGCGGATTTTAGTCCTTGCGCTTGGTGCCTCGGTAGCGGGATGCTCAACGCTTTCCCA
AGAACCTTCACCACCTGTTCCGTTGGGAAACGTTGATACT

>RXA02058
GTGCAGATTGTCTCTCCCAATGGGGAGATTGAGTCTTTTGTGCTGGGGAAGCTGTATGAG
ACCGCATTAGTGGAACGTGGCAGATCTGCATCAGTTCAGCTGATTGACGGCGACTTGGAT
GAGCAACTATCTATGCTGCGAGATGACAGCACTGATTTGGTGATTGCTTGCTCAGGACAA
TTACTGGAATATTACAACCCAGATTTAGCCTCCGAGTTTGCCGTCGAATACGCTAATCAG
ACAGCCTTTGATAAAAACTCTGGTGAATGGCGCGAAAAAGTCTACGATGCTCTCCAAGGA
TCGCTGCCGGACTCCATCGTGGCCACCGATCCTTCCAATGCTATTGGTTGTAAGGACGAT
ACGTCGCTGCCTCAAAACATCGTGCCAATTTATAGAAAGCCCAATCTGGATAGGGACAAT
CGGGACACCCTGAACTTTGTGAGCGGTTCTTTGGGTACAAGCGATTTGGAAGCATTGGTC
AAGGACGCCCAAACAACAGGCACAACCTCTGAAACTGCGCTGGATTTCTTATTGTCTAAA
GGATTTTCACGC

>RXA02058-downstream
TAGTTCAGCCGTGGTGATGCACG

>RXA02059-upstream
TCGGGAAATTCCACTCATGAACGCCTAGTCTACGGGAACCATTTCACCAGCGTGTACGTT
GTAAATGTGAACTGAAAAAGTGAAAAGGAAGATGATAAAG

>RXA02059
ATGACTCAACCACGGCCCGATGCCGCATCTGTGTCGCTGGAAAAGAAGCGCCCAGAAGGA
TGGCCAGTGGGAAGCTTTGAAACATACCCAGAAGCCCAAGCAGCAGTGGATTTGCTCAGT
GATAATGCATTCCCCGTCACCGAATTGACCATTGTTGGTGTGGACCTGATTGAAGTGGAA
CGCGTTACAGGTCGTCTCACGTGGGGTCGTGTGATTGCCGGAGGAATGGCATCTGGCGCA
TGGTTGGGTCTGTTCTTTGGCATTGTCATGGCCTTGATGTCTGGATTCTGGTTCTCTTCC
ATCGCAGCGGGAATAGGTATGGGTTTGGTGTTTGGCATTGTCGGTGCAGCAGTTCCTTAT
GCTGCTTCCAAAGGCAAGCGGGACTTTACCTCTTCAACTCAAATTGTGGCGGGGCGCTAT
GATGTGATTTGTTCCCCAGAACGTGCTCGGGAAGCTCGAGACATGATTGCCCTGAAAACT
CGAGATCTCCGCCAA

>RXA02059-downstream
TAAGTTAAACTAACGCCTATGAA

>RXA02066-upstream
GGAACTTATCACAGGCGACATCCGTTTTGAGTAGTAGGTATCTTGGATAAGAAGTTACCC
ACATCCTTGAAAGTCGAGACACAGGAGGTCATCGGAAGAT

>RXA02066
ATGTTCAATTCCGACACCACCGCGAATCTCCAAGCTAAAAGTCGAGATCGTGCAGGATCT
AAAGCAAAGCGCAGCAGGCCAAGTTTTGATTCAGTAGCGCGGGATGTTTTGGATGTTCGA
ACAAAAACAGCACAAGTTAAAAACAAGGCTAAAGAGTTTTCCTCTGTTGATCACCTTTCA
GCAGACGCCGCAGCCATGTTTGTAGACAATGAACTGTCCCGTGGCGCCATGCATCGCGCC
AGGCTGCACATTGTGCACTGCGCTGAATGTAGGGAAGAGATTAACCGTCAGCGGGAAACC
GTTGATTATCTCCGCTCAGAGTGCAAAAACGAAGAAGTGTCCGCCCCAATGGACCTCAAA
GCACGGCTTGCCAGCCTCGCCACTGAGTGCATGCCTGGCCCTGGCGCAGAGAATTTAGCA
ATGCAGCGCCCAGAGTCTTTTGTGGCTAAAGTTGAGTCCGTAGTGCGCGCAGTTCGTAAG
AACCAAGGCCGC

>RXA02066-downstream
TAATTTTTAATCCTTATTTACAT

>RXA02067-upstream
TAAAGTTGAGTCCGTAGTGCGCGCAGTTCGTAAGAACCAAGGCCGCTAATTTTTAATCCT
TATTTACATTTTCTGAAAGACCGGTCTGATGTTTTCTAGC

>RXA02067
GTGGGTTGGGGAGAGATCTTCCTCTTAGTCGTTGTGGGCCTTGTTGTCATCGGCCCGGAA
CGGTTGCCTCGTTTGATCCAGGACGCACGCGCTGCGCTGCTCGCTGCACGTACCGCTATC
GACAATGCAAAGCAGTCGTTGGACAGTGATTTTGGTTCGGAATTTGATGAAATCCGAAAG
CCACTAACCCAGGTTGCACAGTACAGCCGGATGAGCCCCAAGACGGCCATCACTAAGGCG
TTATTTGATAATGATTCCTCGTTCCTGGATGACTTTGATCCAAAGAAGATCATGGCCGAA
GGAACAGAAGGCGAAGCTCAGCGCAACAAGCAGGCAGCTGACAACAATGCGAATGTGGTG
GAACGTCCAGCTGATGGTTCCACCGCACGCCCAACGCAAAACGATCCAAAAGACGGCCCG
AATTACTCAGGTGGCGTCTCTTGGACCGATATTATT

>RXA02067-downstream
TAGCTTTTATTTAACGCCAAGCC

>RXA02069-upstream
CGCCATCTGCTTGGTGCCGTAGCTGTCGATGACTTGCTCGACCACATGCTGCCAGAAGAC
TGGCGCGACGCCGGAATCCGACCAGGAAAGGAGCACACCC

>RXA02069
ATGGCTGATTTCAACCGCTCTGAATTAGACAGCCCACTTTTTGGATCCCGCAAACGATTT
AAATTCGACGATGACACCATTGGTGCCTACGCCGAAAAAGTAGCCCGGTTCTTTGGCACG
GGACAGTACCTGTTTTGGCAAACCATTTTCGTGGTGGTGTGGATTTTCCTCAACATCGGT
GGTTGGGCCTGGAGTTGGGACCCCTACCCTTTCATCCTGCTCAACCTGGCATTCTCCACG
CAGGCTGCTTATGCTGCTCCGCTGATCCTGTTGGCGCAAAACCGTCAAGAAGACCGCGAT
AAGCACACCATTTTGGCGGATCGTCGGCGTGCTGAAGAGACAAAAGCCGATACTGAATTC
CTCGCACGGGAACTCGCAGGCGTTCGCTTAGCCTTGGGAGATACTGTCACACGTGACTAT
TTGCGCCATGAGTTAGAAGATCTCCGCGGACTTCTTGACCGCATTGAAGCCAAGCTCGAC
GACGAGGCAGCGTCCCGTATTGCAGACCGCCACGAACAGCACGGATCAGGACCTCAAGAT
TTGTCTGACCCCACTCAGGGTGATGTTGCAGACGAATTT

>RXA02069-downstream
TAGGGAGTATCAAAACTTGGGAC

>RXA02070-upstream
AGCACGGATCAGGACCTCAAGATTTGTCTGACCCCACTCAGGGTGATGTTGCAGACGAAT
TTTAGGGAGTATCAAAACTTGGGACTACTATCGATACGTG

>RXA02070
ATGACTCAAGTAACCGAATCCGCTGTCCGCAGCGCGCTATCCCGCGTAGAGGATCCAGAG
ATCGGTAAGCCCATCACAGAGCTCGGCATGGTCAAATCAGTGTCCATCGACGGCTCTGAT
GTCCAGGTGGAGGTCTACCTGACGATCGCGGCTTGCCCGATGAAAACCACCATTGTCACC
AACACTGAAGCAGCTCTCAAAGACATCGACGGGGTTGGCCAAGTTCATGTCACCACCGAT
GTCATGAGTGATGAACAGCGCCGTGCGCTCCGCGTCTCCCTGCGCGGTGAAACTTCTGAG
CCAGTGATTCCATTCGCTCAGCCTGGTTCCACTACCCGCGTTTACGCTGTTGCTTCCGGC
AAAGGTGGCGTAGGAAAATCCTCCATGACGGTGAACTTGGCTGCAGCCCTAGCCAAGCGC
GGGCTGTCTGTGGGAATTTTGGATGCCGATATTTACGGACACTCAGTGCCCGGAATGCTC
GGCTCGGACCAACGCCCACACCAGGTCGATGACATGATCATGCCTCCCCAGGCGCACGGC
GTGAAGATGATATCCATTGCTCACTTCACCGAAGGAAATGCTCCTGTGGTGTGGCGTGGA
CCAATGCTGCACCGTGCCATCCAGCAATTCCTCACTGACGTGTTCTGGGGCGACCTGGAT
ATTTTGCTGCTGGATCTTCCTCCAGGAACTGGTGACATCGCCATCACCGTTGCCCAATTG
ATCCCGAATGCTGAGTTGCTCATTGTGACCACTCCTCAGGCTGCCGCAGCTGAGGTTGCC
GAGCGAGCAGGAACGATCTCTGTGCAGACCAACCAGAAGGTTGCTGGCGTGATTGAAAAC
ATGTCTGCCATGGTGCTTCCTGATGGCACCACCATGGATGTTTTCGGCACCGGCGGCGGT
CAAAAGATTGCTGATCGTCTTACCGCTGTGACAGGTGAAGAGGTCAAGGTTATCGGATCT
GTTCCATTGGATCCGAACCTGCGTATCGGTGGCGATGTGGGAAATCCTATTGCGATTTCT
GAACCACACTCCCCAACCGCTGCAGCGATCAATGAGATCGCTGAACACCTAGCTCACCGC
AAGGTATCGCCCACCAAA

>RXA02070-downstream
TGACCCAGAACCACACCGCAAAC

>RXA02071-upstream
CATGGATTCCCATTTGGAGCCTTATTTACACAGGCCACCTGGCTTGTTTCCCACCGCGAT
GTGCCACAATAACGCCATAACAGAAAGGCATACTGACACA

>RXA02071
ATGTCCAACTCCCCCACCGACGTTTCAACGAGCGCACCTCGAATTATGATCGCGCCAGAT
TCCTACAAAGGAACCGCTACCGCATCAGAAGCTGCGCAATACTTAGGCGAAGGCGTGTTG
GAAATTTTGCCCAACGCCTCCATTACGTTGGCACCCATGGCCGACGGTGGCGAAGGAACA
TCCTCAGTTTTCGGCGGGCAGGTCATAACATTACCCACGACAAATGCCGCGGGACGCCTC
ACCGAAGCCAGCTACACCTTAGATTCCGAAACAAACACTGCCTACATTGACATCGCCGCA
GCCTCCGGTTTGCCCGCCGTTGCAGACGATCTAGTCCCCACCACCGGCGATACCTACGGC
ACCGGCGTTTTGATCGCAGACGCGGTCACCCGTGGCGCAACTCGCATTGCTTTAGGCCTT
GGCGGATCAGCCACAACTGACGCCGGCTCAGGA

>RXA02076-upstream
TAGTTTCCAAGAAACCATTTAGGCTTTTTCACCTTTCCGTCTAGCGATCCTCATCTGATG
TATGTAGTCACGATGAGGTACGAGTAGGATCTTCCTGGTC

>RXA02076
ATGAAATCTCCATTTATTTTTGATGTCGCCGCACTCCTTCGTGGAAGTGCCCTTCCGGAA
CACCTCACCCAATCAGGTCCAAGCCCGACCCGCATTGGTCCGGAAATGATCGCGATCCCC
GAGGGCGGAAAAGTTATCGTAGAAGCCCAGATCATTCCACTCGGTGGAGGCCTGGCCGTC
GAAGCAGATATCGAAGCGCAGCTTCTGGGACAGTGCTCCCGCTGCCTCCGCGAACTCACC
CCAACCAAGACGCTGCACGTCTCTGAGGTTTTTGCTGCCGATCCAGACTTTGTTACTGGT
GAAGATGCAGCAGATGACGAAGATGAGCTGCCAATGGTTAACCAAGACCAGATTGATCTG
CTTCAGTCTGTCATTGATGAAGCTGGTCTGACCTTGCCGTTTAACCCTGTCTGCGAAGAA
CTTGGGTACGGCGCATGCCAGGATGATGAAACGCCAGCTCCTGACGGTGTCTCTGAAGAA
GTAGAAGACGAGGAAAAGGTCGATCCGCGCTGGGCTGGTTTGGAGAAGTTCCTG

>RXA02076-downstream
TGAGCAGGAAAAAGAATCGCCTC

>RXA02080-upstream
CGTAAATTCGAAGCGAGCTTCTAATTCTAGCAAGCTTGGTGATGGAGTATCCTGCCAAAA

TTTGTCCTGTTGCTTATTGTGCAGGAATTCGGAGGCGGAC

>RXA02080
ATGTCAATCGAGTGGTTACAAATTGTTGAATTAGGAGCGATCTTTGGTGCAGGTTTCCTC
GCAGGAAGCATCAATGTAATTGTCGGAGCAGGAACATTAGTGTCGTTTCCTATTCTCGTG
TTCCTGGGCCTTCCACCGTTGACTGCCACCATCGCCAACACCATCGGCATCGTTCCTGGA
AGTATTTCGGGTGTGGTTGCTTATAGACGTGAACTACACGCCCATGTAAAAACCATCAGA
TTTCTGCTGCCAGCATCAATCCTCGGAGGGATCACCGGCGCCTCGCTCTTGCTGCATTTC
TCCGCAGATGTTTTTACAGCAGTAATTCCCTGGCTGATTGGATTCGGCACGCTGTTGGTT
ATCGCAGGTCCATCAATTAAGAAGCATGTTGGCGCTCATACTTCAGGTGGCATCTCTGCT
GGGTTTAGGCAATTGCCTTTCCCGAGCCGAACCACCTTCATCGTCTCAGTATGTGGTGCC
CTGTTGCTGGGCATGTATGGAGGGTACTTCAGCGCAGCTCAAGGCATTCTTCTCATCGCA
TTGCTTGGCATCACATCAACGCTGCAGATGCAGGAACTCAACGCCATCAAAAACCTCACA
GTGGCGGCAGTTAATCTCATCGCAGCCAGTGTTTTTATAATCATCTCCCCTGAGTTGATC
TCCTGGCCGACCGTTGCCTTAATCGCGCTTGGCTCAGCTTTAGGTGGATACATCGGCGGA
CGGTACGCCCGCCGACTTCGCCCCAGTGTTTTTAGAGCATTTGTGGTCATCGTCGGAATC
ACCACGGTCATCGTTATGACGATCGGT

>RXA02080-downstream
TAATGCAGCAGACTAGTAACCCC

>RXA02081-upstream
CCTGGATGATGTCACTGTCTTAAATCCGGTATACGCAGATGATTTGTGGGAAGATCCGGA
AGCTCAACATAATTTTGCGGTGCCACCGGTACAAAAACAT

>RXA02081
ATGACGTTAAGTGGCTTGGAGCTTTTAGAGTTCGAGCGTCGAACAGCTGCGATGGAAACC
AGGCTTGGTCGGCATAATCGGGGAGCGGGTGGCGCATTTCCTGAGGCGGTGGTGTCTCGA
AGCGTGGAGTTGCCACTTTTTGTACAGGCCCGGAATTTCCTCAACAATCAGCAGATCAGA
GCTCAAGTGCATCGCCGTATTTTGGAGCAGCTTCCAACCGAGGGAGAGATTGTGCTGTTG
GGGCACAGTTTGGGGTCGGTAATTGCTGCAGACCTTTTGAGGCGATTGCCGCCAGAGCTT
ACGGTGAAGGGATTTGTCACCATCGGTAGTCCGTTGGCAAATGGTCAATTCAATGTGGAT
GATTTGTTTAAGTTGCTGCGCACGCCGTTGAGCAATGTGTCGTGGTGGGTGAATTTTTGG
AGTGGATCTGATCCTGTTGCAGCAAAACGCGGAGTGTCGGTGGCTGTTCCGTGGGTATTG
GATTTTCGTGTGAAAACCTCACTGGTCCCAGGCCCTGGGCATTCTTCGCGGGAATACTGT
GCCAATGATGCAGTGGCGGAAGCAATTGGGTTTGGGCTGTTCGGATCGCGCAGCAAAGAA
ATCGTCCTTGCGGAGAAAAATCTGCAGATTCCGCTCAATGACGCGGAGATTTTTGTGCTG
CAGGCGCTGCGTTATTGTTACCTCATTTTGCAACGGCTCAAAGGCGATGAAGCCTTAAGG
TATGAGTACGCACTTCGGGAGACTCAGGATCGCCTGATTGAGGAGATTAAATCCAGAAAC
GCCGAAGAGGGCCGGCCGATTCCGAAGGAAATCGCACGCCTGGATTTTGATAACGGTGAT
CCAAACGCAGCAGCTCCTGTTCCAGGTTTGAGCCCATTTATGCCCAAAGAGCAGGCAATT
GAGCGGCTTTTAGAGATCATTGGACAGAACCTGCTGCTGCCTTTTGAGATCGAGGTGCCG
GAGAAAATTCAGCGGGAAGCACTGAGGGATTTCACGGCGGAAACTCAATTGGGTTCCACC
GTGGGCGCTGATATTTTTGATGCATTGCAAATGGCTGTTGGGGTGGTGTCGGGAAGCGCG
AAGAGCAATTGGCGCAAATGGGGAGCGTTTGGTGTGGGGGCTGCAGCTTTGACCGCTGCA
ACGGGTGGTTTGGCTTTGGCGGCTGTGCCGACTGTTGCTGGAGTAGCCACTGTTGCCTCG
ACACTCGCAGCATTTGGTCCAGGTGGGATGATGGGCGGTTTGGTCACTGCAGGAACACTG
CTCACAGTTGGTGGCGGCAGTTTAACCGCTGGGGTGTTGAGCTCGGTGAACACCACGGAA
GAGATCGAAGCGCTCGTTGTACAGAAGCTAAGTTTGGCTATTTTGTGGCAGCGCCATGAG
ATAGATAGAACTCATGAGGTGTGGGAAGAATTCGCGGAGGCAGAACGTCTGATTGTGCGG
GAGCACACGCGTGTGAAAAACGTGTCGGATAGTTCTTCGCCCATTTTGAAAGCTTTCGAG
CAGCAGCGTTCGACTATTGAGCGGGCGTTGAAGTATTTGAGCGATCATGGGATGGAACCT
GGCTGGTTTGAAGAACTGGAACCACCAGCCCCAACACCGTTTCTAAAACTGCGGGCTAAG
AAAACTGAT

>RXA02081-downstream
TAGGAGAAACACAATGGAGAAAG

>RXA02084-upstream

CGTTGATGGTTGGGTGGTGGGTCACAGTTTAGAAAAAGTGACTTCAAATCACGTCGAAAA
GAAATTGAAAGTACTTAAGAAACATGTCACGCTAGGAGAC

>RXA02084
GTGATAATCATTGCAAGCGTTGTTTTCCTCCTCGTTGGCGCAATGTTGGCGAATGCTGCC
GCTGCGCTCTTTAGTGCCAGCGAGCCATTCGGACGAATTTCCTACCTCATTGGCCTACCT
AACGAAGACGACTTCGTGCCGTACTCACTACGGTTCGTGGCCTTTTTCCCACTGATGCTC
TCCGCATCGATGGCAGCATCCTTCTTCGGGGTGTGGGCAGTACTAATCATTCCTTTCGGT
TACTTCCCATCACTGATGATGGTTCATAAGCACAACAAGCAGGTACAGCGAACCTGGGAT
TCCGTCACCGTTGCTGACTTCTACGAGGATTCCACCCCTCTGGTC

>RXA02084-downstream
TAATTTCGATTTCTAAATGTCAT

>RXA02089-upstream
CTAGCTGACCAGTATTAATACCAATAATAGAACATATTATCGAACAATGTCGCTTGGGTG
CTCTACACTTCCCACTATGATCAAACACCGAAACCGCCTA

>RXA02089
ATGTCTTCCATCTACTCCGCAACTCGCTACGCCGCCCACTTCAAAAGCGTCTTCCCCACC
GCCCTGGATGACATTCAATCCATGATGCGCCACCCTCGATCACTGGCCAGAGCCATACCC
ACGTGGCGCCCGCCGAGCATCCCGCTACCGTCACTTCCCGGCGAAGATCCCCTCACCCTC
ACCTTGTCACGTCACCGCGCAGGCCCCGCCGCCCGCCAAATCATCCGCGAGTTCGGTGAG
CAACGTGAACCCGCCTATCTCATCACCATCCGCATCACCAGCCCAGAGGGCTTCAAAGTA
TCCACCCGCCTCGCCGAAGGCTGGATCCGCGCAATTCTCAGCACCGCGCACAGCGGCACT
GTCCACCAGCTCACCGATGAGCCGGCACCGACGTTTTGCTGGCTTGTCGACGCCCACTTT
GATCCGGTGCGTTCCCCTTCCTTCCTTTTCGAATATTCCAAAAGTGCAGCC

>RXA02089-downstream
TAGAAAATGACGAAACCCTGGAT

>RXA02090-upstream
AGGTGAAAGGCTAGGCGCGGATTCGTTGTGGACGCTAGGCTTGTCGGCAGTGTCTTTGGG
GGACGTCCCCAGCACAAACCAGATGGAAGGTCATCAGAAC

>RXA02090
ATGAGCTTTTTTGAGGACATCGCGGCTGGACTTGATAGTGACGGTATCGAGTCCCGCGTA
AACGGCGACACAATGTTCGTTCCGATCACCTCTGACTTGGAAATCCAGTTCGTGGAGATC
GATTCCCTCCTACCTGCAGCAAACGTTTATATCGCTGCAGCCAATGTTGATGAAGACGAT
GATGAGTTCGAGGCAGTTCTCGTTTCGGTGGTGTTCTCTGTTGAGGATGCTGTCGCTGCT
GTCGCAAAGCATGTTGCTACTGATCAGGTGGTGACTGTGCTGCGTGATCTACTTGAAGGA
ACTGATGAACGCATCCAGGATTTGGAGTTTTTCCAGGATGCAGTGAATGCAAATTTGGTT
CGTGCGGAAGTCGGCCAGAATTCTGAGCTTCAGGTTTTGGTCGAGGTTGAAGACGGCGTC
CCAACCGCAACGGTCAATTTCATCGCGATCGGTGAGTCCTTTGAAGATCTGATTGATCAG
GCCATTGAAGAATTGTGGGAATCCGACGGCGACGCAGTTCTATCGGATGAAGATCGCCAA
CGCATGTTCGCTGATTTGACCTCCGAGTTGGAATTTGTCACTGATGAAGTCCTCGACTTG
GGTACCTTCACTGATTTTGATCGACTTTTCGATATCCTTTCCCTCGCCGATGACCAGGCT
GAGGATTGGGAAGCACAGCTCGTTCCTTTTGAGGACGAGGAATTTGATGAGCCGGATGTT
TATGACCTTTTCGTCGATGACTCTGAAGAAGATGACGACGACCTCGATGATGACGAGGAC
GATGAGGATGATGACGAAGAC

>RXA02090-downstream
TAGATTTTAGCCTTTGTCGCGGT

>RXA02091-upstream
AGATCTAGCCAACGAACTTGATTTCATCGAGCCGGAAGAGACAGAAGAAGAGCAGCAATT
GAAGTGGCTTAGCCTTATGCAGTTTTTTGGAAGTAGATAA

>RXA02091
ATGAGCATCTGGAAACGTCTGTTAGTGCAGTACCCGCGCTTCGCCGACACCCTCACAGCC
GGCCAACCCATCACGCTCGAGGAATTAGCAACCCCGGAAGTGATCTTGGAAGCTGTTGCC
AAAGGCCAAGAAATTTTCGGCATTGAGCAGCCAAAACATGCAGCACAACTCTGGTTTCAC
TCCCTGTGCACCGCAATTGTCGGCCCCGCCGTCACCGCCATGGTGGAATTCGATGTCATC
CCCAGCCTCGACATACGTCGAGGTCAGCTGCATAACATCGACGGTTACTGGTTCGGCTTC
AGGCCGGAGGAGATGCTTGTCGACGCCTCCCTCCACCTGTCGGGCACCCAATTCGGCGAG
AGTATCCGCGTGGTGATTGATGCATTATGCGCTGCCACGGATCTGCGACCGGCACCCCTG
TGGGCGGTTGCCTCAGATGCGTTGGGAATCGCAGCTAGCGGCGCAGGTGTCGAGGCCTTT
GAAGAAGAACATGCCCGCGAGGTGGCGGAAGCCCTCATTGAAGGAATGAATAGTGTGAAC
TCAGTTCCATCGCCGCGGTTTAACGACGACGATTATTTCATTCGAGCTGGATGCTGCATG
ATTTTCCACTCACCACGAGCTGATTTTTGCACGTCGTGCCCACAGAAGAGG

>RXA02091-downstream
TGAAAGGCTAGGCGCGGATTCGT

>RXA02094-upstream
TTCCACCTCTACACCGGAGTTCTTCCAACCAACGACCAGATCATTGCTGCGGAGGAGTTC
TCCAAGTAAATTTCTCTCCCCTATTTTTAGGAGGCACCAC

>RXA02094
ATGGCTGAACACAACGCCATCATCACGGATGCAGTACATTCCGACCCCGCTGTTTTAGAA
GACAACGCCGGGTTCAGCGGAAAGTACCTAATCCGTGCCCTGGACAAGGCAGCTCATATG
CAAACAGGTGCCATCGAGGGATACATTTCTTGGCTTCGGAAGCACAATCCTGAGAAAACA
CCGGCGCAGCTGCAGGTACTCGTCGACAAGCATTTTATGCGCCTTGCCACCGGCTCTGGC
GCTGGTGTGGGCATGGCTGCGGCCGTGCCAGGCATTGGCTTTGTCACGGGTGCTCTTGCC
GTTGGTGCTGAATCGTTGGTGTTTTTGGATGCTGCTGCGTTTTACACCATGGCATCCGCG
CACCTGCGTGGCATCGACATCCGCCATCCTGAACGCCGACGTGGTTTGATTTTGGTGGTT
CTGCTGGGCACCGCAGGCAAAGCCATTGTTGACGCAGGCGTCGGTGATTTATCCAAGAAA
AACCACGCGCCGGGCATTGCGATTTCCCGGTTTAATATCGGTGGCTTGATGGAAGTCAAC
GGCCGACTGATGCGCTACGCAGTGAAGGAAGTAAGCAAGCGTTTCCGTTCGGCATTGATT
GGCAAAATTCTGCCGTTTGGTATCGGTGCGGTGCTGGGCACGATGGCCAACCGCAAAATT
GCCAAGAGGACTGTCGGAAACGCATACGACTCTCTTGGTCCTCTCCCCACCCATTTT

>RXA02094-downstream
TAAGTACTCAAGACCCTTCCAAC

>RXA02097-upstream
TTGGCTACAGATGTTTCAGCGCTTGCAGTGGGGTAGTGTGTTTAAACATCACAATTAGTT
CTAGAGGAAAACGCATTTTTTGCGCGGGGAGAGTGTATAC

>RXA02097
ATGCCGGCTGGCATCGCAGACATGACAGATTCATTGCTCGGATGGGCATCACAAACTGAG
CTGGATCTGAACCAGCGTCTTGCAGGGGTAGAGTACTTTCCACAAATTCAGCTGCGACAC
GATGAGCTCGAGCGCATTCATCGGTTTTACGGCACCTTTTTGTCCCGCCAGGTAGGCGCG
GGCGCAAGCCTTGGGGATCTTTTTGAAATGACCCCATGCCTGACAGTCACCACCTTGGTG
TCTCGGGCGTCACGGATCAGCGATCCAGCAGATTTCTTCGGTGAATACATCGGAGGACTG
GGACTTAGCGCAGAACACGCAGCAGTTGTTGAAGGGTTGACCGAAAAGCTCTTCGCACAG
GCTGGCCTGCTCGTTCCTGAGGGAATTGCATCTCCATTGGAGTTGTTATCCATCCACGCA
GGCATTAGTAACCACGAAGTGGCCGCAGTGCTGACCGAAGTGGAAAACGGCACCACCGAA
TATCCATTCATGTTCGACGCTGTCCTGCGCCTAACCCCTGAGTGGGCACAGACCCTTATC
GGCGGAGTTCAAGAACTCATTGAATTTGCCACCACCCACCGAACTTCTTGGTCAGACCGC
CAGCGCGAATCCTCACTGCCAGCCATGATCGATGAGATCGTTGTGGCGGAACTTCGGGAA
CGCCCAGTTGGTACTGCCGACCGTGAAAACTCCGTTGGTGTGGCACTTCGTGAGCTTCGC
CCACGCCTCATCCTGGATGCAGAACGCCGCAAAGTCTGCCTGCGTCTACCTGAACAGCGC
GTCAGCGACGATGAAATCAACTGGCGAGTCAGCCTAGAAGGCACCACCCGGATTTTCTCC
ACCCGCCGAGCATGGGGCGATACTTCTGGATACTCCGAAGCCCTCGACATCACTGTCGAG
CGTCAAATCCGCGAAACCACCGTCACCGACACCTCAAACCAAATCACCTGGGTTGTCCCA
GTCGTGGACTTCAACGACCCAGTGCTGGTGTTTTCCGCGCGCGGTGAAAACCTCACCGAC

AAGGTCTCCCTGCACCATCAAGAGATTTACGTTCTCGCGCCAGCGGAAGCAAAACTCGAA
GACATGGTCACTGGCCAGCCAGTACCAGTTATTGAGCAATTCCTCGTAGAGGGCTGGAAC
TCATGGGTGTGCTCCCGCGTGGACGCCCGTGGCCTGTCCTCTCTGAAGGTCAACAAAGAA
GTCCGATGCATTGACCCACGTCGACGCGTTGCCTTCCACCACCCAGCCGAATTGGTCCCT
CACGTACGATCCATTTCCGGACTCCCCGTACACGCGCAGTCCCTGATCGCCGAGTTCCCA
CCAACCCTGAGCGGACAAGACGAAACCTGGATGCTCTCCATCTCGGCTTTCGCAGGTGTA
GGCGCTGCTGGTGAAGAAATCGCCGAGCCAGAGCCTTTGGAAGTCCCTGCCGACGGTGGC
CTTTTCGCCATCTTCGACCCAGAAATATACGACGCCCCATGGGTGGGTGAATACCTGGTC
CGACTCCGCGGCCCACGCAATGAATCCTTCCGACCCGAATTCGCCATCGTCGAAGACATG
ACCACCGAATTCGAAGTCGCCTCAGGTGCATCATTTCGAATCCCAACCACCACTGGTCTC
AGCGAAGCCAGCCTACGCGTGCGTTCCGGTGAAAAGCACTTCACCGCAGAGCCACGCCTG
GTCACCGTTGAAGCAACCGACCCCAACGCATCATTCGTGGTCACCACCGATGAAGGCGAT
CAAATGCCATTGCGATTTGTGCCACCACAAATCGCCATCGAACTTCCACTGACCACCGAG
CCACCAACCTGGCGCGTCACCCGTACTGTCTGTGGACCACGCGACCTCGACGGTGCAGGC
GAACTCCGCATCCGCACCGGTGTCGATGTCGGCGATCCAAAGGTCAGTGTGCGCAACCAC
CACGGTTCACCACTGCGAACCGTGAAAATGGTCACCCCTGACAACGGCCGTACCTGGATT
GCCAGCATGAAGGAAATCGCAGCCAGTACCTTTGTGATGCCACGCGGATCCATCGAATTT
GAGTGGACTGACCGCAAGGTTGACCGTCGCGTTTCCGTGACGATTGCTGTCATTGACAAA
ACTGAGAACTTTACTGGCATCACCATCGAAGATGGAAAGCTCGTATTCGAAGAACTCGCA
GCCGGTCGCCAACTCGCTGCATGGGTGTGGCCACAAACCGCACCGTGGGTAAGCGCAGTG
GAACTTGCTGTCACCGGACCAGAGCTGGAACTCCCTGAAGTTCTCGTCGGCGCAGGCAAC
CTGATTGTTCAACTCCACACCGCTGACCCATTCACTACCTCCGTGACCCCACTGTCACCA
GGAAAAGCTGCGGTCACCGTTGAGCAAGAAGGCTACTACTCAGCACAAACCGAAGAATAT
GCACAGCTTTCAGCATTCTTCGGTGGGGAAGTAGAAGAACCACCAATCAGTGACGCTGTG
GTCCCCGCACTTTGGGATGTTTCCCATATCTGGACCGAACAGGGAAACACCGAGCATCTT
CCAGTAGTCCATGCCGCCCTGCGCTCCTCACCAGCCGCAGCACTGAAGGGTCTGTCCGCT
TCGCTGGTTCCCGCACAGGCACTACCTGGAAAAGTCATTTCCTCCGGACTGGCAGCCTCA
CCGTTCACCACGGAATCACCAGCAACAGAAGTGCACCGCACCGCATGGATCGGAACCCTG
CAACTCCTGGGTGCACTGCCAAGCGCATTCAAGGAAGCCGAAGAGCTTGGCAACCGCACA
CCACTGCTGCCAATCCTCGGACAACTTGAGGAAGTCGCCGGCAAGAACATCCTGTCCACC
CTTGCAACTGGCCGTGACTCCACTTTGGACACCGCATGCATCGACCAATCCACCGTTGCG
ATTGCCGGCATGAACGAAACCCAGCAAAAAGCCCTGCTGGACATGTTCTTCAGCAACGCC
GACATCGTTCCTGGACCACTAATGGAAGACAACACCCGCCTCATGGCAGTGTTCGAAACC
TTCAAGAAGCGCGATGCACTCCGTGAGGTTCTCCAGACTGAAGGCTTGATTAAGACCGCT
GTAGAACTTCTTCGTGCCATGCGTGGAACCCAGCGTCAGCTGTATTCCTCCGCACGTATT
CGATTCGACAAGCTCGATGGTGTCAACACTGACAACCCAGAAAACATGTGGGCACTCACC
CCAGTTGTGTCACTGGTGTTCGCGTTGTCATCCCGTTTGCATGCACACGAATTGATCGGC
AAGACCCGAACTCTCGATCGTGCATCTGCCGGTTGGGGTCGAATCGCTGATCTGGTGCCA
GACCTTGTCACCGGTGACTTGATCTCCGCGGAGGCAATGGTTTTGGGAGCTCGAAACCCA
GGACTCGTCGAT

>RXA02097-downstream
TAGTCCCTGATTTCATCGGAGGG

>RXA02102-upstream
CGGTAAAACGTCCCGCTAGTGCGATGGAATCTGTGTCGGGGACTAAAACATCAAACTGAA
TCTTCGGCATAACACCACAGTAGACAATAGCCTTGGTGTT

>RXA02102
ATGACTAGCCCCCATTCTTTTTCTGTCACCCCCATTCGCACCATGGCTGACGGCACGATC
AAACAGATTCACCCTTTCACAGGCACCGAAGTGTGGACGGTCCCTGGGCGTGGAAATCGA
CCTCTGTCACATCCCGCTTCTACGATCGTCGAACTATCTGCACACGATCACACCTCTTAC
TGTGCATTTTGTTCCGACAATATGCTCTCCACTCCGCCTGAGAAATCGCGCATCATCATT
GATAGCTCCGGCGACTTTGACATCCTTCCCGGAGCATTGCCTGGTGAGCTTTCAGAAACC
ACTCCGGAATTTCGACGAGTCCCCAATCTGTTTGAGATTGTCTCTTTTGACTACTGGCAC
CAGAATTTTGGTTTCGATATGGATTCAGAAACCGCCATGCGCATGGCGCAATACTTGGCG
ATTCCAGAAGGTCGCGAACATGTTTTAGCCATTGTGCGCACCCGACTTTCTGCCGCTGGT
GAAGATCCCGCGCACATGACCGATGGCGAGTTGTTAGAAAAAGCTCCCAGCTACTTTGCT
GGTGGTCATGACGTCATCATCGGACGCCGACACTTTGTCGATGACGCAACCACCAGTGAT
CAATTGGCCTCATCTGGAACACTGACCGTTAAAGAGCATGAGGCGTTCATCCGCCTGACT

GTCGATGGCATCAGGGATTTGTACCACCGCAACCGTTACGCACCGTATGTAGTGGCGTTT
CAAAACTGGTTGAAACCCGCCGGCGCGTCTTTTGACCATCTTCATAAACAGCTCGTCGCC
ATTGATGAACGCGGCCGACTTATTGCCGATGAACTGCATCATCTACGTGGCAATCCCAAT
ATGTACAACGAACTTGCTGTTGATTACGCCGGATACCACAACCTGATCATCGCGGAAAAC
GATCACGCCGTGGCCTTCGCAGGTTTCGGTCACCGCTACCCCACCATTGAGATTTACTCT
AAGTCCGCTATTCCTGAACCCTGGCTTCAAAGCGACGAGGAAATCCAAGCGATGAGCAAC
CTCATCCATGCATGCCATGCTGCAACCGGCGCAGATGTACCCTGCAATGAGGGATGGGTA
CACAAACCAATCGATGTTGATATGCCAATGCCCTGGCATGTGATGATCAAATGGCGTGTT
TCTACCCTGGCAGGTTTT

>RXA02102-downstream
TGAAGGTGGCACCAAGGTGTATC

>RXA02103-upstream
GAATCTGTTTGATCGTGCCGTCAGCCATGGTGCGAATGGGGGTGACAGAAAAAGAATGGG
GGCTAGTCATAACACCAAGGCTATTGTCTACTGTGGTGTT

>RXA02103
ATGCCGAAGATTCAGTTTGATGTTTTAGTCCCCGACACAGATTCCATCGCACTAGCGGGA
CGTTTTACCGTAGTCGCCAACCTTTTGATCGAAAAAGGCCTCATGGATCATGGCGTTGTT
GTCCATGATCCAGCAGCGAAAATCGCAGAAGCTGTGGAAGAGCAGCTTCGCCAGACTTAC
CGCGACGAGCATGAAGATGCAGACTTGGAAGAATCCTCGGTCAACCGTTACCTCATTGAA
GTTGATGGAGTTAAAGGCTCCGTTAACCAAGTGACCATGATTTTTGCCCGTTTGCTCACC
CCGCCAGCAGAGTTGCCAAAGGACGCTTTCCTCCTGGAGCAGGAACTTGCCTATGAAGTT
CCTGCAGTCTACCCATGGACTGTGGAGATCCTTCGC

>RXA02103-downstream
TAGTTTTGAGCTACGTATTCTTG

>RXA02104
CACGCCTGCGCCCAACTGGAAGTTGATGGCACAAAGCCAGGTATGGGCGCAGCCGGGGGC
ATTGCAATCGGACTGACGTGGCTGTCCACCCTCATGCACGGCAACGACCAACAGATCCAT
ATCCTCCCCGGCGCGCCACTGATTGCCCGCTCCAACGGAATCGAGGATGCGCTGCCAGAA
ACTGACTTGTTGATCACCGGTGAAGGCCGACTAGATTCCCAATCGTTCACCGGAAAGGTT
GTGGGCACCCTCCACGGTTTAGCTAAAGCCCACGATGTGGATCTCGCTGTTGCGGCCGGC
ATCGTGGAAGGCGGTATTCCCGATGATTTCCTAGCGGTAGAAATGATTAAATCCTCCGAC
GTTGCAGCACAATTACGTGATGCAGGCCGAAGGATCGCTCAAGAATACGTAGCTCAAAAC

>RXA02104-downstream
TAGCGAAGGATCTCCACAGTCCA

>RXA02107-upstream
AAGAAGTAGAGCTCAGCGATGAAGATTTCGCGGCAGGCCACGACCTAGTAAAAACCAAAT
ACGCCACCGAGGAGTGGACTAAGCGAGTTCAATAGTTTCT

>RXA02107
ATGGATCTGCACAAGGTAGCTGCAGCGCACGCGGCGACTCTTCCCCTGAGCACCAAAGAG
TTTCCTTTCGGACCCGAGCACGAAGTGTACAAAGTGCGGGGCAAGGTATTTTTGCTGCTC
ACGATACTAAATGATGAGCCGATTATCACGCTGAAATCAGACCCCGAGATTGGCGCTTCA
CTACGCAGTGGCTTCCCCACCATCCAGGCTGGATATCACATGAACAAAGTGCACTGGCTG
AGCATTAGCGATGGTGAACGGATCACGAAAGACTTCATCGAAGGTCTCGTGGAAGAGTCC
TATGAACTGGTAATTTCCACCTTGCCGAAGTATAAAAGGCCT

>RXA02107-downstream
TAACTTGGTTGCTTGCGGGTGGC

>RXA02108-upstream

TTGATCCCGGTACTTTTGGCGCCCCAGATTTAGATGGGCGACCATCCTGATCACCCACAA
TCATGCCGATCACGTTGATCCCGAGTTGCTCAAGCCCGGC

>RXA02108
ATGACGATTTACGCGCCTCGATCAGTAGCACATTCAATTCCAGTAGAATGCCACATCGTG
GAACACGGCCGAAACTTTACCGTTGGGTCCCTATCCGTTGAGGTTCTTGGTTCTGAACAT
GCGATGCTCACCCATTCCATGCCGATCGCGGAAAACGTTGGATACTTAATCAACGGCCGA
GTGCTCCACCCCGGCGATACCTTCCAACCCATTAAAGATGTCGAACTCGCCCTGGTTCCT
GTCAACGGCCCCTGGGTGAAAATGCTGGATGTGGAAGGCTATTTGAAGAAATTTCCACCA
AAGCGTTTCATCGGCATTCACGATGGCATTGTTAATGATCGCGGTTTGGCGATCAACAAG
AAGTTCTTAACGCATCTTGGTGAAACCTATGGCTCGGAATACTCGCCGCTTGAAGAGGGA
GAGTCGTTGGAAATT

>RXA02108-downstream
TAGATTCTTGGTTTAGATTCTTG

>RXA02109-upstream
GACTCTAAGGGAAGTGTTTCGCTTCAACCCGTACAGGTCTAATATGTCGGGAGTCTTGTT
TTAAGCTCTTATATAACCTGTATAGGAAAGCGAAAACCTC

>RXA02109
ATGCTTGCAGTGCTATTCGGGGTGGTGGCCGGTGCCATCATGCCTTTCCAAACTTCGGTG
AATAATAGATTGCGTCAGTCCGTGGGAGCACCACTGCTGGCGTCTTTTATTTCCTTTTTG
GTAGGAACTTTTTCACTCCTGGTTGCAACGTGGATCACCAGTGGGCACCCGTATCCTGCT
CTAGGAAATACAACTGGCCAACCGTGGTGGATTTTCACCGGTGGCATGTTGGGTGTTGTG
CTGCTGACGGGAAACATTTTGCTGTTTCCCCGAGTCGGCAGCGTGCAGACCGTTATTTTG
CCCATCTCCGGACAGATCATCATGGGCCTAATTATCGATACAACTGGCCTGGCACATTCG
CCTCAAGCACCGTTAACCCTGTTCAGAGTATTGGGTGCTGCTGCGGTACTTGTTGGATCG
CTGGCCGCAGTGGGAGTGTTCTCTAAGAAAAACATCGGACAGACCCAATCCCAAGGTGCC
TCCATTTGGTTGTGGCGCCTCTTCGGAGTGGTGATGGGCATGTGCCAAGCAACCCAGGTT
GCAGTCAATGGTTACTTGGGAACTGTCCTAGGATCCCCCATTGAGTCAGCACTGGTGTCT
TTCGCTGTTGGCACCACCGCGCTGTTTATTCTGCTGTTGGTCACCCGAACCAAGTGGCGT
GGAATCAACGGCGCTGGGAAGAAAAACCCATGGTGGATGTGGATCGGTGGCGTCATCGGC
GCGACTGTTATTTTCAGTACTGCTTACCTGGGACCGATCATTGGCACTGGTGTTACCGTG
GTGGTTATGTTGCTGGGCATGATGTTGGCCAGCCTGATGATCGACGCTTTTGGAATCCTT
GGCAGCCCGCGCCGCCACATTCACATCGCGCAGCTTCTCGGGCTCGTGGTGATCATCCTC
GGCGTAACAATGATCAGAATC

>RXA02109-downstream
TAAACCAAGAATCTAAACCAAGA

>RXA02114
TCCATCGGCTACGCCTGGACCACCGCATTTCACGCACTCACACCAGGCCTTGGCGGCATC
GCCATTGGTATTTGGCTGCTCGGTGGTGTGCTCGGTGGGTTGGTTATCCGCAAGCCGGGT
GCCGCAATTTTCGTTGAAGTAGTGGCCGCATGTGTCTCTGCAGCGCTTGCTTCACAGTTT
GGTATCTCCACCATTTACTCCGGCTTGGCGCAGGGAATCGGCGCTGAAATCATCTTCGCG
CTGTTCCTCTACCGTCGCTACAGCCTGCCCACCACCATGCTTGCAGGTATGGGCGCAGGT
GGCGGCGCAATTTTCCTGGAAATGTTCTTCTACGGAAACCTCGCAAAGACGATGTCCTTC
AACATCATCTATTCCACCACTGTCCTTATTTCCGGTGCGATCCTTGCCGGCCTGCTCAGC
TGGTACCTGGTCCGCGCGTTGGCGAGGACTGGTGCACTTGATCGTTTCGCCGCTGGCCGC
GAGGTA

>RXA02114-downstream
TAAATGACCACCGCACTTGGAAC

>RXA02117-upstream
TGAACACAAACTACCACGTTTATTGCATCATGCAACACCCTTGCTAGGATATAAAATACT
CTATGAGTCCAGACGTTTTTAAAGGGAGCGAATTACCATA

>RXA02117
GTGTCTACAGATCCAGAAGAGTTCGACCAAGCTGAAACCCTCGATCAACTCGCGTATGAG
ATCATCCTGCTCACCCGGTATGGTGTCCAAAACACACCGACCAACAAGCGCGAAGCCATC
ATGGATCGCAGCGCCCTCATCTTGCTCACCCGCCTTGACGCTCAAGGACCTATGACAGTT
AATGAGCTAGCTGAAAGCTTTGGACTTAACGTTTCTACCGTGCACCGCCAACTCAAAGCA
GCCATTGCCAATGGCTTAATTGAAGTCGTCGATGATCAAGCATGCCCCGCTAAACTTCAT
CGTCCAACTGAGTTGGGTAAAGAAAAACTGCAGCAGGAGCTTCTTGCCCGCCAGCAGGAT
CTCACCCGCATTCTTCATGATTGGGATGAGGAAGACATTAAAACGCATGCCAAGCTATTG
CGGAAGCACAATGAAAGCTTGGAAGAATACCTCGATATGAAGTGGCCCCGCCCC

>RXA02117-downstream
TAAGTGCCCATAAACGCACCTCT

>RXA02121-upstream
CCGGGAAATCTTCAGGCGTCTCCTCCCATATGCTGCTGACAAATTCCAGAACAGGATCGT
TGGGATACCTTCGAGACAAACTTCCGAAAGCTCCGCAACC

>RXA02121
ATGATCACCTCACCATTTGAGCGCGAGCTGAAGCTGCTCAACGAGGGGGAACTGGGTATT
GTCCAGCAGTTGGTGGAATCAAGCAACATCGGATTCATCGTCGATCTTGAATTAGATGGC
GATTATGGGTGGGCGGTCTACAAACCGGAATTGGGGGAGCAACCCCTGTGGGATTTCCCT
CCTGGCCTGTACAAACGTGAACGTGCAGCCTTTGTGATCAGTGAGTTTTTGGGTTGGAAC
ATCGTGCCTCCAACGGTGATCATGCACGATGCCCCGGCTGGTGTGGGCTCGGTGCAGTGG
TTTATTGAAAACAATGGCGAACACTATTTTCCACTGTTTGACACCCGCGCTGACCTGCAT
CCGCAGTTTGTCCGCATGGCTGTGTTTGATCTGTTGTGCAACAACACTGACCGGAAATCG
GGCCATGTGTTGCTAGACGGCGATCATATTTGGGGCATCGATCACGGGTTGTGTTTTTCC
GTCGAACCGAAGCTGCGCACGGTGATTTGGGATTTCGCAGGCTGCACCATTCCAGATGAC
TTGGTGACAGATGTTGAGCAGCTTTTGGAGGACGTCCCGGAAGAACTTCATCAGCTTCTT
CATCCCGCAGAAATTGATGCGCTGCAGCGCCGTGCCTCAAGAATCAGCAGGTTACCGTTC
CTTCCGCAGGCGAAATCGCATCGTCAATTCCCTTGGCCACTTGTT

>RXA02121-downstream
TGAGTAGGCTGGCGGGCAGGTGC

>RXA02123-upstream
GGATTGAGTCTTTTCGGCAGCTGCGTGTGAACCCGGCTTCATGACATGCAGCATACCTGT
GCGAAAAATTCCTGACCGCCCACTTAAAAAAAGGTCTAGG

>RXA02123
GTGTGGGGTGTGAGTCTTCCACCAAATGTACAAACTGTCGGTGAGCTGAAGGCCGCCGGC
CACATCTACCGACCTTTGCGCGTAGAAATCCGCGACAACCTCCTAGCCAAACTTCGCAGC
GGCGAAGATCCGTGGCCAGGCCTGCACGGCCTGAACTACACGGTCATCCGGCAGCTTGAA
CGCGCGCTCATCGCCGGCCACGACATCGTGCTGCTCGGCGAACGCGGCCAGGGTAAAACC
CGCCTGCTCCGCACGTTAATAACGCTTCTCGACGAGTGGTCCCCGATCATTCCCGGGCGC
GACGTTCCAGAACACCCTCTTGCGCCAAACGTAGAGATCTCCGATGATCAGCCCATTGAA
TGGGTACACCGCGATGCGCGCTATACCGAGAAACTTGCCACCCCAGATACTTCCGTGGCT
GATCTTATCGGTGATGTTGACCCAATGCGTGTTGCTGAAGGCCGCAGCCTCGGTGATCTA
GAAACCATTCACTACGGTCTGATTCCTCGCGCCAACCGTGGCATCGTGGCGATCAACGAG
CTTCCTGACCTCGCTGAACGCATCCAGGTTGCCATGCTCAACGTCATGGAGGAACGTGAT
GTGCAGATTCGTGGCTACAACATTCGTTTGGACTTGGATGTGCTGGTTGTTGCCTCAGCC
AACCCTGAGGATTACACCAACCGTGGCCGAATTATCACTCCGCTCAAAGACCGCTTCGGT
GCAGAAATCCGCACCCACTACCCACTTGAGTTGGACGATGAAGTGGCAATTATCCGCCAG
GAAGCAGAGCTTGTTGCGCAAGTCCCTGATATCTTGGTTGAAATTCTTGCCCGCTACACC
CGAGCGCTTCGTGAATCCTCATCGGTGAATCAGCGTTCTGGTGTGTCTGCTCGTTTCTCC
ATTGCAGGTGCAGAAACTGTGGCCGCAGCAGCTCTTCGACGCGCAGCAGTGTTCGGCGAA
GATGAGGCCGTTGCCCGCCTGGTTGATTTGGAAGCAGCCGTGGAAGTCCTCGGCGGCAAG
ATTGAATTTGAATCCGGCGAAGAAGGACGCGAATGGGAAATCCTTGATTATCTCCTGCGC
ACCGCAACCGCAGAAGCGCTGCGTTCCACTCTGCGCTCGCTGGATCTCACCCCGCTCATC

GCAGCATTAGACGGCAGCATCACCGTTTCCACTGGCACGAACATCACCGCGTCAGAATTT
TTGGCTTCGCTCCCCGAACTCGGCGAAAGCACGCTATATGACGACATCGCTCAAGCTTTT
GGTGCCACCACACCAAGTACTCGCGCGATGGCCATTGAGCTTGCTTTGGAAGGTCTTTAC
CTTTCCCGAAAAATTGCCAAGGATTCTGGCGAAGGTGAAACCATTTACGGT

>RXA02123-downstream
TAACTGGTTTTAAGGAGCACCAC

>RXA02124-upstream
GCTTGCTTTGGAAGGTCTTTACCTTTCCCGAAAAATTGCCAAGGATTCTGGCGAAGGTGA
AACCATTTACGGTTAACTGGTTTTAAGGAGCACCACAGCC

>RXA02124
ATGGCCACTTCACATTCACGACCCCGCCGCAGCCGTTACGGACGCTACACCGGAGGCCCA
GATCCGCTGGCACCTCCAGTGGATCTCAGCGATGCCCTGCGCGATATTGCTGATGATGTC
ATGGCTGGTTATTCCCCTGAGCAGGCACTACGTGAATACCTGCGCAGAGGCGCCCGAGGA
CAGGAAGGCCTCGATGATCTAGCCTGGCGTGCAGCCGAACGCCGCCGAGAATTACTTAGC
CGAAACAACCTCGGTGGCACACTCGCTGAGGTTCGCAAGCTTCTCGATGAAGGCCTCAAG
CTGGAACGCGCTCAACTGGCCCGCGATATCGATATGGATGACACCGATCGAGCATTCCGC
GAAATGCAGATCAGCAACCTCCCTGAATCCACCGCCGCTGCCGTTTCCGAGCTAAATTCC
TACGATTGGCAATCCCAAGAAGCACGCCAAAAGTTTGAACAAATCCGTGACCTGCTTGGC
CGTGAAATGTTAGATCAGCAATTCTCCGGCATGAAACAAGCCATGGAAGGTGCCTCCGAC
GAGGACAAAGCAGCCATCGCCGAAATGCTGCGCGATCTCAACGACCTGCTCTCCAAACAC
CGCGAGGGAACGGACACTCCCACCGATTTCGCCAATTTTATGGCCAAACACGGCGAGCAC
TTCCCCGAGCAGCCGCGCGACATCAATGAGCTCATCGATGCCCTCGCAGCCCGTTCCGCC
GCAGCCAGTCGCATGTTCAACTCCATATCAGAGGAACAACGCCGCGAACTCATGAAACTA
TCTGCCCAAGCTTTCGGATCCCCAGAGCTGCAGGAATTGCTCGGTGACCTGGCTGGAAAC
CTCCAAGGTCTGCGCCCCGACCTCAACTGGGATGGCTCCGAACAATTCTCCGGCGACGAA
GGCATGGGACTTGGTGATGGCACCGGCGCCATGCAGGACCTCGCCGAACTCGACAACCTT
GCTGAACAACTGAGCAACTCCCACACCGACCTCGACATTGATGCGATTCGCCGCCAACTC
GGCGATGACGCCGCTGTCTCTGCCGAAACTTTGGCCAAACTGGAGCGCGCGCTCCGCGAC
AGCGGCCTTCTTCGCCGCAACCCCGATGGCTCATTGAAGCTCAGCCCCCAGGCCATGCGC
CGTCTAGGGAAAGCGCTTCTCGACGCCGCCAGCGAACAATTATCGTCCCGCCCAGGCTCG
CGAGACTCCCGGTTGGCAGGAGCAAACGGTGAAGCGACGGGAGCATCCCGACCTTATGTT
TTCGGAGACACCCAACCATGGGATGTCACCCGCACCATCACCAATGCTCTGCAGCGAACA
GCCGGAACAGATACGGAAGGTCCGCTGCGCATCAACTTAGATGATGTGGAAGTCATTGAA
ACTGAAGCCCGCACCCTCAACGCCGTGGCACTGCTAGTAGACACCAGTTATTCCATGGCT
GCCGAAGGCCGCTGGGTGCCCATGAAGCAAACAGCGCTTGCCCTCCACCACCTGGTATCC
ACCCGGTTTAGAGGAGATGAACTAGCACTAATCACTTTTGGTCGACATGCCCAAAACATG
GACATCGAGGAACTGACTGCACTGCCACCGGTTCACGAACAAGGAACTAATCTCCACCAC
GCATTACTGCTGGCAGAACGGTTCTTTGCTCGCCATCCCTCCATGAAAGCAAGCCTGCTC
ATTGTCACAGATGGCGAACCCACAGCTCACCTCGAAGCCGATGGACACGCCTGGTTCAAC
TGGCCCACTGACCCAGAAACCATGTTCAAGACCGTCACCCAACTAGATAAAGTAACCAAG
CGAGGAACCCACACCACACTCTTCCGACTGGGACATGATCAAGGATTAGAGCACTTTCTC
AACCAACTAGCCGACCGTGTTGGCGGCACCGTGGTGGCTCCCGATCTGGACGGACTCGGC
GCCGCAGTCGTGGGCGAGTATTTACGACACCGCTAC

>RXA02124-downstream
TGAGCATTGGACGTTTTCGCCTT

>RXA02125-upstream
GACCTAAAATTCATCACCTCACCGTTTTTAAGGCTTAGAAAAATAGCAGTGTTGGGATGT
GAATATCCATTTATGCTGCTGTAGTCGGCTATGTGGACGC

>RXA02125
ATGGTGGCAACCTCTCAGTTTATCGATGACAGCGAGGCTGCCCAGGCGGTACGCGCAGCT
ATTGTTGCAGGATACCGAAACATTGATACTGCCCTAGCGTATGGAAACGAGCGCGGCGTT
GGCGAAGGCATTCGCACCGCTGGAGTGCCCCGCGAGGAGCTCTTTATTTCCACCAAGCTA
GCTGCAGAAATCAAAGATTACGATGGAGCAGTCGCCGCGATTGATGAGTCTTTGGCGAAA

ATTGGCTTGGATTATGTCGATCTGATGCTCATTCACTCCCCACAACCATGGAGTGATTTC
CGTGGTGGGGACTATTCAGAGGGAAACCGTGAAGCGTGGCGCGCGCTGGAAGATGCCTAC
AAAGCCGGAAAGATTCGATCCATTGGTGTCTCGAACTTCCTGGAGGCCGATCTGGAGAAT
ATCTTAGACTCCGCGACGGTTGCTCCTCACGTTAATCAGCTTCTTGTGCATGTTGGAAAC
ACCCCAAGCGAGTTAATCAGTTTCTGCGATTCCAAGGGCATTCTGGTCGAAGCATATTCA
CCCATCGCCCACGGAGAGATGCTGAAGAACCAGCAGGTCAAGGCGATTGCTGACAAGTAC
AACGTGAGCATTCCGCAGCTATGCATTCGGTACACAATTCAACTGGGAACGGTGTCTTTG
CCAAAGACTGCCAACCCAGATCATATGAGCTCCAATGCGCAGATCGACTTTGAAATTTCC
GAGGAAGACATGGCGGCACTTCAAGAAGTGACCGCCCGCGATTATGGCGAGCACAGCGGT
TTTCCTGTGTATTCCGGCAAG

>RXA02125-downstream
TAGAAAGATTTTTATCATGGGAC

>RXA02129-upstream
TGTTCTGCCGATCCAGCACCAGCTCTGGTGGCAGGAGCTGAGAGTTTTGCCAATTAACTT
GGCGAACAGACTTGTTGGAAATGAATTTGTCAAGAATGGC

>RXA02129
ATGAAGATCATCTTCAAAATGGCTAGTAACAAGTTCATCGACAACAAAAAGGGGCTGGCT
ATGCTAGTTTTTGCCGAACTTGTGATGGAAATGCTTGATCAGCCTGAAGAACAACTTCAT
AATGTGCGTGGAGTGGCTATTGAGAAGCGGGAGTTCCTCAAAGCTCTCACCGCTGATTTC
ACCAGCAGACTTAAACAAGCTCAAACCGATAAGATTCTTGTTTGGGATTTCGCA

>RXA02129-downstream
TGACTATTATGTGGGCGACCCGT

>RXA02132-upstream
GCAGCCCACCGCCAGCGATTCCTCGCCGAACAAGGCTACGCATACCGCATCCTCGACGCC
GACGACATCCTCTTCCCACTACCCAAGAAAGAGCTATAAC

>RXA02132
GTGCACAACTTCTCCTTCGACGTGGACGAATCCTACGCCAAGAAGAACAACGAAATCCTC
CGCGACGCAAAGCGACTCCAGATCTCAGCACTGTGCCTTGGACTCATCCTCGGCGGCGGA
GCCGTAGCCGTCTACCTGTTTTCTAACGGAGCAGTGTGGATGTGGATGATCGCCATCGTC
ATGGTCTTCCTCGCCCTGTTGAGCTTCATCATGATTCCTGTGATCCCCCGCCAAATGGGC
AACGCACAAACGCTCTACGATGACTACGAACTAGCCCCCGCCATCATCGCAGAAGTAAAC
CCCCGCGATGTGGTCCTCCTGGCACTCGTCAACCGCAATGTGAACCCCGAAGCCAAACCA
GAGTGGGCATTGGCCACCCGCACGATCGTTCGCGTCGGAGCACACGAACGTCGCCTCGGC
GAACGTATCCCATCCGTCGCAATCACCGGCCGACGCACCGTCAAAGACCAAGACCACTGG
GATGAAATCAGCCCCATGCCAATTACCTGGGGCACCACGGACAAAGACATCATCCGTGAA
GCCGAGAAAACTATCCCCCACGAACTCTGGGCCAAACTAGAAAAGAACCGCGGCAAGTTG
GAGGACGTTAAAAAGACCCCCAACAACCTGTTCAAACTA

>RXA02137-upstream
GCCTACTCACCGTCCACAGATGAGTAAACCCGGAAAAACCCGTATTTAGTTATTGGTTTT
ACCTGCGTGGGCTGAAAGTCTTCACTTTTAATCCTTACAG

>RXA02137
ATGGTCGTTCTGATTCCTTTCAACGATGAAGTGTGCACCCCTATTCCCGATTTGGGAGGT
TTTCCTTGTAGCCTATTGAGTGTGAAACTTCCTTGGGATAAAAATAAGAACAACGAAGGG
GCTGACGCTGCAGGCCAAGACGCCAGCTCCACCCCTGAGACCGCTACGCCTGACGCTACT
GAGCAGAAATTGCCAAAGGGGCACACGGCACCGAAGGGCCGTCCCACTCCGAAGCGTCGT
GAAGTTGAGTTAGAGCGAGGTGTCGTTGGCGGCCAGTCTTTGGCGCCTACTGATACTTAT
GCGCAGCAGCGCCAGAAGCGTAAAGAATTTAAAGCTTCTATGACCAAGGAAGAATTCAAG
GCATACAAGCAGAAAGAGCGCGATGCCCGAGTTAAGCGTCAGCGCGAAACCCAAGCTGCA
ATGGATCGCGGCGAAGATGCTTATTTGATGGATCGCGATAAGGGCGAGGTTCGCCGTTTT
GCGCGTGACTGGGTGGATTCCCGCAGGTTCTTGTCTAACTTTGTGATGCCAGTAGCTATT

GCTTTGCTGGTTGTCATGCTGATCGGTAACTTCAACCCATCATTCGCTGCGACTTCTTCC
ATGGTTGCCATGGTTTTGATGTTGGGCTTCCTGATTGAGGGCATCACCACTGGTCGTCGT
GTGAACAAGGCTGCTCGCACGAGGTTCCCTGGTACCACCGAGACTGGTTTTGGTCTGGGT
TACTACGCGTATTCCCGCACCATTCAGCCTCGTAAGTGGCGTACCCCTCGTGCACGCGTT
GAAATTGGTGCTGAAGTC

>RXA02137-downstream
TAGCGCATGCGCACGTTAGTTCT

>RXA02138-upstream
TCACTCGCCGGAGATCCGTAAAAAGGGGAGTACACTGCAAGCCTATGATGTCCCGGCCTA
AAAGTAATTCAAAGGGCCAACAGTTAAGGAGACTAAAGCG

>RXA02138
ATGACCGCTCCATCAACCAACACCGGTGTTATCTTGACCGAGTCCGCAGCGTCCAAAGCT
AAGGCACTCATCGATCAGGAAGGCCGCGACGACCTCTCTCTGCGTATCGCCGTTCAGCCT
GGCGGCTGCTCTGGCCTTCGTTACCAGCTTTACTTCGACGACCGCACCCTTGATGGCGAT
AAGGAAGACATCGTCGGTGGCGTTCGCCTTGTCGTTGACAAGATGAGCACCCCATACTTG
CTCGGCGCTCAGATCGACTTCGCTGACACCATCGAGCAGCAGGGCTTCACCATCGACAAC
CCAAACGCAGGCAGCTCTTGCGCTTGTGGTGACTCCTTCAAC

>RXA02138-downstream
TAAAGAGATTCCGTTATGTAGGA

>RXA02141-upstream
GCCCATTCGTTTCCGATCGCACCGCAACCCGCGACGGCGAAAACACTCAGAGCAACGCTT
AAGAAGGAGTGGCGAAAAAATGAAGTCTTCAGCAAAACTC

>RXA02141
ATGTACGGCCCGACCGTATTCATGGCCGCAATGGCTGTCATCTACATCTTCGCAACAATG
CACGTTAGTGATGGCGGCAGCGTTAAAGGTGTTGAGTGGGTCGGTTCTGTGGCCCTGGTC
CTGTCAGCAGGTCTGACGCTTATGCTCGGTGTCTACCTTCACTTCACTGAAGTCCGCGTA
GATGTTCTTCCAGAGGACTGGGAAGAGGCTGAGGTTGCCGACAAGGCAGGAACCCTCGGG
TTCTTCAGCCCAAGCTCCATTTGGCCGGCAGCTATGTCCGGTGCGGTTGGATTCCTTGCA
TTCGGCGTTGTGTACTTCCACTACTGGATGATCGCAGTTGGTCTGATGCTCCTGATCTTC
ACGATCACCAAGCTCAACCTTCAGTACGGCGTGCCAAAAGAAAAGCAC

>RXA02141-downstream
TAGTACTAAAACCACATATGCTC

>RXA02146-upstream
GGTTCTCTCGCAGAGAGAGAAGGAGTGGGGATAGGGGCCTTCCGCTCCGAACCCGACAGC
TAACTCGGTCAGCAAACAGGAAGAATTTGGAGTTTCATCA

>RXA02146
GTGGGTAAGCACCGTCGCAACAATTCAAACGCAACTCGCAAGGCTGTAGCAGCATCTGCA
GTTGCGCTTGGAGCAACCGCAGCTATCGCCTCCCCAGCACAGGCAGCTGAGGTTGTTGTT
CCTGGCACCGGAATCAGCGTTGACATCGCTGGCATCGAGACCACTCCAGGTCTTAACAAC
GTTCCAGGAATCGATCAGTGGATCCCTTCCCTTAGCAGCCAGGCAGCTCCTACTGCTTAC
GCAGCCGTCATTGATGCACCTGCAGCACAGGCTGCACCTGCAGCAAGCACCGGTCAGGCA
ATCGTTGATGCAGCGCGCACCAAGATTGGTTCCCCATACGGTTGGGGTGCTACCGGTCCT
AACGCTTTCGACTGCTCCGGCCTTACCTCATGGGCATACAGCCAGGTTGGCAAGTCCATC
CCACGTACCTCCCAGGCTCAGGCTGCACAGGGCACCCCTGTTGCTTACTCTGACCTTCAG
GCTGGCGACATCGTTGCGTTCTACTCCGGCGCTACCCACGTTGGTATCTACTCCGGCCAC
GGCACCGTTATCCACGCACTGAACAGCAGCACCCCTCTGTCTGAGCACTCCTTGGATTAC
ATGCCATTCCACTCTGCAGTTCGTTTC

>RXA02146-downstream

TAATCTGCATAAAGTCTTAAGCT

>RXA02151-upstream
ATGAGCGCATCGTCTTTTTTAGGAGTTGTCCGCCACCGTGAAAACTGGAAACTTAAACCC
AGCCCCACAGCAGGTGACGGCTCCCCAGAACAAGGCTCGT

>RXA02151
ATGGATTGGCCAGACATCGCCAAGGGAATATCCATCCTAGGTGTCGTGTTACTACACGTG
TCGTTGGCAATTCCAGGTGGCCAGGACACCATGATGTCCCACCTGAACGCACTGCTTGAT
CCACTTCGGATGCCATTATTTTTTATGGTGAGTGGATTTTTTGCAGTTAAAGTTCTGAAT
CAAAGCTTTGGTGAACTTTTCCGCGGGCGACTGTGGTTCTACCTGGTTCCATATTTGCTG
TGGACTCCAGTGAATCTTTATCTACACCGCCTCGAGGGCACAGTTTTTACCGGTAGAGCA
CCGGGAACATGGGAATGGTACAGCGGCTCGATGCTCTCGGCCACCAATATGTACTGGTTC
CTCTACTTCTTGGTCATCTTCAACCTATTTTTATGGGCAACGAGAAAACTCCCAGCTTGG
GCAATTGTGGCGTTGGTGGCCTCACTGTGGCTACTTATGCCGGCTTATAGCGAGATTGAG
ATTCTACGCAAGTCCATTATTTACTTGCCTACATTCCTCATTGGCGCTTACTTCCGCCCA
CTGATTTCGCGTTTTGCAGAAGCCGCAACAAGGCCAAAAGCAATAGTGTTTGCAGCGGTC
CTTTATGTCTCGGGACTTGCTTTGGGCGTGATCTCAAATGGGCTGCGCGACAGCGAAAAC
CATGGCGCAAGCGTGCTGTGGCTGATGAACCTCCGCGATACTTTTGCTCATGCACTCGGC
GGCAACCTCACTGGATTCGATATGGATCACCTTCCTGGAATGATCATTCGGATTGTTTCC
CTGCCTGCAGGAATTGTGTTGTGCGTATGGCTTGGCCGAATAAAGCCAGTAGGGGAGTTT
TTGAAACTTATTGGTAGGCACACCCTTCCCATCTACATTGGGCATGCAACAGGACTATCG
CTGATTTTTGGTTTCGGCTTGCGCTGGAATTTCATGGAGATTGATAACTTCTCTGACAGT
TTGTGGCACCACACCAATACGTGGATGGTCATCGCGTTTGCCTGCGCGATGCTCGGCGGG
TACCTGACCTATCTGATCTCGCGAGTTCCAGTGCTGGGATGGACTCTTGTTCCCCCTAAA
CTGCCAGAACCAGATAAAACTCCAGCTAAAGCACAAGCTGATTCTCACGTTAAAGCTCAG
TCTGCGAAGCCTATGAATGCTTCTACCTCTTCTAAGACGTACGGTATA

>RXA02151-downstream
TAACTGAAGCATAACCTGTGTGA

>RXA02152-upstream
AAGCCGTTAAAAGTTGAGACTCGCGCTGAGAATCTCACAGAAAACTCCGAAGCTCCCGCT
AAGGTAGCTACCGGAATCAAATCTTAGGGAAGGAAAACAT

>RXA02152
ATGGCTATTTACCGTAAGCTTGCGGCTTCCGCTGCAGCACTGGCCCTGTCCGCATCACTG
GTCGCTTGTGGCGACTCTGAGGACACCACCGAAGAAACCTCAACCACCTCTTCTTCGACC
ACTTCCAGCTCCTCCAGCAGCTCTAGCTCCAGCACCGCGGCTACTTCCGAGGAATCTTCC
GCAGTTGAAGAGCCAGCAGTGGAAGCTCCTGTGGAAGAGGCTCCAGTCGAGGCACCTGTT
GAGCAGGCACCTGTCGTGGAGCAAGCTCCAGTTGAGCAGGCTCCGGCACCGGTTCAGGAA
GCACCTGCACCAGTCGAGCAGGCTCCAGCTCCAGTTCAGGAAGCACCTGCAGCTGACGCG
CCACCTGCACTTCCAGGTGGTGGCGGCGGACACGCTGGCTAC

>RXA02152-downstream
TAAAAATTCATGCTTTTACCCAC

>RXA02163-upstream
AGCCCGTACGATTTCTGCGTTCCCATCCTCTGCACCAGCTGCGCAGAAGATCTCCGAAGC
CAACACCACGACGGGCCGATTCACCCCATTCTATTCGCCT

>RXA02163
ATGGCGGTGGCAACATTCGGAACCATCACCGACATGTTGGAAACCAAGGGGATCGTGAGC
AATGTAGGCGGCACCGACACCATCGATTTGGGCGCGTTGTTGAATGAAACCCAAGCCGGA
ACCCGCTGGAGCGAACTTAGCCCCAACTATCAGTCCAACCGCGTCGTGCAGATTTCTACC
ACCGATGTGCGCACCTCTAACTCGGCGGCCATGTACCTATCAATGATGTCCTGGGTGAAA
AATGGCGGAAAAACGGTGAGCAGCACTGCGGAAGCCGATGCCATCATCCCAGAGCTTAGC
CAACTGTTCGTGGGCCAGGGCTATACCGAAAGCACCTCCGCCGGCCCGTTTGATGAATAC

CTCTCCCAAGGAATGGGTTCTAAACCAATGGTGATGATCTACGAAGCCCAGTTCCTCGCG
GAACAAAACAAGGAAAACTCACGGATTTCCGGCGATATGGAACTAGTGTATCCAAGCCCC
ACCGTGTACAGCACGCATACGGTGGTTAGCTTGAGTGACGTCGGCGCGGAGATCGGCGAA
CTCCTAGAAACCGACGAAACCCTGCAGCAGTTGGCAGTCAAACACGGTTTTAGGCCAAAG
AACTCCGCAATGATCGCCGATGCTGGCATGACCGACCGCATGCCCAACAACCTCAATGTC
ATTGATCCGCCGGACTATGACTTCCTAGAACGACTCATTGATGGCGTGGGCGCATCGTAC
AGTGCCACCCCAGCAGAAGAGGACACAGATCTA

>RXA02163-downstream
TGAAAAATCTTGTAAAAGGTACA

>RXA02164-upstream
TCAATGTCATTGATCCGCCGGACTATGACTTCCTAGAACGACTCATTGATGGCGTGGGCG
CATCGTACAGTGCCACCCCAGCAGAAGAGGACACAGATCT

>RXA02164
ATGAAAAATCTTGTAAAAGGTACAGCGCTGGGCTTGAGCTTGGTGCTTCTGGCAGGTTGT
TCAACTGTTTCGGATTCTATCGATAGCCTCGGCGGGGGCCTGGGTGGTTCCTCTGAGACT
TTGAAGATTGTGGCCGCCACAGAGCTGGAAGATCTGCAGCCCGCGATCGAGCAAGCCTCC
GACGACTTGGGTTTTGATATTGAACTGAGCTTTCCAGGCGGCACACTCAGCAACAGCCAA
GCCCTCATGGATGGCGCTTTTGACCAGGACTATGATGCCACCTGGTTTGCCACCAACCGT
TACGTCGATCTGATCGGCGCTTCCAACAAGCTGGGGGAGACCACCAAAATCGCGACCTCT
CCCGTGGCGTTCGGTGTGAAAACTTCCATGGCCCAGGAGCTCGGCTGGGATCAGCGCCAG
CCAACCTGGGAAGAGCTGGGCCAGGCCTCGCAGACCCAAGATTTCACCTTCGGTATGACC
GATCCGGCCACTTCCAACTCCGGATTTTCCGCGCTCGTTGCCATGGCCACGGCATATGCT
GATACCGGCCAGGCCTTAACAACCAACGACATCCCCGCGATCGCCGAGCCGATGTCCACA
TCCCTTTCCGGCCAAACCATCACCTCCGGTTCCTCTGGCTGGCTCAAAGACACTTTCCTG
GAACAGCCTGACCGCGCGAATGCGATCATCAACTACGAGTCCGTCCTGCACACCATGATC
AGCGAAGACGGCGCCGATATCACCGTCGTGGTGCCCGCCGATGGCGTGGTCAGCGCCGAT
TACCCGCTCTCTACGATCACGGGCTCCGACCAGGGCGAGCATGTAGCAGAGCTGGCCGGC
TGGTTCGCTGAGCACCCCGACGCTTTAACAGATACTTATCGACGTCCGACCACCGCGAAC
GCAACGCTCCCAGCGGAGCTTAGCTCGCAGACCATCATCGAAGCTCCCTTCCCAGGGAGC
AAGACGGTCACCGACGCGCTTATCGACGCCTACACCAATCAATTCCGCGTCCCAGGCGAA
ACCACCTTTGTGCTCGACGTTTCCGGATCCATGCTGGGCCAGCGCATCACCTTGCTCAAA
GACACCATGTCAGACCTGATCAGCGGCGGCGCGACCACTGACCTTGCCAACGTGTCCCTG
CGCGACCGCGAAAAAGTATCGATCATTCCTTTCAGCTTCGGGCCACACGAAGTAATCAGC
GAAACCCTCGGTGCGGTGGGCAGCCCAAGCCGCACCGATCTGCAGCAGCGCGTTGAAGCC
TTGCAAGCAGACGGCGGAACCGGAATTTACGACGCAGTGCTCGCCGCCTACGCAGAGTCC
GCTGGTGGCGACTACATCCCATCCATCGTGCTCATGACCGACGGCGAACTCACCGCAGGA
CGAACCTACGATCAATTCCTCACCGAATGGAACGCGCTTCCTAGCAATATCCGATCAATT
CCAGTGTTTGTCATCCTTTACGGTGAAGCCAATGTTGCGGATATGGAACAATTGGCAGCA
ACAACCGGCGGTGAGACCTTTGACGCCATCAACGGTGACCTAGACGAAGCATTTAAGGAG
ATTCGTGCCTACCAA

>RXA02164-downstream
TAATGGAGGATCCTTCTTTTTCT

>RXA02165-upstream
GAAGCCAATGTTGCGGATATGGAACAATTGGCAGCAACAACCGGCGGTGAGACCTTTGAC
GCCATCAACGGTGACCTAGACGAAGCATTTAAGGAGATTC

>RXA02165
GTGCCTACCAATAATGGAGGATCCTTCTTTTTCTCCCGCAAGAATCTCGCGGGTATCGCT
ATTGCAACGCTGATTATCGCGCTGCACTTAGTGATCGGACTCGGAGCATTTTGGCCTGTT
GTCGCCATCGCCGGATACGGCGCTGCGGTGGCACTTACACCTAAAAACCCTCCGAAGAAG
GAACTCCCTCCGGTTCAGGCAACTCCCGAATTAGATAGCCCGGGTCTGCTTGCAGCCAGG
TCTCAAGAACTCGTGAGAACTATGTATAGCCACGGTGCTGCAGCACCAGTGATCGAAGCG
ATTAAGAGGCTAGACAGCTCACTGCAATTGGTCATTGGTAACTGGACAAGCCTGACCAAT
TTTCCCGAGCACCAAGTCACCATTCGCTCAATTATCAACCAGTACATCCCAGGCATTATC

GACGCTTACCTGAAGATCCCCACCCGCAACGATCCTCGGGCAGTCGAAGACCTCATTGAA
TCCTTCGACCTCCTGAACTCCGAGACGATGAAGATCTTCAATGCGATCCAAGAACAAGGC
CTTAATAACCTTGAAGATCACGGTCGCGCACTGCGCATGCAATTTGGTCAACTGCCAGAA
GAATTCCGGGAA

>RXA02165-downstream
TAGCCACTCAATGCAGTTAAGTT

>RXA02166-upstream
CGGTCGCGCACTGCGCATGCAATTTGGTCAACTGCCAGAAGAATTCCGGGAATAGCCACT
CAATGCAGTTAAGTTTTTCCTGCCCGGTAGGATGGTCCGT

>RXA02166
ATGAGTCTTGATCCACAGCTTCTTGAAGTCCTGGCCTGCCCAAAGGACAAGGGCCCACTT
CGATATCTGGAGAGCGAACAGCTCTTGGTCAACGAACGCCTCAACCTGGCCTATCGCATT
GACGACGGAATTCCGGTGCTTCTCATCGACGAAGCCACCGAGTGGACCCCCAACAAC

>RXA02166-downstream
TAGAAGTACATCAAGGACATTTT

>RXA02168-upstream
AGGGTTTAGTCATCTATTTCGGCTACGCTCACGTAACCTACGCATTCGTAAGTGGTCATG
GGTCCAAGAAGCCCATTCCAAGACTTAGGAGCTTTATTTC

>RXA02168
GTGAGTATTTCTTCACTGACACCGCTGCACTCTTTCAAAGAGCCAGCAATTCTGTACGCC
GGTCAGGCTTCTGCCTGGCAGCAGGTGATCGCTGATTCCAGCGAAGACCACATCACCGCA
ACGCACCTGCGCGAGCTCCTGTCTCGCTCCCGTGCAAAGACTGCACCTTTCGCTCGCCAA
ATCACCGCCATCGTGCCTGGCTCACTTGCTCGTCTTGAGGAACTGACCCGCGAAGACGCA
CAAATCGGTGCAGACATCGACGCACAGCCTGCCGTTTCCATTCCAGGCATTCTGCTGGGA
CAGATCGCTGCAACCCGTCAGCTGCGTGACCTCGGACTCGATGTCGCAGCAGCTTCCCGC
CTTGGACACTCCCAGGGCATTTTGGGCGTTGAAGCAGTAGACAATGAAGAAGACGTTTTA
GCTTTCGCCATCCTGCTGGGCGCAGCAGCTTCCCAGTTCGCTGGCAAGGGCGCACATATG
CTCTCTGTTCGCGGCCTGTCCCGTGAGATCATCCAGGACACCATCGCTGGTGTCGATGGG
GTAGAGGTCTCCCTGCGCAACGCTCGTGCACACTTTGTTGTCTCTGGTAAGCCAGAGGCA
CTGAAGAAGGCTGCTGCTGCTCTACAGCGCGCAGCTGATGTTTACAACGAAGACATCAAC
GAAAAGCGCAAGGGTGGATCCCTGGCAGAGCCTAAGTTTGACTACTTGGATGTGGCCATT
CCTTTCCACCACTCCTCCATGCAGGACGCAGCCGACTTGGCTGTCGAGTGGGCAACCACC
TGTGGCCTAAACGTCAACGCGCGCGCGTTGGCAGAAGCAATTCTAGTTAACCCAGCTGAC
TGGGTTGAGCAGATCGCAAACCTCAAGGCTGATTACGTTCTTTCCCTCGATGCAGGCGTC
AGCCGTTTCACCGCTCCATTGCTAGACGGTCGCGGAATCTCTTTGGTTCCTGCGTTCTCC
GCTGCAGAGCGCGACAACTTGGCTCGCCCTGGCTTCCACGTTCCTACCGCTGAGGATTGG
TCCGAGTTCGCTCCAAAGCTGGTTAAGCTTCCAAACGGTGAGCACAAGGTTCTCACCGGG
TTCTCCCGCCTGACTGGTTATTCCCCAATCGTCCTGGCTGGCATGACCCCAACCACCGTT
GATCCTGAGATCGTTGCAGCTGCAGCGAACGCTGGACACTGGGCCGAAATGGCCGGTGGC
GGACAGTACTCTGAAGAAGTCTTCACCAAGAACAAGGAAAAGCTCGTTTCCCTGCTCAAG
GTTGGACGCTCCGCACAGTTCAACTCCATGTTCTTCGACCGCTACATGTGGAACCTGCAG
TTCGGTGCACAGCGCATCGTTTCCAAGGCACGTGCAACCGGTACCTCCATCAACGGTGTT
GTTGTCTCCGCTGGTATCCCAGAGGTTGAGGAAGCAACTGAGCTGATCAACGATCTGAAC
GCTGATGGCTTCCCATACGTTGCATTCAAGCCAGGCACCGTGGATCAGATCCGCGCAACC
CTGAAGATTGCTGATGCAAACCCAGAGACCAAGATCATCATCCAGATCGAGGACGGACAC
GCTGGTGGCCACCACTCCTGGGTCAACTTGGACGATCTGCTCCTGACCACCTACGCAGAG
CTGCGTTCCCGCAAGAACGTTGTCGTCATGATCGGTGGCGGCATCGGAACCCCTGCAAAG
GCTGCTTACTACCTGACCGGTGAATGGTCCACCGATTTGGGCTTCCCAGCAATGCCAGTG
GACGGCATCCTCGTGGGTACCGCTGCCATGGCAACCAAGGAAGCAACCACTTCTCCTCAG
GTCAAGCAGGCACTGGTCGACACCCCAGGTGTTGATCCACACGACGCTGGCGGCTGGGTT
GGCCGTGGCGATGCTCGTGGTGGCGTGACCTCTGGTCTGTCACACCTGCACGCTGACATG
TACGAGCTGGACAACGATTCTGCTGCAGCTTCCCGCCTGATCTCTTCCATCGATTCTGAT
GATTACGCAGATCACCGCGAAGAGCTCATCGAGGCTATCAACAAGACCGCTAAGCCTTTC

TTCGGCGAGGTCGAAGAGATGACTTACGCAGAGTGGATCCAGCGTTGGGTTGAGCTTGCT
TACCCAACTCAGGACCCAACCTGGGATGATCGTTTCCTCGATTTGGTTCACCGCATTGAA
GCTCGTCTCAACGAGGCAGAGCACGGCGCCATCACCACACTGTTCCCAGACCATGCGTCT
GTGGAAAATGAGGAAGAGGCCGTCGAAAAGCTTCTTGCTGCTTACCCGCAGGCCCGCGAG
ATCCAGGTCTCTGCGCGCGACGCCGCGTGGTTTATTGGTCTGTGCCGCAAGCACCACAAG
CCTATGCCTTGGGTTCCAGCAATCGATGCTGACCTAGCACGCTGGTGGGGCCTTGACACC
CTGTGGCAGTCCCAGAACGAGCGCTACGGCGCGAACTCAGTCCGCGTTATCCCAGGACCA
GTCTCCGTCGCCGGCATCGACCGTGTTGACGAGCCAGTTGCAGAGCTGCTCGGCCGCTTC
GAAGCTGCCTGCGTTGACGCTCTCGACGGCGAGCCAGAAGAGATCTTCGCTCGCCTCAAT
GAGTCCAAGAACGAGCGCGAATTCCTGCTGGCTACCCCACACATCGTGTGGCACGGCAAC
CTGATCGACAACCCAGCTCACGTCCTCAACGAGGGTGCTTTCGAGCTCATCGAGGAGGAT
GGCTACTGGGTCATCCGTATCCTGGCTGATTCCTACTTCGACGATCTGCCAGTTGAGCAG
CGCCCATACCTGGTTCAGCATGTTGACATCCCAGTTGAGCTGGGTGACGCTGGT

>RXA02168-downstream
TGAACCGGTGGTTTCCCAATTGG

>RXA02169-upstream
GTTAAAGGTCGAAAAATCCCACCCCTAGCCCTTTTAAATGAGTGTTGTTATTGTTAACCA
CTGTTACTGGTGGGATTAATACTTATTTTTGGGAGAACTT

>RXA02169
TTGGACATGCAAATAAACCGCCGAGGCTTCTTAAAAGCCACCACAGGACTTGCCACTATC
GGCGCTGCCAGCATGTTTATGCCAAAGGCCAACGCCCTTGGAGCAATCAAGGGCACCGTC
ATCGACTACGCAGCAGGCGTCCCCAGCGCAGCATCCATTAAAAATGCAGGGCACCTTGGA
GCTGTCCGTTACGTGTCACAGCGACGCCCCGGCACTGAATCCTGGATGATCGGCAAGCCA
GTCACACTGGCAGAAACCCGAGCTTTTGAACAAAACGGCCTCAAAACCGCATCCGTCTAT
CAATACGGAAAGGCAGAGACCGCCGATTGGAAGAACGGCGCCGCAGGAGCGGCAACCCAC
GCTCCACAGGCAATTGCGCTTCACGTGGCAGCTGGTGGCCCTAAAAATCGCCCCATCTAC
GTGGCGATCGACGACAACCCAAGCTGGTCTGAATACACCAATCAGATTCGCCCCTACCTC
CAGGCATTCAATGTTGCGCTGTCCGCTGCCGGCTACCAGTTAGGTGTCTACGGCAACTAC
AACGTCATTAATTGGGCTATCGCCGACGGCCTTGGAGAATTCTTCTGGATGCACAACTGG
GGATCAGAAGGAAAGATCCACCCACGCACCACCATCCACCAGATCCGCATTGATAAGGAC
ACCCTCGACGGAGTCGGCATCGACATGAACAATGTCTATGCAGACGACTGGGGTCAGTGG
ACCCCAGGCAACGCGGTTGACGATGCCATCCCCACCATTCCTGGAAACTCCAACACGGGA
ACAGGTACTGGAATTGATGCTGACACCATCAACCAAGTAATCAAGATTCTTGGCACCCTA
TCTAGC

>RXA02169-downstream
TAAACTAGCCGTGCTGACTCACA

>RXA02170-upstream
ATTTAAACCGCCCACTCTCCAGTCGGAGGATGGGCGGTTTTCGCATGCAGTACTATTAGT
GGACGTGTCAAGAACTTCTAAGGTTCACCCGGGATGGCGG

>RXA02170
GTGTCTACTGTCCTTTTAGCAGGAGTAGTTATTATTGGCGGAATTTTTACTCTCCCTCAG
AAGGAGGAAGTAAAGGTTTCCGAATTGCAGCCACAGGCCAGCGCTGCATCCATCCCGTCT
TCATCTTCCACAGCTGGGAAAGCAGTGGAAGAAAGCCCTCTAACGCAGTTTGTGGAAAAC
TCGACAGGCTCCCAAATTACGTACATGAGCCTGAAAGACGATTTCCATACTGGCACGTCT
ACGGAACGTTTTGCGCGCCCAGCGTTAAGTTTGTCTAAGCTCTACATCGCTGAATATGTG
CTCGAGCACGGCACGAATAATGAGAAGTCTTTGGCGATGGAAATGATCAAAGATTCCTCC
GACGTATCCGCCGAAATCTTGTATGAGGCGTACCCAGAATCAATTGAGGAGATTGCGGAT
CAATACGGATTGCTCTCCACAAGGGGAGACGCGCACTGGGGATACTCGGTGACATCCACT
TACGATTTGGTGAAATTTGTCAGCGCTCTCATTATCGATGATCCAGATTCACCGATCCTT
GAAGCGATGCGTAATGCCAGCGCAGTCGCGGCTGACGGTTATCCGCAAGACTGGGGGACA
GCGGTGCTTGATGAGGCAGAAGGATCCAAATGGGGATGGTCTGATGATCTCATGCTGCAC
TCCTCTGTGACCTTTGGCGAAGACTATGTTGTGGCAGCTGCTGTGACTGGATCAAAAGAA
GACCTCACCCAATTGGTGGAAAACCAATTGGGTGAGGTTGTGAGTCAGCACGGC

>RXA02170-downstream
TAGTTTAGCTAGATAGGGTGCCA

>RXA02172-upstream
GAGAAACATATAAGTTGCTTTATTTTAAAGCCGGCATTGCTTAGAGAGTGGCCGATCACC
GACTCCCGCTCGAGGGATATGAAAGCGAGATAAGTTTCCA

>RXA02172
GTGAATGCAGAACAAATCACCCAGGGGCGTCGCCAGCCGACGGCTCAAGAGTTTCGGGAC
ATGCAGGCGAGCCCAGAATTTGGAGAGCTCCGCAGCAAGTTCCGTTCCTTTGCTTTCCCA
ATGACCGTTGCCTTCTTCTTGTGGTACGTCGTCTACGTTCTGGTTGCATCCTTTGCATCA
GAGTGGATGGCAACCCCAGTTTTCGGCGCAATCAACATTGGCCTAATCTTCGGCTTCCTT
CAGTTCGTAACCACATTCGTCATTACTTACATCTATGTCATGTTTGCGAACAAGAACTTG
GAGCCTCGTCAGGCTGCTATTCGCCAGAAGATGGAAGGT

>RXA02172-downstream
TAATCAGATATGAATTCCACTAT

>RXA02177-upstream
AATACCCCCACTTTGAAAAACACCCCGTACAGTTACACCAGTACGGGGTGTTTTTTAGTT
AAGCTTGGGTGATCACTTAACCCAGCTAGAAGGAGTCAAC

>RXA02177
ATGCGGGAAATATTCCTGATCAGCGGTGATTCCACCGAATCATCCTTGGTTTTCAAGACC
TCCGAAGAGGACGGCGCTGAGGAATTTTTCATTGCTGTAACAGATGAACTCCACGCCATT
CTTGCAGGTCATAGCGAGATTAAGAGCGCCCCAGAACCCGAAGAACACAAAGAGGTCCCA
CCTCCTGTTCTAGAGCCGGTCGCTGCGGTAGAAGAGCCCCGTGAGGAAAAAGAAATTGAC
CCTCGTATCAGCGCTCCCCTGACGATGTCACCCCGCGAAATTCAGATTCGGGTTCGCTCA
GGCGCCACCATCGAAGAATTAGCCGAAGAAATCGGCGTCACCGAAGCCCGCGTTGAGCCC
TATGCCCACCCCGTTTTGCTGGAACGTGCCCGCATTGCCGACTTGGCTAAGCAATCACAC
CCCATCAGGGAAAATGGTCCTGCAAAACTGACTCTCTGGGAAATTCTTGCAACGGCGTTT
GCCACTCGCGGCCACGATCTCACCACAGCACGCTGGGACGCCTACAAAGACGCCACCAAC
CAGTGGATCGTGCGAGTTGATTGGAAAGCAGGACTCAGCGACAACTACGCGGAGTGGACG
TTAAACCTGCACAACACCAGCAATCCCACCGCTGATCCGCGGACCCCAGTCGCAGCCGAT
TTGATCGATCCTGAATTCATTCAGCCGGTACGTACCTTGACGTCCGTAAACTCCACCCAG
GAACAGTACGACGACGAAACCGATGTTTTCGACACCGTACCAAGCCCTGACGACGCACCA
GACTCAGAATCCGATGCCGTTGCTGAAATCACCAACGACAACGAACCTGAAGTCGATGCG
GAAGGCCCACGCAACAGGCGTCGAAAAGCAGTAACCCCACACTGGGAAGATGTTCTTTTA
GGAGTTCGCGCAAACACAAAGCGCCCGAAGAAA

>RXA02177-downstream
TAGGATGTGCTGATGCCAAGTCA

>RXA02178-upstream
CCCACGCAACAGGCGTCGAAAAGCAGTAACCCCACACTGGGAAGATGTTCTTTTAGGAGT
TCGCGCAAACACAAAGCGCCCGAAGAAATAGGATGTGCTG

>RXA02178
ATGCCAAGTCAATTGGGAGAAAACGCGGCGATCGTCACCCTCTGGTTTGTTAGCGCATCC
GATCCCCAATCCATCATCCGCTCGGAACCTCGGGCGGATCGTGGATATGGCCGAAAACTG
TTGGCACAGCTCAACCCAACGTGGCCAATTACCCCCATCGGGCAGTTCGCCCTCAACAGA
TCCGTTCCTGCTAGTGCCAACGAGTTCTACATCGCTGGTTTTCCCGGCATCACCATCATT
CAAACCGTGTTGGAAGATGTCACCTCTTTATCCAAGCTGAATCCTCGGTTACTGCGCAGC
GTCCCGGCAACAGATGTCTACATTTTCGCCGTCAATGAAGAAACCACCCTTGGTGGCTTC
GCACACATCTACAACGGTGAGATCAAACGATCCTTCATCGCCTATGAAGAGCGCGTCTTC
GAAGACAACGGCATCCCCGGCGGCTTTGAAACCCCCTACTGGGCAGGCAAAAAAGGCACC
CGGAAAACTGCGCTGTCGTTGCCCTTCAACCCCATCGAACTAGTCCACGAAGCACAACGT

GCATGGCTCGGATTCGACGCCACCACCTCCCCTGACATCAACGTCGTTGCCTATGCCACC
GATGGTCGCCCCGAGCCGCGCATCGCTGCACCCCGCATAATTAACAGCGAGGAAGTGACA
AGGTCCGCCGTCGAAAAGCTAGGACTGCGCGAATCCGCCTTCTACGACGACTACGAAGAA
TACGAGGCACCCGATCGAGTGGTGTCCAAGCGCATTACCTCAAACGCGAAAAAAGCGGCC
AGCTCAGCACAGAAATTTGGTAAATCTCTGTGGCGAGCCAGCCGCGAATTCGGGTCAAAC
ATGGCGGAAAGACTCCGCCACACTGACCGC

>RXA02178-downstream
TAGCGCTACTACTTAGCGCTGTT

>RXA02180-upstream
GTTTCAGCTAAAAGAAGAATCCTTGCTAGTGGAATCAGCTGAGTTTTCCACGAGTTTTCC
AGCTTTCTCACAACTTGAATAGAAATTGAGGTATCCGGCA

>RXA02180
ATGACGTCAGGGAAATCAACGAGTACTAGGGGAGCCCTAGACCGGTATTTCAAAATCTCG
GAGCGAGGATCAAGCATTGGCACGGAAATCCGTGCAGGTGTGGTCACATTCTTCGCGATG
GCCTACATCATCATCCTCAACCCCTTGATCCTTGGCACCACCCCTGACGTAGAGGGCAAC
ACCCTAGGCATCGCACAGGTTGCAGCGGCAACAGCGCTTGCCGCTGGTGTCATGACCATC
GCGTTTGGTTTGATTGCGCGTTATCCATTCGGCATTGCTGCTGGCCTGGGAATTAACACC
ATGGTCGCCGTGACACTGGTTTCAGGTGAGGGCCTGACCTGGCCGGAAGCAATGGGACTT
GTGGTCCTTGACGGTGTGGTCATTGTTATTTTGGCTGTGTCCGGCTTCCGTGTTGCTGTG
TTCCGTGCGATCCCAGCATCCATGAAGGCGGCCATCAGCGTGGGTATCGGCCTGTTCATC
GCCATGATCGGCCTCGTGGATGCAGGCTTTGTTCGCCGTATTCCAGATGCTGCCGGTACT
ACTGTGCCAGTGACTTTGGGCATTGATGGTTCCATTGCGTCTTGGCCAACGTTCGTGTTC
GTTGTCGGTGTTCTTCTCTGTGGCATCCTTGTTGTCCGTCGAGTTCGCGGTGGACTGTTT
ATCGGCATTTTGGGAACCACCATTTTGGCGATCATCGCAGAAGCAATCTTTGATTCCGGT
GCGTCCTTTGAAAATGGTGAAGCAAACGCAGAAGGCTGGTCACTCGCCGTTCCTGGTCTC
CCAGACTCCTTCGGTGGCATCCCGGATCTTTCCATCGTCGGCGCAGTTGATTTGATCGGT
GCGTTCAGCCGCATCGGTGTGGTCGCCGCGACCTTGCTGATCTTTACCCTGGTCCTTGCA
AACTTCTTCGACGCCATGGGCACCATGACCGCTCTTGGTAAGCAGGGCAACTTGGTTGAT
GATGAAGGCAACCTTCCAGACATTAAGAAGGCACTGGTTGTGGAAGGCGCAGGTGCCATT
GTCGGTGGTGCTTTCTCTGCATCCTCCAACACCGTGTTCGCTGACTCTTCTGCAGGTGTT
GCAGACGGCGCACGAACCGGCCTTGCCAACGTGGTCACCGGCTCCTTGTTCTTGGCTGCC
ATGTTCTTGACCCCACTGTATGAAATCGTCCCCATCGAAGCAGCAGCACCAGTGCTTGTA
GTTGTTGGCGCGATGATGATGGGGCAGGTTACCGAGATTGATTTCTCCAAGTTCTACATC
GCATTCCCAGCGTTCTTGACCATTGTGATCATGCCTTTCACCTACTCCATTGCAAACGGC
ATTGGCGTTGGATTCATCATGTACGCCATCATGGCTGCAGCGGCAGGCAAAGCAAAGCAA
GTGCACTGGCTGATGTGGCTGGTCGCTGGACTCTTCGTCGTGTTCTTCGCGATTGATCCC
ATCATGGAAGCTGTCGGC

>RXA02180-downstream
TAATGACAACGCGCACGGTAATT

>RXA02181-upstream
TTTGGCTAGTAGGGTGATAATCTCAAATAAAATGCACTTTCACCAGCTTTTTCGATTCCG
GAAGGTCTAACTACACGTCGTGGTGACCACAAGTTTTCTC

>RXA02181
ATGGTTGACGGACACATCCGCAATCTTCAGGGCCACATCGATCGCCTCGAGGCGGCAGCC
CCTACTGCTTCACAGTTCCATGATCGCATCATCACTCAATTGCGTGAAGCTCCGGGCAGT
GTTCAGGCAGCTGTCACGATTGAAAATAACCACTATAACGTCGAGCTGCGCCCGCCCCGC
AAGTTAAATTCACTGGTCACCCTTGATACCCACGGCCACCGCGATGAGCGCCTACATCCA
AAGATTAAAGGCCACGATATCGCGTGGCAGAACACGGCCACCGCAAACAGCCGCCGCCAG
GGCGCCGATGATGGATTGCTTGTCGACGAGTCCGGCCAGGTGATCATGGCTATCAATGCC
TCTCTCTTGGCGATTAAGGGCGACACCGTGTTTCATTCCACGCACCCCAGGTCGCTGCCG
TCTGTTCTGGAATCAACGGTCATTGCCTACCTGCAGGAACAAGGCTGTAATGCAAAGCCT
CGAGAGCAAGGCTTCAACATCAATGATTTGCGCTCTTCGGAAGTGTGGCTGGTGGATTCT
TTGTCCGGCATCCGTCGCGTCGCTGCATGGCTCGAATACGGTTCCAAATTCCCAGTCTCA

GAAACGCGACCTGTGGCAGCTTTCGTGCCGACGTTTTCTGAAGTCAATGACTACCTATGG
AGCACTGCACAGCAAGTG

>RXA02181-downstream
TAGGTCGCTCGACTGTTATTCTC

>RXA02183-upstream
TTGCACATATTCCGGATTCCGATCGTTTTTATATCACTGGTAAGCGTTGGCCTGACCTCT
ATGAGGTTAGATTCGTCCCTGCTGACTAGAATCAAGACTC

>RXA02183
ATGGCAAGCCGGAAGACCAAGCGTAAAAACCTCATTCAGATTCTCAGCCTTATCGTTGCT
GTGTTATTGGTGGTGATTTTGTCTGTGGTGTTCCAGCAATGGTGGAACAATCGCCCAGAG
CCACTCCCCCAAGAGATCTCTATCTCAGCATCTTCTCCCGCTGGTGAAATCGAGGTATTC
CCATTCAGCATGTGTGAACCAGGTGTTGAATGCGAAGAGAACGAGGTGCCAACGCTGGAA
GTTGGTGCTGATGAAGAGTTGCACCTGACGATTCCAGAGGCAATTCATGATCATGACTGG
TACTTGTTGACCATTTATGATGATCCGGCTGCAAATGACGAGTTCTACCACACCAGTTAC
GACGCCACCGAGGCAACCGTTCCTGGTTCTGTGGATCCAACCGAAGAGGGTGCGGAGCGC
CCACGTCTGGTCGTAGTGGAAGTGTCCGCTGTGATGATCGGTGAGGATGAAAATGGTGAG
GAAAGCCCTTACACCGTCACGTGGTCGCTATCCACGATGAACGAG

>RXA02183-downstream
TAACTCACTCACAAACAATAAGG

>RXA02185-upstream
CAACTCCTTGGGGTGAAGCCAGACATCCACTGGCAGAGCAACTCCTCCGCTCTAACCCGA
CAGCTAACCTCGACGGCGACAAATGAGAGGAAAACTTTTC

>RXA02185
ATGGGACGTCACTCCACTAAGACTAGCTCCGCGTTCACCAAGCTCGCAGCTTCCACCATC
GCTTTCGGTGCTGCTGCAACCATCATGGCTCCTTCTGCATCTGCTGCACCTGATTCCGAC
TGGGATCGCCTCGCACAGTGCGAGTCCGGTGGTAACTGGGCAATCAACACCGGTAACGGC
TACCACGGTGGTCTGCAGTTCTCCGCTAGCACCTGGGCTGCTTACGGCGGCCAGGAGTTC
GCTACCTACGCATACCAGGCAACCCGTGAGCAGCAGATCGCTGTTGCAGAGCGCACCTTG
GCTGGTCAGGGCTGGGGCGCATGGCCTGCTTGCTCCGCTTCCCTTGGACTGAACTCCGCT
CCAACCCAGCGTGACCTCTCCGCTACCACCTCCACCCCAGAGCCAGCTGCAGCTGCACCA
GCTGTTGCTGAGTACAACGCTCCTGCAGCCAACATCGCAGTTGGCTCCACCGACTTGAAC
ACCATCAAGTCCACCTACGGCGCTGTCACCGGCACCCTCGCTCAGTACGGCATCACCGTT
CCAGCTGAGGTTGAGTCTTACTACAACGCTTTCGTCGGC

>RXA02185-downstream
TAAATCTAGCTGCACTTTTTAAA

>RXA02186-upstream
AGCTGATCATCACTTTGAGTATCCAACCACCCCTTGAGGGTGGGGATGGGGGAGTCTTTT
TTCATGATGTTGTTAAGTTTAAGCCTTGTTGAGGTGACTT

>RXA02186
TTGTTCCCAGAGTTTGAAAGAATGTATGACATGGCAAACGTAGAGAAGAAGCACTTCGTC
GATCCGGCATGGCCGGAGCACAATCCAGCTGACGGACACGTCGTTACTGAACTCATCTCC
AAGGTCGCAGGCGCGTCCAGCCCATGGGGCGATGACAAGGAATTCCCAGTTTCTGCAGAA
GAGACCGGATACGTTCACCCGTACACCCGGATCAACCGC

>RXA02186-downstream
TAAGAAACTTAAAAAAGAGGCAA

>RXA02187-upstream

GGATCGACGAAGTGCTTCTTCTCTACGTTTGCCATGTCATACATTCTTTCAAACTCTGGG
AACAAAAGTCACCTCAACAAGGCTTAAACTTAACAACATC

>RXA02187
ATGAAAAAAGACTCCCCCATCCCCACCCTCAAGGGGTGGTTGGATACTCAAAGTGATGAT
CAGCTCTCCACAATCCTTAGAAATCGACCCGATACGGTTCTCCCTTTACCACCTAATTTG
GCCTCTCTTGCTGCGCGTTTACAGCTGAGGGCGTCTGCGATTCGCGCGGTGTTGAAACTC
AATGCGTTGGAACTTGGTGTGTTGGAGGCCGTGGCCAACCTTGGTGGTGAACTCCACCCG
GTTACTGCCCCCGAAGTGGTGGAATATTTGCATGTGGCGTTGGCAGAGGATCTTCCAGCG
CAAGACACGATTGGTGCGGCTCTTGCCACGCTGAAAAATTTCGCGTTGGTTTATGGCGAT
GACCAGTTGATGATTGCTCAGGAGACGATGGCTGCGTTGCCTGTTCATTGGCGGTTGCTT
CCGGAGGTAAGTGATCGCGGGCAGAGTGAGGAACAGGTGAGGGAAAGCGTCGATAAGCTT
TCTGATAGGCACCGCAAACTTTTGCACACGCTTGCGGCCTCGGGTGGCTTCGGTCTGACG
CGCGATGCGGCGCCTGATGCGGATCCGTCGCGGCCGATTCCGCAGTTGCTGGCGTCGGGG
TTGTTGGCGCGCGTGGATGAGCAGACCGTGCGCCTGCCGGCGATGGTGCGGCGTGTGATT
GAGGGCCGCGAGCAGCTGCCCGCTCAGGTGCGCCCAATTCCGCGCACGGCGGCGCCAGGT
TCGAATGATGGCGGCATTGCAGCCGGCCTTGAGGTGGTGCGGCACATGCGATTGCTTATC
GACGCCCTCAGCCACGTTCCCGCCCCCACGCTGAAAGTCGGAGCCCTCGGTGTGCGCGTG
GTGACTCGCCTGAGCAAGGAATTAGACCTTGATGAGACCGAGCTGGCACGTCTACTGAGT
TTGGGTATGGCCAGCGGTCTAATCCGTAAAGGCGTGCCCGATCCATTGCCCATGGATGAT
GATGGCGGCGATTACGTCGCTCCCACCCCGCTGGCTGACGAATGGATGGAATATGATCTG
GCGCACCAATTGGGCACGTTGATGTCTGGTTGGTGGAAGCAAACTTACGCGCCGTGGTTG
GTGGGTCGGGCTGATGATAAGGACAAGCCGATCCATGTTCTCAGTAAAACAAGCATCATT
GATTCGCTTCCTGATGCTCGTGCGAAGATCCTGTCCTCTTTATCTAGGGTTTTAGTGGAC
AATCTGCACGCGGATTTAGCATTCCATTATCCCCTTGCGGCGAGTCGGATGAATCCTGAC
ACCATCACACAGCTGGTACAGGAAGCCCAGTGGATCGGAGCATATTCTCAAGGCGTGACC
GCAGCGGGTCAGGCCTTAATTGATGGCGAAAACCCTACGGAGGTAATCAAGGCTCCTGCG
CCGGTGGAGAATTTCATCGTGCAAGGCGATTTCACCATCATGGTTCCAGGACCACTAACC
CCTGCGATGCAAAAAACCATGGATTCGATCGCATCGTTGGAATCACCTGGTTTGGCCTCG
GTGTATCGACTCAGCGAGAAATCCATCAGGCATGCTCTGGATCTTGGGCTCACCACCCCG
GAAATCTTGGAGTTTCTCAAAGAACATTCCATGACAGATCTGCCCCAATCTGTGGGCTAT
TTGCTCAGCGATATCGCCAGAAAGCACGGCACCCTCCGAGGCGGCCCTGCACTGTCCTAT
ATCCGTAGCGACGATCCCGCTTTGCTGCATTCCGCAGTGGAGGCGGGCGCCGATGTGGCG
CTTCGGCAGATCGCTCCCACCGTTGCGATTGCTCAAGCACCCCTGCTTCAGGTGATCACT
GTGCTGCGTGCTGCCGGGTTCCAACCTGTGGCAGAAGACGGCGAAGGCGCAAGTCTGAAT
ATCTCGCCATCCCCTGCACGTGTGCCCGCAGCTTCCCCACCACCAGTTGTTCCGGCACTG
GATGAAAGCCGGGTACAGGCAGCAGTCAAAGCAATCCGACGGGAAAATTCAGCATCTCAA
GGAACTGTTTCCACACAGCCAACTCTTTCGGTGCTGCAGGCTGCAGTGCGAGGGCAGCGC
ACGGTGACGTTGGGGTTCGTCGATAAGCAAGGCGTGGCCGTGCACCGCGTCGTCAAGCCT
TTAACCGTCAACGCCGGGCAGGTGGACGCTGTGGATGAAGCCACAGGTGCGGTGCATCGT
TTCATGTTGCACAGGATCACAGAAGTAATAGTGGATAAC

>RXA02187-downstream
TAGCCTAGAAGTGACATAATGGA

>RXA02199-upstream
ACAGCTTAGTACGGATTAGACAATTCCCGAACTTTTCATTCGTAGTTCATTTTCAACGCC
GCCTAAGCAACACAGGCAAAGCGCCACTAGTCTCGGTCGC

>RXA02199
ATGACTGACTCCACTCCGCAAGGCTCAACACCAGGCATGTCCCCTGAAGCTATCCTCAAC
GGCACCGGAAAGCCGTGGGAAGAGTGGCTAAAATTGCTTGACGACGTAAAAGCCACCTCT
TGGACTCACACCCACATCGCAAAGCACATCGTGGACAACTTTGATGTCAGTGGCTGGTGG
GCTCAAGGCATCGCGATTGGTTATGAATACGAACGTGGCATGCGCAAACCCGGGATGACC
AGCGATGGGTTCGCGGCCAATGCCTCCAAAACCCTTAACCTGCCGGTCGAAAAAGTGTGG
AAGCTCTTCGGAGACGATGACCTGCGGGCGCAGTGGCTCGATCCCGCACTAATTGAGAAA
ACCTCCGCCTCCGAACCTAGAACATTCAATGCCAAATGGTTGGCCGATGATTCTCGAGTG
AGCGTCAACTTCACCTCCAAAGGCGACAATAAATCCAGCTTCGGCATCCAGCACAGACGC
CTGCCTGATCAAGACAGCATCCCTGTCATGAAAGCATTCTGGAAAGAACGCATCGCTGCA
TTAGTTGAGGTGTCAAAACAATTTTCGCTT

>RXA02199-downstream
TAACATTAAGTTCTTAGCCTTCA

>RXA02203-upstream
CGATTCAAAAGAGTTCACCGAGGTAGGAAACATCGTGGTCGCAGCCATTGATGCCCTCCT
GGGCGTGCAGCTCTAGGAAATTTCAGGAACAATACATCTC

>RXA02203
ATGACCATTCGCGCCACTTTCCAGCCTTCCGTAGATGAATTCATCTCCACTCTCGAAGAG
TTTGCAACAGGTTCATACCTTAAAGAGGACGAAAAGGAATTCTGGGACGAACCTTTCGAT
GTCAAGGCACTTCCAGATCTTCGTTTCATCTTGGAAAACTACCTTGATTCCCTAGATAAG
CTCGGTGAAGCACCAGACCTTGATGCTGTTAACGCCTCCGCTCAGTCCACCCTTGATGAG
CTGGAGAAGTTCAACACAAAGCACCACGGTGCTGTTGTTGAGCCTGAAGAAAAAGAAGAG
ATCACTAAATTGATGTTTGATGCTGCAAAGCAGACTGGTGCAGATGATCTTTCTGCAGAG
GCTTTCCCTGAGTTTGAG

>RXA02203-downstream
TAAATTTCAGTAGAAGTTTTTTA

>RXA02206-upstream
GGCAGGATCTGCTGCTGCGGCTAGGAGGGTTATCTCTTCATTCACCCGATCTACCGTACT
ACCTTATGACCTCAGTAGTGTGGTGGGCGTGAAACAGCGA

>RXA02206
ATGGTCGGTTCAAGTGGTTTGCGGGTATCCAGGCTCGGTTTGGGCACCTCAACATGGGGC
TCGGGCACCGAGCTGGCTGAGGCAGGCGATATCTTTAAGGCGTTCATCAATTCTGGTGGC
ACGCTTATCGACGTCTCCCCCAACTACACCACCGGCGTCGCGGAAGAAATGCTCGGCACG
ATGTTGGATGCGGAAGTCTCTCGTTCGGCTGTCGTCATTTCCTCCAGCGCAGGTGTCAAC
CCCGCTCTGCCGCTCGGCCGACGTGTGGATTGCTCCCGCCGCAATTTGATTGCCCAATTA
GATGTCACCCTGCGGGCATTAAACACTGACTATTTGGATTTGTGGTCTGTGGGCTATTGG
GATGAGGGCACCCCACCGCATGAGGTGGCCGATACTTTGGATTACGCCGTGCGCACCGGC
CGAGTCCGATATGCCGGTGTCCGAGGATATTCCGGTTGGCAGTTAGCGGTCACCCACGCT
GCATCCAATCATGCAGCGGCCTCCGCCCGCCCCGTGGTCGTTGCACAAAATGAATACAGC
CTGCTGGAACGCCGCGCAGAACAAGAACTCCTCCCTGCCACCCAACACCTAGGTGTCGGA
TTCTTTGCTGGCGCTCCGCTGGGGCAAGGCGTGCTGACTGCTAAATACCGCTCCGAAATT
CCCCATGATTCCAGAGCTGCATCCACAGGACGCGACGCAGAAGTCCAAAGCTACCTAGAT
AATCGAGGCCGCATCATTGTCGATGCTCTTGATACTGCAGCCAAAGGATTAGGCATTAGC
CCCGCTGTCACAGCCACCACCTGGGTGCGTGATCGTCCCGGAGTGACAGCTGTCATCGTG
GGCGCTCGCACACATGAACAGCTGTCACATCTTCTCAAGGCGGAATCGGTGACTTTGCCA
ACACCAATCACACAAGCCCTTGATGATGTCTCCCTG

>RXA02206-downstream
TGACTTGGTCCAATTACATTCAC

>RXA02207-upstream
GAATCGGTGACTTTGCCAACACCAATCACACAAGCCCTTGATGATGTCTCCCTGTGACTT
GGTCCAATTACATTCACTGGTAATCTGAAACCTTGTGAAT

>RXA02207
ATGCGCCGTCGATCCCGTGTGTCCCGTTTGCTTCCCGCCACAGCTTTGCTGGCCTCAACT
GCACTTCTTTTTAAGTGCATGTACGCAAGGGGTAACGGACTCCCCGGATATGGGCAAGGCA
ACTCCCGCTGTCTCCCCCGCAGCAAGCAACCCGGATGGCCAAGTAATTGAGTTCGGCAAC
ATCACTGACATGGAAGTCACTGATGGTGACATCCTCGGTGTACGCACCGAAGACGCACTC
GCTATTGGTACAGTCTCCGACTTCGAAGCGGGTAGCCAGGTGGAACTGGACGTCGATAAG
CAATGCGGCGACCTGACCGCAACCGGCGGCACTTTCGTGCTCCCCTGCGCCGATGGCGTT
TATTTGATTGATGCCAAGGACCCGGATCTGGATGAGTTGCGTGCAACTGACAAGCCAGTC
ACGGTGGCAGCCTTGACCAGCGATGATCAGCTTCTGGTGGGCAATGGTGAAGATGAAGAA

CTCACCATCTACCGCGAGGGCGAAGAGCCAGAAACCTTCACCGTCGCGGGTCCCAATACC
CAGCTCATCGCCGTTCCTGTCATTGATCGCCACGACGCCGTTGTGCGCACCTGGAACGAA
AACACCACGATTCAAGATGTGGACTACCCCAACGACCGTGAAGGCGCGACCCTTCGCGTG
GGACTCGGCGTTGGTCAAATGGCTGGTGGCGAAGACGGCCTGCTGGTGGTCTCTGATGAA
ATGGGTGGCCAAATTGCCATCTACAACGCTGATGATGTC

>RXA02211-upstream
ACTGTCCGAAGTATTGGATCTGGTCGAGGGAACTGTCCGTAAACGCGACTAAACGACCCC
TGATTCACACTTTCAGACTACAAGAACTAGACTAAGCGGT

>RXA02211
ATGGTTTCAGTTCTTTTAATTCAGCCCCGTCAGGGAGAAGCAGTCGCCGCAGCTGAGCGA
CGTGACTTTTTGCAGGCCACCGGTCTTAAGCCTCAAGAACTGACCTCCCGAATGTTGGAT
ACCACCACTTCTCGAATTGGCAGTCTGGAAGGTTTCGACGGCGTGATTGTGGGCGGAAGC
CCACTGAATGCCACCAACTTTGAGTACAGCGATTGGCAACGCCACGTCCACCGCGAATTG
TCCTTGCTGATCAATCACCCACTGCCAACAATCTTTGTCTGCTACGGCAATACCTTTTTG
ACCTTCTTCTCTGGCGGACAGATTGGTCGCACACACCCCGAAGATTCCGGCGCCACCACA
GTGTTGCTAACTGACGCCGGCAAACGAGACGTACTCACTCAAGACCTACCGGATAGCTTT
ACGTCCTTTACTGGTCACACGGAAAACTCCGTA

>RXA02212-upstream
GTGATGTGACTTTCTATCACCCCCTTACTCACCCCCATTGCTTATTGAGTAAAGTCGGTT
CCCGCTCTTTCGTGAGCCCGACACTAATGAAGGTTTTTAG

>RXA02212
ATGATTCCAGAAAATATTGATCTCAAGCAGCTCGCTTCGGAGCTTGGTGATGATGCCGTG
GCAATGGGGGAGCACACAGGCAACCAGTTTCCGACTTTGGAAAAAGACCTTATTAATGTT
GTGACAGATGCAAAGGAATCAGATTTTGGATCTTTAGGGGTCGTGATTCTTGATGAAACT
CCAGTGATGACTTCCAACCTGAGGGATATTGCGCAGGAGCTGTTGATTCAAACGGATCTG
GACACCGTTGTGGTGCGGGCTCCAATGTCGGCTGCGGTGGTGAGTGATGTTCATTCGAGG
GCGGCGCTTGAGTCAGGGCAGCATGATTTGCTTGGGACCACTGATTACGTGCTGGGAACG
GAGCTTTTGGTACAGGATGTAACGGAATCGACGGTGGGGAATATTGATTGGGGTCAATTG
CTGATTTGGGGGTTGGTTGCTTTGGCAATCGCCGTGGTTGTTGCGGGTGCGTCTGTGCGT
CGAAAAGCAATATCTTTA

>RXA02212-downstream
TAAGTAAAGTTCTAAAGCTTTAC

>RXA02216
GTAGCGCCCGCCCCTGGACACGTGGTGTTGGCAACGGGACCAACCTGCCCCATCCAGATG
CTGCGCGCCAACAAGAACACCTGGTCAGTTCAATTCCATGCGGATATGGATGCCGTAGGC
ATGAAAAACCGCATGGATTTTTACTCCAACTACCGGTTCTTCTCCCCAGAAGATTATGAC
CGCATCATTGCAGAGCTACCCTCTGTTGACTCCATTTATGCCAACAGGGTGCTCCGCAAC
TTCGTGGAGGTCTGCGAAGGAATTCGTGTTGCTGATGGTGCTGAGCACCAACTCCCAAAG
CTTAAC

>RXA02216-downstream
TAATCGAGGAGACTGGTGATTCG

>RXA02217-upstream
CCAAATGGGTATGGGCGCTTTTGACCATCGTCAATGGTGTTGGCCCCGCTGCCTACTGGG
CTTTCGGCAGGAAAAACTAAGAGTTGTTAGGGTGGCGCTC

>RXA02217
ATGACTAATAAAACACGAGCTCTACTCATTGGTGGCCACGGCAAGGTGGCCCTCCTAGCA
ACCCCCATGCTTATCGACGCCTCGGTGCAGGTCACTTCCATGTACCGCAATCCGGACCAC
AGGTCCGAAATTGAGGCGCTGGGCGCCACAACTTTAGAGCGTGACGTCACCACACTCAGC
GTGGAGGATTGGGCAGATCTGCTCAAGGACTTCGACGTAGTGGTGTGGAGCGCCGGAAAC

GGTGGCAAGAACGGCGCGGATGCAACTTATGCCATTGATCGTGATGCCGCGATCGCATCC
ATTGATGGTGCAGCTAGCCTAGGGGAGAAGGCACCTCGCTACATCATGGTGAGCTACATT
GGATCCTCCACGCACACCATTGATCCTTCAGCATCCTTCTACCCATATGCAGAATCCAAA
AAGGCCGCTGATGAGCACCTAAGCTCCACCAACCTGGATTACCTTATCCTCGCACCAGCA
GCCTTAACTCTGGATGAAGTCAATGGCGTTGAGGTGATCGCCGATACCAACGAAGCAGCC
GCAGGCCGCACCACATCAAGAGTCCTCGTTGCGGAAGTTATCACCGAGTTGGTGGTTCGC
GACTTCCCACAAACCCGTGTGCTGCCTTTCGTGGATGGCGAATCACCAGTCTCCTCGATT
AGT

>RXA02217-downstream
TAAGCTTTGGGAGTTGGTGCTCA

>RXA02218-upstream
CAATGATTTATATGTCTTGGACGAGCGATTAAATAGAGTTGGCATACCCCAAATGATAGA
CCCAAAGTGTCGTGTCCACCGCTCGTTGTAGCATGAACCC

>RXA02218
ATGTTTGCAATCATGACTGTCACAGGGCAGGACCACACCGGAATTATCGCCGCAGTTTCC
ACCGCGTTGGCTGAGCTAGATGTCAATATTCACAACGTTTCCCAAACCATCATGGATCAA
TGGTTCACCATGATCTTGCACGTTGGTTTCGATGAATCGGTCTTGGATATCGCCACAGTT
CAGGAACGCATGAAGCCAGTGGAAAAGGAACAGGGCTTGGTTATTCGTATCCAGTCTGAA
GCCTTGTTCAACGCGGTTAATGAGATC

>RXA02218-downstream
TAGGGGGTGCACATGGATGATTT

>RXA02219-upstream
TCAGGAACGCATGAAGCCAGTGGAAAAGGAACAGGGCTTGGTTATTCGTATCCAGTCTGA
AGCCTTGTTCAACGCGGTTAATGAGATCTAGGGGGTGCAC

>RXA02219
ATGGATGATTTTTCTGCATCGCTAGGTTTTACTGACCGTTCCTCGAGGGGAATTCTGGAC
ACCATCGAGATGATTGAGAAGTATCGTCTTGATATTCGCACCGTGACCATGGGAATCAGC
CTGTTGGAATGCGCGCGTGGCTCGATGGAAGAGACCGCGACGGCTGTTTATGATCGCGTG
ACGTCACAGGCTGCACGTCTGGTTGAGGTTTGTGAAGGCATTGAGCGTGAATTGGGCATT
CCCATTGTGAATAAGCGCATCTCGGTGACTCCAATTGCCCTGGTGACTGCTGGTTGCAGT
GGCGATCCCGTTGACGTTGCTCGAGCCTTAGATAAGGCAGCAAAAGATGTCGGAGTGAAC
TTCATCGGCGGGTATTCAGCACTGGTTGAAAAAGGTGGAACCACCTCCGATATTCGGCTG
ATCCGCTCCATTCCCGAGGCATTGAGCACAACCGATGTGGTGTGTGGATCCGTCAATGTG
GCGTCGTCTCGCGCGGGTATCAACATGAACGCAGTCAATGAGATGGGCAAGGTGGTCAAG
CAAGCAGCTGAATTGACCAAAGATCGCTCCGCCATCGCATGTGCAAAGCTAGTGGTCTTT
GCCAATTCTGTGGGCGATAATCCATTCATGGCTGGCGCTTTCCACGGCATTGAGGAGCCG
GATTGTGTGGTCAGCGTTGGTGTCTCAGGACCAGGCGTGGTTAGTCGCGCGCTGGGCAAT
CTTCAAGGTGCCACCCTTGATCAAGTCGCAGAAGAGATCAAGAAAGCGGCCTTCAAGATC
ACTCGTACTGGACAACTGGTTGGTGCGATGGCCTCAGAACGCCTAGGAGTTCCTTTCGGC
ATCGTTGATCTTTCGCTCGCTCCCACTGCTGAAGTGGGCGATTCCGTGGCAAATATCCTT
GAGGTCATGGGTCTTGACCAGGTGGGCACACATGGCACCACCGCGGCACTCGCACTGCTC
AACGACGCGGTGAAAAAGGGTGGCATGATGGCCTGCTCACGTGTCGGCGGCTTGTCCGGA
TCCTTCATTCCAGTTTCTGAAGATAAAGGCATGATCGATGCGGTTCGCACAGGAGCAATT
TCTATTGACAAGCTCGAAGCGATGACCGCGATCTGCTCAGTTGGTTTGGATATGATTGCG
ATCCCTGGCGACACCCCGGCGGAAACTATTTCGGGCATGATCGCGGACGAAGCAGCCATC
GGTGTGATGAATCATAAGACTACAGCTGTGCGTGTTATTCCTGTTCCAGGAACTGTCCCT
GGCGATGAGGTAGATTTCGGTGGCTTGCTGGGTTACGCGCCGGTCATTCCAGTAAATACC
GTGGGAAATAGTGAGTTTATTCACCGCGGCGGCTTCATTCCAGCACCCGTTCACGGGTTT
AGAAAC

>RXA02219-downstream
TAGGAGATCCGGGGCCTTTACCT

>RXA02221-upstream
TTCAATGATATTTGCTCTGATTTTTGGTTCTCGTCTAATTTCATTATTTTGTCACGCCAG
CCATCACGACTTCATACCCACCAATTGAAAGTAAAGTCCA

>RXA02221
ATGTTTACCGCATCCATTCCTACTTATGAATTAGGGTCTTTCAGCAAGGGCTCCTACGTT
GAGATCAAAGGAACTTACTTCTACCCTGACACGCTAAATACTTTATTTAGAAATTCTGGG
GCAAAAGACAACGAAGAGTTCTTTGTAGACGTAACTCTTGTTCCAGAACCAGATAATCCG
CATAGCACTCGAGGCCATGCCATTTCAGTCCGCTGGAATGATCTCGTAATAGGACATATT
GCCTCGGATATGACTGAAAAATTCCAACAAGTGCGACGAGTTGCAGCTAGTGGCTACGAT
GCTCGAGTCTCTGCTCGGATTTGGACGAATACAAACTATAAGAATGAACGAGATTTTTGG
GTATCTGTTAAGCTCCCCGATCCAGATTTCCTTGTTCCTCTTAATGATCCTCCCCATGAC
GGGTTTACCCTCCTCCCTTATGGAACAGCAATCCAAGTCACCAAGGAATCTGATCACATG
GACGTGCTCTCAGAATTCGTGCCTCCATCTGGACAAGGTCAGATTCTCGTATCGCTACAC
ATCATTAACGCAGGCGTGAGAAAAGAATGGGATGGCATTGAAGTTCGGCTCGATAATCAA
CGGATCGGAGAGCTTACAAAGGCCAGTTCAGAAAAATTCGCACCCGTAGTGCGACATTTC
GATGACCTAGGACTTAGTACACTATGTCGTGCGCTCATCAAGGGGTCATCACTAGCTGCT
GAAGTAACTCTATATGGAGCTCGTGCACATGAGCTTTCCGAAGAAGACTTAGAACCTAAA
AGCTCTTCCCCATTGCCCAGGTTGGTTGAATACCAGTCAAATCCGTTTAATTATCAAGTC
CCCAACAGGTGGCCCGGCGAGCAGAATCAACGTGCTCCTAAGTCGCAAAAGTCTTCTTCA
TCACCTTTCGCAGCGTATCGCGGGCCATCGCAACCTAGTAAATCACTCACACCGTTTGTA
GCGCAGACACCTGCGCCTCAGCCTAGTGATCGATTTATTGATTGGGATTCATTGCTTCAA
CCGGACGGAACTCCAAGAGCTACGCCATTCCAAAGAGGAGTAACCCGCGGGTTAATTGGC
AAGCATTTTTCGAATCAAAAATCTCCAAGAATTGACTTTGCAACGGTGGGGCAATGTGAT
GCAATTCTCCGAACTTTCGGAGAGCCGACCGACAAGCTTTATAAAGACGGCAGGACTTCT
TGGCCTTTGTGGTGGGCGCTCATGGCGATAGTCACCCTTCTCGTCATGTTGCTGAACTTT
ATTCCAGGAATTGGTCCGATCTTCCCACTTATCGGATTGATCGTACTTGGTCATCACTTT
TGGACTCGCCGAAAACTTAACCCACCATTCGGTAGATCAAAA

>RXA02221-downstream
TAGATATTCTCATCAAATATCGC

>RXA02223-upstream
CTTGCTTTTGAGGGCCGCTACGCGCAGCTGTATCAACGATGGAGTGCTCAATAGTTCAAA
TCCACCACAAACTCTAGAGATTTGGGGTAGAAACGAAGAC

>RXA02223
ATGAGCACCTACCAAGACGATCGTTTCCCAGGCCCAGACCCCTACGCACCGCTTGGTGAA
AAGCCAAGCTTTACCCTCACCTCCACCGACTTGGAAAACGGTGCAAAGCTGGCCGAAGCC
CAACTCGGTGGCACCGATATTTCCCCACAGCTGTCCTGGTCAGATCTTCCAGAAGGCACC
AAATCCCTCGCGATCACCTGCCTCGACCCAGATGCCCCAACCGGCGCTGGTTTCTGGCAC
TGGGCAGTGTTTAACATCCCCACAACTGTCACGGAGATCCCCACCGGTGCTGGCGATGAA
ACCCTCGGCGGCATCGAAGGCGTAGTTTCCCTCAAGGGTGATTCCGGCAAGCGTGGCTTC
TACGGAGCGCAACCTCCAGCTGGCCACGCACCGCACCGTTACCTCTTCGCAGTTCATGCA

>RXA02226-upstream
CTGACACCTCCTATGGCACGCGGTATGTTTAATAAACGTAATTCGAGTTTCGGCGGCCGT
GTCGCGCGGCCAGGACGACCCTAGCTTTTAAGGACCCACC

>RXA02226
ATGACTGAGAACCAGACTCCCAGCTCCACCTCTGCACCGAAGCCGGGACCTCGCCCGGGC
CCACGGCCAGGACCCCGACCTGGGGCTCAGGTTGCTGCAAAGAAAGCTGCGGTTGCTACA
CCTGCGCCGATCGCCAAAACTTCTAACGATCCTGCAAAGTTTGGTCGCGTTGAGGCAGAC
GGATCTGCATATGTCACCACCTCTGCTGGCGAGCGTCTGATTGGTTCTTGGCAGGCCGGC
ACCCCTGAGGAAGGTCTTGCTCACTACGGCGCCCGTTTTGATGATCTGGCCACCGAAGTT
GAGCTCATGGAACAGCGCCTAATCTCCCACCCTGATGATGCGACCTCCATCCGCACGAAG
GCTGAAGAACTCAAGGCAACCCTGCCCACCATCGCTGCGATCGGTGACCTTGATGGCGTT
GAAGCTCGCCTGTCCAAGATCATCAACAACTCCGAGGAAGCCAACGAGCGCGCCAAGGAA

CAAAAGGCTAAAAACCGTGAGCGCGCAGTAGCTCGCAAGGAAGAGCTCGCTGTTGAGGCT
GAAACCTTGGCAGAAAACTCCTCCGACTGGAAGGTTGCTGGCGACCGCATCCGCGCCATC
CTGGATGAGTGGAAGTCCATCCACGGCATCGACCGCAAGACCGATGATGAACTGTGGAAA
CGCTACTCCCGTGCGCGTGACTCCTTCAACCGTCGCCGCGGCGCACACTTCGCAGAGCTG
GATCGCACCCGCGCATCTGCACGCAAACTCAAGGAAGAACTCGTTGAGCGCGCCAATGCT
CTCAAGGAATCCACTGAGTGGAACGACACCGCCCGCGCATTCCGCGATCTCATGACCGAA
TGGAAAGCCGCCGGCCGCGCACCACGCGAAATCGACGACAAGCTGTGGGCAGCATTCAAG
GGCGCCCAGGACTACTTCTTTGATAAGCGCAACGCCGTAGCCAAGGAACGCGACCAGGAA
TTCGAAGCCAACGCAACCGCAAAGCAGCAGCTCATCGACGAATACGACGCACAGATCAAC
CCCGAGCAGGGCCTCGATGGAGCGCGCAGCAAGCTC

>RXA02227-upstream
ACCGCGTGCCATAGGAGGTGTCAGCCAGATAGGGTGCACTATCTTGAAAAACCGCGCTCA
GGAGAGGTGTTTGCCCAGCAATTTCGGTGGGCAGGATAGG

>RXA02227
GTGGAAGACGTGAATGCAACGCTGATTATCATGCCTGGAAGTCCGGCGCTGGTACCTGAA
CTGGCACCAGCGGATGCTGCGGGGGCGCGCTTGTTGGCGTCGTTACGTGCAGTTTTTGAT
GCGGAACTGGCTAATGATGATCGCCCGATCGAGTTGGTTGGCTCCCGGGATGAGGCGTGG
TTTACCAAGCATGCGGGAAATCTGCGGGCCTGGGGTGCACCGAGCGTGCAGGTTTCTGAC
GGACATTATTTGCCGGAAATTTTGCAGCGTGTCGCGCTGGGTGGTTTCGAATCGCGTGTA
ACTCATGTGCGCGATCGGTTGGGTAGCGTCAACGACAACACGGTTACGGTGCTTGCCCTT
GACGGCCCCACGGGCTTGACCACCCGCGCGCCGTCCGCACTCGTGCCCGGCGCGTCCAAC
ATCGACGCCTGGTGCCGCTCATTGCTGTCTGGAAAGCCCGGGGAAGTGCCCAGCACCAGC
ACGCTTATCGACGCCTCCCTCCGCGAACCACAGCTCTGGCTCGACTTATCCGCCGTGGCA
ACAGAAGCGTCAACTGCTCAACTTCTCGACAGCGACGACACACACGGCGTGGGACGCTAC
GTTGCTCGCTGGACTTTT

>RXA02227-downstream
TAACTTAAGGGAGATCTAGATCG

>RXA02230-upstream
CATCGCATAGAATACTGGTGCAATCGTTTACGTTCGCTATTAATGTGACACGTATAAGCC
GACACTTTTAACGAAGCGCAGAAGGAGTGAGAGCAAGAAA

>RXA02230
ATGGGAGAACAACTTCCGTTTGCTAATGGTTCACGCTCCAACAAACTGCCGCTCATCGTC
ATCGGTTTGTGCTGCATAATGCTGATCCTGTGGCTTAAACTTCCCGGCGTACTGCTTGCC
ACCATCATTGGGGTTGCCACGATGAGTGTGATGCGGATGCGCACCTCCACCCCAGAAACT
GCCTCGCTGGTTACTTCTATTCGGCTGTCTGCGGAAGATATTTCCGATGTGCAACATGAG
TGGCAGCAGTTTTTGACCTCCCCCGAGGCCGATGCGCTGGCTGATCGCACGCTTGTCCGT
CCCGCACTGGCGGATCCAGATTGTGGCGATAAGGCTATCGAGAAATTTCATTATGAAATC
AGCAATGCCAATCGCTTCTTGGGCAGGTTGGACGCTCGTCTGCAACAAAACCTCGTGGTC
AGTGAGCTAGAAACACTTCTCAAAGTAACGGACGAGCGCGCACTAGAGCTGCGGGAAACG
TGGCTGGATGCGCGTAAAGCGGCCCAGAAACTTGGGCCGAACTACAATCGCGAATCT

>RXA02230-downstream
TAGATCTGCACCTCACCGAGTGC

>RXA02231-upstream
TAAACACCTAAATTGAGCGCTCTATTCCATCAACGCGGGGGCAATTTCTCACGTGTAGGA
AAAGTGACTATTGCCTGTTAAGGGAGTTAGACTAATCGCC

>RXA02231
ATGACTAGCGATCTGAAGACAATCGGTATGGATTTCGCCAAGTGGCAAGATGCAGTGGAA
GCAGCAATTGCTTCACAGCGTCTCGAGGTAACAGGCGAGGTCCGTGGCGGCCAGCTCATC
CAGTTCTCGGATGATTCCGGCGCCCAAATTAACATTCTGGCTGTCGAGCCTTTTGCCACC
TTCGCCGGCTTTAACTCCGCAACAGTCGCTTACGGCCACGTCAGCATGATCAATGATGTG

CTGTCCCTGGTCGATATCATCGATCCTTTCGGCACCCCTGTTGCCACCATTACCTGCAAC
CTTGCTCAAGGCCCACTGCTTGTTGATGAACCAGTGCAGCGCTGGCAGCAGATCCGCATT
ACTGCCCTGGGCATTGATGTTGAGGTCCACGACAATGCAGATGCTTACATCCGCAATGGT
GGCGAAACTGTCGGCATGCTGGTTTCTGAAGGTGCAGAGAAGATTGCCAGCGGCAGCGGC
GCTGTCATCCCGGACGCATCCGCAGAGTTTTCCGCACGCGTGTTGTCTGCGGAGTACCGC
ACCAACACTCTTACCGGCCAGCGTTTTATCCACGCAACAGTTGATGGCCTCTTCGCTTTT
GATGTGTGCCTTCCTGATGCACCAGAACTACCTGCCCGTGACAGCGTGTTGTCTGGCAAA
GTCATGCTGACTGCTGCCGTTATCCCCACTGAGGTCACCGGCTGCGGTGGCTCCGGTGGC
GGCTGTGGCTCAGGTAGCTGTGGCTGCGGCGGACAC

>RXA02231-downstream
TAAAATTCTGCACAATTTTTTAA

>RXA02238-upstream
GGCGCTTAGCCAAAACATAGAGCGGTAGGGTATGCTTATCCGATTGAGCAACCTTTCCCG
CTCTTAACACTACTGTCCATATACTTTTGAAAAGGTGTCA

>RXA02238
GTGACCAACGTGAGCAACGAGACCAACGCCACCAAGGCCGTCTTCGATCCGCCAGTGGGC
ATTACCGCTCCTCCGATCGATGAACTGCTGGATAAGGTCACTTCCAAGTACGCCCTCGTG
ATCTTCGCAGCCAAGCGTGCGCGCCAGATCAACAGCTTCTACCATCAGGCAGATGAGGGA
GTATTCGAGTTCATCGGACCATTGGTTACTCCGCAGCCAGGCGAAAAGCCACTTTCTATT
GCTCTGCGTGAGATCAATGCAGGTCTGTTGGACCACGAGGAAGGT

>RXA02238-downstream
TAAAAGACCTTATAACTTCACAC

>RXA02244-upstream
CACCAATTGTTCTGGGCAATATCCAACCCCCGGGAAAGAAAATGATGAATGCAGCAGACT
GGGCGCGTGGTGTCCAACTTGATCAGGAAGCGAAATTCCA

>RXA02244
ATGAGCCTAGAAAAATCCGGCGGATTCCGCTCCAGGACTCCAAAAGCGCAGCAGGAACCT
GCTAAGCAGAAGCCGCAGGCGCGTAAATCTCCGTCAAAGAAGGCCCCGGCTCGGGGGCAG
GGGCAGAGTCAGGGGCAGCGCCAGGGCCAAAGCAGTGGCAAAGGCGGCGGAAACCGCAAG
CCCCCTGCGCAGGCCAGGGAAGTGAGGGCTCTGGGCGTCGATAAGCCGAGAGAAATTGCG
TTTGAGGTGCTTGATCGTGTGCGTACCGGTGAGGCGTATGCCAACTTGGTGTTGCCACGA
CTGCTGAGCAAGCACAATCTTTCTGGCCGTGACGCGGCCTTTGCTACGGAAATTACCTAC
GGCACCTTGCGTAATGTCGGCTTGCTGGATGAGGTCATTAAGGCTGCATCTGGGCGTGAA
CTGTCTGATATTGATCCAGAGGTTTTGGACGTGCTGCGTTTGGGCGCGTACCAGGTGATG
TTTACCCGCGTGGAGGATCACGCTGCGGTCGATACTTCAGTAAAGATGGTCGGTGGGCTG
AAGAAATTCCAGGCCACTGGTTTTGCCAATGCAATTTTGCGCAACATCACGCGCAAGGAA
CCAGAGCAGTGGTTGAAGGAATTGGAGCCCGCGGAAGAGTTGGCTCGCGTTGCGTTCCGT
ACTGCGCACCCACGCTGGATTGCGCAGAGTTTCTCACAGGTGCTCCCGGCAGATGAGTTG
GAAGCAGCGCTTGCTGCGGACTCTGAGCGCCCAGTGGTGCACTTGGTGGCTCGCCCAGGT
GAGATCAGTGCAGAGGAATTGGCGCTGATCACCGGTGGTGACGAGGGCAAGTATTCCCCA
TACGCGGTGTACCTCGAGGGTGGCGACCCGGGTGATATTGAGCCAGTGAAGGATGGTCTT
GCAGCAGTGCAAGATGAGGGTTCTCAGCTGATTGCTCGCGCCTTGGTGGAAATCCCCGTG
GAGGGCACCGATGCCGGCCGTTGGCTGGATATGTGTGCAGGTCCTGGCGGTAAAGCGGCG
CTCATTGGTGCGTTGGCTCGCATGGATCGTGCCACCGTTGATGCCGTGGAGGTCTCTGAT
CACCGTGCCCGACTGATTGAAAAGTCCGTGCGTGGTTTGCCCGTCAAGGTTCATGTGGGC
GATGGCCGCACCATCAACTTGACCGGTGGTTACGATCGTGCGCTAGTCGATGCGCCGTGT
TCTGGTTTGGGTGCACTGCGTCGTCGCCCTGAGGCGCGTTGGCGCAAGCAGGAAAGCGAC
ATTGTTGAGCTCAACACCCTGCAGTACGAGCTGCTTGAATCCGCTGTGAACAAGGTGCGT
TCCGGTGGCGTGATTGTGTACTCCACATGTTCACCTGATCTGCGTGAAACCCGCGGAATC
GTGGACAAGGCACTGGGGGCTCTGGAGATCGAAGAGCTTGAGGCTGCGGAGTTCATGCCA
GGCATGACCGATACCGGCGATGAGAAATCAGTGCAGATGTGGCCACACCGCCACGGCACC
GATGCGATGTTTGTGGCAGTGCTGCGAAAGAAG

>RXA02244-downstream

TAGACCTGTGAGCTAAGTGGGGT

>RXA02254-upstream
TTGATCGCCGATGCCGAAGAAGGCGGATTGTGGGAAAACCTCCTGCAGCACCGCTTCAGG
TGGACATGGTGCGCTAGCTGGTCACGCCTTGGGAAACCTC

>RXA02254
GTGATCGCGGCGTTGACCGACATTTTGGGCACCTCCCAGCATGCGCTTGATCAAATCGCT
CAACTCGCTGGAGCCAAAGGACGCATCATCCCGGTATGTGCTGAACCTTTGGATCTTGAA
GCGGAAGTATCAGGTCTAGACTCTGATGCTCGAGTCATGCGTCAAGTTCGTGGTCAAGTG
GCGGTAGCTGCAACCCCCGGGCAGGTGCGACGCGTTCGAATCATTCCGGACAATCCAGAA
CCGAACCCCGCTGCCATCGAGGCCATTCTCGATGCAGATTTGGTCACCCTTGGCCCAGGT
TCCTGGTTCTCCTCTGTGATTCCACACATTTTGGTCCCAGGGATCGTTGATGCCTTGGCG
CAGACAAAAGCAACCAAAACCGTGGTGTTAAACCTGACGTCCGAGCCAGGGGAGACCGCG
GGATTCTCTGCAGAACGACACATCCATGTGCTCCGCCAGCATGCTCGAAACCTTCAGGTT
GACCAAGTCATTGTCGATGCCAAGACACTGTCCTCACAAACCGAACGCAATCATGTAGAA
CGAGCTGCTCGCACCCTTGGTGCAGAAGTCTCCTTCCATGATGTCCAGGCTGAAGATGGC
CGTGGTCGATTCACCAGTATTCACGATCCAGCAAAGCTGTGTGCAGCGTTGCTGGCAAGT
TTTGCTGGAGCACGAAAGCGT

>RXA02254-downstream
TAAGGAGTAGGCGTGTCACTGAC

>RXA02255-upstream
GTGTGCAGCGTTGCTGGCAAGTTTTGCTGGAGCACGAAAGCGTTAAGGAGTAGGCGTGTC
ACTGACGAGTGATATCAAACAAGAATTGGCGCAGGTCCAT

>RXA02255
GTGGCCAAAAACAGTGTTCGTGCTGCGGAAGTGTCTGCAATTTTAAGGTTTGCTGGTGAG
ATGCAAGCTGTCGGCGGCAAGCTGGTCATCGAAGCAAATTTGGACAGCATGCAAGTCGGT
ATGAGGCTTCAGGAGTTTATCCAAGGTTTGTACAACTCTCGAGTCGATGTGCACACCGTG
AACCCGACTGTGAGCAGGAAAACGCCACGGTATTTGGTGCGCATCATTGACAATGCCGAT
GAAATTGCGCGACGCACCGGACTGGTCACCAGGTCTGGACATGTGGTTAAAGGTCTAGCG
CCTTCTGTGGTCAGCGGAACAATCAGTGACGCTGAAGCTGCATGGCGCGGTGCGTTTCTA
GCCAATGGATCTTTAAGTGATCCAGGTCGTTCCTCTTCGTTGGAGGTGTTGTGTCCTGGT
CAAGAATCAGCATTGGCACTGGTTGGATGTGCGCGAAGAATTGGGATCGCGGCGAAAACG
AAAGATTCTCGAGGATTTGATCGCGTCAATGTTCGTGATGCGGAAGCAATTGGGGCACTG
CTCACTCGAATGGGTGCCCAGAAAACTCGCATGTTGTGGGAAGAAAAACGCATCAAGCGG
GAAAGTCGAACTCCGCAAACCGGGTTGGCCAACTTCGACGATGCCAATCTGCGCAGGTCA
GCCCGAGCAGCAGTTGCCGCTGCAGCGAGGGTAGAACGCGCCATGAAGATTCTTGGTGAT
GATGTTCCTGAGCATTTGGCTGAGGCTGGACAGCTGCGTGTGCAGCACCGTCAGGCATCG
TTGGAGGAGTTGGGCCGGTTGGCTGATCCTCAAATGACCAAGGATGCTGTGGCCGGTCGT
ATTCGTCGTCTTTTGACGATGGCAGATAAGCGCGCCGAAGATCTGAAGATTCCTGATACA
AATTCTGTTGTGACGGAAGATTTGTTGGAAGAAATT

>RXA02255-downstream
TAGATGATTGAAGCCTAAAAACG

>RXA02266-upstream
GAGGAAAGTAGCGCTACATCTGCATATCTACCCCCTTAAAAATGAAGCATAAAACCGCCG
TGTACCGGCCTTTTATTGATTTTGACGTAAGCTTGCACCG

>RXA02266
ATGACTCAAGATGAACACCCCCGACAGGCCGACTCCCATTTCAACATGCTTTTACCGGAT
GGAAATGAAAACGCACACCAGCTTTCTGTCGCTCTAAATCAGGTGGCACATCTGTTGGCC
TATGATGCGGACTCTTCAATTCATCGGCCTGATGGGCTAAGTCTGGCGTCCTATAGAATT
CTCTTTTCACTGTGGACTGATGGCCCGATGAGTCCACTCCAGGTGACTGACAAGACTGGA
ATGAAAAAGTCTGCGATTTCTAACCTGTTAAAGCCATTGCTCGCTGAATCTCTGATTGTG

CAGGTGACGGCAGAAAATGATCGACGCTCAAAGGTTTTAAGCCTTAGCGAAAAAGGCACT
ACATACATTCAGAAAACAGCCACCCGCCAAAATGCTTTGGAATCCGAGTGGTTTGGCACC
CTGACCGACATCGAGCAGGATTTATTGGAGTCGTTGCTCAGGAAACTGCTCGACTCCAAC
CGCGCATCCAAGGTTCGTAAAAACCGATCTAAC

>RXA02266-downstream
TAGCGTCGATCCTTAGGGATGTA

>RXA02267-upstream
TGCGCTCGGCAAGTGTTTTGCTTATCGACGTCTCCCCACATAACAATCCCAACTCGAAGC
ACCAACGATTCAAGCCTTATCAGTTTTGTACAGGAAAATA

>RXA02267
GTGCAAAAATGGGGTTTAAGCTTCGTGGAGAGGATTGTCATCGTGAACAACGTGCAACAG
TTTCATCGATTTTTTGATGATTCCGCAGTCTATTATCCCTGCTTCGTCCCGCTTGACCGA
GCCATCGGCGAACACTTTGATCGTCAGAACAAACCGATGTCCAGATTCATCGGAACGCTC
ATTCTGCCGTTAGCCAAACTGGAAGAAGCCGCCCAATACACCGGCGATGAAGTCCTTCGC
GTGTCGGCAGTAATCAGTACTGATGGGCTCGCTGATCTGCGAAGGGATTTTTACGAACTC
CCCAACATCGACATCGCCTCGGTGGAAATCAAGCTGGTCGGCGCAGCCCTCACCAACACC
GCTTGGTTGGGAGATGTGGAAAAACTCATCCAACAACATCGCAACACTTTCGTATGGGTT
GAGATTCCGACAGCCCTGGTCACCGCAGATATTGTCCGAAAACTCCGCCACATGGGAGCT
GGCCTGAAATACAGAACTGGAGGTGATAGGGAAGAGCTCTTCCCCTCACCGCAGGACTTG
GTCACTGTGCTGCGCACCGCCATCGATGCTGCATTGCCGTTTAAACTCACTGCAGGCCTG
CATCGTGCTCTCAGGTATCGTGACGAGAAAACCGGCCGACTTCACTTCGGATTCCTCAAC
ATTGCAGCCGCCGTGGCGACACTTCGTGCTGGAAAAGGCGAGGCAGAGGCACTGAAGATC
CTTGAAGGCGATGATGCCGCTCCGCTTATTCACGCACTACAAAGCGGCGAAAACTGGCGG
GATTCCTTCCGCAGCTTCAGTACCTGCAATGTTGTTGAACCACTCAACACTCTGATTGAT
CTTGATGTGTTGGCGGAAGGAGACGTACATCCC

>RXA02267-downstream
TAAGGATCGACGCTAGTTAGATC

>RXA02271-upstream
CACTCCCCTATCCTAAGCCACATCTCGGTTTATTAAACTGTTAGTGAATTCTCACCCGCA
ACACTGGTGTATTTCAGTTACATCCGTATGGTTATTGGTT

>RXA02271
ATGAGCTTTCTTAACTCTGCAAAAACCAAGACCGTAGCCCTCACCGCAACCTTCGTTGGT
GCAGCAACCCTTGCAACTCCTGCAATCGCATCCGCTGACATCGTCGACAACGCCCTCGCA
GCCCTCCCATCCGGTGAGATCAGCTGCTCCCAGGCTGAAAAGTACTGGACCACCGAAGCT
GATTACAACAGCAAGGTTGCACAGGCCAACGCCTTGGCAATGTTTGACTCCCGCGGCCCA
CAGATCCAGGCAGCTCTCGCACGCGTTGACGAAGCAGCAAACCGCTGCGGACTCAAGGGC
GGCACCGTAGCTGCGCAGGCTGAGGCAACTGAGGCTGCGCCTGCCGCTCCAGCACCTGCA
CCGCAGGATAACACCGGCACTTCTCAGACTGCCCCTGCCCCAGCAGCACCAGCAGCACCA
GCAGCTACCCCTGTGGTTAACCTTGCACCTGCAGGATCACCAACTTTCACCATTGAAGTT
CCAGGAGTTGGCGGGGTTCAGCTGCCAGATCTATACCAAATCGTCCAACAGTTCTTGGCA
CAGTTCGGAATCAAGATC

>RXA02271-downstream
TAAATCTATTCACATCCCTTAAC

>RXA02279
NCNGCCAGGGCTACCGCGCTTGTCGATTTCTTGGAATCCCAGACTGTTGACCAGCTGAAT
AACCCCGATGTCCAGACTTACCTCACCGAAGCGGAACTGATTCGCGATGACTTGAGGTCT
TGGGCAGTCATCAAATCAAATGGCATTGGACAACATCGATCTTGTTCCATACGGCGAGGA
AACGACGAGCCACTTGCAATCGCCCGCAAGATCATCGAGGAAACCGCTTCCCATCCTGAG
CTGAGATTCGAAAACCTCGAGGCCCAGTTCTCCGAGTTCACCATCTTGCTTGCTCAAAGC
CCGGAGAACCTCGACGTAGCCCGCTACCAGGAGCTTCGTACACAGGGAAACTTTGTTCAA

GAACTCGCCTTGGACAGCATTTTCGGCCAACATGCCGTTGTTCAAGACACCGGAAACGGC
GAAGCCATCCTAGATGAAACTATCGGGTACATGATCGGCGCCGGCATGCGTGAAACCACT
GCCCGCACCGCCAGCCAGTTCGCGCAGCTTTACTCATTTGTGGGCAGGCAGGAACGCTCC
ATTGAAATGGCACGACTCGCTTTCGAGGAACTTCAAGCGGCAGGACTTCCCCACCGTGAG
GAAGAACTGCGATTGGGCATGCAACTCGCCCAGGTTGAACCAATTGAAGCCCGCGAAATC
CTGGAAAAGCTGCTGCTGCCTAAATTCGAGCAGAATCTGACACTTGATGAACTTGAAACT
GAAGCACTCCTTCCTTTGGGTGCTACCGTTGCTATCCACGACCCCCAGGCTGCCGCAGCA
ATTTTGCGCCACGCTCGCGAAAACGCCGCAGGGTTCGGCAACTTCGAACTCGCAGTCCAA
GCGATGACCATGATCACGGATGTCCTCTACACCCAAAACATGCACGAGCAACTGCTGGAG
GAGCTCAACCACTCTCTCCCCTATGCTCAAATGCTTGATGATCAACACCAAGCTGAACTG
AAACTGCTGGACAGCATCGCCATCGTCCAGGCAGACCTCGGTTCCACCGAAGCGCTGGAA
ACCCTGGGCACCGCAATGGGACTCGCAGAAACCACAGCTCAGAAGCTATACGTGCAGGAA
TCCCTCAACCGCGCATACTTCACTTTTGCCCGCCCTGAAGATTGCATCAGCGGAGCAGCC
GACGCTTCTGCCCTGGCCATGCAAAACGATGACCCTTCCAATGCAGCTGCCCAGTTGGAG
CAGTGTGCACAGTACTTGTTCCAATTGGGCCACGAAACTGACGGCGCAAGCCTGCTGGAA
TCTGCATTCAGGGTTGAAGGCATCCCCACTGAGCAGGCACTGTACTACGCAAATGCACTG
TCTTCCATCTATGAAGATTTCGGCGATTCCGCGAAGTCGCAGTACTGGGAGCAGCAGGCG
CAGGAAAAGCAGCAGCTTCTGGAG

>RXA02279-downstream
TAACGGCCGTTTAAAGAGTCGAA

>RXA02280
GCGGACCTGGCTGAAACCATGTTGGGTCTTCTCACCTTGGAGACCTCCCGTGGTCGCATC
TCGATCGGTGAGATCACCACGTTGTCCATCACCGAGGATGTGTCGCTGCAGCTGGCTACC
ACGTTGGATGATTTCAGGCAGCTCAACACCATTGCGCGCCCGGACACCTTGATTATTAAT
GGCGGCTACATTCACGACAGCGATCTGGCTCGGCTCATTCCCGTTCACTACCCACCGCTT
ACGGTATCTACTGCTGACCTGCGCGAATCCATGGATCTGATGGAGCTTCCGCCGCTGCAG
GACATTGAGAAAGCCAAGGCACTGGATGCGCAGGTCACGGAATCATTGAAGGATTTTCAG
ATCAAGGGCGCAACGAGGGTTTTTGAACCCGCAGATGTTCCTGCCGTGGTGATCATTGAT
TCCAAGGCGCAGGCCTCACGGGATCGCAATGAAACACAAAGCGCAACCACTGATCGTTGG
GCTGACATTTTGGCAACGGTGGATAACACGTTGAGCCGTCAAACAGCCAACATTCCACAG
GATCAGGGACTGTCGGCGTTGTGCTTGAATTGGAACAATTCGCTGGTCAGGAAATTGGCG
TCCACTGATGACACCGCCGTGGTGTCGCGCACGGTGCGTTTGCTCTACGTTCAGGCATTG
TTGTCCAGCAAGAGGCCACTGCGGGTGAAGGAACGCGCGCTGCTTAATGATTCGCTGGCA
GATCTGGTTTCTTTGTCTTTGTCATCCGATATC

>RXA02280-downstream
TAAGACAATCCTCCGCTAATCTT

>RXA02285-upstream
TTAGCTTGTCGACGTCCCCCTCTTCCAACACCTCCGGCTTTGTTTGTTTTTCCAACCAAC
CGGGCTCTGCTGCGGTGGCGACGGCTTTTGTGGCCCACTG

>RXA02285
TTGGTTTTGGATGAGCGCTGGGTTGGTGTCGGGCTCGTTGATAAATGGGACGAGGGGGGC
GTCGAGAAGCGTCTCTTTGCTGCGGTCTTGTGTGTGGTTGGGGCCGGGCGCGGGCACGTC
GATGAGCGTGGCGAGGTCAGATATGGAGGCGCGGAAGCGGCTCTCCTCTCGCTTGAAGGA
CGGGTTGTCGGCGTCGAGGTCGAAGATGGCGGACATGAAGTTTTCGCTCGCGGCGTTTTC
CTCGAGGCGGCGCACGAGGTAAGAAATGGCCACGTCGAATTCTTGTGGGCGCACGGCTGG
TACGTAAAGCAGCAGCTCACCGACGTCAACGCTGACGGCGCGCGCCTGATCGGACGCCAT
GCCCTGCAGCATTTCGAACTCCACACGGTCCGCTACCCCACGCTCCACAGAGAGCAAATG
TGCGAATGCTATGTCGAAAAGGTTGTGGCCGGCAACGCCCAGGCGCAGGCCCTCCATGTT
TTCTTTGCGCATCGTCCAATAGAGGACGCGCTTGTAATTGGCATCGGTGGCTTGTTTGGA
AGGTTCTGTGGCAACTGGCCAGCCGGTGATCTGCGCGTGGACGTGCTCCATAGGCAAATT
AGCACCCTTGACCAGGCGAACCTTAACGCCCGCCCCGCCTGTGTTGACGCGCTCGCGGCC
GAACTGCGCCAAGTCCTGGATTGCACCGAGGGCATCGGGAAGGTACGCCTGCAACACAAT
TCCGGCTTC

>RXA02285-downstream
TAGTTCATGCAGCTCTGGATTGG

>RXA02286-upstream
GCAGCGCACACGCTTTCCCCTCAGCCTGCTGATACCCCCGTTTTGCCACCTAAAACAACC
TCTCATCTTCATTTCATATTCACTTCATAGGGTTGAATAC

>RXA02286
ATGAAGAACGCAAAACTTTTCCTCGCGCTCATATCCGCTCCTCTTATCCTCGCTGGCTGC
AGCTCCACCGATACTGGAACAGCAGAATCCACCATTTCCAGCGAAACTGCTTCTGCAGTA
GATGCCACCACTTCTACCTCCTCAAGTACCGCCACCTCTGCCGTGATTGATGACGATCCG
GTATTCGACATCATCGACATCGTCCTTGCCCAATACCCCGACAGGATCATCACCGACATT
GACCGCGAAGACTCCTCCGATCAATACGAAGTCGATGTTGTGGTTGGCCAAGAAGTCCTT
GAACTTGATGTCACCACCAGTGGCCAGATCCATACCGACGACCGCGACAACGATGATGAT
GACGACATCCGCGAAGCTCACGCAGCCACAGTCACCGCAGCTCAAGCCATTGGCCTAGCG
CTGGATCAATACCCAGACGGAATTATTGATTCTGTTGAATTAGACGAAGACGACGGCCAG
CTGAAATGGAAAATAGACCTCGATGACACTTCCGGCAATGATCTTGCTGACGTTGAAATC
GCAGCAGTT

>RXA02286-downstream
TAAGCACGCGCACGGAAAGCCAC

>RXA02287-upstream
TTGAAAAAGGAACATTAGTGCCAGTAACAAGAGCCCAGTTGAATTCAAGCGGGCAGAGAC
ACATCTGGCCCTCAAAATTTTCCTTTTACTGGAGACCACT

>RXA02287
GTGTACTCAATTTCAGAAACTATCGCCCGAACTCTTATGCCCCGCACCGATCACGTTTTC
GACCTGATGGGCAACGGAAACGCCTGGTTCGTCGATGCCCTAGAACGCCTCGGGCGAGGC
ATCATCACCGTCCGCCCCACAGTTGAAACCGTGGCCGCCGCGGACACCTACCACCGCGTC
ACCCGCCGCCCGGCGGTCGCTACCACCACCTATGGTGCTGGTTTCACCAACACCATGACC
ACGCTTGCCGACGTCGCCCTCTCCCGTATCCCACTTCTTTTAGTTGTGGGCACTGCCCCG
AGCGCCGGGCCTCGCTGTTTCGACATTGACCGGCAAGGACTCGCACGTGCCGTAGGTGTG
GAAACCTTCACCGTGCATGCAGATGACGTTGCTGCGGTAACTCTTCAGGCTTGGAATAAT
ACGCCGGAAAACACACACGTGATCCTGGAAATCCCCTATGACCTAGCAGCTGCCACAGCC
ACCGATCCAACAGTGACTACATACCTGCTGCGCCCCGGATTTCAGAAACTCCCGATGTCA
CCGACCTTGTCC

>RXA02287-downstream
TAGCTCTACGCAATGCCCAAAAT

>RXA02294-upstream
TACCTCACCTGGCAACAAATCCAAGGAATGTAGATAAGTCGGGGCAAACTCTAAGAAATC
ATCCTGGTTTGTGGCAGGGAACATTCCTAGGATGGGAGGC

>RXA02294
ATGGCAAAGACAAAACTAGAAAGCATCTCCGAGCGCAACTCGGATGATCCGCTTAGTTAC
CCCGACCTGACTCTTGCACCAATATCCACAACAGTCACAGTCGTGGTCGCCGAAGACACC
CCAAACGATAACTTCTCAGAACTTCTCCTCGGCGCAGCAGAATCAACCCGTCTTTTAGGA
CTCGACGAGCTCCACATCATCGCTCCATCAGTCCACCTACCCGCTCTCGCAGTAGCAGCC
GCCGACATCGCACACCATCTGCCAGAGAAATTCCAATTCTGTGAAGCCGAAACCTGCACT
CATCTCCACCCCGACGATGACACCTATCTCACGGCTGAATCCGTTGCTCAATTGGGTACG
AAGCTGAAGTCTGCG

>RXA02294-downstream
TAGTTGTTAGGAGCCACCACAGA

>RXA02295-upstream
TTCCCATGCTAATCCGCGAAAATGGCACTTCAACAGCCATATACTTTAAACAACACAAAT
GATGCAAGACTGATACCGGGATGTGATAGGAGCGCACCAC

>RXA02295
ATGGGGTTGGAATTAGCAGCTAGCGGGTGGGGCATCCTCATCGCAGGCGCCGCCGTAGCC
GGATGGATCGACGCAGTAATCGGCGGTGGCGGACTCGTCCTCATCCCGCTGATCCTCGCG
GTCATGCCGCAACTCGCACCTGTGACAGCGCTGGCCTCCAACAAACTGGCAGCCGTCACC
GGCACGGCATCGGCGGCATTCACCCTGGTCAGGCGCGTCAAACCCGACAAAAAACTGCTT
GCGCTCTACGTTCTGGTGGCAGCTGTGTGCTCCGGTGCAGGCGCCCTGGCTGCGAGTCTC
ATTGACAAACAAATCATGCGACCGCTGATCATCGTGTTGATGCTGGTCGTTGGCCTGATC
GTGGTGTTCAAACCAAACTTCGGAACCGGCGAAAGCAAAGCCCTGCCCACCGGATGGAAA
CGCTGGGCCGCCATCGTTGCAGTCGGACTCATCGCAGCCTACGACGGCATCTTCGGACCC
GGAACCGGCATGTTCCTCATCATGGCGTTCACCGCACTGCTCTCCCAAAATTTCCTGTCC
TCCGCAGCCATGGCGAAGGTCGTAAACACCGCAACAAACCTGGGTGCGCTAATTGTATTC
ATCATCGGCGGCCACATGTGGTGGACCCTAGGACTCGTGCTGGCAGTCGCCAATGTCGCA
GGCGCACAACTCGGTGCCCGAACGGTGCTTGGTGGCGGTACCAGGCTAATTAGATACGCA
CTACTAACCCTGGTTGTCGTCATGAGCGTCTACCTCACCTGGCAACAAATCCAAGGAATG

>RXA02295-downstream
TAGATAAGTCGGGGCAAACTCTA

>RXA02296-upstream
GCATCATTTGTGTTGTTTAAAGTATATGGCTGTTGAAGTGCCATTTTCGCGGATTAGCAT
GGGAATCACCAGTATTTCTGGACGGTTAAGGATGATTCAT

>RXA02296
ATGCGTAATCAAACAATCGCTGCGGTCGCAGCTTTGGTCCTGCTCACCGCCGCCACGCCC
GCGATCGCTGCCACCCCGGCGACAGCTGGAAACGGACTCTATTCCATTGACATGGGCGAC
GAGCAAAAGCTTACCTGCGTGCTTTTCGATGAGCCCTCCACCGAAGCGCACGTCGTCGCC
AGCTGTGCTGCGACTTTCCCGGTGACCTGGAAGCTTCTCGACGGCGCTCACGAACAAGCC
GCGAAACTTGAAATCACCCAGGCTCAAGACGGTGAACTCTCGGTGACAGCCAGCAAGCAG
CCGTTGATCACCACGATGATTGCGCCCACCAGCATCACTAAGCCCATCACTGTCAATAGG
CTTGTGGTTGTTCCTGGTGAGAATGAGGTTCGCTTTTATGCTACCGATCCTGATGTTTTA
CCAGTGCTGATCACGCCTGACTCCTATGAAGTGTTGACCGATTCCGCTGCTAAAGTGAAA
GCGACATTA

>RXA02296-downstream
TGAAATAAACGTGGATCAAGGAG

>RXA02297-upstream
TGCTGATCACGCCTGACTCCTATGAAGTGTTGACCGATTCCGCTGCTAAAGTGAAAGCGA
CATTATGAAATAAACGTGGATCAAGGAGTCCGGTGCCCAA

>RXA02297
TTGAGCGATAAAGAACCAGACCCCCACGAACAAATTCCAGAGAAGCCATCCCGCAAGGTT
ATTGCACTTCGTTGGTGCATCGTAGCGCCGCTGTCGCTAGCCGTGGGGTGGCTTTTTACT
ATGTGGGGTGTGCCAGCCGCATGGATCCTCGGGGCGATCCTTGTTGCCGGTGTATGTGCG
CTGACCACAGGGCAAGATCTTCCGATGGCCAAGGGGGTGCATGTTTTTGGTCGCTCAATC
GTGGCGATGCTGGCGGCGCTGCCTTTGATTAGTTCTTCTGGTTCGGAACTTGTTCGTTTC
CTCATCCCGGGTCTTGTGATTTCCTTTTTCACCATCGCGGTAGGCATCGTTGGTGGTTTG
TTGCTGGCAAGATCCAGGCCGGAGATTTTGCCGGAAACTGGTGTGCTGTCCATGCTGGCG
GGTGGCGCGTCGGTGATGCCGATTCTGGCCCGAGAGTTGGGCGCTGATTTCCGCTATGTG
GCGCTGACGCAGTACCTCAGGTTGTTGGTTGTGTCCATGACGTTGCCGCTGGTGACGCAC
TTTTTCGTCCCTGGCGGGGCGGATTTGGGATCGCCGCCTGAGAAATGGTTGGACGTGTTG
AGTTTGGGAGAGTTCGGGACGTCGATAAGCGTTTTATCGCTGCTGGTGCTCTTCGGTATT
GTGCTGGCCGGCGAACCTCTCGGCAGGTTGCTGCGCTTGCCTGCCCCTGCGGTGATGGGG
CCGCTGATCCTGACCGTGCTGGTGAGTTTTGTGATTCCAGATGATCTCAGCCTGCAACCG
CCAACCGTGTTTAAGATTATCGCGTTCATGGCGATCGGTTGGATGTGTGGCGGTCCCTTG

AATATGACCGCGCTGAAGGTGTTTTCTAAGCAGCTTCCGGCCACGTTCTTGTTTATTTTC
GCGCTGCTTGCGGTGTGCGCAGGTGCGGCGGGGCTGCTCACCTGGTGGTTGGATATCAGC
TTCTTCGAGGCTTACCTAGCAACCAGCCCTGGAGCTCTGGAGACGGTGTTGGCGCTGTCC
TCGGAAGGATCTGCAGGCCCGGTGGTGGTCACGATCCAGATCATTCGACTACTGGCAATC
TTGACCATCGCCGGTTTGATCCCCACGCTACTGCGACGCATTTTGCGTAGGGATCGT

>RXA02297-downstream
TAAAGGCCTTCTAGTTCAGCACC

>RXA02298-upstream
AAATCATAGCGTGAGATGACAAGGAAAGGAATATTTCGATCCGGCAACAACCCCCGCGTC
AGGTGGGATTATGCCGAAAAAATCGCTACGATAGCCACTT

>RXA02298
ATGACTCTTCAGAGTTCTGATAAACGTTCTCCTTCACTGTTAGACGCCTCCTCCGAGGTC
TTTGTCCATGATTTGGCAGCTTTGTCTCCCACTGATGCCACTGCATGGGGTATCTCAGGC
TTCGAAGGTGATCTTCAGGATTTCTCTCCTGACTATTGGAATGCCATCGCCGAACGCAAC
CGCGACATGGTTGCCGATGTTGATGCTTTTGATGACGGCACTGATGACAACGATGACGAA
GAAGATTTCGATGACGTTGACCGCGTCACCGCTGATGTTCTCCGTGATCGCGTATGCCTG
GATCTGGCCCTGCACCACCAGGGCGAAACCTTAGCGAATCTCAACAACATTGATTCCCCA
GTCCAGACCATCCGCGATACCTTCCTCATCATGCCCCGCGAGACGGACGATGATGTGGAA
AATCTCCGCGAACGTCTCTCCCGCGTCCCCGACGCTCTCCACGGATACTGTGAATCACTC
GCTGAGGCTGCCAGCCAAGGCCATGTTGCAGCGGTCCGCCAGGTGGAAGAAGTGGTGTCG
CAATGTGAGGACCTCGCTGATGAGGACTCCGTTTTGCAGCACCTTGGCTTGGATGAAAAT
GATCCAGTAGTTGTAGAGGCCCAGGAAGCTTTTGCACGAGTTGCCGGTTGGTTAGCAGAG
CAACTGGCTCCGCATGCTCCTCATGTGGATGCGGTTGGCCGGGATCGCTATGAAATGTTC
TCCCACCTGCACGTCGGCGAGTTTGTAGATCTGGATGAGGCTTACCAATGGTCCCTGGAA
CAGCTGCGTGACATTGATGCTCAGCAGCTTCAGGTAGCCCAGCAGCTGTACGGCCCTGGC
ACCACGATCCGTGAGGCCATGAAGAAGCTCAATGCTGATGAGCGCTACCTCATCCGAGGC
ACTGATGCTCTGCAGGAGTGGATGCAAAAGACCGCTGATCAGGCAATCGCTGATCTAGAT
GGCGTTTCCTTCAACATTCCAGAGCAGGCTCGACAGGTTGAGTGCCTCATCGATCCTGCT
GGAACTGGCGGCATTTTCTACACCCCACCAAGCGATGATTTCTCCAGGCCTGGCCGCATG
TGGTGGTCTGTGCCTAAAACCCAGGAAGTCTTCCACACCTGGCAAGAGCTCACCACCGTG
TTCCACGAGGGTGTTCCTGGCCACCACCTGCAGATCTCCCAAACTTTGGTGGAAAAGGAT
CTGAACCTGTGGCGTCGAGTCGCTTGCTGGAACTCTGGCCACGGTGAAGGTTGGGCGCTG
TACGCAGAATCTCTCATGAAGGAATTGGGATACCACGAAGATCCAGGCAACCTCATGGGC
TACCTTGATGCTCAGCGACTCCGTGCAGCCCGCGTGGCCATTGACATCGGAATTCACCTG
AACAAGAGGAACCCAGAGTGCACCGGCCTGTGGGATGCGTCTTATGCGCGCAGCTTCCTG
CGTGAAAATACGTCCATGAATGAAGATGCGCTGTACTTTGAGCTCAACCGTTACCTTGGT
TGGCCAGGTCAGGCCGCATCGTATGCCATTGGTCAGCGACTCTGGTTGAACCTGCGCGAT
GAGGCCATTAGCCAGGGGCAAACCTTGGCGCAATTCCACAGCAAGGCATTGTCCTATGGC
AGCATCCCGATGGGCATTTTGCGCGATCAGGTGCTGAAC

>RXA02298-downstream
TAGAAGGCCTTTAACGATCCCTA

>RXA02300-upstream
GGGTCATTCCGGTGAACACGGATTTCGCGCCGGTGAATCTGACGGTCAGCCAATTGCGGG
CAATGCTGTCCAAAGCGGAGCGTAAAGATAAGGATCAGAA

>RXA02300
ATGAAAACTTATGCAGTACTAATTGCGGTGGCAGGGTTGGCACTTGCTGGGTGTAGCTCG
TCGGCTCCTGGAATCTGGCGTGCCACTGAACCCGCAGATGCCTACCTTGAAATAGCCGAT
GACGGCACGCTGTCCGGAACCGACGGCTGCAACAGACTTTTTGGTGGCTGGGAAAAAGAC
GGCTCTACCATCACTTTCGGCGCCATCGGTATGACAGAAATGTACTGCGAAGGCGTCAAC
GATTGGCTGTCCCAGATGCACACCGCCACCGTCACCGATGCCACCATGACCATTTTCAAC
GAGGCCGGCAGCAATATTGGCGAGCTAAAACGC

>RXA02300-downstream

TAAATGCTTCTCGACGTCAAAAG

>RXA02301-upstream
GCTTCGCATATGTCTGGATCTTATTGGATGTATGAGTCAGAGATCAGGGAGATCGCGCAC
TAACCGAACCTGGCCAGTGCAACAGGATTATGTTTAAAGC

>RXA02301
ATGGATCTTGCACTGGCTCAGGTTGATTCCACCGTTTCGGGGCTTTATGACGCCCTCGAT
CTCATCGGCGTGCTGCTGAACGGAATAATCGGTGGAACGATCGCCAGGCAACGAGGCTAT
GACATCATTGGCTTTCTGTTCCTGGCGTTATTTTCTGCGCTGGGTGGCGGAATGATCCGT
GACATGCTGATTCAGCAGGGGACTGTCGCGGCGATCGATAATCAGATCTACCTTGCGCTC
GCGTTTTCTGGCGCGCTGATTGCCATGGCGGTGAACTTTAAAGGCAGGGTGTGGGAGCTG
TTTAAAGTTCACGGCGATGCCATTGTGTTGGGCGTCTGGGCGGTGACGGGTTCCGTGAAG
GCGATGAATGCGGGGGTGGCTCCGCTGCCGAGTATTTTCATGGGCGTGCTCACCGCGGTG
GGTGGTGGCATGGTGCGTGATGTGGCTACTGGCCAGACGCCGACGATTTTTGGTGGCGGA
ACTCTTTACGCTGTGCCTGCGACGCTTTCTGCCACGTCAATGGTTATTTTTCATAGCTTT
GACCAGGTAATTCTGGGTATGATTATTTCACCGTTCTTGGGTATCGCGTTGGCGGTTACT
GCGTATTGGTGCGGTTGGGTCATTCCGGTGAACACGGATTTCGCGCCGGTGAATCTGACG
GTCAGCCAATTGCGGGCAATGCTGTCCAAAGCGGAGCGTAAAGATAAGGATCAGAAA

>RXA02301-downstream
TGAAAACTTATGCAGTACTAATT

>RXA02302-upstream
GGCCAGGTTCGGTTAGTGCGCGATCTCCCTGATCTCTGACTCATACATCCAATAAGATCC
AGACATATGCGAAGCTAATGAAGGAAACGAGGAGCTGATA

>RXA02302
GTGGCAACAAATCGTACATCTTCCGCTGGTGTCATCACGTCTGTTCTCGCATCCGCTTTG
TTCGGAGCGATCTTTTTCATCTCTGGGGCGATTGAGGCAAAGGCGGAAACACTTGTTGCT
TGGCGTGTCCTTCTAACAGCGGCATGCTATTTGCTTGCCCTTCTGCACCCTGCTGGTCGG
AAGGTGTTTAAGGAATTTTGGGACACACTAAGGTCCCAACCTCGTCAAATTCTGTACTTT
ATCTTCCTCGTTGTACTCATCACGCTTCAGCTGTGGCTGTTTTCTTGGTCGCCTAAGAGT
CATGCTTTAGATGCCTCACTTGGTTACCTGTTACTGCCCATTTTCCTAGTAATTGTGGGG
CGGTTTTTCTTCGCTGATTACATCACCAGGCTGCAGTGGATTGCGGTGGGAATCGCGCTG
ATCGCAGTAACCTTGAAATTTGTCATTAGTGCGCAATTATCGTGGGTAACTTTTGCCATC
GCTGCGGGTTATGCACTGTATTTTGCGCTTCGTAAATACTCGGGGCTGAACAACGCTTTT
GCTTACGGCGCAGAAGTTTTAGCGTTAAGTCCCCTGGCATTTTTCATGCTCGCCACTGTC
GAGGATCCGCTGTCTAACGCCATGTTGTCAATGGTTATTCTGGCGGGCCTCGCTGGCGCA
TTAGCTATGGCGTTGTATCTAGCCGCCTCAACTCTGCTTAGTATGCCGATGTTTGGCCTG
CTCAGTTATGGTGAACCAATCTTGCTGTTTGTTGCAGCACTATTA

>RXA02303
GATCCTGATCCAGCAGACCGCTATATTGCACATCTTCCCGATCGCACCACGCATACTGCG
ATGATCATGTTGGGTTCTGGCCTTGATCATTCCATGCCGGGTGTCGCATTTATCGGTGGT
GTGAGCGTCGATGACGTCCCGGAGGTCGGAGGCGCGATTTTCCACCCGTCGAATCCGACG
GGCCGCTGGGCTGTATCGTTCCACAGCGGTGGTTGGTGGCGCGGTTCCGGTGATGCGTTG
GAGTTCCAGTGGCGTCCAGAGGTCGCGGCAGCTGCGGAATTGTCCGGCACAACCATCCTT
GACCTGGACTATCCGCTGGCCCCAGGCCATAACCTCCACGATATGAATGAGGTTGTGGGC
AAGGCGGTCGGTTACGCCCGCCACCATAATCCGGTGTCGATCACGGGTTGGGGTTATTCC
TCGGGCGCGGCGTTAGCCGCGATTAATGCATCGCTTTTCGACGCCCTGGTCCTCACCTTT
CCGGACCTGGGTAGCGTCGAGAAGCTCCCTGCCGAAATTCGTGGAGACGCTGTAGTGCCC
GCGGCGGCTGCGTGGCCGACGACCTTTGTGCAGATCGCGGCGCAGGATGAGATCGCGGAG
CGGCCAGGAGAGCTTGGCGACGCGACCGTGAAGGAATACGTTTCCCGCCACCGTATTTCC
ACACCGAAGGTCGCGCGCGAAAAAATCACCGACGTGGCGGAGTTCCTTAAAACTGTTTGC

>RXA02303-downstream
TAATGTGCCAGCAGGTTGTAAAT

>RXA02304-upstream
CTAGCCATCATTGGTAGTTCCTAATTGTTTCCGTACAGTATAGCTCCAGCACAACTTCTG
AGTGCAAGTTTTTTATAACAGGGCAGTAACGTTTACTGGT

>RXA02304
ATGAAAACTCCCCGTCTGCTGAAGATCCTCAGCGCGATGGTGGCTGTCACTGGACTTCTC
ATTCCAACGGTGGTCCCCATGGCCGCCGCTGATGCTGCTGAACTGTCCGACAACGTTCCC
GATCGCACCCAAATTGCCATCATCAACCCTGATGGCAGCGTGCAAGAATCTGACAACGCC
GAAGAATCCCGCCCGGCATTATCCCTGGCCAAGCTGTATTTGGGTTATTATGTGTTGGCT
CAAGGCGCGGAAGAAGATATTGAACTAGTCCCAGATATGATCCGCTACTCTGATGATTTC
ACCGCGGATTATTTGGAGAGCGAATACCCGGAAGCAATTCCTGAGGTTATTGATGCCTTC
GATTTGGAAGACACCGAATGGGCTGGTTTCTGGGGCAATGCAACTACCAGTGCGGTGGAT
ATTGCGACGTTTGTAGCAGCACTCATCGACGATCCCACGGCGCAGCCCTTGCTTGACGCA
ATGTCTGACACCGCTGAGTATGCGGCGGATGGCTACGCCCAGAACTTTGGCACTTTTACA
TTGTCCGATGTCACCGGTACTAAATTTGGTTGGTCTGATTCCCTCGATGTGCATTCATCG
GTCAGCTTTGGCCCTGGTTTTGTGATCGCTGCCAACACCTACGGTGACGCCGAAACGCTC
ACCGAAGATGTCCAAGATTCCGTGTCTTCGCTGTATCCGGAGGAAGTAACCACCGCGATC
GAGGAGCAGGTGGATCAGCTGTGTGAGTGCGCTGCAGAGACTACGCATTTGGGAATGCAC
ACTGGCGCGGAGCTGAAAGCACAGCTTGAGGGCACTATTTATGGAAAAACCCTCAGCTTT
TTACCTAATTCAGCCCCAGCGCCAGCGTTTATTTACAACCTGCTGGCACAT

>RXA02304-downstream
TAGCAAACAGTTTTAAGGAACTC

>RXA02307-upstream
TTTTGCATTAACCCCAGGTAGGGGCATTGTCGCAAAGCCCAACTACAGCAAGGTGCGTAC
GCTGGTGGCCAACTGAATACGTTTGAGGAGAAGGTTTTCT

>RXA02307
ATGAGTGGCACCGCCATCATGTACGACACGACAGTTGTTCCATCGAAGAAAGAAATCGCG
CAGGCTTGGACTGGTTATGTGGATCTTCAGGGAAGCTACCGCCTGGTAGATACGGTGGAT
GGGGAAGTTGGCGTTGAGGTGCTGATTTCCAAGGATCGGGAGGGGCGTTTACTCCAGATT
CCGTTTAGTTATCGTTCGGCAGAGATTAACCCAGAGCAGACACTTTCCACATTGGAGCAT
GGTGTGTTGGGCAAGCGTTGGGTGACTAATGCGTTGGGTGACCCGGTGGCAGTGCGGGAG
TTTATTCGCACTATTTTGACGGGCGATGATGGTGCAGCTCGTAGCGATGGCGTGAAGGGC
TATCTGGATATTAAAGGTTCCGGCGATGCT

>RXA02308-upstream
GGGTGAGATTGGAATGATTTCGGCCCGGGCGCTCGAAAACCGTGATAGACACAATGAACC
GAGCAAATCCGCCAGGAAATAAATTAAGTAAGGAATATCC

>RXA02308
ATGAGTGAAACCCAGTCGAATTCAGTGTCAGCGGTAATGCCTGCGCAGCTCCCTCCAGGG
CCTGCCGAGCGTACTGTGTACTCCTACGGTGTTCGCGCAGGGGATCAGGTGCACATTTTA
AGAATGGAGGCTTTTGATTCTGACGCGAATATTGTCGGCGAAAGGGACATTGAGGCGCAT
GCTGAACAAGTCTTTAAGAACCTGCAAGCAGTAATCCACGAGGCAGGAGGAACGATCAAC
AACATTGTTTCCACCACTACTTATCTTGCCGATGTCACCGATGCTCCCGTTGTTAACGCT
GCTCGCTCCCGCTATTTCACCGGAGAAGTATTGCCCACCCACACCGTAATTGGAGTTGCT
GCTCTTGCTCGGCCACAGTTTCTAGTCGAGATCTCAGCGGTGGCCTATTTGGGGGACCTT
TCAAAAGAC

>RXA02308-downstream
TAGATACATGATTATTTTTGCAT

>RXA02314-upstream
TGATACCACCGAAGTATCCGGATTCACCATTATTGAAGCTTCGACCGTCCGAGATACCCG

CCGTGCACAACAGCAAGCTCTCATGGACACGGTGCACTAA

>RXA02314
ATGGAGTGGTACCAAGTGCGCCGACGGGCCCGACAACTGCTCATTGTCCTTTTTATAGCA
GCGATGCTCGGAGCAGCCTCCATGGTGATCGGGCCATTCCTTAACGACCGCACTATCGAA
GGCAACTCCGGGCGCGCCTTGGCACAAGTAACCAACGTCGGCAGCTACCGCACAACGGTG
GATTTCCAAGATGAAAACGGCATCTATCACTCACCAGCCACCGGCCTGTTGTTCCCCACG
GGACTGGGCGAGGGGCAACGCGTGTGGGTGAACTACGCCAAATCAGATCCAGACCTGGTC
AAAGTAGAAGGCCGCAAGTGGACACTGTCCATCATCCCAGCGCTTAGTGTCGCAGCTGTC
GCCACCGCTACCTGGTCAGTACTATGGCTGGGAGTGGGCAGATTCGGAAGACGATCCGAC
GACGCCAACGAAACCACAGTG

>RXA02314-downstream
TAAAGCTCTATGCCGGGAGCATT

>RXA02324-upstream
GAAGGTCAAAAAACTTGACTTTATTGAAAACAATTTCCATTAAGAAGTGTACACTTGCGT
CGACTCTATTGAAAATGATTCCCAAAAGGAGGGCTTTCAC

>RXA02324
ATGGCCACAACGACCCCAGTCACCGTGCTATCAGGATTTCTCGGCTCCGGAAAAACCACA
TTGCTCAACCAGATCCTCCACCACCGAGGATCCCGGAAAATCGCAGTCATTGTCAACGAT
TTTTCAGAAATCAACATCGACGCAGCCCTCATCGCATCCGAAGGCCACCTCACCCGCGGC
GAAGACCGCTTCGTGGAACTGACCAACGGATGCATCTGCTGCACCCTGCGCGAAGACCTC
GTGGATTCCGTCGGCGAACTCGCCAGCAGCGACCGCTTCGACCACATCGTCATCGAATCC
ACGGGTATCTCCGAACCAATGCCGGTAGCCGCCACATTTGAATGGCAGTGGGATGACGGC
ACCCGCCTGGCTGACAAAGCACCGATCGACACCATGGTCACCCTGGTCGATGCCACCCAA
TTCATCGACCTCATCCGCAAAAACACCTCCCTCACCGAGGCTGACATGGGCGCAACCGAG
GACGATGAACGCACCATCGCCGACCTACTCACCGATCAAATCGAGTTCGCCGACCGCATC
TACATCACCAAATCCGACCTGGTGGACCGCACTGTCCTCGAGCAAACCCGCGCACTAATC
GCCAGCATGAGTCCACGCGCCCGCATTGACTTACTCATCGATGGCCTCAATGACGGCTCC
CCCATCACCGACGACATCCTCGGAGCTTTCCTCTACGACGAAGCCACCGCCCGCGCCTAC
GAGGGCTACACGGAAGAACTCGAAAACCCGCACACTCCCGAAACCGAGGAATACGGCATC
AGTTCCGTGGTATTCCGCTCTGACCGGCCGTTCAACAAGGATCGCCTACTTCAGGTACTG
CGTTCCACCACTGGACTCGTTCGCTCCAAAGGCTATTGCTGGATCGCTGATCACCTCAAC
ATCGTCCAGGTCTGGCACCAAGCCGGCCCCAATTTGAGCATTCGCCCGGCCGCCTATTGG
GCCAATTCAGAGATCACCCCCGGCACTGAATTGGTCCTGATCGGCATCCACATCGACGGC
CCCACCTTGCTCGCACTGCTACAAGGCGCGACGCTTACCGATGCGGAAGTGGCGGCACTG
GTTTTG

>RXA02324-downstream
TGAGTTCCTCAAGTCCGTGAATT

>RXA02325-upstream
GGGCAGAGATTTGAAGATGGAGACCAAGGCTCAAAGGGAATCCATGCCGTCTTGGTTTAA
TACTGCACCCGTCTAATGAAAATCATTACTATTAGGTGTC

>RXA02325
ATGATGGACCATGCACACGATTCCTGCTCACCAACTCTGCGCCGTGATTTGGAGGTCACT
GGCCAGCTCCAACCTGAGAAAGCTGTCGATTTAGCAGCGCCGCACGAAGGGAAGGTTGCC
AATATAACGAAGGTGACCTCCTCAAATATGGAGCACACCATCACGCAGGCCTCAAAAGCT
AAGGAGGTGGTGGTGCTCATTGGTCACTCCCTGCTGCCCACATTTCAGGATTTGGAAAAA
GACATTCTGCACTTTCAGGCAGGTAATAAAGGGCGATTTTCTGTAGCGATTGTTGATCCT
GATCGCAGTGCAGATGTGGTTGCCAGATTTAGGCCAAAACAGATTCCGGTGGCATACGTG
GTGAAAGATGGCGCCAGCATTGCGGAGTTCAACTCGCTCAACAAGGAGCCGGTTGCACAA
TGGCTTGATCATTTTGTGTCGCGGGAAACGATCCCCAATGAAAAAGAGGGGGACGTCGAT
AAGCAAATAGACCCGCGCCTGTGGCGGGCAGCGGAATTGGTGAACGCCGGTGATTTTCGC
GCGGCGTTGGCGTTGTATGAGCAGTTGCCGCAGGATGCGACGGTGAAGCGGGCGCACGCG
GCGGTGTCGGTATTGGCGCGGATGTCTGTGGCGGATCGGGGAGAGGATCCGATCGAGAAG

TCGCGCCGGGATCCAGACGATGTGAACAAGGCGCTGGCGGCGGCGGATATGTATGTGTTG
ATGAATCAGCCGGACACAGCGCTCGCGCACCTTGCAGCACTATTGCCAAAACCGGAGGCT
GCCCGGCGGATCGTGGAGTTGCTGAACTTGTTTGATCCGCTGGACCTGGTCGCATTGGAA
ATCAGGGCGCAGGTGGGGAATGCAATGAGC

>RXA02325-downstream
TAAGAAAACACTTTAAATATTCT

>RXA02331-upstream
TGCAGCGTGCATTCCCACCATCGGGTCAAGAATCTATCCGCCCAGCCCCTGTCCAACTCC
TCAACTAAAAAGGCAGCACTTAAAAAACACTATGGAACCC

>RXA02331
ATGGAACTAAACGGCGGTCGTTTCTACGCCCGCAAGCTCACCTCAGATAATCGGATTGAT
GATGTCCCGGCGCTCTCACTGATCCTTGCCGATGCAGCACAGTTCATCGCGGACGCCACC
ACAGCCTGGCACGAGGACACCGAATACACCTGGGCTATCTGCGAGCAGACCAGTGTTGAA
CTACTGGCACTGGCACGCCTTGATCCCAAGCAGCGCACACTCGAGGTCGTGCCCGCAGGT
GATCCCGCCACCCAATTGCCCAATGATCCAGTGCTCGCTCCGAAAACCATCGGCGATGCT
GTGGCGGAGGGCCGCGACACCATCACCAGATGGGCACAAGGCTATTTAGAAATCAGCCTC
ACTGAT

>RXA02331-downstream
TAGGTTCTCTCCGAAATGGGCAC

>RXA02336-upstream
CAAATCCACACGACACAATTACACAAATTTTACCTTGTGCATTGAAAGCCGTCAGCCGAT
TAGCGTTAAAGAAAATAAAAAACCACAAGGGGAGCACACC

>RXA02336
ATGAAAGACACCACCGAGATCAACTGGCAAGGCTACGCCGATGGAACCGCAATCCGCGAA
GCAGTCATCCACTCCATTGAACGAGAAGTATCAGCGGGCGAGCAGCCAACCCCAAACGAT
CTTAAATTTCTCGGGCTGTTCCAGCACCGCGCCGGGTATGTGGGCTCGTTGATCACCGGT

>RXA02336-downstream
TAAGTGTGGGGAGCAGGCTGGCT

>RXA02337-upstream
CACAAGGTAAAATTTGTGTAATTGTGTCGTGTGGATTTGAAGGTTTTTGTAAATCTAGTT
AAATCATGAGGTCATAAGCTTTTCGGGAGGTTGTCAAAGG

>RXA02337
ATGTCGAAGCTTTACGCGGGGGCAAGGATCAATGCACTGCGCCGAACCCATCAGCTCACC
CAATCAGCATTGGCCGACAAGCTTGATCTCTCCACCAGCTATCTCAACCAGTTGGAAAAT
GACGGACGGCCACTCACTGCCACGGTGCTTCTGCAGCTGATGAAAGTGTTCGATGTTGAG
GCCAGTTACTTCTCCCCTGACCGGGGTACGGCCACTGCTACCCGACTGGCTGAAACCTTG
GCGATGAATCAGGGTCCGACGATGTCGATGGATGATCTTTTAGATTTCGCGGATCGTTTC
CCTCAGTTAGCGCAGCATATTATCCAGCCTGCTGAGGTTGATCCCACGCATAGTTCTGCG
CATGATTTTGTTCGGGATTATTTTGCCACCCACAAAAACTACATTGATTCGCTCGATCGC
CTTGGAGAGGAGTTGGCAACTGCCATTGGTCAGCCGGGACTTCGGGTTACTAGGCTCGCG
CAGTTGCTTGATGCGGAGTACAACATCACGGTGCGTTTCCGGGCGCCGGATATTACTGGC
CGGAGGCACTTTGATCCCCAATCGCGTCAGATTCTGCTGCGGCAAGATCTCAGCGAGGCG
CAGCAGTGTTTCCAGTTGGCGGAGGAATTGACGTTTCTTGCTCATGCAGAGCTCTTGGAT
ACCCTGACCACAGATCAACCGGATCTCCCTTCTGAGGCAGCTATCCGCCTGGCTAAGGTG
GGTCTCTCCCAATATTTCGCGGCTGCTGTTGTCATGCCGTACACCCGCTTTTTGGAATTC
GCCCAGGATAAGCACTATGACATCGAGTTGATCTCTGAGGCGTTTGGAGTGTCTTTCGAG
TCTGCATGCCACCGCCTGTCTACTCTGCAGCGTTCGGGGGCGTCAGGGGTGCCGTTTTTC
TTTGTGCGCTCGGATCGTGCAGGA

>RXA02338-upstream
AAAACGTGTCTAAAAATTCAGTTTTTATTGCTGCTGATCACCTCTTGAAGAACTCAACCC
AAAAGTGCTTCAAGTTATGAGAAAGTGAAATCCAACACCC

>RXA02338
ATGAAAAAGAGCATCGTTGTATTTGAAGTCGAAGGCGGCTCCGACAAGCACTTCGACGGT
CACCGTAAAGACACCATGCCTATCGTCAACTCCATAAATGATGCTGGCTGGCAGGCAGAG
GTTGTGTACTACCGCCCAGAGTGGACCGAAGGTCTCTTTGAGTACGTATCTGAAAACTTC
GACGGCTACATCTCACGTGTCAACCCAGGCAACATCCCAGGCGGCGAGCGCGGCTACTTT
GACCTGCTCACCCGCCTGTCCGAAGCAGGGCTCGTGGGCATGTCCACCCCTGAGGAAATG
ATGGCATACGGCGCGAAAGATGCGCTGGTCAAGCTATCCCAAACCGACCTGGTGCCATCC
GACACCGAGGCGTACTACGACGTGGAGACCTTCCACAAGGTTTTCCCAACCTCCCTGTCC
TTCGGTGAAGCGCGTGCTCAAGCAAAAACCTGGCTTCACCGGCTTCCGCATTTGGCGCGT

>RXA02339
CCCACCGACAACCTCTTTTCATATCCTGCACAACGCTATGATCTTCTCACACTTGCCTTT
GAAGTTAGGATTGGGGACATGGTTCAAATTAATGACATGCTTGCCCCTCCTCCAGTAAAA
CTTCCGGAAGATCCTGCCCTCGGCGCCGATCCAACTTTGACCTCGACAGCGATTGCGCAT
CCTGACAGCCCATTGGTGTGGGCGTACCGAGCTGAAAATCTTATCAAATCTGCATCAAAT
GATGAAGAGAAGATTCAGGCCTACGCTTTTGCGCGCACGGGTTACCACCGCAGTCTCGAT
CGTCTGCGTGCCAATGGTTGGAAGGGTTGGGGTCCTGTCCCCTTCTCTCATGAGCCAAAC
CAGGGAGTGTTGCGGGCTATCGCTTCCCTAGCTCTTGCTGCGAAGCTGATTGGTGAGGAC
AACGAATACGATCGTTGCCGCCAGATGCTCTCTGATGCGGATCCAGAGTCCGTCGCAGTC
CTACTCGACAAA

>RXA02339-downstream
TAAACCACCAAAAATAAAACAAT

>RXA02340
GAGCGCGTGCTCAAGCAAAACCGTGGCTCCACCGGCTCCGGCATTTGGCGCGTCCAGTTG
GTAGACAAGGAACTGGCTGCATCCATCGAGCCAGGCACCGCACTGCCATTGGACACTGAA
ATCAAGTGCACCGAAGCAGTCGACAACCACACTGAAGTCCGCAAGCTCGGCGAGTTCATG
GATTTCTGTGACCAGTACATCATCGGCGACAACGGCATGCTCGTTGATATGCGTTTCATG
CCACGCATCGTCGAAGGCGAAATCCGCATCCTTCTCGTCGGACCACACCCAGTGTTCGTC
GTGCACAAGAAGCCAGCAGAAGGCGGCGACAACTTCTCCGCAACCCTGTTCTCCGGCGCG
AAGTACACCTACGACAAGCCAGAGCAGTGGCAGGAACTGATTGACCTCTTCGCAGACGCT
CGCCCAGTCATCGCAGAAAAGCTCGGCGGCGACAACATCCCATTGATCTGGACCGCAGAC
TTCATGCTCGGCGATGTCGTTGACGGCAAGGACACCTACGTGCTCGGTGAAATCAACTGC
TCCTGCGTCGGCTTCACCTCCGAGCTGGACATGGGCATCCAGCAGCTTGTGGCATCAGAG
GCCATCAAGCGCATCGAGGAATTCGCGCAGCTTACTGTT

>RXA02340-downstream
TAAAACTTTGCTTCTCGACGTCT

>RXA02341-upstream
CGCGACTGGCGGAGAAATTCGTGTTCGCGATGCTTCGGGCACCGTTCACACCCTCAACGC
CGGTGAAATTACGCACCTTCGCCTGCAGTAAGGTGACGGT

>RXA02341
ATGGGGAATTCACTTGAGAAACATATTGCAGAGGGAGACCGGATCCACGTCGATCTGACA
TCTCCTTTATCCGCAATGTTGTTCCCCATTTTTGAACTCATTGTGATTACTGGAATCTGT
TGGATGGGCATCGGCTTTTTGGATCAGCTTCCAGGAATCGATGGCACCAACCCCGCCGAT
AGCTTCCCCGAAGGCACCCGCAATCTTCTAGTGGGTGTGTGGGCAGTACTTGCTGCATGG
CGTTTCGGTCTTCCTTTAATAAGGCAACGTCGACTCCGCGTGATCTTGAGCGACCGCAAA
CTGCTGGTCCGACGCGCGGGTCTGCGCACCGGGTTCGATTCCATTCCACTGAGCTACATT
CAGCGAGTCCAACGTCGGCGAAACACCCTGGTCTTAGGTGTTGGTGGACAC

>RXA02347-upstream
ACGGTTGGAACAGAGCTGCACCTTTAATCAGGCAGTTGCTGGCCAACTGAGTTAGCCTAA
AACGATGAAGAAAAATCCTTTGGTTGAATGGGTCTGGGTT

>RXA02347
ATGGATGAACTCGGGGTTGGCTGGTGCCAATGCGAGAAAGATTCCATCACCGGAAAAGCA
CCACATCCCGTGAACAAGCCACTGGTCACCAAATCCATTATCAGGGCTCTAGGCGATGTC
CCCGATGTCATGAGCAACCAGGACATCAGCCTTGTGGTGGTGGATTTGTGGAAATTCGAT
ACCATTACTCCTCCAATCGCAGAATCCCTCATGCGTTCCGTCAAAGCTGTTAACGGTGAG
ATGCACCCGCAGTATCCCACCGCGACAGCAATGGCTGCGATCAAGCATTTCTCCAACACT
TTTGATGGACAGATTAACGCT

>RXA02347-downstream
TAAAAGGCCTGTTATAGACTGAT

>RXA02349-upstream
CTTCGAGTGCTGTGGCGAAAAATCCGAACTCCAAAGAACTAGCCTAAGAACTAGCCCCAT
GAGCTATCCCTCAAAAAATTACTGATAGTGAGGTTTTCGC

>RXA02349
ATGTCAACTGCATATTTTATTGCGCACGGAAACGATACGTACCGCCCAACGGAGCATTCC
AGCGGTGCGTGGCGCGATGATGAACTCCACCTTGCACCGGTTGCCGGTTTGGTGATTCAC
CATATGGAACGTTGGCGCAGGGAAGTGGTTGGCGATGCTTTGGTGTTCAGCCGTTTTAGT
TTGGAGGTCTTGGGCCAGATCGCTCGGGATGATGTCACCTTGAGAACAGAGATCGTTCGT
CCCGGGCGCACCATTGAACTTATTGAAACCGTGGCTGAAATCAACGGCAGAGTGACGATT
CGTGCACGCGCCTGGTTGCTGAAGACCTCTGATCTTGCCCATATTTCTGGCGATACTTTT
GAAGCGTTGCCGTCAATGACTGAACTGGCA

>RXA02352
ATCTACAACACATCGAGCACGCTCAACGGCTTCATCGCAGACAAAGACAACTCCCTGCAA
TGGCTTTTCGACGTCCCCGGCAGCGACGGTGCCTCTGAAGACTTCGGTAATTTCCTTTCA
AAAGCCGGCACCATCGTAATGGGATCCACCACCTATGAATGGCTGCTCAAGGACCTAGAT
TTCATCAGCGATCCCCACAAGTGGACCGATGTGTATGGCGATCGCCCCACGTGGGTGTTC
AGCAGCAGGAACTTGGAAACCCCGGAAGGAAAACCTGTCAAGGTAGTAAATGGAGATGTC
GCCGATGTTCTCCCCGCCATACTGGAAGAGAGTCCAGAGAACACTGATATTTGGATCGTC
GGTGGTGGCGATCTGGCGGGTCAATTCTTTGATGCGGGTGCACTCGATCGGATCATCTTG
ACCATGGCGCCAGTGTTTCTCGATGAAGGGCAGCCAGCGATGCCCCGCCGGATCGAAAGT
AATCGTCTCCGCACCGTAAATGTCCGCGAGGTTGGACAATTCACCGAGATCACCCTGGAG
ACGATTAAAGGGGCT

>RXA02352-downstream
TAATTTGTAGAGTTTTGGGCAGA

>RXA02356-upstream
TTGGCAGTAGCCATGCGTTCTGCTCCTGACCTTGAACAGCGGTCCCAATTTAGACCCGCT
AAACCCACAATGTGTACTGGTGCTGGTAATTTAGTAGAAC

>RXA02356
ATGGCAACGGTCACATTCGACAAGGTCACAATCCGGTACCCCGGCGCGGAGCGCGCAACA
GTTCATGAGCTTGATTTAGATATCGCTGATGGCGAGTTTTTGGTGCTCGTCGGCCCTTCG
GGTTGTGGTAAATCCACTACGCTGCGTGCTTTGGCGGGGCTTGAGGGCGTGGAGTCGGGT
GTGATCAAAATTGATGGCAAGGATGTCACTGGTCAGGAGCCGGCGGATCGCGATATCGCG
ATGGTGTTCCAGAATTATGCTCTGTACCCTCACATGACGGTGGCGAAGAATATGGGTTTT
GCGCTGAAGTTGGCTAAGCTGCCGCAGGCGCAGATCGATGCGAAGGTCAATGAGGCTGCG
GAAATTCTTGGGTTGACGGAGTTTTTGGATCGCAAGCCTAAGGATTTATCGGGTGGTCAG
CGTCAGCGTGTGGCGATGGGTCGCGCGTTGGTGCGTGATCCGAAGGTGTTCCTCATGGAT
GAGCCGCTGTCCAACCTGGATGCGAAATTGCGCGTGCAAACCCGCGCGGAGGTCGCTGCT
TTGCAGCGTCGCCTGGGCACCACCACGGTGTATGTCACCCACGATCAGGTTGAGGCAATG

ACGATGGGCGATCGGGTTGCGGTGCTCAAGGACGGGTTGCTGCAGCAGGTCGCACCGCCC
AGGGAGCTTTACGACGCCCCGGTCAACGAATTCGTTGCGGGCTTCATCGGCTCGCCGTCC
ATGAACCTCTTCCCTGCCAACGGGCACAAGATGGGTGTGCGCCCGGAGAAGATGCTGGTC
AATGAGACCCCTGAGGGTTTCACAAGCATTGATGCTGTGGTGGATATCGTCGAGGAGCTT
GGCTCCGAATCGTATGTTTATGCCACTTGGGAGGGCCACCGCCTGGTGGCCCGTTGGGTG
GAAGGCCCCGTGCCAGCCCCTGGCACGCCTGTGACTTTTTCCTATGATGCGGCGCAGGCG
CATCATTTCGATCTGGAGTCGGGCGAGCGTATCGCT

>RXA02356-downstream
TAGTTTCGGACGTGGGGAGGCGT

>RXA02358-upstream
TGAAGGTTGGACGCTGCTTTTTGCAAATGACCTCGAGACCTCCGATATTCCCGCTGCCCT
TCGTCCCTAGTACACCCAAAGTTTATGAAAGATAAAAATC

>RXA02358
ATGGTTTCTTATAGCGTGCACGGCGCACTAGATATCGACGGCAGCCTCAAAAAACTCACC
CTCGATTTCCTCAATAAACTAGCCACCAATCCAGCTTCCCCGGGGCTTCATATTGAGCCC
ATCAAAAACAGCATCGACTCCCGCGTCCGCACAGGTCGGGTCAATGATCAATTCCGCGCA
GTGCTTTTTGAGCTTCACGACGAATTTGATCATCACTTTGTAGTGGGTGGGTTTATCCCC
ATGATGATGCCATCACCAAGGCAGGAAAAATCCGCCTTGAAGTCAACTCTG

>RXA02358-downstream
TAACGGCATTACTCGACTCATCG

>RXA02360-upstream
AAGTAACTAAAGTTCGAAAGTATTTCCGAACGGTGTCGGCCTCTGCGCATACACTGTATT
TTTAAAGAAAATTCTTCTCAATTCTAAGGGTGAATATCCA

>RXA02360
ATGCGTGGTGACGTTCAAAAAATAACCAAGGTTTATGACGGCAAGCACCGAACCTTGGAA
ATCCCGGTTTATCAACGCAATTACGACTGGACTGAAAAGCAATGTTCACGCCTCTTTGAT
GACCTCAGCGAAGTGGTCAAAGAAAACCACCGTCAACATTTTTTTGGAGCTGTGGTTGGT
AAGCCTCAAGGCAGCTGGACCTGGGTTGTCATCGATGGACAGCAGCGTCTTACAACAATC
AGCTTGTTCATGCTTGCGCTGGTACATTCCTTGCGCGCATCTGAAGTTGAAGAAGGTGAG
TTTAATGCTGGCTACAACATTGATCTAGCCACATTGATTGAGGATGACTACCTCCGATCC
GGCAATGAGGGAAACCTCAAGTTCAAGCTCAAGCCAGTTAAAAACGATAATGAGGCTTAT
CAAAAGCTCTTCGGCCCAGAATCTGAATTCATAGAGTCCTCAAACCTCACTGCTAATTAT
CGCTACTTCCGCAATGTCCTTAAGGCAACCGATCTCACCGCAGCTCAACTATGGGAAGCT
ATCGAGAAACTCAGGGTCATGTATCTTGACCTTGAGGAATTTGATGATCCGCAGCGAATC
TTTGAAAGTCTCAACTCCACGGGATTAGAGCTCAGTGAAGCTGATAAGGTACGCAACTTG
GTTCTTATGGATCAGGAGCTCAAAACCCAAGAAAAGCTCTATGAGCAGCGTTGGAATCCC
ATTGAAGTCTGCGTGAAATTTGATACCGACAATTTCATTCGCTGGTACTTAACTCTCAAA
ACCGCGCGCACCCCAAGAAAGCAAGATGTTTATGAGGAATTCAAGAAATTCATCCGTAAC
TCCAAGCTCCCGGTCGAATTCATCCTCGACGATATGTACGAGTACGCGAAGCTGTACCGA
GATCTCTTAGGTGCCACTACTGGGTTTATAGCTGCCGATAGGTGTCTTAAGCGTTTTGTC
CCTGTCATGGGCGATGTGGTTTTGCCTTTTCTGCTGCCTGTTCTCAAAGATGCTAAAGAC
GGCATCATCACCGAATCAGACTTCCTCGGAGTTCTAAAAGTTCTGGAATCCTATTTATTC
CGCCGTTTTGCAGTCGGGGTTGCTAGTAACGCCTTAAGCAAGATCTTCTCCACTGCTTAT
AGCGACATCAAGAAATTCTGGACTCCAGGGCAAAGTTATAGCTCACTGCTGGCCTACATT
CTGAAACGTCGCGATGGTTCCGGGCGTTTTCCCTCCGACAGTGAATTCCGTGAGAACTTC
GCAACCAAAAATTTCTGGAATATTCATAACGAAAACAGGCGTTACTTATTTGATTGTCTA
GAAAATGCCGATTCCAATGATGTTCGTGACATCCAAACAAGTCTGGATGAAGGATCTCTC
TCCATTGAACACATCATGCCACGTAGCCTAAACGATCAGTGGAGAGCTGAACTCGGCCCT
GAATATGCTCGAATTCATGAGACTTGGATTAATAGAATTGGTAACCTCACCATCACCGGC
TACAACTCCGCCTATTCAAATTCTTCCTATGAGCGCAAGCGGACGATGGAAAATGGATTT
TTGGTATCCCCCTATCGCATCAATAATTTCATCAAAAAGCAGAAGCATTGGTCTGAAGAA
CAGCTAATTGAGCGAACCGAGCTGCTCACTCAAGCAGCGCTGGACTACTGGCCCCTTCCA
AAAGAAACCTTCCAGCCACCACAAGCTGTGCTTCCTACAGAATCCTTAGATAGTGATCTT

TCTTTCCGCGGACGCGAAATTGTCGCCTTTGAATATGAGGACTACAAGGAAACGGTAACG
TCCTGGGCAGACATGCTCCAGAGCGTTCTAAAAGTCTTGAACCAATCCTTCCGCCAGGAA
CTCATAGCTTTGACCAATGAAGAAATCTGCCTGGCAACTTCAAACAACAGTAACAGCAGT
CTCCGTGAAATTGACCACGGGCTTTTTGTAGACACTGGCTCTAGTACGAGTGTAAAGATT
GGCTTCCTCCGCAGAGTTTTTACTCAACTGGGGCTAGAGCAGGAAGCATTGGTTTTCACC
CTTCGACCACTGGCAAATGATGTAGAACCCCGAGATGATGAACTCGAGGTAGAGGTAGAA
AAGAAATATTCCGATTTGACTAAATTCATCCCACAGTTAGAAGAAGCTGAGAATCTCGAG
GGGGCGGATACAGAGGTTATTCCTCTCCTCTCAAAGCTCAAGGAACAACTGACAGCCTTT
AGCCCGGAGAATCCTCAAGCAGCCCTAGGGGGCCTACCTGTTCCAGAATTCCTCAAACAA
AATGTGATTGAACAACTAAGCGCAGAGCACATCCTTGCTGTACTCACTCAACACTTTAAT
ATCGCATCCATGATGGGTGATGACTATTTGCTCGAAGAGCTCAGGTCAGGCCGCTTAAGG
GAATTACTGCAGCGTTTAGAGGAATTGGATAGC

>RXA02360-downstream
TAATAGCCGTAGTCGGTGGTCAA

>RXA02361-upstream
TAGAGGAATTGGATAGCTAATAGCCGTAGTCGGTGGTCAAACTTTGACCACCGGACTCCC
CTTTAAGCACAATCTCTAGCTTTTATTTAGGCTTGGAGTT

>RXA02361
ATGGAACTTCTCTCCCACTTGCTTGCTCTTGATCCTGCCTCCCCTCGTTTGACTGTTTAT
AACGAGTCCACGGGTGCGCGTTTGGATTTCTCCGCCATCACTCTTGATAACTGGGCGTCC
AAGGTTGGCAATATGCTCCTTGAGGAATTGGATCTGGAGGAAGGCTCGCTCATCACTATT
GATTTGCCGGTGAGCTGGCAGGCCGCAATGATTATGCTCGGCGCTTTAGCAACTAGTGTT
GAGGTCTCTTTTGATGATCCCGAGGCAGATGCCATCTTTACCTCCCTCGATAGATTTTCC
CACTACAAGGGCCATAGTGATGTGCTGATTGTCAGCGAGGATCCTTTTGGTCGTGGAGTT
GTTGAAGGTGGCGGTGAACTGCCTAATGGTGCCATCGATTTTGGCCCCACAGTGCGTTTT
TATGGCGATCAATTCTTCCAGCCTACCCGCACATTGCCGGAAATCATCCAGCATTCTGAT
GTTCCGGTTGGCGCCAGAGTTCTTGCAACTGGTTGGTCAGATATCGAGTCCTTCAATCAC
CAGGTTTTAGAACCACTCGCAGTGGGTGGCTCTGCAGTAATTGTGACCGGACTGGCTGAT
ATTGAGCGTTTAAACCAGATTGCAACCAATGAGAAGACAACCCACCGTATC

>RXA02361-downstream
TAGGCAAATTTCGGTTACTACTA

>RXA02362-upstream
ACAATTGTTCCCATTCGCATATCTCGTGTCCACCAGAGTCGCTACAGTAACGAGAAACTT
AATTATTTGATCCGATTCTTCCGTTCAAAGGCCTCATTCC

>RXA02362
GTGACTATCTCTCGCCGACTCAAACAAGAGCGCAGTTTCGCTGACGATCTTCAAGATCTC
AAAACTCTCAATGATCAACTGCGGTTTACAAACGCCAAATTGCAAGCTCGCATCAGTGGT
ATTGGCAATGATGGAAAGAAAATCACGCGCCCTACCCCACTCCTTGCGCTGGATTTTCAG
CTGACCGTTGAAGAATACGAAACGATCATTGCAATCTTGGTGGAAGCAGTTGGCGGAAAT
CAATCCAAGCCAGCGATTCTTAAAGATCTGTTTATAGAATATCCACTCGTCTTCCTGGCA
GCGCTTTCTGGAACCGCCATGCTCGATGCTCAAGAAGGTTTCTGGCCTGCGTTCTGGAAA
CGCACTCAGGTGTCAGTTCCAGAGCATGTATACGACGCGATCCGTAAAGAACTAGTTAAT
AGCATCCGCAAAAATGGCCTAGAAACTTTTTCTCTCGCTGACCTCAATCGACGCGAATAT
GTCGGACTCATCCAACTTCACAGTGGCCTTTCTGCAAAAGACATGCTCGCCTTGGTCAAA
TTTATCGATCACACTCGAGCAGAAAACCAAGGATGGGATTCTGGTGAGGACTTTGCATCA
TATGCGAAGAGTGTCTTCTCCTCCGGGGACAACCTATTAACCACGGAGTCGCTCAAGCAA
TTAGTCACCCACATCCCTGCGCGTTCCGTCGACTTCATCGCCAGAGTCTATGAACTAACC
AATTGGTACCGCGACCTCAAAGACCTCAATGAAGTAGAAGCCTTCGTAGGTACTCATGGG
CTGCCGGAATTGTCTTTCAAATTTCTTCTGGAGTGTCTGAGCGGCGAAGCTGAACAAATT
GCCGAAAAGACGAAAGCAGCACCAGCAAGCCTGGAAAACCTGGAACCTCCGCATCTCTAT
CTGGATCCACAGAGTTTTGAACTCAGTCTTGTTTTCCCAGCGATCTCTAAAACTGCAGCA
CTTCAGATTCCAGCACCAGAATGGACAGTGATTTATGACGGAAACTCCATTAAAGTTCGT
CCCGAACAGGACTGGTCCTACGGAGGTTTCGCCGAATACCGTTTGCCTTTAGACAAACCG

CTCTCCAGCTTGAGAGTCATCACTCCAACAGAGAAATCCCTAATTCTGATTGAAGGATTT
GGCCACAAGAATCCCATTATGTTCTTTAAGAACAACGGTCAGCCATATGCAAACCAAGAA
ATGCTCAGTGGCAACGCTGTCACAGCTATAGTCCCAGCTGCAGCAATCATTCGTGCACGT
ATGCGAGCTTCCAAGACTTTCAACTATCAAGACTTGGGTCCCTTGTCCGGATGGAACAAG
TGGGTCATTCGTTCGATCCCACTCAAACGAGCTGAATCGATCACAGTCTCCCACGGTGGC
TTCAGAAAAGAACTCCCAGTTCGACGCAAAGTTGATGTTCAATGGATTACTGAGGATCTC
ACGATCGAGAATCTTCAAGGTCTCGATCATGAGCCCGTTTTCCACACGAGTCCCCGCATC
GAATTCCCCACCTCTGGATCAAACTGGGTAATTCAGTATTCACAGATTCTTCCAGATGGC
AGCCTCATCGAAATGGAAGATTACCCAGTCGAACCTGAAAACTTCGGATACGAACTAGAC
CTCTTCGAAGAATCCGACGACCCTTGGGTCGGGCAATTTTTAGTAACTCTGCTCAAGGAT
GAAAAAGTCTATGAAACCCGCAAATTCAATCTCGCGGAAGGCCTCGATCTTTCCCTAACA
TTCAGCGGAGGCGGACCTGAAAATCGATTTAGGTACCCCAGCATCAATCAGGGACAAACT
GGCTTAACAAAGACTTTCGCCCGTTTTAGTTCCAATTCTGAAAAGCACATCAGGTTCCCA
GATGAGATCATCGGGCTTGATGCATTCACCTCTCAAAAAGCGTTTAACATCGCAAGCGGT
GATTTCCCTGAGGACTACAACCTCGACGTTTTCATCACGCCTCCGCAACTTCACTACCAA
GTACCTGTCACACACAGCCAAACAAAGTGGGAAAGCACAAAGACGACACTAGATTTCAAT
GACTTTGCCGATGGAAACCTCCAGATCAGATTCCCTAATGAAGTCTATGATCCAAACTTG
AAAATCATTAAAATGGTGGCATACAAGAAACCTGAGTCCAGTGAGCCTAAATACTTAAGC
AAAATTGGTTCAAGCAAAGTGTGGTCTATCCCTATGGATCGCATCAAGGAACTCATGGAT
GATGATGCCCAATTCCTTTTGATCGCGGAGTGGTTCGCTGAAAGTAAAGACCAGCACCGA
GAGAAGATCATTAGCGAAGCTAAGCGAACTGGAAAAATCTCCAATGCAGCGCTTAAGAGT
GCTCGTCCTCAACCTCAAGCAAGTTCCCACATTGCAACAATTGAGAAAAAGCCCCTACTA
GCTGCGGCTGAAATTAAGCTTTCTACCGTGGAGTTGGAACTTGGTCGGCACACTTCTAAG
AGACTGGAAGGCTGGGCATGGTCTGCGCTCAACCCGCTTGATCCACCAATCAAAGTCGAT
TTCCAAGGAACCTCAGGCTCACTTCCAGACACCCACTTCGTCGTTGGCCCTTTAATCGTG
GAAGTGAGAGAAAAAGAGTTTCTCTCCCAATGGCAGCCAAAAGTTCCCTCAGTTAAAGCC
GTGGTTGCAAATGATCCCTCATTTGAATTGGACCCTCAATTTGATCCTTTCCTCACACAC
CGATGGATGTTCGCTCCACGAAGTGGGAAGGTCTTACTCCCACAAGAAATCCGCACAGTG
TGGGACGCCCGATTCAATATGCGCCATGTCTTAGCGCAGCGTGAAAACCTTCATGTGAAA
TCGATTCAAGATTTTGACGATGCCACCAGTACCTATCTCACCAGTGATCCTCGGGTGGCA
TTAGATGAATTGGATAAGAGCTCAATTCCGTCTAATTCCCACTTTGAATCATTCATCCGA
TCCGGATTAGCTGAGCTTTCTTTCGAAGTTGACGACACAGCCGGAGATATCCATCGCGTT
CCCTGGATCGGCCTGATCCAGGAAATGAACGACCTCAGAATTCTGCAGATACAAGGCTAT
GAAACAGAAGAACGAGCCATCGAACGCCGAAATTCGCAGAGCTACATCCGTGAGATAGGA
GGCAGTGAATTGTGGAATATCCTAAAAGGAAATTCAGAGGGATTGTCTCTTGCTCAAAAA
TGCGCACCACAAGCCACTGAGATTAATGTGATTCGTAATTCAGGCTTGGAAGCTATGCGC
AATGGGCTGGGCGCCGATCAGTTCAGCGCCGAGTTTATTTCAGCAGACTCACGCCTACGA
GCTCAGCTTGAATGGTTGGAAAACCGCCGAGAGCTCAATGATCTCGGCCAGCTCCCAACG
CTCTTCGATTTCGCCGAGAAATACGAGTACCTCATCGATCACTTAGGTGATGATCGCATC
AAGGTCACTGCACGTGAGCTGTCTACTCTTGCGTCGGAACACCGTCGCGGCAACGCTGAA
AACTGGCTTTATGCACCATATGTGTCATTCATTTACAGCTTGCTTAACCGAATGATCGCT
CATGAAGTAATACGTCCGATCGCTCAGATCAATTACTCACGGCACGATTGGGCAAACGCT
GCTCGGCTGATTCCTCGTCTCACAGGATTTGACCTGGTGAGTGCCGAAGCGAAAGTGCTC
AGCGCAATAAACAACAACAATATAATCCCAACTGCAATT

>RXA02362-downstream
TAAGGATCACTATGTCCAACGCA

>RXA02367-upstream
GGCACTTGAATCCGGACGCTAAGTTGTTGATACATCAACTTATTTCTTGGCTATACTTGA
GGTCACGTTTCCTCAGCTCAGGAGAAGTTCGGAGAAGTCC

>RXA02367
ATGTCAAACGCAGAAATTAATCCCGTTGAATATGAAATCAACAACCACGCCCCTGGTACC
GCGCTAAACCCACAGTGCGAAGACGGCGCCAACGTAGAAATCATCACCTCCCGTGAAGTC
CCCCTCGGCGGACCACGCGCCATGACCGTGCACCGCACACTCCCCCAACGCCAGCGCTCC
CTCATCGGTGCCTGGTGTTTTGTGGATCATTACGGCCCCGATGATGTCTCACTAACCGGT
GGCATGGATATGGCCTCCCACCCGCACACCGGATTGCAAACAGTCACGTGGCTTTTTGAA
GGCGAAGTCACCCACCATGATTCCGGCGGAAATCACGCAGTCGTGCTTCCTGGCGAAGTC
AACCTCATGACCGCCGGCGCAGGCATCTGTCACACCGAAGTTTCCGCCACCTCCACCACG
ATTCTGCATGGTCTGCAGTTGTGGACAGTTCTTCCCGACAAAGACCGCGAAGGACCACGC

CGCTTTGATCACTACGCTCCAGAAGAAATCACACTCGAAGGCGGAAGTGCACGCGTTTTC
CTAGGTTCGCTATTTGGTCAAACCTCCCCTGTTCATACGTTTACTGGCTCTTCCTGTTTT
AGAGTGCAT

>RXA02367-downstream
TGATCTTATGGACCAACTGCCCT

>RXA02368-upstream
CTTAGGTCAAGCTTGCATTTATTGGCTAGTGTCGGAAATCATGGGAGATTTAGCAAAGCA
CATGGGCAGTGAACCACCAGCATGGTGGAAGTTTTTACCG

>RXA02368
ATGATTGTCCTCGCTGGAGCCACTCGAGTTACCTATGAAGTAGAACCTTGGCTGGCGATC
CCATTATTCATTTTGGCTTTTGCATCGATATTGATCCCATTCCCGATCTCTAAGACAAAA
GGACTCCGTGATATCGATGCCTGGAAAATCCACACCACGCAAGGCGATAAAAAGCGTGCC
ATCCGCCAACTGATCATTCCGGCTACGGCTTTGGCCATCGACATCATTGGGCTGCCGACA
TTATTTAATGCCCCTCCCCTTGCTTCCGCTGCACTTTTTGGCGGTGTTTACGGCGCTTCC
CTAGCTTGGGCTGCGTACAGAGCTGATCAGCTTCCACGCATTCGAACGAAGGAACGCCTC
GCAGAACTTTCACAAAATGCATCTCTGGATGATGTGCGCTCAGATGACTTAGATGTTCTA
GAGCAGCCGGAATCCCGTGAATTAGTGCGCTGTCTGCTTGCCCACGGTGCGATGGATGGC
ACTCGGGTGATGGCCAGACAGGTCGCGCGAGTACTGGATACCGAGGTAGACGAAGTACAT
CAGGTAGCACGCTCACTAGAACAGCATGGTTTGGTTAGTCGCTCCACCATCATGCCGGGT
GGGGATCCAGGAAAAGTATTCATCGAAGTTTCCCTGAAAGGGATCTCAGCCATCAAGGCA
CTTGAATCCGGACGC

>RXA02368-downstream
TAAGTTGTTGATACATCAACTTA

>RXA02374-upstream
ACCCACAACAGACATATTTTCTCCTTGATGCGCACCAAAATGCGCCTTAGGTTGAGATGA
ATTGGATAGCCCACCGTACGCCTATCTACACTGAATTACC

>RXA02374
ATGAGCTATGACTTTGTCCTCTTTGAAACCGATGGCGACCCAGGTAGCGCCCGTATTTCC
AAAACCCCACTGACCGAACGCATCGATTTCGCCACGCCATCTACAACCCCTGTGTTGGAA
TCTCTTTCGGCAGGGCTTGCCGAAACGGTGCCAGACACCGTCAAGCTTGAAGAAGACGCC
ATCCACTTATCCGGTGATCGTTGCCTTTACGTTGTGACCAACTACAACTCCGCCGAAGAA
GCAGCCGAATGGCTCACCGCCATCGCTTTCGATTACGGACTGGGCCTTGCCGACATGAAC
GCGGACACCATCCTGCTTTTCGGCGATGAAGATTCCGACGCTGTCGTCCAAATCGATGAC
TGGTTCTCCCCCGCTTTCTCTGCGTACGGCCTTCCCCACCTCCTGGTGGAAGTCATGCGC
CTGAAGGATTCCAAAACCCCTTATCTTCGAGTCACACTTGCTGCAGATGACTCGAAATTT
ATCCAAACCCTTTACGAAACCGACAACAAACAATGGTTGGTGGAAACCTCTTCCTCCACA
GGCACGGACGAAACCCACGTGAAGACCATTAATGATGTGCTGGAACGCATCGAGACATGG
TTCAACCAGGAGACTGCTGTC

>RXA02374-downstream
TAAACCTTTTGTCGTGTTCTGGG

>RXA02381-upstream
AAGTTTGAAGAAGTAATCAAGCTCCCCTGTGAGGACTCGTTGTAGTCTTTTATTTAGTTA
ATAAAAGATTTCATACCAACTTGTCAGCAGGGGAGCTTTC

>RXA02381
ATGTCTGTCACAAACTTCCGTCGGTTTCTTGCTGGCATAGCGGTCATCGCGGCGTGTGTT
GCTGCGACTCCAACAGCTCAGGCACAAAGCAGTGGCTCTTCTGGATCCTCTGGTTCTTCA
GCGGGATCTAGCGGGCTGTGGGATTTACTTTTTCCAGAATCCCATGAGTCTTTTATCGAG
CGGCTTCTTGATCCTTTGGATGACAGCCATATATCTATTCACCCTGACCTCACCCCAGAC
CTGTATGAAGAGGTGTTTGATCCACCGCAAATTGGTGAATGCCCAGCCGTTGTTGCTGTG

GTCGCACGAGGCAGTGAACAAAACCTTCAAATCCGACCCGCGCGATACAGCGAGGAATCT
CCATGGACATCCAATGGATTTGAGGAAAAAAACTTTCGTAGTTTCTTTGGCCGAATGGAA
AAACACTACCGTGAATCGACTGGCGAGTCGTTGATGAAAGACGTCTACGTGATGGGTCTG
AATAATATCGAATACCCTGCTTCTTTGCCACTGTCTTCGGAGGGAAGCAGCGCCATTGAA
TTGGGCACTTCCATTTCTAGTGGTCGCGACAATGTCATCAGCGCGATTGATCGCTTTGAA
TCAGCGACAGGGTGCACGCCGAAGTACCTGTTGGCGGGTTATTCTCAAGGTGTCCTCATC
GTTGATGGCTATGAAGAGGAGTTGATTGCGAGGGATCAGTACCTCGGCACCCTGCACATC
GCGAATCCAGCGCAACAAGTTGATGATCCAACACTTGTTGGGCATGAAGTAACCACGGGA
GGCTTGGCTAGTTCCGTGGAGCCCGTCGAGGACAATCCTTTCAAGGTGAGCTACTGCCTG
CCTGGAGACATCGTGTGCGATCGTTCTTTTGAACAGTTCTCTGCTGCGGGATCCTCTATA
GCAGCTGCGCAATTGAGCACCGGAAATATCCGTCCAGGTCGAGTACACGTGCAATACTTC
GTTACCACCCAACCGTGGGATGAGCAGATTTTTGACGAAGTCGCATCGTGGATTGAAGCT
GCC

>RXA02381-downstream
TAAAAACTCGCGAGGACGCATGC

>RXA02383-upstream
GGGCAACAATGTGGAAAACGCCCAGTGGTATCTTGACGGCTGGAACATGGGTGTTACGCA
GTAAAGAAGATGGCAATAAAAATGTGGAGGAGTAAAGGCG

>RXA02383
ATGCCAGTTCGGGTAATTGTTGATTCCTCCGCATGCTTGCCAACGCATGTGGCCGAGGAC
CTCGACATCACGGTGATTAACTTGCACGTGATGAATAACGGTGAAGAACGCAGTACATCC
GGGTTGTCGTCGTTGGAACTTGCAGCAAGTTACGCCCGCCAGCTTGAACGCGGTGGCGAT
GACGGTGTGCTTGCGCTGCATATTTCTAAAGAGCTCTCGTCCACGTGGTCCGCAGCGGTG
ACAGCAGCCGCTGTGTTTGATGATGATTCTGTGCGCGTGGTGGATACCAGTTCGCTCGGT
ATGGCTGTGGGTGCTGCCGCGATGGCTGCTGCCCGCATGGCTAAAGATGGCGCGTCTTTG
CAGGAATGCTACGACATCGCGGTGGATACCTTGAAGCGTTCAGAAACCTGGATCTACCTG
CACCGCATTGATGAAATCTGGAAGTCGGGACGGATTTCCACTGCAACCGCCATGGTGTCA
ACGGCTCTGGCAACCCGCCCCATCATGCGTTTCAACGGTGGTCGCATGGAGATCGCCGCT
AAGACCCGCACCCAATCTAAAGCGTTTGCCAAATTGGTGGAATTAGCCCAGATCAGGGCA
GAT

>RXA02387-upstream
GCTAGCCCCGATTCGCTTCAGGTCACCACCTTGAAGGCCAGCGAAATTACTCAGGGTGAA
TTGTTGGATGCGTTAAGCCCATCCTTGTTTGCTGAAGACC

>RXA02387
GTGTGGTGGTGCTTACCAACATGGATCAAAGCAGGCCAAGATGCTGTAGATCTAGCCTTA
TCCGCAGCAGTTGATCCCAGCCCTGGTACCTACTTGATCGTCATGCACTCTGGCGGTGGA
CGCTCTAAGTCGATGGTGAAGAAGCTGGAAAAAGTCGCGGTGGTGCACGATGCCGCAAAG
CTGAAAGACCGGGATCGTCCAGGTTGGGTAAAACAAGAGTTCAAAAACCACAAAGTCCAG
GTCACCCCAGATGTCATTCATGCTCTTTTAGAGGGCGTGGGTTCAGATCTTAGAGAGCTG
GCGTCCGCCGTATCCCAATTGGTTGAGGACACCCAAGGCAACGTGACGGTGGAAAAAGTC
CGTGCCTATTACGTGGGTGTTGCTGAGGTATCGGGTTTCGACATCGCCGATTCTGCATGC
GCCGGTCAAATGTCAAAGGCCGTGGCCAGCACCAGACGTGCCCTTCAATTGGGTACCAGC
CCGGTTGCATTGGCAGCTGCGTTGAGTATGAAAGTTGGCCAGATCGCCAGGCTGTATTCC
ACCAGGGGACGCATCAACGGTTTTGAGCTGGCCAAAGAATTGGGCATGCCGCCGTTCGTG
GTGGAGAAGACTGCGAAAGTGGCCCGAAACTGGTCGGGAGATGCGGTCAGCGAGGCCGTG
ATTTTGATGGCCGATCTG

>RXA02390-upstream
GCTGGTGGTGCTGACCCATACGCTGGAACTCCAACTGCTGTTGATACCGCCAAGATGTTT
GGCCGCGAGGATCTCGTAGCTCGCTTCGAGTCATAGGCCG

>RXA02390
GTGGAGTGGACCGCTTTTGGCACCCTGATTCTGCTCAATTTGGTGGGCAGTTTATCCCCG

GGGCCTGATACCTTTTTCCTCCTCCGCTTAGCCACCCGCTCCAGAGCGCACGCGATCGCT
GGCGTCGCCGGCATCGTCACCGGACTCACGGTGTGGGTGACGCTGACGGTCGTGGGAGCA
GCGGCGCTGCTCACCACTTATCCGTCGATTCTCGGAATCATCCAGCTCGTCGGCGGCACG
TACCTAAGCTTCATTGGGTACAAGTTGCTGCGCTCGGCGTCGAGAGAGCTTATCGACGCC
CGCCAGTTCCGTTTCAACGCCGATGCCCGACCTATCCCGGATGCGGTAGAAGCACTGGGA
ACCCGCACTCAGGTATATCGACAAGGTTTGGCCACCAACCTGTCAAACCCTAAAGTTGTC
ATGTACTTCGCGGCAATTCTGGCTCCGTTGATGCCAGCGCACCCATCACCGGTGCTGGCG
TTCTCTATCATCGTGGCGATTTTAGTGCAGACCTTTGTTACCTTCTCTGCTGTGTGCCTC
ATTGTCTCTACGGAGCGTGTGCGCAAAGCAATGCTGCGTGCAGGTCCCTGGTTTGACCTG
CTTGCTGGCGTTGTCTTCCTCGTTGTGGGTGTGACTCTGCTGTATGAAGGCCTGACCGGT
TTACTCGGG

>RXA02390-downstream
TAAAGGCATAAAAAATGGCTTCC

>RXA02393-upstream
GCCACCTTCATTTTTCNCANGCCNCNGCAAATCAGAACNCNACCTTCTGGCACTCCCNGC
TCAAATNNGGGACGTCCATGCNGANGTTTTAGACATCTTC

>RXA02393
ATGGCGGAATCTTTAGTGATTATCAACATCGACGAGAAAAGCGCCAAGCTGCTTATCGAC
GCCGCCCGCCACCACATCCCCACCCGCTTCACCGGGCCCAACGCCCGGCCGCTCAGCGTC
ATCCCCATCGAGGATCCCCGCTCACGCCCGACGCTCCACCCAGATCATGGTTGGATGATG
CCGCTAAGCCCACCAGTGGTGGATGAACTGCTTGGCGGTGGCTTGAAAATTGGAGAAACA
GAACTAGAAAGCACCAACATTGCGTTCATTGTTGATGCTTCC

>RXA02393-downstream
TAAAAATCCTGTGCCGTGAGGTT

>RXA02395
CTCATCACCATGGCTATCCCCTCCTTCATTTTGATCCTGGCGTTCACCATTTTCGGTGGA
ACTGCCATCACGATGAACCGCGAGAACGTAGATGGTTTTGACGGCAGTTCATCCAAGGAA
CAGGTGCTGTTTGATATGTTCAGCAACCTTCCGCTGTACTCGATCACACCGTTCATTTTG
ATCTTTGTGCTGGCAGTATTCTTTGTTACCTCTGCCGATTCCGCCTCCGTGGTGATGGGA
ACGATGAGCTCCCAAGGTAACCCTGCACCAAACAAATTAATCGTGGTGTTCTGGGGACTG
TGCATGATGGGCATCGCGGTGGTCATGCTGCTTACTGGTGGCGAATCCGCGCTGACTGGT
CTGCAGAACCTCACCATTTTGATCGCCATTCCGTTTGCGCTGGTGTTGATCGTGATGGCT
ATTGCCTTTATTAAGGACTTATCCACAGACCCAGCCGCTATTCGACAACGCTATGCAAAG
GCAGCCATCTCTAACGCGGTGGTTCGTGGCTTGGAAGAACACGGCGACGACTTCGAGCTC
TCCATCGAACCTGCAGAGGAAGGTCGTGGAGCGGGTGCTACCTTCGATTCCACCGCTGAT
CACATCACCGACTGGTATCAGCGCACCGACGAAGAAGGCAATGATGTTGATTATGACTTC
ACCACCGGCAAATGGGCCGATGGTTGGACACCGGAATCGACCGAAGAAGGCGAAGTGGAC
GCGAAAAAGGAT

>RXA02395-downstream
TAAAAAATAACGACTGGCTGGGA

>RXA02396-upstream
GAGTGCTTGTAGGTTGATAGAAAGTAAACTAAAGTAAACATCAGGTTAACAGCCGGGGGT
TCAAGTATTAACTCCCTCGGAAACAGAAAGGAACACGACA

>RXA02396
ATGGCTACCACAGCTTCCAAGATCTCCACGATCCGTCCAGCACAGCAAGATGCTCTTTGG
AGCGTACGTGAGGATCTTCACGCTCGCTTCGATGGCCTGGTCGATCCTGTCCAGGTAGAC
GCAATTTTGGACCATGTCGCATCTAACCGCGAAGCCAAGATCACCGTCTTCAGCAAGATT
TTCATCGCTCGCGAGGCAACCGCTGCACTTCAGCAGATTGCTGGCAACGTTAACGCAGAC
CTGCTTGACTTCATTGCCCTCAACCGTGGCATGGCAGCA

>RXA02396-downstream
TAAGTTTTAGCTGCCCATAAATT

>RXA02398-upstream
GTGTCCAATGAATGCGTTCAATAAATGCCCTCTTTAAGCATATTCTCTGAGTGCATTCAT
TACAGGCGTTAATTAAATGCGTTCATAGAAGAACTTGAAA

>RXA02398
GTGGTTGAAGTGAAGAAGCGTAATCTCCTCGTAGCTCCCCTCACTGCTTCCCTGGTGTTC
TGTAACTTGGCTGTTGCAGCAAACGCCGTTGAAGTTGAGGCCGAATCACCAGTTGTCATC
AATGAAGTTGAATCCAACAGCGACCCAGTTGGTGACTGGGTGGAGTTGGCTAACACCGAC
AACAACAACTCCATCGACATTTCCGGTTGGTCCTTAGTCGATGACAAGGAAGACCTGGAA
AATGCCCTCGTCCTTCCTGAAGGCACTGAGATTGAGTCCGGTGGATACTTTGTTATCTAC
ACCGACTCTGCTGATTACGTGCCTACCAACAACACCTTTGGTGGCCAGGAATACTTCGGC
CTCGGCAAAGATGACACTGTTACTCTGCGCAACGCTGAAGGCGAAGTAGTTGCTACCTAT
TCCTGGAAGGATCTGGGCGAGCACGCAGAAAACACCTATGGTCGCATCCCAGATATGACT
GGTGATTTCGCAAACACCGGCGTTCCAACCCCAGGTGCAAAGAATGTTGCTGCTGAAGGC
TCCGGCGAAGAAGAAGGCGTTGTTGCAAACGCCCAGCTTCCATTCCACAACGTTGAAATC
ACCCCAATTCACCTCGGTGGAGATTTCACCGGTGAAGATATGTCCGGCGTTGATTTCGAT
GCAAACAGCACCGCATGGATCGCCAACAATGACATTGGAAAGATCTACTCCCTCGCCCAC
GACATAGCTAACAACACCTACAAGCTGACTGGCGAATGGGAAACCGGCTACCCAGAAGGC
GGCGGAGAGCCAGACGCTGAAGGCATCGTCGCAGCTACCAACGGTGACATCTACCTGTCC
ACCGAGCGCAACAACGCTGACAAGAACGTCTCTCGCCCATCCATCCTGCGTTTTGCTACC
CCAACTGGCAAGACTGGCGTACAAAACGCAGTTCAGGAATGGGACCTGTCTGAGTTCGTC
GGCGACATTCAGCCCAATGGTGGTCTTGAGGCAATCGCGCAGCTCGAGGACAACATCTTC
GTTGTCGGTGTCGAAGAGACAGGTGATGTCATCGTTGTTGATCTTTCCGCTGACCAGCCA
GTTCTGGTTCAAAGGTACGAATCTTCCTTCGACGGTGTCATGTCGCTTGATTACAACGCA
GCAACCAAGCAGCTCAGCGTTGTGTGCGACGAAGCATGTGACGGCTTGTCTGAAATCCTC
GAATGGGATGGCGAGAAGCTGTACAAGTCCGACGACAAGATCTACGAGCGTCCAGCAAAC
CTGGGCAACTGGGCTAACGAAGGCTTCGGCACCTACACCTCAGAGCTTAAATGCGAGAAC
GGCAACACCGTTTCTGTCACCAGCTACCTCTGGGCTGACGATGCAGCAACCAACGAAGGC
ACCTCCCTCAACTCCGCACAGGTCATCAACGGAGATTGCGGCGACGTCAACATCCCTGGA
GAGTCCTCTTCCGACAATTCCTCTTCTGACTTTGCAACCGGCAGCATCGCAGGCGCCTTT
GCAACCGCAGTGCTCGCAGTCGTAGGCATT

>RXA02403-upstream
GCACAGAATTAAATCGCTGGTGTGCGAACTTTCATACCTTAACGCAGTAGTGATGCTTAA
GGCACAACGTGGGGGCAATTCCGGCCTATACTTTGGAAGT

>RXA02403
ATGACTACTTTTATTACCTCCGGTGGCTTGGAAATCTCCCCCGCTGGCGCTCATATTGTT
CACGCCGAATCACCTGAAGGTGAGCTGTTGTTTGTTAGCTCCGCTTCCCAATATGGGGAG
GGAAATGCAATTAGGGGTGGTGTGCCCATCATTGCTCCATGGTTTGGTGGACTGCTTGGT
TTGGACCCTGCACATGGTTGGGCGAAGCGTTCCGCGTGGGACGTGACTGAACATGACGGC
CAAATTCACGCTGAATATGGCCGCGATGGTTTACTGCTGGATATTCGTGCGAACAGCACT
AAGAATGGTTTTGAGATCACCCTGCGCGCTTACAACGACACCGATGAGGCACGCACTGTG
CAGTTGGCCTTCCACCCTTATTTCAAGGTGGATGATGTAGAAAAGATCGAGGTCCGTGGC
CTTGATGGGGTGGACATTCTCAATCGCCTGAACAATGAGGTGGAGACCCAAGATGGTCCC
GTTACTTTTGATGGCGAGTTCGATCGCATTGCGCTAGGGACTCCGGTTGTGAGGATTTTT
GATACCGATCGCATCATCACCATTGAGGGCGATGGTCATGATTCCACTGTGGTGTGGAAT
CCAGGCGAAAGTCGCGCCTCCACCGTGGCCGATATTGGCGAAGGTGAATGGCGCGACTTT
GTGTGTGTTGAACCGGCGCTTTTGGGTGCTGACCAAAAAGGAGTGAGGGTGGCTCCGGGG
CAGTCAGTCACCGTTGGGATGCAGGTAAGCGTCGAAAAGCGTGCT

>RXA02403-downstream
TAGTTTTTTGCTTTGAACTCGCG

>RXA02406-upstream
CACTCTGATAGCCTTTTCTCTGAAATTGTACCGAGCATTTGATTTTGTTCCCCTATCAAT

GCTGGTTTTGGTGACAAAAACTCGGCGGAAGGACCACCGA

>RXA02406
ATGGAAACCCTTGCAGCACAAGCGCGCACCCTGCTAGAAAAATGGGGCGTCGCGCCGACG
CACGCATCTTTCGTCGAATCCATTGCAAAGGCCATCCCGATTCTGTCGATCCTGCTGACG
CTGATTGTCACCGTGAATGGAATTTCAAGCGGAAATCCGGTCCAGCCACCAGCACTGGAA
CAGGTACGGACCGATGTAGTGAACAAGATCAACTACGAACGCAACCTAAAGGGCCTCGTC
TCGATCAGCCCGGAGCTTGAATTACACACGGCAGCCCAAACAATTGCGCAGCGAAATGCA
GACTCAGATTCCGAAGAAAAAGTACCGGATCCAGAGGGAACCTTGGTGGTTCTGCAACAG
AATCTGCCCTATGCAAATGCCAACGCCGATACCATCGTTGATCGGTTCTTAAACTCTCCT
GATCATGTCAAACTACTGCTTGCAAACGATTATGAAGCCATCGGAGTTGGTGTGGCCTAC
AAGGGTGATCATGCGTGGATAGTGGTGGAGTTCACTGTAGCTCCCGCTGATTCCGTAGAA
TCAACAGAG

>RXA02406-downstream
TGAATACCAATCCGTCTGAATTC

>RXA02407-upstream
GGATAAAAATTTGGATGACATATCACCTAAGCTTGCAATTTCTACTGGAATAGCGCGACT
ACTCTGCACCAACGCATAGTTGTTGACTAGGCTATTTGTC

>RXA02407
ATGAATAGGCAAAACCAACTTCACTACCCGCAGGAAGTGAAGGCAGTGGAAAGTGTGGAA
TCAAGCTTGAACATGTCGTCACCTTCTGCACCGCTTGCCACGCCAGATGTTGAGCTTGAT
GTGCACACGTTGTCGAGCGAAAACCTGCCTTGGTTGTGCATCGTGTGGGATGATCCGGTC
AATTTGATGAGCTATGTCACCTACGTTTTTCAGACTGTGTTGGGCTTCAGTAAGAAGAGG
GCCACTGAGCTGATGATGCAGGTGCACACCGAAGGTAAAGCCGTGGTGAGTTCTGGCGAG
AAGGAC

>RXA02408-upstream
GTGATGTACGCGGCGGGGAAGCCGCCGAGGAAGACCGCGAAAACCTCGTGCAGTGGCTTG
CCTACAATCAAGAGTCCTTGCTGGAAGCGATGATGAATTA

>RXA02408
ATGCTTATCGACGTCGCGGGCTTCCTTTTAGGCCACGTCACGAAGGGGGATACGGGTTGC
TCAGTGGTCATTGCACCTAACGGTGCATTTGCGGGCGTCGATGTCCGTGGGGGAGGCCCA
GGCACCAGGGAAACCGACCTTCTAGAACCACACAATTCTGTGCAGCAAGCACATGCCGTG
GTGTTGTGTGGCGGTTCGGCGTTCGGGTTGGCTGCTGCCGATGGAGTGATGACAGCCCTA
GAAAACCGCGGTATTGGTTTCCCTGTCCGTCCCGAAGGGCCTATCGTGCCAATCGTTCCA
GGCGCTGTGATTTTTGATTTGTTGGTGGGCGATCCCAAAAACAGGCCCACGGCAGCTGAT
GGGGAACAAGCAGTTGAAAACGCTTTCGCTGGTACACACAACGGTTCGGGCAGCGTCGGT
GCAGGAACGGGTGCTACAGCAGGTCGGCTGCGTGGCGGTTTTGGCCAAAGCTCGCGCCGG
GTCGGAAAGTACACCATCGCGGCAGGGGTCGTGGCGAATCCTGTTGGGGAAGTCGTGGAC
CTAACAACTGGAGCTTTGTTTGGTAGGCCCGAAGTGATGGGGGTGGGCGTCGATAAGCTA
AAAAGCGCGGCAGAGACGCTGAACACGACCATCGGCGTCGTGGCAACTGACGCGCCGGTG
ACAAAAGCCCAAGCGAAGCGCTTGGCGCTGGTGGCCCATGATGGTTTGGCGAGGGCAGTG
CGGCCGTCGCATTCACCGATGGACGGTGACACATTTTTCGCCATGTCATCGGGTGATGGT
AGTGGCGTTACCCCGGTTGAGCTGGGGGAATTGTCGGCTCATGCTGCA

>RXA02409
CGTGCACAGTCTGTGCCGAAGGATCCTCTGGCAGAGATGACCGGCATGACAAGTGGACAC
AAAGAAGCACCAACCGATCCGGCGCTTGCGCGTTTGCTCCCTGATTTTCAGCACGAGGGC
GATGAGGAATACGACGGCGATAATTCTTTCCTCCGTTCACTCCATGAAGGCGACATCACC
CGAGCAAAACTGGAAAATCTGCGCGTGATTAACGATGCGCTGGGACCCGACGGAAATGTT
GCGGTCACCGCCTCTGAGGAGGAAGCGCACGCTTGGTTGGCTGCGCTCAATGACATCCGC
CTGTACGTTGCCTCCGGTGATGTACGCGGCGGGGAAGCCGCCGAGGAAGACCGCGAAAAC
CTCGTGCAGTGGCTTGCCTACAATCAAGAGTCCTTGCTGGAAGCGATGATGAAT

>RXA02409-downstream
TAATGCTTATCGACGTCGCGGGC

>RXA02412-upstream
TGCGGTGCGAGCAACTTCGGAGACTATTGGCTCTCCTACAGCTGTGGCATCCGCGAAACG
TTCACCCAAAGGCAGTCTCATTGGGTTGATCTTGATCTTG

>RXA02412
GTGGCCATCATCGTGATTGCGTTTGTCTTGTTGTTCAACAGCCTCGTTGCACCAAATAAT
TCCTCGAGCCCTGTGGCAAGTCCAAGCACCTCTGAATCTGTGGAGCAAACTATTTCGGAA
TCCCCTGAGTCACCGAGCGCGACAGAGGATCAGCCCCCAAGCAGTGCAACGGAAACTCCC
CGAAACCGCCCTGCGCAACCATCACTTCCTGCGGGAGCATCACCAGCCAATGATGCTGCT
GCCACCCAGACCGATGCCGGCAATTTAAACAATGTGTACACCGGGTCAGCGTCCACCTCA
GCAGGTTTTGCTCAAGCCGTCCGAGATGCTTTTGTAAACCACTATTTAGACACCAATGAA
CTATCCGGCAGGGTGACAGCCACCAGCCCTGTCACTGGCGGAAACTACACCATGAACTGC
GAAGACAACGGCGAGTACGTCACCTGCACAGGTGGCAACAACGCCGTTGTCTACATTTCT

>RXA02412-downstream
TAAAACTTCTAACTACACCCGGG

>RXA02417-upstream
CGCTGTTCAGAGGACTTCCGCGGGGGTCGACAGTATAACGAATTAGCGTCACTAGAATAA
TCGGGCTGTTTAGTTCTTCACACCAACATAATCTTATGTA

>RXA02417
ATGGACATGAACTCTTCTGACCGATTGGCTCTACGCACCGCGTTAGAGAAATTGTCGGCA
TCGGCTACCGCCATGGCGTCAGCGAGCAATGACATCAAAGATCTCGTTGCACGCCTTGAT
GCCCAAGAGATGTCGCTTATCGACGCAAACCCGGCTCCCACCCCAGCGCCCACTGCCCCA
CCCGAGGCTCAGCTTGAGCCCCAACCACTGGTGTATGCAACCGCCTCAACGGCGCCTGCA
CTGGCGGATGTTTCCGGGACCAACCGTATTCCACGTTTCGTTCGGCATCGCGCCCTGGAT
CCAGCGAGCGAAGGCTGGCCACTTGGCGTCGAGAAGCAAAAAGTGCAGGCTCCTGCGTAC
CCGCACCCCGTCCGGCCAGCTCGTCCGGCAAAGCCGCCGATGACGTCGGAGGAAAAGATC
ATGCGTGGCGTGGCGATCGGCGGTGGTGTGATCACCGTGGCCGGCGTGATTTTGCTGGTG
TCGGTGGCGATTCAACGCGGTTGGCTTGGTCCGCTGGGTCGTGTGATTGGTGCGTACCTG
CTGGCGGTGCTGCTTCTTGGCGCCGCACATTATGTGCGCAAGCGCGGAACCCGTGTGGAA
GCACTCGTTGCGTTGACGGTTACCTCCCAGATTGCGTTTCTTGCCACAACGAGTGCAATC
ATCTTCATTTTGGAATGGTGGCCGCCTGGATTGGGCTCGCTGGTGGCATTAATAGGCAAT
ATTGGGTTCTTAATCGTTGGTCGATTGTGGAGCCTATCCAAAACCGAGAAGTCCGCGGCC
GAAGGCCACACAGTATTTGTGGGAGCCATCGCCGTTTCAGGATTCTCCGCGATACTCTTC
GCGCTCTCCGCCGATGCCTGGTGGCCAATTTTCTCCATTGTTGCGGCATTGTTGCTGTCG
TACCGCATCTCCACGAATATCATCCGAGCGAGCATGGCGGCATTCGCGGTCATTCTGCAG
TTTGTTTTGTCGGCATCCTGGCAAACCATGGAATGGCCAGCAACAATCGTCGGCACAATT
ACTGCAGTCCTACTCGTAGCCTTGACATTGTGGGATCCGTTTAAGATCACCGCCACCGAC
AGCCACGACATCGCGTTGGAGGAATACTGGCGCAGCTTTGAAACCAACCCTGTTTCCACG
TGGGTGGGTGCTGTTTCTCCGGTGCTCATCGTGTTCATCACCACCAGCATGTTCATTGCA
GTCGACTGGCCATGGCTTGCCCTGATACCAGCGTGTGCGGTGGCAGCTCTCGGAATTTTC
GCGCTGCGCTCATCAGACACCGCGTCCATTGAAAATCAACGCATGTCTCGCCTCATTGCT
GTTGTTGGCCTTGCGTTGATTGCTGAAACTTTTGTCCAGCTGTTCTACGGCGATCTCCCC
ACCAACCCGCTTCTCGTCATGGTGTTCCTCATCGCCGGAGCTGCACTATTTATGTGGTTG
CGGATGCTTCCACCGCAGCGTCAATTAGGTGTCGTCCCATGGGTCGCTTGGCTGATTGCC
GCCGTGGCGATGACCGGCGTGCTACTGCGCAATGTCGTTTCAATTTCTCCACTGTGGCTC
ACCGATACCCAAGCGCTCATCCAAGCATTGCTGATCTTGGTGTTCATTGCCGCCACAATC
CAAGTCCGCCGCAGCTTCTACGGACACAAACTGTGGCTGCAAATTTTGGTCGGCTTGACG
CTTCTCACGCTGTCCGCAATTTCCATCGTGACCATCACAACCTTCATCGGTCGCCTCATC
GCAGGAAATGCCGGCATGATGCTCGGATTCCTCATCGGCCACGCCACGGTTTCTATCCTG
TGGATGGTCATCGCCGCAGCACTGATGCTTAATAGGAAGCTTCTCGACGCGCCCGGCGCC
CTTTGGACCGGCGTTGGCTTGGCGGTTGCGGGCACCTTCAAGCTGGTGTTCTTTGACCTG
GTCGCGCTGTCCGGAGTTCCCCGCGCAATTGCCTTCCTGCTCTCCGGTATCGCACTGCTG
ACAATCGCTGCTATGAGGGGCCGGAGAACCTCAGAAAACAAGGCCGACGTAGCTAGACCT

CAGGTGGCTAGACATGGGGCGACTAGCCATAAAAATGAGGAGCCTTCCCATGAAAGCCCC
TCATCTTCTCCTACAACAACTCTT

>RXA02417-downstream
TAAGGAATTGGCCGGTGTAGGAA

>RXA02421-upstream
CGGTGTACTTTAGCAACAAGGAAAAATAACTATCTACGGCCTGTTAATAGTTCAACCTAC
AGGCCAAACCCGCCTTCATTAATGAATTGTGAGATCGACC

>RXA02421
ATGACATTGCTCTTGAAGCCAATTTTGCAGGCTGCGGGAATCAATCCTGAAGATGCGTTA
GCAATGCGTCATGTATTTATTTCGATCCACGAGGACACCAATTCCAATGGTATTACCCGT
GAATCTAAAGACGAAGAGATTCTCGCCTACACAGCTAGCCAGTCAAGTGATCCGCGTAGA
TTCCCACTGAATCCGCCACGCTTTTGGATGGTGTTCATCCGAGAAGGTGGCTCGCAGGCT
CGACTATGGAAAGTGGTGGAAAACCACGGCGAAGTCACCAATGATGGCGTACGCAGAGTC
TTCAACCTTACTGAGATTGAACTCATGGATGACCTTGCAGGCAGACTCGTTATTCGTTGG
AATTCACCACGCAAGTGGTGGATTAAGGGCACTACTGCTGCCCTATACACCGTGGATACT
ATTGCCGATGCGGAGCCTATTCCGTTTCCAGGTTTCGACAATCTTGTCCTGAGCTACCCA
TTTCTTCAAGAAGTGATGCGTGAACCTGCCTATGCTTCGTGGCGCACAGCTCTTGGTGCT
GTCAAAGGTATTTACCTCATTACCGATACCCGTACTGGCCGCCACTATGTCGGCAAAGCT
GAAGGACTAGAAAACATACGCCAACGCTGGAACAGCTACGCCACCAATGGACATGGCGGA
AACGTAAAACTCAAACAGCTTAAGCCCGACACATTTCGTTTTTCGTTGCTTCGGGTCTTT
GATCCCGCAACTCCAACTAGCATTATTAACGCTGCTGAAAGCCACTTTAAAATTGCTCTC
GACACGATCAAGCACGGATTAAACGCAAAC

>RXA02421-downstream
TAATCGCAGCTCCCCAACCCCAA

>RXA02423-upstream
TAGGTACGATCGGACGAGGAGAAAAAATCTGAAAACAATCCAGTGGCCCACCTCGGCTTA
TAAAACTGGACAACAGTATTTTGATTGGAGCATCACCATA

>RXA02423
ATGATCCGCAAACTTGCTCGACCAATGCTTGCATCGGTCTACGTCGCAGATGGCGCAGAA
ACAGTATTGAACACCAGCGCACACGTCGAAGGCACTCAGGTAGTTCTGGATCGTATCCGT
TATGTGCTGCCCCGTAAGTACGCAAAGCGCATTTCCAGAGATCCAGAATTGGTCACCCGC
GTCATTGGCGGCACCAAAGTCTGTGCGGGTTCTTGT

>RXA02425
CCCGGCGCCTTTGATGAATTAACCAGTGTTTGGGGAGAAAAAGGCGGAAGTTGGGCCGCT
GTTATCGGCTTCTTCGGTGGCATCGCGCTGATCGCCATCATCGACCGCTTAGTCCCCACG
GCGATTAACCCCCACGAGCCCTCCACCGTGGGAGGCGCCGTTGAAGGATTCGAGCGCCGC
AACCGCATGATGAAAATGGGTGTGCTCACTGCGCTGGCCATCGCGATCCACAACTTTCCC
GAAGGTTTCGCTACATTCTTGGCCGGATTGTCCGATCCAATGATCGCGATCCCTGTGGCC
GTGGCAATTGCCATTCACAATATTCCAGAGGGCATTGCGGTGCCGGTGCCACTGAGGGAA
GCTACAGGGTCACGTCGAAAAGCATTAGGTTGGGCGACCCTCTCCGGCCTTGCTGAGCCC
GCCGGCGCCCTCATCGGATTCCTGCTGCTCATGCCCTTTATCGGACCAGAAGCACTCGGC
CTGTGCTTCGCCGCAGTTGCCGGCGTGATGGTGTTCATCAGCGTCGATGAACTACTGCCC
ACTGCCATCTCCAGCGGCAAACACCACACCGCCATCTACGGACTCATCGCTGGCATGGCA
GTCATGGCGATCAGCCTGCTGCTGTTTATC

>RXA02425-downstream
TAGCGTTCAGCCGCAACAAGCAT

>RXA02427-upstream
AGCGATGCTGACAGTGCTTCACTTCGGGCCGCATCTAATTCCTGCTCGATTACCCAACTG

CTCGCGCAGGGAATCGTCATCGACGACGAGGTGAACTAGC

>RXA02427
GTGGATTTTGAGTTGGGTAAACGCTGCCCCTGCGGAACTGGCCTTACCTACGGTGAGTGC
TGCTACCGCTTTCACTCCGGCGAATGGGTGGCCCCCACCGCTGAAGCGCTCATGCGATCT
CGGTTCACCGCCTTTGCTGTTGGAAATTCCCAGTACCTTCTTGACACTTGGGATCCAGAA
ACCCGGCCAAGCGAACTCGGCCTCGATATGGGAATTGATTTCTACCGCCTCGACATCCTC
GAGACCACCGGCGGTGGACCCTTCGATTCCACCGGCACCGTAAAATTCCAAGCCTTCTAC
AAGGGGCTCGCCTCCGGCGTCCAAGAAGAAGACTCCACATTCCGCAAGGTCAACGGCGCG
TGGGTCTATTCCACAGGAGATGTCGAC

>RXA02427-downstream
TAGTTTCCCCACACGTGCAATAG

>RXA02428-upstream
CGAAAGATATGCATAAAGTGATGATGAAATAGCTTTGTCGAAAGGTTTGCTCCCGGTGCA
TTCAGTTAGCGTGAAGGTGCCATCATCACAAGGGTTGATG

>RXA02428
ATGGCCGCGACGTTAGATCTTCCAGATACAGATCCCATTGCCTATGCAATGTTTGCCCAC
TGTTTCACCGGCTCACGGTTCACGCCAGCCGCCGCGCGAGTCAGTAAAACACTCGCAGAA
TCCGGCGTCGCCTGCCTGCGTTTCGATTTCCCAGGACTGAGCCAATCAGAAGGTGACTTC
TCCAAAACCACCTTCAACTCCAATGTGGACGATATCGTGGCGGCCTCGCAGTGGTTGACG
GAACACTACTCCGCTCCACAGTTGCTCATTGGACACTCCTTGGGTGGTGCAGCATCACTG
AAAGCTGCCACCAAAATCTCCTGCCTCAAAGCAGTAGCAACGATAGGTGCACCTTTTGAT
CCTGCGCACGCAGTCCTGCACTTTGCTGATCGCATATGTGATGTAGATGATCAAGGTGCT
GTCACTCTGCAGCTCGGAGGCCGGGATGTCACCATTTCCCGCGAATTCCTCGAAGACCTT
GCAGAGGTCAACCCCGAAGATCACCTCCGCAGGCTCCGCAAACCACTGCTTTTACTGCAT
TCCCCCACCGACCAAACCGTCGGCGTGGACAACGCGCAGCTCATCTTCAGAGTCACTCGC
TACCCTAAATCCTTGATGACTTTGGACAAGGCAGATCACCTGCTCACCAAAGATGGCACC
GCACAGCGTGCAGCCCGGATCATCGCGAACTGGGTCGAGCCCTACCTGGTTCCAGAAAAC
GTCTGTGAGGATCTTCCGGAGTTTGTCGCCGAAGCCTCAACCATCAAAGCCAGCAAATAC
GGCGCAGCCATCCGCACCGGTGGTCACAATTTCATCACCGACCGCGACAAATCCCAGGGT
GGCAAAAACCTCGGCTTCACCCCTACTTCCCTGCTGGTTTCCGCGCTTGCTGCTGCAAAC
TCTCAAACGATCAAACAAGCAGCCATCGACAACCGCATCAAAGGCCTTGACGATGTCAAA
GTGACGATCTCCCAGGAACAATCAGCCGACCACGGCCAGATCAAACTCCGCCGAAAGATC
TCTTTGATCGGCAACCTCAGCGATGCTGACAGTGCTTCACTTCGGGCCGCATCTAATTCC
TGCTCGATTACCCAACTGCTCGCGCAGGGAATCGTCATCGACGACGAGGTGAAC

>RXA02428-downstream
TAGCGTGGATTTTGAGTTGGGTA

>RXA02430-upstream
CTTGTAGTCAAGCGTGGACCAAATGCAGGCGCTCGATTCCTTCTGGACCAGCCAACCACG
ACCGCTGGTCGTCACCCAGAAAGTGACATCTTCCTTGATG

>RXA02430
ATGTCACCCGTTTCACGTCGCCACGCAGAGTTCCGCATCAATGAAGGTGAATTTGAAGTC
GTGGACGTAGGGTCCCTCAACGGAACCTACGTTAACCGCGAGCCACGCAACGCTCAGGTC
ATGCAGACCGGTGATGAGATCCAGATTGGCAAGTTCCGCCTGGTTTTCCTCGCAGGCCCT
GCTGAG

>RXA02430-downstream
TAAAAACACTTCCTAGGAAAGTT

>RXA02433-upstream
AGGCACGAGATCATCCATCGTCGGTTCCATAGAATGGGTAGCTGTCGAATGCTGATAGAT
ATTTGGTGACCAGAGATTAGAGCAAAGGATCATTTTCATC

>RXA02433
GTGAAGCTTTTCAAGGCAACCGCAGTTACTTTTACTGTTGCAGCAGCATTGGCGCTCAGC
GCGTGCTCCAGCAGTGATGATTCCTCTTCGGAGTCAAGCACCTCTTCTTCCACCTCTTCG
GCTGCGTCTGATGCTGCGACTCAGTACCCAACTGCTGAGGAACTGAATGCAATTTTGGCT
GTGGCAACCGACCCTGAGGCACCAATCGAGGAGAAGGTGAAGACTGTTCAGGGTTCTGAG
AACGCTCCTGAGCTGTTTGAGACCATGACTCAGGCAAAGGTGGAGTCGGGTGCTGAGTTC
CAGGTTGTTGGTTCTGTGCTTCCTGGCTATGACCCAACCTCTGAGGTTCTGACCACCGTC
ATGTTCCAGCTTCCGGACCGCGCTGAGCAGGAAGCTGAAGGCGTGGAGTTTGTGAACACT
GATGGTAATTGGCAGCTGTCCCAGGATTGGGCTTGTATCTTGATCACCAATACTGTTGCT
CCTGAGCAGGTTCCTGCAATGTGTGTTGGAACTGATGCTTCTTCCGCTGGTATTGAAGAG
GCCCCAGCTGAAGAGGGTGCTGTTGTTGAGGAAGCCCCTGTTGAAGAGGTTCCTGTTCAG

>RXA02433-downstream
TAGGGTTTAACGGCTCAGGCTGA

>RXA02437-upstream
GCCCATCATAACTACATCGAGCGAAATGCCAACCACATGTCCCATGCTTTTACTAATGTG
GGGTCTTAGAAGAACGCGACCAATTTAAGGAGAGTTGAAT

>RXA02437
ATGAGCACGATTGGCAACCTCAAGTTAGTAGTGGATGGCGCACGTAAAGCTTATGGAACT
TATGCGGATTACCGCGACCGCAAGGTGTCTGAGACTTATGATGCGTTGTCCCAAGCTGCT
GGTGAATATGCACCAAAAGCTGAGCAGGCTGTAGAGACTGCGCGGGAATCAGCGAAGGAA
TTTTATACTGAGTCGCGCGATAAGGCTGGAAATGTCACCAAGGCTGCTCGTGCTCGTCTG
GAAAAGGCGCTCGCTGAGGCTGACAAGCAGGGCACTTCTGCGTTGAAGGACGCACGTGAA
TCGGGCAAGAAATTGAACCGGAAGGCGCGTCGAAAAGCAGACAAGGCCGCTAAGGCAGCC
CGCAAGGCGACTGAAAAGAAGGAGTCGCACTGGGTGCGCAATCTGTCGTTGGCGGCGCTA
GCGACCTCCGGCATCGTCGCGGTGGCCTACGCGTTTTTGAACAAGACCAAGAAGGAAACC
CCAGGCACCCAGCCTCCACGGGTTGAGGTTCAGTTGAAGAAGGCCGTGGAGCAGGATGAG
CCTGAGGTTGTGGCTGAGGCTGCTGTGGAGGAGCCAGAGTTGGTGTACTCCACAGAAAGC
CCAGAAACCACTGAAGCCCCAGCTGAGGCCACCGAAACTCCAGCAGAAACCACCGAAGAA
GAAGCCAAAACCGAAGCTGAACTAGAGGCAGAGCTCGAGGCTGAGGCCGATGCGGAGCAG
GAAGCGGCAGAAGAGGCGGAAGCTGAGGCCATTCAGGCTGAGTTTGATAAGAAGAATGCA
CCTCAGCGCACCCAGAGCGAAAAGAAGAAG

>RXA02437-downstream
TAGGTTAACGCTTCAATTCGTGG

>RXA02443-upstream
CAAGCACTGCCGCGGGAGCCACTATCACTTTGTTAAGTGCTGCGATATTTTTTGCCACCT
TATTGACAAAGAGTGCCATTAGTAGGTTAAACTTCACCGC

>RXA02443
GTGATACTGAAAGACATTTTCAATAATGGGGAGCTCTTTGGGGCTTCCTCCGCGAAAAAT
TTCCGAAAACTACTAGCTGTTCCAGCCGTTGCCGCCTCACTAGCTTTTGGTATCACCGCC
TGTTCCGCTGTAGATGACACCCCTGACATTGTGGTCACCACCAACATCCTGGGTGATGTT
GTAAGCCATATCGTGGGAGATTCCGCAGATGTCCAAGTACTCATGAAACCCAACGCAGAT
CCACATTCCTTCGGAGTCTCAGCACAAGACGCCGCTGCCATGGAACATGCCGATCTCATC
GTGGCCAATGGACTAGGACTTGAAGAGGGCCTTCAATCCAATGTGGACAATGCCAAAAGC
CAAGGGGTTCCCGTCTTGGAAGTCGGCGAACACATCGATGTCATTGACTACTCCCCCGGC
GTTCCAGATCCTCACTTTTGGACAGACCCGGCGCGCATGATCGCCGCCACGGAAGTTATA
GAAGCTGAACTGATCAAAGAACTCGATCCTTCCCTGACTGAATCGATCACACAATCAGCC
CAGCACTACCGTGAGGAACTTGTTGCCCTTGATGAGGAAGTCACCGAATTGCTCAGCGGC
GTGGCCCCAGAAAACCGCAAGCTGGTAACCAATCACAATGTTTTTGGATACCTGGCCAGC
CGGTTTAACTACACCGTCATTGACACCATCATCCCAGGTGGAAGCACATTGGCGGCGCCT
TCAGCATCTGACCTCAATGACATCTCCACCGCCATCGAAGACAACAATGTTCCCGCAATC
TTCACCGATACCTCAAGCCCACAACGGTTAGCTGAAGTGTTGGCCAGCAACGCTGGCATT
GATGTTCAAGTGGTGTCCATTTTCACGGAATCACTCACCGATGCAGATGGTGAAGCACCC

ACCTACATCAGCATGCAAAAAATCAATGCCGAGCGCATTGCAAGCACTTTGTCC

>RXA02443-downstream
TAAACAGTCCTAAACAGTCTTAA

>RXA02444-upstream
AAAATCAATGCCGAGCGCATTGCAAGCACTTTGTCCTAAACAGTCCTAAACAGTCTTAAA
CAGTCCCCGTTTTACTAAATGTTTTACTAAAAGGAGAACC

>RXA02444
ATGAAAAACTCCAAGCTACTTCTTATTGCTGCGGTATCCACCGCATCTATCCTGCTGGCA
AGCTGTGGCACTGACAGCTCTGCAGATACTGCAACTGCGTCTAGCTCTGCAACAGCAAGC
TCCGAGGCACACGATCATGATGGCCACGAAGCCGAAGGCAGCAGCACTGCCGTTGAGGTG
TCCTCCCCGCAGGCCCGCATCGTCACCACCTACGACGGTGGCATCATTACCCTCGACGCC
AACACTCTGGAAATCCTGGAAGACACCGAACTAGCAGGTTTTAACCGCCTCAACAGTGCA
GGAGACGGACGCCACGTATTTGTCTCCACAGGTGGCGGCTTCCAGCTCTTTGATACCGGC
GCATGGACCGAACCACACGGCGATCACACCCACAGCTACACCGCCACCCCAGAACTCACC
GACATCACCTACTCCACCGATAAGCCTGGTCATGTAGTGAACCACGCCGGCAAGACCGTG
CTGTTCGGCGATGGTGACGGCAAAATCCAGATCTTCGACACCGCTTCCCTCCTCAAGGGC
GATGAAGTAGAACCTGAGATCAAAAACGCCCTCAAAGCCCACCACGGCGTGGCAGTAGTC
CTCGAAAACGGCGACCTGCTGCACACTTTGGGCGATGAGGATTCCCGCAACGGCGCCGTC
GTATTCAACGCAGCCGGTGAAGAAATCGCCCGCAACGAACAGTGCCCCGGCGTTCACGGT
GAAAGCGCAGCACTCGGTGACGCCATCGCAGTTGGCTGTGAAGACGGTGTACTGATCTAC
AAGGACGGCGAGTTCACCAAGGTCCAGGCACCTGATTCCTACGGTCGCATCGGCAACCAA
TCAGGCAGCGACGTCTCTCCTGTCGTCCTCGGCGATTACAAGGTAGATAAAGACGCCGAC
TTGGAGCGCCCAGAGCGCGTTTCCCTCACCAACACCGAGACCGGCGAGCTCACCCTCGTT
GACCTCGGCACCTCCTACTCCTTCCGCTCACTTGGCCGTGGCCCTGCAGGCGAAGCAGTA
GTTCTAGGCACCGACGGCGCACTCCACATCATCGATGCCAACACCGGCGCCATCACCAAC
ACCTACCCCGTCATCGATGCCTGGACCGAACCAGAAGTATGGCAAGAAGCACGCCCAACC
CTGTTCATCAACAAGGACCGCGCATACGTCTCCGACCCATCAAACAACGAACTCCATGTT
GTTGACCTGGCCAACGGCAACATCCTTGCCAGCGCCACCCTGCCAGGAACCCCCAACGAG
CTCACCGGAGTGAGCGGC

>RXA02444-downstream
TAAAAAGAAATTGCTTTTCGACG

>RXA02452-upstream
TTTGCGCGACTAATCGCCGGATAAATGAATTGATTATTTTAGGCTCCCAGGGATTAAGTC
TAGGGTGGAATGCAGAAATATTTCCTACGGAAGGTCCGTT

>RXA02452
ATGACGCCTGCAGGTCCAGCACAATTACTCATTGTTGCTCTTGTAGTAATTGTCCTCTTT
GGTTCCAATAAGTTGCCTGATGTTGCTCGGTCCGTTGGCCGTTCGATGCGCATTTTCAAA
TCTGAGATCAAAGAGATGAACAAGGATCAGATCGAAAGCTCCGATCAGACCTTGAAGAAC

>RXA02452-downstream
TAAGGTTCCTCGCATCTAAAAAC

>RXA02454
ATGCATCTGCTCAACTTCTACTGGGGAGATGTGTCACTGTCTAATACTCTCTTTCGTCGC
GATGCTGAAACCTATTCCGCCTATCTCGTCGATGCCGAAACCGGGGAGTTCCAGCCCAAC
CTCTCTGAATCACGCAGGCTTTACGACGTCGACATCGCCCGCGTCAACATCATTGGCGAA
CTCATGGACCTACAGGCGGGTGAATGCCTAGATAAGTCCATCGATGTCATCGCCCTAGGA
GGCCTTGTCGAAAGCTCTTATCTTGAATTGTGGACGGAGCTCACCGCGGAGGAATCCGTC
GATGCCAGTGAATATTGGCGCCTCTCTGAGAGAATTGACCGGCTCAATCAACTGGGCTTT
GACGTAGGGGAGCTCAAGGTCACGAAGGACGATTCGCGGCAGGTTGTGCGCATTCGCCCT
GTAGTGGTGGATCCGGGCCACTATCGTGCAGAGCTATTGAGCTTAACCGGGCTGAGCGTC
GAGGAACACCAGGCCCAACGCCTATTGGGCTCGATCCAGGCCTATCAGGCCGTCGAATGC

GGACCGCATGTAGGTCTTACCCAAGCCGCGCATCTCTGGATGACGAATGAATACGAACCG
ACTATCGCCGCCGTCCCCGTGGAGATGTTAGACAAGCTGGAGCCAGCACAAATCTTCCAC
GAAATCGTCGACCACCGCTGGTTCCTCGCCCAAGAAAGGGGAGGGGCTGTCACCCTCCCA
GAGGCCACGGCATCCTATCTTGAATCCGTGCTTCCGGCCCGCCGCGACGAGGCTCGCCTC
CTCAGCACAAACCCTTCAGACGAAGACTTGTCA

>RXA02454-downstream
TAACCTCTCGCGTGCCCCAACGG

>RXA02457-upstream
CTGTAAAGCCACGTGAGCTGTTGCTTAGACTTTACTCTACCCCCGCGTGTCCACCACATC
AGTTAGAACATATGTACCACTTCAAATCTAGGGGGAAACA

>RXA02457
ATGTTCTACTTCACCGTCAATAATCCGCAGGATCCTTTAAGCACCGAAATTGTTGAGACT
AATCGCCGTGACCTCGCATTTTGGCATCGATTACGCCCCAAAGATGACGATGATTTAGCC
ACAGCCATCAACAAAATATGCGTGCGCACAGGCTTATCCCGCAAACTGATCGCCGCTTGT
TTATTTAGCATCTGCTTCCTGCCGTACTTACCCAACTTCCACAAACTCGTCGAAAAGCTT
GGTCATCTCGACATGGCGCGCATCAACGCGATCACTAAAGCTGGCGAAAAAGTGCCAAGC
GAGAAGAGAGAGCTTTTCGACGCCTACCTCGTCGATTACCTGACGCCTCGAGCGGAGGCT
CAGTGCTTGCCCCAGGCAAGCTCAATTTCCGCAATGATGCGGAAATTTATCGCACAACAC
TGCCCCGACGACAAGGCCTCCTCAGCCACCAATGATGGCTCCATCCGCTACCGCAGAAAC
AACAAAGGCGGGATCAGTATCACCGTCGATGCCACCGCCAGCGAAGTAACAGAAATCAAA
GCTGCCCTGGAACAAATGTCCAAAGATAAGGACTGCACACCAGGCACTTCCCTACTCCAC
ATCATTCGTGGCCTGCCGACAAAAGTCGTACTCAACACCTACGGCACCAAAGACAGCCCT
GAATACTTAGAAGGAGGAACCTGGCTGTCAAAGGAACAGTCTGAGTTCTGGAAAACCCGA
ACCACGTCCAGTCGGGATATGGACGCCGCCCACTTCTCTTACACCACCGCCTACGCTCCA
ACCCGAGAAATGCGCGTCTACATCAAAGGTCTACGCACCACCTGTAGCGTCCCTGGCTGC
AGTGTAGCGGTCGAAAACTGCCAACTGGACCACATCATCCCCTGGGGTGAAGGAGGGCCG
ACAACACCGTGGAATATTCATCCCCTGTGTGTCTTCCACCACATCCAGAAGACTGAAGGG
AGGCTCCAGTGCTATCCACTACCGGACGGCACCGTCCTATTCCTAGTGGATGGAATACCG
GTGTTCTCCATCCCCGACGGGCCTTTATCTAAATCGAATAAAACCTGGGGGACAAAGTTC
GGCAAATACATGGAGCGTCGAATCGCCGCC

>RXA02457-downstream
TAATCCAGCAAGCCAGCGTGATC

>RXA02459-upstream
GGTGCGATCATTGGCCTCGCGGTTGATGGCGTTCAGGTTGAAGACATTAAGACCACTTCC
AAAACTTTCCCTGGTTTTGAAAATGTTTGGGAGGAGATGG

>RXA02459
TTGGCTAGACGCAGCTATGACGAATCCGATGTTCGTGTTCGCCCAGGTAAAGGTACCCGC
CCTCGTACGAAGGATCGGCCATCGCATGAGAATGCTCTAGTGGGCATGGTTGTGACGAAG
GATCGTGGTCGTTGGGGTGTTGTTCTCGATGGTCGTCAAGATGCCATTGTGACGATGCGT
GCCCGTGAGTTGGGGCGTACGGCTATCGAAGTGGGTGATCGTGTCGGAGTTGTCGGCGAT
ACGTCTGGCCGTCCGGGCTCGTTGGCTCGAATTGTCCGCCTTGAGGAGCGCACGAGTGTG
TTGCGTCGTACGGCTGATGACACGGACCCGTTTGAGCGGATTGTGGTGGCTAATGCGGAT
CAGTTGTTGATTGTTTCTGCTGTCGCCGATCCGCCGCCTCGGGCGGGTTTTGTGGAGCGT
GCTCTAATTGCTGCGTTTGTTGGTAATTTGCAGCCGGTGTTGTGTTTGACGAAGTCTGAT
TTGGCGGATCCTGCGGAGTTCGCTGCGGAGTTTGAGGCTTTGGAAGTGCCGGTTGTTGTT
TGTGGTGTTGATGATCCTCTTGATCCTGTTTTGGAGGTCGTGGAAGGCCATATTACGGCG
CTTATTGGGCAATCTGGTGTGGGTAAGTCGACGTTGGTTAATCGTTTGGTGCCGGAATGC
CGATCGTTAAACTGGTGTCGTGTCGGGGGTTGGCAAGGGTCGGCATACGTCGACGCAGTC
GGTCGCTCTTGCCAT

>RXA02459-downstream
TGATAATGGTTGGATTATCGAAA

>RXA02460-upstream
GCGCCGTCGAAGCCGGACTCGTAGGCGTCTACTACCAGCAATTTGACCGTGCAGTCGTCG
AAATCGTCGGACTGTTCGGGCTAGAAGGAGAATTCTAATC

>RXA02460
TTGCGCGTCTACATCCCAGCAACGTTTTCCACACTCCGCGGACTCAATGAATCCCGCGTC
ATCACAGCACGCTCCGGATACGGTTTCGCAGTCACCCCAGCACTCCTTGACTTCTACACC
GACGGTGACGAAGAAGAAATCGCACATGCAGCCTTCCAAGACGCCGCAGAAGCCTCCATC
CGACTCCTCGCAATCGGCGACGAAGAAACATTTCCCTACCGCAGAGTCGTCGTCTCAGTA
GATGTTGACGACTCCGTGGTGACCTACCAGCCTGAAAACGGCGAATCCGTAGTCAAACTC
AGCCCAGCGCACATCAACCTCGACGACGTGGCAGCAATCCACATCGACGTTGAAGCCTCC
GAAGCAGACACCAAAAAAGCTATCGAAGTCATCGACGAATCCGACCTCGGCGAAGAAGAC
GCCGAACTCACCGTCGGAGACGCCCAAGACAACTTCATGGCCTGGTACGACCCAGAAGAG
CTCCCCTTCCTAGTCGAGCTCCTC

>RXA02460-downstream
TAGATCACATATCCCACGCGTCG

>RXA02461-upstream
AGAAAATCTCAAGGCAAAAAACAAGCCACCCCAATCTGTGCGACAATCAAACCACAGACT
ACGACTATTATGTCACGAAGAAACCAAAGAAAGGGAAATA

>RXA02461
ATGCGCGGACTAATTGTTGACTACGCTGGAGTACTAGACGGAACCGATGAGGACCAGCGT
CGCTGGCGCAACCTGCTCGCCGCAGCAAAGAAAAATGGCGTCGGAACCGTGATCCTCAGC
AACGATCCAGGTGGGCTCGGCGCAGCGCCGATCCGGGAACTCGAAACAAACGGGGTAGTC
GATAAGGTGCTGCTGTCGGGAGAACTTGGCGTCGAAAAGCCAGAGGAAGCAGCTTTCCAG
GCCGCCGCAGACGCCATCGACCTGCCCATGCGTGACTGCGTGCTTGTCGACGACTCGATC
CTCAACGTGCGCGGCGCCGTCGAAGCCGGACTCGTAGGCGTCTACTACCAGCAATTTGAC
CGTGCAGTCGTCGAAATCGTCGGACTGTTCGGGCTAGAAGGAGAATTC

>RXA02461-downstream
TAATCTTGCGCGTCTACATCCCA

>RXA02464-upstream
ACAACCACATCCGGAATGCTCGATTACGTCCGCCATGACACGCAAAGATCTATTGGCTAT
CACCGAGGATTGCCCTGACGGATCTTCTTACTTGAGGTTC

>RXA02464
ATGGGCACAACACCAGACGATTCCCGAACTCCTGAAATCACCCAAGACATAGAAATAACC
GATGGCAGGATCGTTGCCATCGGTCAATCAGTGGCTGCGGTGTATACAAACGATCCTTCG
CCTCGAATCGTCTCCTACAACGATGATGGTGAACTAGTTGGAGAACAAGCAGTCGATGAG
GTTGAGTTCCCGGATCCGCCGTTTCAAAGCGCGACCGCTGATCTTCCACACCATATGAGT
TGGTTCAACGGAGACAGCCTCGTACTGTTCTCTCCCACTCAGCTCAATGTACGACAAAGC
TTCAATGATGCTTTAGGAACCGGCATTGCGTTGAACGGAAGTCTCCTCTACCCCACCGCT
GAGGGCATCACGGTAGCTAATTGGGACACCGGAGAGGTGCAGCGCACCATTCCGGTGGAC
CGTGCGGGCTACGACGGTGAAGTTGCGCTCGGCGTTGTAGGGCAGGTGATCGTCGAAAAG
CGTGGCTCTGAGATCGTTGCTCTAGGC

>RXA02464-downstream
TAGATCTCGTTGTTAGCCCAAAG

>RXA02465-upstream
CTGGTGCAATATAAAAGTTAACCAACCAGTCATCCAATATGTCGCCTAAGTAGTCTTCCC
AAAGTTAACAGCTAGAATCATGGCCGTGACTTCTCCGAAC

>RXA02465

ATGCCTGCATCAATTCGCTGGGGCGGCATCGTCGCCCTCATTCAATCCACCATCGGATTC
GGTTACGCCTTTTTCCTTATTTACAGGGAAGCTACGGGCGAGACGGATCCAAGCATCGTC
TACGAAACCGATAACGCCAACACGTGGGTTGGCTACGGTACCGCTGCATTCTTCATCATT
GTGTTCGGAACGGTTGTTGCAGGCGCAATCAACATGATGAAGGGGCATCGCTGGGGACGC
GGAGCTGTCGTCATGCTGAATATTATTTTGTTGCCGGCTGCGTATTACATGTTTATCGAA
GGCCGATTCTCCTGGGCGATCGTCACAGGAATCTCAGCTCTCTTCGTTTTGGGCGCACTG
TTTAATAAGCGCGCCGTCCTTTGGGCTAACAACGAGATC

>RXA02465-downstream
TAGCCTAGAGCAACGATCTCAGA

>RXA02466-upstream
CGAACCGCAAAGCGTTCCGCTGACGGAACTGCCGCCTGGCGGCAGCTACACCGAAACCGG
TGCTGGCACTTTCCGCCAGGTCGGCGCTGCTCTTCCTCGC

>RXA02466
GTGGGCGAGGGGCAGGAACAAACTTTTACGTACGTCATTGAGATTGAGGATGGCGTCAAC
ACGGCCGCTTATGGTGGCGACGATGCG

>RXA02467-upstream
GTGAACGTAGGTCTGGGGCTTTCAGAAGACACAACTTAGATACTATCGTTGCACGGTTAC
AATAGGGTCATTCCAATACAACGATTCTTTTAGGAGAGCT

>RXA02467
ATGGATATCAAGATCGGATTTGCCGATACTGCCCGTGAACTGGTCATTTCTTCTGCTTTG
CAGCAGGATGAGGCCGCTGCGAAGGTGTCGGAGGCTTTGGCTAATGATTCTGGCGTTTTA
GATTTGAGCGATGAAAAGGGTCGCCGTTACATTATTCGTAATAGCCGAATCGCTTATGTT
GAGGTCGGCACGAGTGCTCCTCGTACTGTCGGCTTCGCTGGCGCA

>RXA02467-downstream
TAGGGGCTTTTAGACACGTGTCG

>RXA02472-upstream
ATGATTCTCATAAGGCTATAAACAATGTAGTTAGGTTACACTAATGGTGTCCGGTTGTGA
ATAGTGCAGCGGACGGGGTTCCGCTGCGGAGGAGGTCATC

>RXA02472
ATGTCATTTGTTAACATCACGGCTCTTACGTTCCCTGCAGGGGCTGAAAAAGAAATCGAA
CAACGCTTCGCGGCTCGTAAGAAGGCTGTAGATACGGCCAAAGGATTCCAAGAATTTGAG
TTGTTGCGTCCACAATTTGGTGAGGATCGCTACTTCGTAGTTACTCGTTGGGATTCCCGC
GAAGACTATCAAGCATGGTCGGATGCCCGCCCTGCCGGTAACCATGCTGATGATGAACAA
CGTGGCATGAGCGTGGAAGTTCTTGGTTTCGATGTGGTTCCTTTGGAAGGC

>RXA02472-downstream
TAAAAGTCCTTGGCGTGGCATAG

>RXA02473-upstream
TGCAGTTATGATTAAACTAACTCCTAGCAGTGGCCAACTACATGTCTGGCTTAATAGCCT
ATGAACGCCTAAGCCTGGAGCCACAACAACCACATTCCGA

>RXA02473
ATGGTCGCAGAGTACCCTGACGGATCCTCGGAAATATTCCCGGTAACGTTAAATTTAATT
CCGGAAGATACCCTCGTTTATGACGCCGTCTACAAATTCAAAAGCATCCGAACTGGTTCC
GAAGATCAAATAACCCCATTTGTATCAAACCAACCTGATGTGCCTTTCCCTGCAGGAACA
TCGTTCACATTAACTGGATATTATGAAATTGATCAGCTGAGAAGTGCAGGATGGAAATTT
GAGCTTAATCCTGTAACAGGTGAACTTTCAGTCACAGTTCCTATCTCTGTAATTTACCCT
GATGGGTCTCGTGATAACACAATCGCGACCATGGAATCCGTAGGCCCTGATGATTCTGAG

CTTTTCAAACCAGACTTTGATTTAATCCCAATAAAATCAGGTGACTATATAGAGATAGGT
GTACTCGCACCAGGGCTTCCTGCTGGTACGGAATTCCATCTCGATTACTACGCACTTCCG
GATCGATTCTTTGACTTAGGCGGTTCTACAAGCCTTTCAGGCAACGGTAAGTTCTCTCTT
GGAGTTCCACTTACCTGGAATGATGATCTCCAGCTCCCGATCTCGATTACTTTTCCTGAC
GGAAGCCACACAGTTGAGAATTTGCATGTTGACGTAACCCCCGCAAACTTTGCTGGCAAC
CCCATTGACGAGCCTAAGGACGATGACAAGGATCATCCACAACCGGCTCCTAAACCAAGT
GGCAGCTCATTTGGTTCTAGC

>RXA02473-downstream
TAGTTCCTACTAAACAGTTCAAA

>RXA02475-upstream
TCGCTCATTGAGGACGGACTCGCGGAACAAAATGAGGCGGGTTATTTCCACCTGCCACGG
TAAACCACTGCGCGCCTGCAAAAAACAGTAGGTTTAAGTA

>RXA02475
ATGCTTGGTCTCTCTCGTCGTAAGTTTGCCATGCTCGCTGCCTTAACTGCGGGAATCGTT
GGCGTTGTTGCCACTGGTTGTAGTACGCCCGCAGAACCTGAAACGATCGATAATCCGGTG
TTCATTGGTATCTCCATCGATCCAATTAAAAACCTAAGTCCGAATCACGCTGCAAACCTC
TTCGCTTTATCTGCAGATGGCTCGGGAGGAATTTTCCAAGAACTCGCTCCCACATACTTT
CCGTCGATCCATCGATTAGGAAACGGATTCATCGCACCCGATAGAGATTCTTTGGTAGTT
GTCGACGCTTCTCTAAAGGAAGTTTATCGACACGAAGTGGCCAGGCTTGGTGTTGGAATG
CAAACTCAATCAGCTAGGTCTCCACTGCATAAATCAGTTGCCTTCTCCTTCAATGAAGGA
ACAGCTGAAGCCCCATATAGACACCGCATCGTCTCCGCAACTGAGAAAACATCAGCTTCC
GCAATGACAGATCAGCGGCACTTCGCGCTTACTGCATGCGATGACGGATCCACACGGTGG
GTCGAATATTCCCCTGACCGCGGAATGGAAGATCCAATGGGCCCCGGCTCAGCACGCATC
GTGACTCTCCAGGCCGACGGAGAACTCAGTGAAATTGACGTTGAGTGGAATTTCCCGGAT
CGGCCCTCCGCCCCAATTATTCTGTCTTGCGAAGATCCAAGCGCTTATATAGTTTCAGAA
GAAGACATCATCTATGTAAAAGACGAGGTAAGCCCTGCCGAATCCATAGGAAAATTACCT
GCATATGAAATTCCGGACCGCGCCCGATTCGATACAGTTTCCGGCGAAGACTACTTCGCT
TTTACGTCAACTGGGATGCTGACACGCATCAATATTCCCCAAGCAAAAATCGTCTACGCA
CAATCCATTGACCTCTACGGCAAGCATCCGGTTTCCATAACTTTCGATTCCGACCGTGCA
TACGTGGTTACTTCCGGGGATTCCGGGGAAAGCCTTCTTGAAATCGACTTGAATGATCCA
ACATGCACTTCAGATCAGCTCTCGCTCACTGGTTTCAACAAATTACTCACAGCTCGGAAA
CCTAAGCCAGAACCGTCGATCATCATCGAAACCATCTTGCCAATTGACCCAAACTACTCA
CTGGGTTGTAAGAGT

>RXA02475-downstream
TAGATTTTGGACGGAAGTGTGTA

>RXA02478-upstream
GACATCGTCGAAGCGCTCTCCAGCGGCAACATCGACGATTATCGCAGCGCCGTGCTCGCT
CACTACGCGCCGTTTCGCCGCATGATTTCCAACATGCTCG

>RXA02478
ATGCGCACTAGCCTCATTGCGCGCGGGTTGTACCGCATTCCCGCGCTGGTCTGGGATCAG
GGTCTTTTAACGCTTTTCGACGCCCGCCTCAGTGTTGACGACCTCCCCGCACCCATCGAC
GTGGTGTCAGCGCGATCCTCAGACGGCATCACCTGGACCACCCCAGAACCAGCAATCGTC
GAAACTGAACACCGCGGTGTGGGCGATGTCTGCCTTGTCACGGGCGATCTGTGCTTCCAC
GGATTGTCCAACCTCGCAGGATTTTTTGAGGATCCCACCGACCTTGAACCCCGGCTGGCG
CGCCGGGATGTGAGTGGGTGGACGTCGATAAGCATGGCCCACTATTTTGCGGATGTTGAT
GCCGCGTTCGCCTCGTCGGGGACGGGACTTGTCCTGGCGGATGGGCGGTGGATTCAGAGT
TTTGTGGTGCGGCGCGGGCGCGAGATTTCGCTTCGGATTCTGCGCAGCGATGGCCACATC
ACCGATATTGCCGGCGGTAACGAATCCGCGATGACGCAGCTGCCGAGCGGTCGGATTGTG
CTGCATTCCAGGGGGGGTGGGACACCGTCTGAGCAGTGTGTCCGATGATTTCGGGGAGACA
TTCACTCCGCTGGAGCCTGTGCCTGAACTAATCGACCCCGGCTGCAACGGCCACGTGTTC
TACTGGAAAGCGGCTGGAATGCTCGCCGCAACGCACCTGGCGGACCCTGATCTGCGACGC
CACTTGGTGGTTGATTTATCCAGCGACGAAGGAGCGACCTGGGCGCATCGCATCACCATC
GAGCGCGAAGAAGCCGCCTATTCAACCGCTGCGGAAATGCCCAACGGAGATGTTGCCGTG

GTGTGGGAAGCAGAGGGAACGCGCGCGATAAAATGCACGGTGATCAGCGTAAATGATATT
TCGCTGCGGATCGATGAGCCCATTTCCGATGCCATATCCCTCCGCCATGTGGTGATCAAC
GATGACCATGACGGCATCGAAGTCGCACTGCCTGACGCATCGCAATGGGGTGAAGGTGTA
TTCAAAATTGTGTCCAATCCAGACGCGAGCACCCAAAAAATCCGCACTCGAGGCAAGCCC
GCGCGACAGACCCTGGAAATTGGGGATGAATTGGTTTTTGATATCCGCAAGGGTGGAGAA
GTGGCTTACGGCGTCACGGTTCCTTATGATGGTCGCTCGTTGGGGAAGTTAAACAGGATT
TTGGAGTGGGGCTGTAGAGGCCGATTTGCGGTCCTT

>RXA02478-downstream
TAATTGCGG

>RXA02482-upstream
AAACGGTGGCGCCTTAATTGTTTTACGCGTGCTGACAGGAACCTTTTAGGTGATTAACCT
GGTTTGCAACTTTCCAACCTCAGCCGGATAAGGAACACTA

>RXA02482
GTGGGCGTGGCTAAATCAAAGAAATCTGCTTTACCTAAAGTCCTGCTCACCATCGTGGTG
ATCCTGCTCCTGCTCGTGCTGGTAGCAGAATTCGGGCTGCGCTTCATGATCGGAAAACAA
CTGAAAGATGAGTTCCAAGCTCAGGCTTCCTCACAAGGAATCTCTGCAACTGAAGAGCCC
TCCATCAGCTTCGGCGCATCCCCACTCCTGTTAGGCATCGCTCGGGGAAGCATCAATGAA
GTCACAATCGACACCCCCGACTCCGTATCCATCACTAACCAAGACGGTGTCCCCTCCATC
AGTGGCACACCAGAGTCAACTATCCAACTCCAAGGGCTTGATATCGGTGACCGCGACAAC
CCAGTCGCAGACCACCTCACCTTAACCACATTGGCAACCGACGATTTCATCCTGGCAACC
ATCCAACAGCAGATGGCCGAAGCAACCGGCGGGAACAGCACCTCCCAAGGATTCGCAGAA
CAGCTTATCCAGGAACTCATCAAAGTCACCGACATTACTTCCGATGCAGCTAATCAAACC
ATCGAAGTTGAATTCACCGACGGCGCCGCCCGAGCCTCACTGCACCCCATCGTAACGAAC
GGCCAACTCGGCTTTGAGATCGTAGATTCCCAACTCTTCGGATTCGGCCTCCCCGATGAA
ATCTCCCAAATGCTCACCGACGCACTGCAATCATCAATCAATGAAGTAGCCGGTGGCCTG
CAAATCCAAAGCCTCGAAGTTGTCGACGCTGGCATCAACGTCACCCTGACCGGAGACAAC
ATCAACATCCAGACCCTAGAAGCCGCACAG

>RXA02482-downstream
TAAAGAGCGCTTTCGCGTCTGTG

>RXA02483-upstream
CATGGGCCCTGCAATCGAGCCTAAGGTTGCCGACGCACTCGGCGAGCTCTTCGCAAACGA
AGGCGCTCTGACCGAAAAGTGGATCTCCGAGAACCTCTAA

>RXA02483
ATGGCTGATCACGCCCACAATCTGCGCGCCTCTTTCCGCAAGGGTGCAAACGGAAAGCAG
AAGCCAATCGGCGTGATCACCCGCGGCACCACCGGTGTGAACCGCCTACGGCGCTTCGAT
CGGTGGTGCTTTCATCATCCCAAAATACGTTCGCTTCTCGACGCCACTTCCCTGGCGTTA
GATGTCGGGTACGGCGCCAGCCACACAACCACCGTCGAATGGGGACGTTGGCTCCACCGC
CTCCAACCCGACATGGATGTCATCGGCCTAGAAATCAACCCCGAACGAGTCCTCGAACCC
CAAAACGGCGTGTCCTTTGAACTCGGCGGATTCGAACTTGCCGGCTACACCCCACAACTC
GTGCGCGCCTTCAACGTGCTGCGCCAATACGACGTGGACCAAGTCGAAGCCGCATGGGAA
ACCGTCACCTCCAGACTTGCCCCAGGCGGACTGTTTTTCGAAGGCACCTGCGATGAAATC
GGCAAACGCTGCACCTGGATCACACTTAACTCAGACGGCCCACAAGAACTCACCCTTGCA
TGGGATCCTTGGGGAATCTCCACCCCCTCCGATGTGGCCGAACGACTGCCCAAAATGCTC
ATCCACCGCAACATTCCTGGTGAAAAGATTCACGCACTGCTAGCAGCCGCTGATTTAGCC
TGGGACTACTGCGCCGGCTGGGAACCCCACGGACCGCGCGTGCGCTGGGAAAAAGCCCGC
GAGATGCTCATCGACCAAGGTTGGCCCATCGCAGTGTCCAGGCGACGCGTGGGCGATAGC
CTGCTGACTGTACCGTGGGAAACGGTGGCGCCT

>RXA02483-downstream
TAATTGTTTTACGCGTGCTGACA

>RXA02484-upstream

CGGCGAAAGTGACTTCCGAATCGAGTTCGACGCCGTCGATCGCGGCGATTTCCTGGGCTA
GCGATGAATCCAACACCCCACTAACGGTAGTCTTATCCTC

>RXA02484
ATGGCAACGCGTACAGAAAACACCATTACGATCAATCAGCCCGTCGGCAAGGTGCACCAA
GCACTGACCACCGAAGCCTACTGGGCATACATCGCAGAGAACCTCTCCCCCGAAGCTGGC
GAGGTCAACGAGTTCACCGCAGCTGACGGTGGCGCAACCGCAACCCTTTTTGAGGTCCTC
CCACTCGAGGTCCTCCCAGAGGCAGTTCGCGCAATGATCAGCCAGGCACTGAAGGTCAAG
CGAGTCCTCACGGTTCCTGCACTGACCAACAACGCCACAACCGTCGAGTACAACGCTGAC
GTCAAGGGCACCCCTGTTGATTTCAAGGGCACCATCGCCATCAACGGCGACGACGCAGCA
ACCACCTTCGACTACAGCAACGAAGTGTCCGTGAACATCCCATTCATGGGCCCTGCAATC
GAGCCTAAGGTTGCCGACGCACTCGGCGAGCTCTTCGCAAACGAAGGCGCTCTGACCGAA
AAGTGGATCTCCGAGAACCTC

>RXA02484-downstream
TAAATGGCTGATCACGCCCACAA

>RXA02486-upstream
TCCGACCTCGTCGCATTAGCCAAAGAAATCCGCGACGGAGTCCTCGAAACCTTCGGCGTC
ACCCTCGTCCCAGAACCCGTCTGGATTGGAATCAGCATCG

>RXA02486
ATGACTGAATTTTCCGACGTCCCTGGCACCGCCGCCCCACTGCACAGGGCGTTGGAAAAT
GCCGGATACTCCACTTTAGAATCCCTCGACGGTGTTCCCTACAAGACGTTGATTGCCCTG
CATGGTGTCGGAAAAACTGGCCTCGGCAGGATCCAGGCAGCATTGTTGGAACGTGGCCTT
TCCCTGGGGGAAGAAACAAAAGGCGCCACCATCACCCCAGGTCACACCGGTAAAGTGGCC
TCAGATATCAAAACTCACATCACTTCCGTGGATCCCGTCGCATACGTCGATGGTCTAGAG
GGGCGTCGGGTTGCTCACGGGCACCAATTGCTATCGATCTTCGGTCGCGTCACCGGCGCG
GAACCCAAAATGTGGGGACCCTCCATGATCGGATACGGCTCAGTCCACTACGTTTCCCAC
ACCGGAAGGGAAGGCGATTGGTTTCAGTGTGGTTTCAGCCCGGCGAAGTCCAAAATCTGC
CTGTATGGCCTGAAGGATTCGCCTCGCGGTGAGGAATTGCTGCAGAAACTTGGAAAATAC
ACCGAAGGCCGCGGATGCGTGTACATCAATAAACCGGAAGACATCGATTTGGATGTTTTA
GAGGCCATGATCAGCGAGTCATGGGCCGGCCAAGGC

>RXA02486-downstream
TAGGTTGCAAATCCCCACCACAA

>RXA02488
AAGCTGACTGCAACTGGTGTCGATGTCATGGGCACCTTCTACCCAGAAGGTGAAGCACTT
GCGCCAATCACTTTGAACCTCACCAACGAAGTTGTATGCGACGAGCCTGAAACCCCCGTT
GAGCCTGAGGTTCCTGTAGAGCCTGAGACTCCAGTAGATCCGGAAACCTCGGTCGACCCA
GAGACTCCAGTAGATCCGGAAACCTCGGTCGACCCAGAAAAGCCTGGCGATGACAACAAG
GATGACGGAAGCAACAGCAGCAGCAACGGCGATATCCTCGGAATCTTGGGCATCCTCGCA
GCGCTTGGTGGCGTTGGTGCACTTGTGTACAACTTCCTGGTAGCTAGCGGATTCCTTGCA
GCGTTTAAG

>RXA02488-downstream
TAAATGAATCGTTTTCCTAGTGC

>RXA02489-upstream
TATCCTCGGAATCTTGGGCATCCTCGCAGCGCTTGGTGGCGTTGGTGCACTTGTGTACAA
CTTCCTGGTAGCTAGCGGATTCCTTGCAGCGTTTAAGTAA

>RXA02489
ATGAATCGTTTTCCTAGTGCCTTATTAGCAGCCTCTGTCGCGGGGGCTGCGTTGGCCATT
CCAGCGACCTCTGCACATGCAGCAGAATCTATTTGTACATTCACCGGCGATGTTGGGTGG
AATGTGCGCGATTCTTTCAACAGTTATCTTTTGGGAAACATCGCAAATGGTAGTGCTTAT
AAATATAAGGGCGGGTTGGACGTTCGTGACGGCGTCCAGACCGACGGTAACGGCAAAACT

CCAGCACTGACCTGGCCAGTTGATTCGGTGACGTCTTCGAAGATTTCCACTTCCGGAGGC
GCGCACTGGACCGGACACAACCTGTACCCCGGTGATGACCTCGCGGAAGTCCCTAACAAT
TTCACGTTGGATCTTGATTTTTCCAACATCACTGTGGAGCTGAGTGGTTCTACAGGTCGG
TTGTTGGTGGATTACACATCTCGGGAATACATCAACACCCACACGTTGGGTGAGTTTCAA
ACTGGTGAACAGGCTGAGCTTGCCACGATTACTTTTGCCAAAGCTCCAGACCTCACCTCT
AATTCAGTCAACGTGACTGGCGATGTGGCATTGACTGCTGATGGTGTGGAAGTTTTCGGT
GGTTTCTACACGGCAGGGGAGGAG

>RXA02495-upstream
AAGGAGGAAAATTATCACCGTCTTAAAAACGGCTAAGGCTTTTCTAAATTCGCCGCTGCG
CACCATCACGTGGCGCAGCGTTGTGGCGAATAAACTCCGC

>RXA02495
ATGGCATTAACAGTGCTTTCGGTTGTGCTAGGAACCGCATTTTTGTGTGGCTCCCTCCTC
CTCACACATTCCCTTGAAAGAACATTTTCCTCCATCGTTGATGCCGGCGTGGAGGGCGTT
GACGTGGGCGTTATCGCGCAACAAAACAACCCCGACGGCGTACCTTTCTCCGTCATCGCC
GAAATTGAGCAGTATCCGGAAGTCCGCGCCGTCAACATCATCGGCGACGGCCCCGGCATG
CCCTCCGGCACCACCATGACCGGCCAATCCGCGCTGATCCTCACCGACTCCGACGGCAAT
CCCCTGCAAGCAGGCAGCTCCGGCACGCACCCGCTAGCCATTTATCCGCAGGGCGAGTGG
GTCTCGCCCGAGCCAACGCTTATCGACGGCCACTTCCCCACAAAACCCGACGAGGTAGTA
GTCAACGCTTCGGCCGCCAAACGTGGCGGGCTCTCCCTCGGTGATCACCTAACGATCGTC
ACACCCACCGAACGCATCGACGCCACCCTGTCTGGAACCTTCGAATCAAACACCGACGTC
GCAGGCTGGGTCGGAGTCGGATTCACCCCACAGCGCTACGTCGAACTGCTCACCAACGGC
ACCGACGCCAGCCAAATCACCATCGCAGTCAACGACGGCGCCGACCCCATGGCAGTCCGC
AACCGCATCGGCAAAAACCACCGGGACCTGCTGCCCCTGCTGCCCGAGCAAATCATCGAC
CAAACCACCGGCGACACCGACCGCCAACTGGAGTTCATGACCTACGTGCTCCTGGCATTC
GCCGCGATCGCACTGATTGTTGGCTCGTTCATCATTGCCAACACCTTCGCGATGATCGTC
GCCCAACGCACCGGCGAATTCGCCCTCCTCCGTTCCATTGGTGTCTCCACGTTCCAAATC
GGATTCTCCGTGATTATGGAAGCAGTATTCGTCGGACTTATCGGCGGTTTCATCGGCATC
GCAGTTGGCTTCGGAGTGGTCAATGCACTTGTCCAAGTGCTCAACCAATTCGGCGACACC
CTCTCCTCCATCGACATCACCTACAACGCCGGATCCTTCATCTTCCCTGTCCTCTTCGCC
GTCACTGCCACCGTACTAAGCTCCATATCGCCTGCTCACCGCGCCGGTAACCTCCCACCA
GTCCAAGCATTCGAATCCTCCGATGCACGCAGCGACGCCCTCGGAAGGATCCGCTTCCTC
GTCGCCGCCGTCATGCTCACCCTTGGAATCAGCCTGACGATCGCAGGTGCCGTGGTATCC
GCCATCAACGGAGATGAATTCAAAACAGAAACACGCCTCGCATTCATCGGCGCTGGACTT
CTCTTAGTGTTCTTCTCACTCTCCCTGTCCGGTCCCGCACTGATGGTGGCGACCTCTCAG
ACTCTTGGCGTGGCGATAATGTCGCCGTTCCGAGCCGTCGGCAAGCTCGCACAACGCAAC
ACCCTGCGCAATCCGCGACGCTCCGCAACCACCGCACTGGCCGTCACTTTGAGCGTTGGC
CTCGTCGCCTGCGTTGGAGTCATCGGCGCCACCACCCGCGCCAGCGTCTTCGGGTCCATG
GAATCCACCATCAAATCCCCATATGTCCTCGACAGCATCGGTGGCACCATGATCCCTGGA
CAACCCGCCGGCGGTTCAAGGTCACTGTCCATGTCCGCAGCCGTCGCACAGGAAATCGCA
CAAACCCGCGGAGTCGGCAAAGTGGGCACCCTCATGACCGGCAGCGTCCAAGTCAACGGA
TGGGACAACGAAAACACCACAATTTTCGACGGCGACCTCTCTCAGTTCCTCGACCTCGCA
GTCCGCTCCGGCGACGCCTTCGACGACGAAACCCCCGGCGTCATGATCTCCACCACCTAC
GCCGACCAATCCGACCTCGAAGTAGGCGACACCGTCACCGTCAACCCCTACGGATCCGAC
GACGGCATCCGCGTCCCCATCACCGGCATCTACGCAGAAACCAACCTCGTCGGACACCTC
ATGGTCAACGCAGCCGCCACCAACCGAGTCCTCACCTCCGCGGACACCTACCACCGGTCC
CAAATCTTCGTCAACGGCGACGGCTCCACCACCAACGAAGAACTCCGCGACATCCTCGTC
GACGCCGTAGCCCCCTTCCTCATCGTCCAAGTGAAATCCAAAGATGAATTCCGCGGAAGC
CTCGGCACCCAAATCAACCAATTGCTCGGCATCATCTACGGACTGCTCGCCCTGGCAGTG
ATCATCGCAGTCCTGGGAATCGTCAACACACTGTTCCTCTCCATCAGCGAACGCACCCGC
GAAATCGGAATCCTCCGCGCCACCGGCGTCCAACGAGGACAAATCCGCCGCATGATTACC
CTCGAATCCGTCATCCTCTCCATCCACGGCGCAATCCACGGACTCCTCCTAGGTACATTT
ATCGGCTGGGCAATCGTCAGTTGTCTCCGCACCCGAGGCATGGCACCCGTCGAATTCCCC
TGGACCCAAATCGGATTAATGCTCATCTCCGCAATCATCATCGGAGGCATAGCAGCCCTC
ATCCCAGCCAACCGAGCCTCCCGAATCTCCCCTTTGGAAGCAATCAAC

>RXA02495-downstream
TAACAGTCTGCATCGGCAACCTC

>RXA02496-upstream
CGGGACGCGCGTCTACTGCAACTAGGTGGACAGTATTGCTGCCCACATCTAATACACCTA
ATCTCACACCTAAAGGTTAGACGGTCTAGGGTGGCAAAGT

>RXA02496
GTGAATCGGTCAAATTCTTCTTCGGTATTTTTAGGTTTCCCCGAGTCTTCGCCAGCGGCG
GCATCGATTCGTGCTGGGGAGGAACTCCCTCTTGATTTCCCACGTGAATGGTATGAATTC
ACGGATCCAACTGATATTGAGCATGTATTTAGCATCGATTTAACGTGGCTTGAGTCTAAT
TGGAATTGCACCTTTGGTACCCCCGATTGTTTAGGTATTGATTCCGAAAACGCCGACGTG
GGTTGTTGCGGCCACGGTGCATTCTTAGCAGATGAGACAGATCGAGATCAGCTTTATGAT
GCCGTTGCTCAGATGCCCGCTAAGTATTGGCAGCTACGCCCCGCCTCCACGGACTCGTTT
TTAGCATCCGATGACGGCACCGACATTGAGCCGTGGCTGACATGGGATGAATTAGATGAT
GAAGACGGCAATCCCGAGCCCGCTTTGAAGACAACTGTGGTCAACGGCGCCTGTATTTTT
GCCAACAGGGCGGGTTGGGAAACAGGCGCGGGGTGTGCGCTGCATCAGTGGGGCGTGAAC
GCAAATGAGGATCTAACCGTCGTCAAGCCTGAAGTTTGTTGGCAGCTCCCGCTGCGCCGC
CTGGAGGCCTGGGAAGAGCGCCCCGACGGGCAAGAAATCTTGCGCACCACAATTACTGAA
TACAACCGGCGCGGCTGGGGCAACGGCGGCGAGGATTTCGACTGGTACTGCACCACCTCT
CCGCGCTGCCACACCAATGCCGAACCCATGTGGAAAACACAGGAAACAGAACTCCGTGCA
CTCATGGGACCAAACTCCTACGAGGTG

>RXA02496-downstream
TGACGTAAATATTTGGAAGCACG

>RXA02498-upstream
CAAGGTAGAAATTTGTCCGTGGGCACTTCGTGAAGGTGTGATCCTCACCAGGATCGACAA
AGGACTCGAGTAACATTTACCCGGAAAGGAGTTGGCGAAA

>RXA02498
ATGAGTGAAGAGAAACTCACAGTCGCTGAGCTGATGGCGCGTGCCGCGAAAGAGGGACGC
TCCACCGATGCTCCCCGACGACGCAGGCGCCGCAGCATCGAAGACGGTGGCGTATCCGTT
GCTGAGCTGACCGGCTCCATTCCTGCCGTTAAGGAAAAGCCCGCGGAGTCCAAGCACTCC
AGCGTGCCCATCGATGCACCAGCAGAACCTGAGGTTGTTGAGGCCCCCAAGCCTGAGCCC
GCCGAAGAAGTAGAAGTGGCTTCGGTGGAGGGCGACGTCGATAAGCAGGAAACCCCTGAG
CGTCCGGCGCCGAGCAACGAAGAAACCATGGTGCTGCGCATCGTGGATGAAAAAGATCCA
ATTAGCTTGACGACGGGCGCGTTCCCCGTGGTTCCGGCAGTTGCCGCCAAGCCGGCGCCC
GTAGTGCGCGCGGAGAAGGACGCCGATGTGGAGACTGCCGTAAAGGCAGATTTCGCAGAG
GTGGAAGTCGATAACACTGACACCACGCAGATGGCTGTGGTGGAAGAAGTTGACGAGGAG
CCAGAGCAAGAAAACAAAATGTCCGTATTCGCGATCATCATGATGGCGATCGTCGGAGTT
GTTCTCGGTGTCGTTGTATTCCTCGGCTTTGAAATGCTGTGGGAGCGCCTGAACAAGTGG
ATCGTCGCTGTTCTGGCAGTCGGCGTGACCTTGGGAATGGTGGGCATCATCCACGCTTTG
CGCACCTCACGTGATGGTTTCAGCATGGTTCTCGCAGGAATCGTGGGCCTGGTCATGACG
TTCGGGCCGCTGGCAATCGTCATG

>RXA02498-downstream
TAATTTGTCGTTTTGGGCCCCCG

>RXA02500-upstream
ACGCGGGTTAGATTTTTGCTCGCGATCCGAAAGTGCACTTCGGCAAAAAGTGCTGGCAGG
TTTTGTACGTACAACATCGATTTAAGCGAGGGAAACCGTA

>RXA02500
ATGGGTTCTGTCATCAAGAAGCGCCGCAAGCGCATGTCCAAGAAGAAGCACCGCAAGATG
CTGCGCCGTACTCGTGTCCAGCGTAGAAAATTGGGCAAG

>RXA02500-downstream
TAAGCCTTCAATTGAGCTTCAAA

>RXA02505-upstream
TCGGAAAGCAATCCGGAACATTCAGGTTGTAGACAATGTCATCAGTTCAGTTGACCGTCC
CATTAAGCGCACTGGTCGTTTGCGTATTCCGGGGGTCTTT

>RXA02505
GTGGCTGGCACTCATGCGTATGTCAATGAAACTCTTTCGGAAAATGAGTTCAGCATGTGC
CGAAAGAATGAACCTGGTTTGGTCATTGAGCTGGAGAACATCAGCATCGATCGCATTGTC
ATTTCCACACCAGATGCCCACCGCTATGCGGATGAGCTCATGGCGGCTGTT

>RXA02505-downstream
TAGAACTCAGTTTCCGTCAATAA

>RXA02506-upstream
CCTTTCCCTGAACTCTAAGCAATTGTGATCTATAGTACAAATGCATAAACATTAACCGTG
ATATCCATCTCTTGCATACCGGCCGAAAGGTTTAGCACAC

>RXA02506
ATGCACCTCAATCAGCTCGAATTTTTCATCGCAGTAGCCCAACACGGACAGATCAACCGC
GCCGCCGAAGAACTCCTCATTTCCCAACCCGCTCTCAGCCGACAGATCTCCGCACTTGAA
AAATCCGTCGGAGCTCCACTCTTCGAACGCCATTCCCGCGGTGTCTCCCTCACAAAGGCC
GGAGAAATCCTCCACGAAGAAGCCCTCCGAACGCTTAGCAGGATGCAATCGGTAGTCGAT
GAAATCCAATCCGGTGAGCACCTCATCACCAGCATCAACATCGGAGTTCCCCCTGGAATC
CCCATCGACTGGTTGCGCTGCCAACTCATCGATTTAGGCCCCGAGACCCGCATTTCACTG
ATCGAATCCCCCACCGATGATCAGCTAAAACTTCTTAAACAACGCGAACTCGACATCGCC
CTTTGTCGACGCCAAAGCGAGGCCTTTGCCACCACACTTGTCCACGAACAAGAACTGGGA
ATCGTCGTCCGAAAAAACTCCGAACTGCACCAAAAAGTCGCAGGAAAAGACAACGCCACA
CTCTTCGATCTTGAAGGGCTTCGAGTCCTCGCACACTCCCGCGGTGAAGTAAGAATTCAG
GAAGAAATCCTCAAAAACGCCATGCTCGCCGCAGGAGTTAATGCCACGTGGATCTTCCGA
AAATTTGGGCAATATAGCTCACTGATCGCAGACCTTGTCCAGGCCGATGTCGCACTCACA
ACAGAGGAATCCGCCCGCACCAACTTCCCCAGCTGGCAATGGGTCCCCATCGAAGGCGAA
GACGCCTCCGGAAATGACCTTGTTGTTCGCACCTGGATCACCTGGAACCCCCAACCCACC
CCCGCGGTGAAGGCCCTGATCCAGAAATTTATTGACGGAAAC

>RXA02506-downstream
TGAGTTCTAAACAGCCGCCATGA

>RXA02510-upstream
CCCGTCGATGAGGCAATCGCTGTGATTTCTTCCTGGATTGGTGACCGCATCAATGATCAG
CCGAGCGAGGACTCCATTGCAGCTCGCAGGTAGCCCTGAG

>RXA02510
ATGGACTCATCTGACAGCCACGTTGGTCAGGATGTATATGTTGATCAAGGTCTAGGGGAG
CCCGACAGACTGGAACGTCTGTGGGCGCCCTACCGGATGAGCTACATCAACACTCGATCT
GGCGGTAAGCAATCAACTACCGCCAAGCGGGACCCCTTCATTGAGGTTCCCAAAATGAGT
GATGAGGACGGCCTGATCGTTGCGCGGGGTGAGCTGGTGTATTGCGTACTCAACTTGTAT
CCCTACAACGCTGGACACATGATGGTGATCCCATTCCGTAAGGAAAAGAATCTAGAGGAT
TTGAGCTTGGCAGAATCTGCGGAGTTGATGCTCTTTACCCAAACGGCCATCAAGGCGCTG
AAGCAGGTGTCAAACCCTGATGCTGTCAATGTTGGTTTAAACCTTGGCAAAGCATCGGGT
GGCTCAGTGGGAGATCACCTTCATGTCCATGTGGTGCCTAGGTGGTCGGGTGATGCTAAT
TTCATGACTGTGATTGACGGTGTCAAAGTGCTACCGCAGACCCTGCGTCAAACCAGGGCC
ATGCTTGCGCAAGCATGGGGCACCATTGATGGGGCACCAGGCACTGTCGACCCAACGCTG
ACTTCAGCGATCCGTACCGCAGCACCGAAGGAGCAC

>RXA02510-downstream
TGATGCTGGGACTTCATGGACGT

>RXA02514
AACTCCCACAACCCAACCCCAGTAACCATCACGGTTACTGGCAAGGGTGAAGGCGTTACC

TCTTTCGGCGCAATCTCCATCGAGGTTGAAGCGGGCGCAGACGCTATCGTCGCACTGCAG
TACGTCGGATCCGGCACCCACGCTGACAACGTCGAATTCATCGTTGGCGACAACGCACGC
CTGACCGTCATCACGGACACCCACTGGAACGCTGACGCAGTTCACCTGAGCAACCAGCTT
GCACAGCTGGGACGCGACGCAACTCTACGCCACACCGTGGCAACCTTCGGTGGAGAAGTA
GTCCGCATCGTCCCACGCGTGCGTTTCACCGCACCAGGTGGCGACGCAGAAATGCTCGGC
GTCTACTTCGCAGATGATGGACAGTACTTCGAGCAGCGCCTGCTGGTTGACCACGCTGTA
CCAAACTGTCGCTCCAACGTCTTGTACAAGGGCGCACTTCAGGGTGACAAGAACTCTGAC
AAGCCAGATGCCCGTACCTGCTGGGTTGGCGATGTGCTCATCCGCTCAAACGCCCACGGC
ACTGACACCTACGAAGCTAACCGCTCACTCGTCCTCACCGAGGGTGCACGCGCAGACGCT
ATTCCAAACCTCGAGATTGAAACCGGCCAGATCGTTGGCGCAGGACACGCAGCAACCGTC
GGTCGTTTCGACGACGAGCACGTGTTCTACCTCCAGGCCCGTGGTATTCCTGCAGAGGAA
GCACGCCGCCTCATCGTCCGCGGTTTCTTCAACGAAGTGATCAACAAGGTCCCAGTTGAA
TCCATCCGCGGGGAATTGGACAACCGAGTCAGCTCGGAACTCGCAGTTCTTGGCATG

>RXA02514-downstream
TAATTAAGCCAAAGTAACTAAGC

>RXA02518-upstream
CGCGTGAAGTGCGCGCTGCTTGGGTGGAAGGCTTTCCAGGCGGCAACCGCTGACGCTGTT
GCGCACGCACATTAGCCCGCTGTATTAATTGGAGGAAACC

>RXA02518
ATGAGCGAGCACACCGAGAACACGACAGAGGTTGAAGACCAGAACGCTTCCACCTTTGAA
GCACAAAGCTCTGAGCGCCCAGAGCAGTCCGAGGCAGACCTGGCTAAGGCCAGCGATGTT
GAGGAGTACATGCGCGACGTTATTGACCCTGAACTGGGCATTAACGTTGTTGACCTGGGC
CTTGTCTACGATATTTACATCATCAACGGCAACGAAGCTCACATCGATATGACTCTGACT
TCACCAGCTTGCCCGCTGACTGACGTCATCGAAGATCAGGCACGCACCGCAATCGTCGGC
AACGGCATTGCAGAGAAGATGTCCCTGAACTGGGTATGGATGCCACCTTGGGGTCCACAC
ATGATTACCGAAGAGGGCCGCGCTCAGCTGCAGGCCCTAGGATTCGCGGTT

>RXA02518-downstream
TAAAAGGCTGCTTATCGACGCCA

>RXA02519-upstream
TGTTTTAAAACTTCATTCCAATTACCGAAAATGAATATAATTTGAGATTTAGCTCACACT
ATCCCCCTTCGGGTCACCACCAGACTCTGATGCGAGGTAA

>RXA02519
ATGTTCTCCGCTCCCTTGCGTAGAATGATGCGAGTGACGAAGGACGAGCAGATTCAACCC
AATTCGAACGCCCCTGAAAACAGAAAATGGTTTCCTCGGGCACCTCGTCCCCTACGCCAA
TTTCTCGACACTTTGCCGCGCATCGGCACCGCTGGTTCCAGATCAGCGACCCTCCACGTG
GAAGACGAGCAGAGCCCTTTAGGGGCAACGCTTTTCGACGTCGCGACCGGCGCGAGCTCC
ATCAACGACCGCGATACCGACGCCTCAGGGCTTGAGCCTGAAAAGATTCGCCGATTTGCA
TGGCTGCGCCTGATCGGCACCATGGGTGCGTTAATGATCGCGTTTGGTGCGCTGGGCGCG
GGTGCACTTCCGGTGGTGAATAATCCGTATGTGGATTTCCCTGGCGGAAACTTCATGAGC
CGAATGCTGCAGACCTCTTCCATGATCGTGCTCATCGGCGTGGGATTTTTGGTGCTGGCG
TGGGTGTTAATGGCACCGCTGGTGGGTATTCCTTTTAAACGCAGCGGAAACAGAACAGCC
AGCGTGAGTTTGTCCATGCTGCGCCGCACATTTGGCGCCTGGGTAGCGCCCATCATGCTC
ACCGCCCCACTGTTTACTCAAGACATTTATTCTTATCTGGCACAAGGCTCTGTGACCGCG
CAGGGAATGGATGCCTACGCCGGTGGACCGCTTGAACTATTGGGGCCCGATAATCATCTG
GCACGGTCCGTGCCCTTTATTTGGGCCCAGTCGCCCTCGCCCTACGGCCCTGTTGCGCTG
AGCATCGCGGCGTCGATAAGCGTTATTACTAATGACAGCATCGTTGGAGGCGTGCTGGCG
CACCGTATTGCGTCGCTGCTGGGCGTTGTGGCTGCAGGCTGGGCGATCACCATGCTGGCC
AGGCGCTGTCGGGTATCTGAAGAAGCGTCCTTTTACCTGGGCGTACTTAATCCGCTGCTG
ATTCTGCACCTGATCGGCGGTATTCACAACGAATCCATCCTGCTGGGATTTTTACTTGTT
GGCCTGGAACTCGGACTGCGTGGCACCGACCGGATTCAAACAGGGCTGTGGGGGCCTGCG
TGGACATATATTGCACTGAGTGGCGTATTGATTTCTTGCGCAGGCCTGGTCAAGGTGACC
GGCTTTATTGGGCTCGGTTTTGTGGGCATGGCCTTGGCCAGGGCGTTTCATGCACGTGGA
CATCGACACGTCGTTGCGATCGGCGTTGCAGGCCTCGTTCAAGTAGCAGCCCTGGTGATC

ACCGTGGTTGTTCTCAGTGTGATTACCGGAATCAGTTTGGGGTGGATCACAGGTCAAGGT
GGCGCTGCGACGATCCGAAGCTGGATGTCTATGACCACCAACATTGGCGTTATTTCTGGA
TTCATCGGAATGAATTTGGGGCTAGGCGACCACACCGCAGCCATGCTCGTTGTGACCCGT
GCAGCCGGAATCGCGGTAGCTGCCGCCTTCATGGTTCGTATGTTGTTTGCCACATATAGA
GGTCACATTCACGCTGTGGGCGGACTGGGCGTGGCGACTTTCGTCCTCGTTATCCTCTTC
CCCGTGGTGCATCCGTGGTACATGCTGTGGGCTATCGTGCCGCTAGCTTCCTGGGCAAAT
AGACTGTTCTTCCAGCTCGGAGTGATTGCCTACTCCACTGCCTTCAGTTTCTTTGTGCTG
CCTCGCGGGCTTGCACTTCCAGTCGGAACTGTCTTTTCCATCTACTTCGGCGCAGCGCTC
GGATTCAGCATTCTCCTATTAGTTGGATGGTGGAGTTTGAGGCGGAATCCAACCTTTGGT
TTACAC

>RXA02519-downstream
TGATCAACTGTGACTACTGATTT

>RXA02520-upstream
TTTGCGCTGGTAGGGGGGAAGGGATTGGACACGGGAATGGAATTAGGGAACACTTGTGTT
GTCTAAAGGTGAAAGCTAAATCAAGCAGGAGGTGACACCA

>RXA02520
GTGGGAGATGTTGTAAAAGGCAACGACGCGCACACCGGAGACGGTGATACGCGCCGAAAA
ATTCTTCTCATCCTGTTGGAACGTGCACCGGTGATCGCTTCAGATATTGCTGAACAGCTT
CAGCTTTCAACTGTGGGAGTGCGCAGGCACCTAGACAACTTGGTTGAAGAAAATCTGGCG
GAGGCGGCAAATCCGCGCCAGAACCCATATGAGCCCAAAATGCGCGGTAGGCCAGCAAAA
ACTTATCGGCTTACTGATAAAGGTCGCTCAATCTTCGGCCACGAATATGATTCCCTTGCT
GCGGCAGCTCTAGCCACTCTTCGAGAGGTCGGCGGAGATGATGCAGTAAGGCAATTTGCT
AGAAAGCGGATCGAAACAATTGTTGAGGGTATTACCCCAGCAGATGTCACAGATCAATCA
ATCGAAGATACAGCCAAATCTTTAGTTGAAGCTTTTAGTCGGCATGGTTATGCAGCAACT
GTCGATGCCACTCGAAACGGGTTGCAACTCTGCCAGCATCACTGTCCAATATCTACAGTC
GCCACGGAATTTCCGGAACTGTGTGAGGCAGAGCATCAAGCAGTCTCAGAACTTTTGGGG
CAGCACACGCAACCATTGGCAACAATCGCGGACGGCCACGGCATCTGCACAACAAATATT
GCATTGACACCCATCAAACACTCC

>RXA02520-downstream
TGATGAAAGGAGCGGATCATGAC

>RXA02521-upstream
GCACACGCAACCATTGGCAACAATCGCGGACGGCCACGGCATCTGCACAACAAATATTGC
ATTGACACCCATCAAACACTCCTGATGAAAGGAGCGGATC

>RXA02521
ATGACTTCGGCAACGACGAACCCAGGGGTTAACGAGCCCTTGACCGATGACCAGATCATT
GAATCCATCGGTCCGTACAACTATGGTTGGCACGACTCCGACGACGCTGGTGCATCCGCA
CAGCGTGGTCTCAGCGAGGATGTCGTACGCGACATCTCTGCGAAGAAGAGCGAGCCAGAA
TGGATGCTTCAGCAGCGCCTCAAGGCCCTGAGCATTTTTGATAAGAAGCCAGTTCCAACC
TGGGGTGCAGACCTTTCAGGCATTGACTTCGACAACATTAAATACTTCGTCCGCTCCACT
GAGAAGCAGGCACAGTCCTGGGAGGATCTCCCAGAAGACATCAAGAATACCTACGACAAG
CTGGGTATTCCTGAGGCCGAGAAGCAGCGCCTCGTTGCAGGTGTTGCAGCTCAGTACGAG
TCTGAGGTTGTCTACCACCAGATCCGCGAGGACCTGGAGGAAAAGGGAGTTATCTTCCTT
GACACCGATACCGCACTGAAAGAGCACCCTGAGATCTTCCAGGAGTACTTCGGCACCGTC
ATTCCAGCAGGCGACAACAAGTTCTCCGCACTGAACTCCGCTGTCTGGTCCGGTGGATCT
TTCATCTACGTGCCAAAGGGTGTCCACGTGGACATTCCTCTGCAGGCTTACTTCCGCATC
AACACCGAGAACATGGGTCAGTTCGAACGCACCCTGATCATCGTTGATGAGGATGCCTAC
GTTCACTACGTTGAGGGCTGTACCGCACCTATTTACAAGTCCGACTCCCTGCACTCCGCA
GTCGTTGAGATCATCGTGAAGAAGGGTGGACGCTGCCGCTACACCACCATTCAGAACTGG
TCCAACAACGTCTACAACCTGGTGACCAAGCGCACCAAGGTTGAAGAGGGCGGCACCATG
GAATGGGTCGATGGCAACATCGGCTCCAAGGTCACCATGAAGTACCCAGCTGTCTGGATG
ACTGGCCCACACGCAAAGGGCGAAGTTCTCTCCGTCGCTTTCGCAGGTGAGGGACAGTTC
CAGGACACCGGCGCCAAGATGACCCACATGGCTCCTTACACTTCCTCCAACATCGTGTCC
AAGTCTGTGGCACGTGGCGGTGGACGTGCGGCTTACCGTGGTCTGGTTCAGATCAACGCA

AACGCTCACCACTCAACCTCCAACGTTGAGTGTGACGCACTGCTGGTCGATGACATCTCC
CGTTCTGACACCTACCCATACAACGACATCCGTAACGATCACGTGTCACTCGGCCACGAG
GCAACTGTTTCCCAGGTTTCTGAAGAGCAGCTGTTCTACCTCATGAGCCGCGGACTTGCG
GAAGAAGAAGCAATGGCAATGATCGTTCGTGGCTTCGTTGAGCCAATCGCTAAGGAACTC
CCAATGGAGTACGCCCTTGAGCTCAACCGACTGATCGAACTGCAGATGGAAGGATCGGTG
GGC

>RXA02521-downstream
TAAGCCCAATGACTGAAGTAGCA

>RXA02524-upstream
GACGCGATCAGGCGCTCCTACGCACCCAGGCAATTAGGCCTGAGCTTATCGACGCATCCC
TCCTCGATTCCACCGACCTCAAAGTATTGGGACTGGACAA

>RXA02524
ATGACAGAGACCACACCTCAACCCCCAAAGCCAGAGCCCGAGCTCCCGAAATTTCTCAGC
AACCCAGAACGCGCCGACATCATTTTGTTCATCGCACTCATTGTGATGGGCATTTTCTCC
CTCTGCATGATCCCACTGCGCGCCTGGATGCTCACCCAACCTCTGGCCTACACCCTCATC
GTCGGTGGTTACACCAGTGCAGTCGTGGGCGGCGCGAACGCTTCGGTAGAAAACGGCATC
TGGTGGGTCTACTGGCTCTGCACCCTGATCGGCGCGCTGAAGTTCATGCCCGTCTATTGG
CTGATGGGTAAGCGCTGGGGCATGGAATTTATCGACATGTCCCTCCAATACATGCCCCGC
TTCCACCGCATGTTCAAAAAATCCGTCGACTCCGAATCCACCCGCCTCTACGCCTGGATC
ATCGGCCTCATTCCACTCGCATACCTCCCAGGACCAGTGCCGGGAACCATCCTTAACGCA
GTGGCTGGGCTGGTGAAAATCCCCTTCTGGATCATCATGGCCTGGAATGCGATCTGCGTA
CTATCGGTCAACGGACTATTCATGTGGCTGGGATACACCTTCGGCGAACAAGTCCTCGAC
ATCGTCAACGTGGTCAACCGCTACATGCTTTGGATAACCTTAGGATTGCTGGCGCTGATG
TTTTTCCGCGCACGGAAGCAATTTGCCAAG

>RXA02524-downstream
TAAATGGTTGAAAGGAATATGAC

>RXA02525-upstream
CGTGGTCAACCGCTACATGCTTTGGATAACCTTAGGATTGCTGGCGCTGATGTTTTTCCG
CGCACGGAAGCAATTTGCCAAGTAAATGGTTGAAAGGAAT

>RXA02525
ATGACCACCATGCGAGAAGTTTCAACCGACCTCAACATCCTCATCGTCCCCAGCGAATGG
GAAAAAGTACTAGAAAACCTACCAGCGACATTGAGTGAGTCCGGATTCGTAGCCTCTGAA
ATCCACTCCCAGATCGTCGACCTCACCTGCGAACCCGACAACATGCTTGTCACCCAGTTC
TCCCAGCTAGAGGGCCACCCACCAATTGTGGAAGTGCTCCACCGCCTAGTAATTAACGGC
TCCTCCGACCTGGAGCTTAAAGACCTCACCAAAAAGGTGGTGGGGGCGTTGCCTCAGGGG
ACCTACTGGTATGGAACTTCCCTTGAAGGTGCGACCGAACCTGGCGTTAACGCATCATGC
GCGTGGCAGCATCGGGGC

>RXA02525-downstream
TAGTTTTCCGCGTTTAGTCAGTT

>RXA02534-upstream
TTACCAGTAATCTATGCAGATTTACTGTCCGTTGGGGATCCGCGCCTATCGGAAGTTGCC
TACATTATAAAAACTCAGATTCAGGAATACACAGACCATG

>RXA02534
ATGAATTCACCGAACGCGGACATTATTTTAGTAGTTAACAAGCTGTCCAAGTTTATTGAT
ATCGAAAATATTATGCTCGTTGGAGCACGATGTAGAGACATTCACCAGCAAAAATATCGC
GATCAAACAGCGGGTAGAAGAACTAAGGATGTTGACTTCGCTTTAGCTTTAGAAAGCTGG
GACGACTTCAATCTATTAAAGCAACAATTCTCACCGACTGGTAACGCATGGCAAGGAATC
ACCATTGGAAATATTCCAGTAGATCTCGTGCCATTCGGAAATATTGAAAACCCACCCGGT
GAAGTCTTGTCCAGAAAAGGTCATCTACTTAATGTCGCTGGGTTCAAGGAAGTATTCGAG
CAAGCTGAGCTATATCCCCTAAATGATGCGATAGACATTAAGTTGTCTACAGTTCCCGGA

CTTACTGCGCTAAAGCTACATGCATGGCTCGACCGTAAAGAAAATAACATCAAAGATGCA
AGCGATCTAGCATTAATCTTGTCGTGGTACGAAGAGGATGTAGAAACTTTATGGAATCGC
TATTTTGCCCTGGAAAATCAAGGATACATAGGTGAACCAGAGGCAATGGCAGCTGAATTA
CTAGGACTTGACACTGGAAGAATACTCGGCCACAAGGAAACTCAAGCCCTCCTTGATCGA
TTTAATGAACAGTCTCCTCCTGAGCTAAACCAATTTGCTGAATCACTTGAAGCCCCTCCT
GAACACAGTCACCCATTAGAACGGCGTCGTATCCAGGTCGAGGCACTGTTAGGTGGACTT
AGAGATTCCCTCGGTTACGATGAA

>RXA02534-downstream
TAGCTTCCAATCCCGCATTGTTC

>RXA02537-upstream
ACCTCCATCTCAACAATCATCTTTCCGATATGCGCACTGTCAGCGAGCAGATGCTCAACA
TAGACGTCGATCTTGGCCACACACTGAATAAGTTGCACTG

>RXA02537
ATGCTCGCCCTCAAAAGTTCAGAATTAGAAGGCATAGCCACATCACTCACCGCCGTGGCG
GGTGCGCTCCACGAATCAAACACTGACCGGTTGCAGTCCTGGCAGCAGCTCGAAACGATG
ACCTCTGCCAGCTCCCTTATCCAGGGCTTTATCAAGCTTGTCGATTACAACCGACCCACA
GTGAATATCGTGGAACAAATGCACAAAACCGCATCCACGCTTTTCAACACCGCTGATTTC
CTACGCACTTTGGAAGGCTATGTTGATGTACTGGAAAAACAAGCCGATAAATCTATAACG
CTCACCGTCATGCTTCGATATATTGCCAGCTTGAGTAGCCTTTTAGACCTCATGTGTGCA
CGCGAGATCAACGCGTTGTGCACAGCGATTACTCCAGAACCATTGAAGCATCTGGGCGAT
TTTGGCACTCTACCGCCTCAGCAATCCACGAGTTTCATTTGG

>RXA02537-downstream
TGAATGCCCCACCAGAAATCCGT

>RXA02538-upstream
GCGAGATCAACGCGTTGTGCACAGCGATTACTCCAGAACCATTGAAGCATCTGGGCGATT
TTGGCACTCTACCGCCTCAGCAATCCACGAGTTTCATTTG

>RXA02538
GTGAATGCCCCACCAGAAATCCGTGCCTTAGCCGAAGCCCATCCCGATATGCAGATCCTA
GAAGCCGGCGATGGTTCATTGGTAGCATCGTTTGGGGATATTGATAGGGCTACGACCGTG
ACCACCATCGTGGCAGGTGTGGGTTCCTCCAACCCAGAAGGGTGGAATACATATGTTGAC
CGTGCCCGCACAGTATCTGCTTCCACCGGTTCCGCAACGGTGTTGTGGCTGGGATATCAA
GCACCCGCTTCGATTCCTGCTGCGGTATCCGGCGCGGCAGCGAATCGCGCTGCCGCGGAT
CTCCAGAGGTTTCAAGCGGCACTACAGTCCCGCAATCCCCACCAAAGAAAAGTAGTGATG
GGCTACAGCTACGGTTCCACAGTGGTGGGAAAAGCTGCGTCTTCCGGCGAGCTCAGTGCC
GATGCGTTGGTATTGGTTGGCAGTCCCGGCGCGGGTGTCTCGCACTCTTCCCAGCTTGGC
GCACCTGTGTATGCGGTAACAGGGTCTGCTGATCCCATCGGTTTTGCCGGCACCCAATAT
GACGGCATCCACGGCACTGATCCCACCGCTGCCCTATTCGGTGCAACAGTGTGGGATTCG
CCCTCAACGCATTCCGGTTATTGGAATGACCAGGAGTTCCTGGGCAATGTGGCGGAGGTG
GTTCGCGGCAAA

>RXA02538-downstream
TAGAAAAGCCGCCGCACACTGGA

>RXA02540-upstream
GCATATGCTGAAGCAGAAACTAATTCAGGTTTTGATCCCCGCGCTAACTGGGCGGGCCAG
AACCGCTAGACGTTCTCTTTGAGAAAGGAGGTGACGAAAC

>RXA02540
ATGGCATCCACACCGAAAAAATCCAACGATGAAGGTCAGTTTGACCGTGTCGATTTTCAA
GGGGAAGTCTTCGTTATCTCTGTCGCAGCCGAGCTTGCCGGCATGCATGCCCAAACTTTG
CGAACCTACGATCGCATGGGTTTGGTCACCCCGATACGCACTCGCGGAGGCGGTCGCCGT
TACTCCCGCGCTGACGTGGAATTACTCCGAGAAATTCAGCACCTCAGCCAGGAGGAAGGC

GTAAACCTCGCCGGAATCAAGGCGATCATCGAGCTCGGCGAAGAAAACCGAAACCTCAAA
GAATCCCTGCGTAAGGTCACAGCTGAGAATGAGCAGCTCAAAGATCAATTACGCAGCGGG
CGTCCGCGTGGCGAGCTGGTGCACGTGCCCCGCTCCACCGCGGTGGTCATGTGGGAACGC
CGCAAGGGGCGTTCCAAG

>RXA02540-downstream
TAAAAACATGCTTGTCGACGCCA

>RXA02544-upstream
CCAATCAGGGAAGATAAGAGCTGTTTTCAACAGGTCCCACTCAACTTTGACACCAAGTCT
CACGCAAAATTAACAGCCATAAACTTTAGAAGGACACCCT

>RXA02544
GTGTCCCACACCTGTGGCATAGTGATTTTTGTGAGCACAGAATCAGGAAACACCCCAAAA
AGGGATGATGCAAAAAGCACCATCCCTCCGAAAGATTTGCCTGACACCGTCTTAGACGCG
ATTGAAGGCAATTTTGAGCCACCGCTAAATACCCAGAAGTCGGCGGTTCCCCCTAATGCC
GAAGCAACTGTCGAGGCTGATTCTGAAGGAACTACCGACCGCTCTGTCATTTTGGGCAGG
GACGGCCGCTGGCTGTCCGGATGGGCATTGCGCTTCATCGTGCTGGTTATCGCCGGCGTC
ATTGCACTTCGTATGCTGGGCTTCATCTGGGTTGGCATCCTCCCAGTCGTCCTCGCACTT
CTAGTCTGCACCGTGCTATGGCCACCAGTGAAATGGCTGCGCGAGCATAAGATTCCCACG
GCGCTCGCCGTTGTCATCACAATTTTGGGTTTCTTCGCCCTCATCGGCGGAGTTTTTGCA
GCCATCGCGCCAAGCGTGTCTTCCCAGACAAAGCAAGTGGTAGACCAAGCAACTGTTGGT
ATCGAAGATCTAATGGATTGGGTTCAGGGCCCACCTTTTAACTTAGATATCTCACAGTTT
GAAGGCGCGCTCAATGACCTAACATCCATGCTGCAATCACAGTCTTCCACCATTGCTTCT
GGTGTGTTCTCTGGACTGTCAACGGCATCATCCATCGTTGTCACACTAGCAGTGATGCTG
GTGTTGACCTTCTTCTTCCTCAAAGACGGTCCTCGTTTCCTGCCATGGATGCGCGGCTTC
ACTGGTGAAAACGCAGGTTGGCACCTCACAGAAGTCCTGACCCGTACCTGGAATACCTTG
GCCGGATTCATCCGTGCTCAGGCATTGGTGTCCATGGTTGACGCAATATTCATTGGTATC
GGATTGCTGCTTCTTGGCGTCCCAATGGCCCTCGCGCTCGCGGTCATCACATTCTTCGCG
GGCTTCATCCCCATCGTCGGTGCGGTGTCTGCAGGCGCCCTGGCTGTCATCATCGCGCTA
GTTACCAACGGCGTGACCAATGCGCTTTTGGTACTTGTATTGATCCTGGCGGTTCAGCAG
ATCGAGGGCAATATCTTGTCCCCATTCCTGCAGTCCAAGGCTATGAACCTGCACGCAGCG
GTTGTTTTGCTATCCGTCACCGTCGGCTCCACCATGTTCGGCATCATCGGCGCATTCTTG
GCTGTTCCAGTAGCCGCGACGTTGGCTGTCTGGGTGCGCTACCACTCTGAAATGGTTGCT
TTGCGCGCCGGTGAGATCACCAGTGATGACATTGAGATCGCCACGACGAAAGGTTCCCCA
ACCAGCCTCAATGGCCAAGAAACCCTTGCTGCCATTCGAAGCAGATTCGCCATCCTTGGC
CGCAAGAAGCCGACATCTGCCACTGCAGAAAAAGCAGACTCAGAAAGC

>RXA02544-downstream
TAGCCAATAATGCTCACTCCCGA

>RXA02545-upstream
AAGAAATCGAGAAAGTAATTCGTGGGTGAAGTTGTTTCAGAGTTGTTTTTTTATTAAACAA
CTCAGCCTGTAACCTCTTGGTCGTTCTATGCTTGGTCACC

>RXA02545
ATGACTGAGACTCTTTTTGTATCCGCCACAACTGAGGAAGCGGTGTATCTTCCAGATGGA
ATCGACTTGCTGGTGACTGGCATCGGAACGACCGCAGCAACGATGATTTTGACTAAGGAG
TTGGCTACTCGGGAGGTGCTTCCTGCCCGAATTGTCAATATTGGTACGGCGGGAGCTTTG
GTGGATGGATTGGCTGGCGTATACGAGATCGAATACGTTCTGCAGCATGATTTCAGTAGC
GAGTTAATCGCTGAAATGACAGGAAAGCCATGCTCAAATGGTTCAACTTTGGCCACGAGT
GGGCACTTCCCAGTAGCGAGTTTGGCAACAGGAAACTCATTTATTGCAGATTCAGAAACC
CGCAACCACCTGGCCACCCGGGCCTCCCTCTGCGATATGGAGGGCGCGGCGCTGGTGGGC
GTCGCAAAGCATTTTGGTGTTCCGATTACGCTGCTGAAGCAGGTTAGTGACAGCGCGGAT
GAGGAGGCTTCGGGGTCGTGGTTTGATGCGGTCGATGCGGGCGCACGACAGTTGGCGGAG
GCTGTGAAGGAGTTTAAA

>RXA02545-downstream
TAACAAAAACCCGATGCCTGGCG

>RXA02546-upstream
GATTATGTCGGCTCCACCATCGTGGTCAGCTACACCGAAAAACCAAACGCCCAGGGCGCA
ATTCAGGGCAATTCCAGTTTCTCTAGGATCGAGAAATAAC

>RXA02546
ATGCCATTGTTTATCGACGACGCCCTCCACCGCAGCAAAAAATACTTCCACGCGCACTTA
AGCGAGCTGCTCCTCGGCGAATTTGCAGGCCTCAGCCTGCCCCTGCACCCACCGACGGCA
GCTAAAGCCGCCGCCGATATTGATGCCACGAGGGAATTTATCCGCCAATGGGAGGGGCGT
GATGATGTGGAATATGCCATTCGAAACTGGTCTCCTGTGGGCTTAGGTAAAACTGAAGTA
CCCGTTAGGCTGACGTTGAACACGACTGAGGAATTAGTTGTGTTTGCGCAGGTAGAGGAT
GAATGGTCTTCACTTCACGAGAGGTTTTCACAGCTGTCTGGTTTTACAGCGGAGGTGGTG
GCGAAACATGTGTCGCTGTGGCGTTCGCTGTCTAACGATGATCTCTCTAAGGCAGTGTTA
GTTGTGGATTGGTTTTTGAAACACCCTAACTCTGGCCTGCTGAAACGCGCCGTCGCAGTT
GAAGGCGTGCATACCAAATGGCTCGAAAACCACCGCGTACTCATTGAAACGTTAGTGGCC
GACAAACGTGGTGAACCTGGTCGTGCCGATCTTGGACTTGGTGACGCCGAAGCTCGCGTC
CGGCTCCGCTTCCATTCCGTAGATGCTCCCGCTGGGCTCACAGACATTGAAGTACCGCTT
TCCAACCTGTGTGAATTACAAGAACCGCAAGTAATTCTGATGGTGGAAAACCTCGATTCA
TTTCTCGCTTTACCCACTTGGCCGGGCGTAACAATTGCTTGGGGTGCGGGCTACCGTGCA
GTAGACATTGTTCGAGGACCCTACTTTTCTAATGGTCGGTTGCTGTACTGGGGTGACCTT
GACCTGGACGGTTTCAAAATTCTCGACGGCGTCCGCAGCCATGTTCCTCACACCGAATCC
GTGCTGATGAACTCTGAAACCGTCTCCCGCTGGCGCTACCTTGGCGTTGCCGACCGAGAA
TTCAAGGCAGAGAGCTTTGACAACCTTCATGATTTTGAATCTGACGCACTTGACCTACTC
ATTACAGACGGTGAGCTCCGCATTGAACAAGAACGCATCCGCCTCGATGTTGCTGTTGAA
GAAATCGAGAAAGTAATTCGTGGG

>RXA02546-downstream
TGAAGTTGTTTCAGAGTTGTTTT

>RXA02549
ACCCTCACTGCAATCTCCTCCGAAACTTGGCCTATCATGCTCGCGCCATGGGTATGTCTG
CCTCTGCTTTCGCGAAATGTGGATGCACGGGCCATCGCGTTGTCCTTACTTCCCGCGGCA
TGCATGGGTGCAGTTAATGCCACCGCCACGATGGCAGCACTCATCCCGGCAGCGCTGATC
TTGCTGTATAGAGGGCTCTTCTTAAGGCTGCTTCTGTGGGGAATGGGCGTTCTCGCTGTT
AATTCATGGTGGATCGGACCTTTGTTGGTGCTTGGCAAATACGCCCCGCCCTTCACCGAA
TTCATCGAAAGTTCCTCCGTCACCACTTCCTGGCTCAACCCAGTAGAAATACTCCGCGGA
ACCACCAGTTGGACACCCTTCGTAGACACTGAACGACAAGCCGGATATCTCCTGGTCAAC
GATGCTCTCTTTGTCACCCTCAGCGTTCTCGTCGCAGCCCTCGGCTTGATCGGCCTCACC
TTGATGAAACACCGTGGACTGTGGGCATTCATGCTGGCCATCGGACTCCTCATCCTCGGC
AGCGCCCACCTAACGGCTGTTCAAGAATTCCTCGACGGCCCAGGCGCAGCACTTCGAAAC
ATCCACAAATTTGATCTATTAGTCCGCATGCCGTTGATGGTGGGCGTTGCCGCATTGGGG
TCGCATATCAGTCTGCCCTTGCTTGGGACGACTGCATTGACCAGCGGACAAGGCAAACAC
CACACCATCCCGCTGCCTCTCCAAAAACGCCAAGCCGCAGGACTCCTCGTGGTGATCATC
GCTGTCGGTGCTCTTGCTCCCGCATGGTCGGCACGGCTGCTACCTCAGGGAACGTGGGAT
GAAGTGCCTGACTACTGGTACGAAGCCACAGAATTCCTCAACCAAAACGCCACAGGCACC
CGCACGTTGATTTGGCCTAGCTCGCCGTTTGCCCGCCAGGACTGGGGATGGACTCGGGAT
GAACCAGCTCAACCACTTCTTGATGTTCCGTGGGCTGTCCGCGATGCCATTCCTTTGGTT
CCCCCGGAGGCGATTCGCGGATTAGATGGTCTCGACGACCTAGGCACTCTAGGCACCGGT
CTAAACGACGAGGCTTTAAAACGTCTAGGCATCGGCGCAGTACTGGTGAGGCATGATCTG
GAAGCCGACCCAGATATTGAGGTGGATCTGCCTGGGGAAAAGCACACTTTTGGCTCCCAA
GGCCAAGTAGACGTCTACCTCACCGACCCCGACCGCAATATGTGGATCACTTCCGGCACA
TCCAAGCAGCTGCCCACCGTCGCTGGCGGCGGCGAAATCCTCTCGCTCCTAGACACCATC
AACGGC

>RXA02552-upstream
TCCTTAAATACCCACTGTCCTCTATTCTGGGTTAGGCTTCACTGGGTAAAAGTGCCTGCC
TATGCCTGAAACTTGAGCATGGCAACAGCAAGGAGACACC

>RXA02552
GTGGGAAAACATGCAGCTGAAACATCGGAACCGAAGAAAAATTCACCGTGGCGCATTGGT
TTGTTGACGTTTTTGATTTCTTCAGTTGTCGTGACGCTGGTGGGCATGGTGATGCTGTGG
CCGGATTCTGATGATGTGGTGTTGGCGGATAACTTTTCGCAGACGTTTGCGGGAAATCAT
GAGCAGGTGGATGGAACGATCACGCTCGTTGATAATTCTGCGTGTAATTCGCCAGACACC
GGCCGAGTTTTTGCGGAAAGCCCCACGATTTCTGCGGAGCCGGCAACGTTGGAGTGCGTG
CGTGCACTCGTAGACATCACATCGGGTGCCAATGAGGGGCAGAAAACTCAGCTGATCACT
TACGCGCAACCTGGTGATCCGGAGTTTTCCGAGGGCGACAAGATCCGCATGGTGGAAACA
CCGGATACAAATGGCGAGATCATCTACACCTTTGCTGATTACCAGCGCGGACCGGCGTTG
ATCATTTGGGGTGTGGTTCTCATTGTGGCGATGGGAGCTTTCGCGGCGTGGCGAGGTGTG
CGTGCGCTGGTTGGTTTGGTCGTCACCTTGGGAATTGTTGGTATTTTCTTGCTGCCAGGA
TTGGCCAGCGGGCACGATGCGATGTGGTTGGCGCTGGTGTGTGGCGCGGCGATCTTGTTG
ATTGTGGTGCCGATGGTTCACGGAATCAACTGGAAATCGGCAGCTGCGTTGGCGGGCACG
CTGGTGGCATTGTTGTTGTCGGCGGTGTTGTCGTGGGCGTCGATCGTCACCACTGAATTT
GCGCGGACTGGGCGA

>RXA02552-downstream
TGAGAATCATCTGAAGATCATCA

>RXA02554-upstream
GCTTTTGAAGTGTGTCGCGTGTGCGGACTGAAATAGTTTCCGCTTCAACTTGGTTGCTAA
GGATAGGCTCCATAAAAATAACCAAAGGCGGAAAATTTCA

>RXA02554
ATGTCACACACTAAGCCATCCATTGCCATCCTCGGTGCTGGCCGAGTGGGTTCTTCACTT
GCCAGGTCAGCGGTCGCCGCAGGCTATGAGGTAAAGGTTGCTGGTTCAGGTGCTGTGGAC
AAAATCGCTCTTACCGCTGAGATCCTTATGCCCGGCGCGGTTCCAAGCACTGCTGACCAG
GCTGTAAAGGATGCAGATATTGTGTTCTTGGCTGTTCCCCTGCATAAATTCCGCAGTGTC
AATCCAGCCACTTTAGAGGGCAAGATCGTTATTGACACGATGAACCACTGGGTTCCGGTC
AATGGTGAGTTGGAGGAAATTGATCAGGATCCGCGCAGCACTTCGGAGATTATTGCGGAG
TTTTTCGCGGGATCAACCATGGTGAAGTCTTTTAACCACATTGGTTATCACGAGATTGAG
CAGGATGCGGGTACCGGGCGTGCGATTGCGTATGCCACGGATGATGTGGATGCAGGTGCC
CAGGTTGCACAGCTAATTAAGAGTTTTGGGTTTGTTCCTTTAAATATTGGCGCATTGGAA
AACGGCCGTATTCTGGAACCTGGCCAAGAAGCTTTCGGCGCGCACCTTAATAAAGATTCG
CGCCTAGAACTTGTTAATCAGCGG

>RXA02554-downstream
TAGTACCTCGATCTTCAGCCAAC

>RXA02555-upstream
GTTTTATCGCTATTTAATACAGGCCTACCCCCACTACCCCCATTCAGTTCAGGGAATCCC
CGGATTTAAAACAATTAAAAACCCTCTAGAATGAGACATT

>RXA02555
ATGGGCGAACAATTTCCAGGCGATAAAAACATCCGAGTCAGCGACACCGAAAGATCAGCA
GCACTAGCAGCACTCGGCCAGTTCTACGCAGAAGGTCGCCTCTCCCTAGAAGAAACCGAC
GACCGCTGCGAAGCCGTCGCCGACGCCAAAACCCGCGGCGACCTCAACGCCATCTTCTAC
GATCTGCCCAACCAACAAATCGCAGTCGTCGACCGCTCCGAACAAACCTACACAGCCACC
GAAGTTGCCGAACTCCACCGCAAAGGCGCACGCCCACGCGCCGGAATCCTCGGACTCACC
ACAGTTTTAGCCATCACCGGTACCGCTGCTTTCGCCAGCACCACAGCTTTTGCAACAGTA
CTTTTAGCCCTGATTCCGATCGTGTTCATCATGCTGTACGTGATGAAAATTGGTCCTGAA
TCCTGGCACGCACCAACACCTCGCCAACTTCAGCGAAAGCGCATGATCGAACTGCGTGAA
AAGGAAAAACTCCGCGACATGGAGCTCAAAGCCCAGCGCAAGGAACGCACCCACGCATTA
ACCAACCGCGCGTTGGATGCTGCTGAAACTGCTTTCAACACCAAGCCCTGGAAGAAGAAC
AAA

>RXA02555-downstream
TAGGGCTTTTGAAGTGTGTCGCG

>RXA02564-upstream
ACACCACAGTGAAGCGGTGACGTGAATCACCCAAGCACTTAGGCATCAAACATTCAAGAG
CTTGTTGTCCAAAAGTCCGACCGAGAGGGATTCCCCCAAA

>RXA02564
ATGGCCGAAGTAGGAGCAGAACCCGCAGGGTCTGCACAATCCAAAACTAAACAATTTGTT
GTAGGTACCGCAGCGGTGGTCATCACTGCAATCGCTGCGTTTTTCTCCATCCAGTCTGCA
TCCGGTGGCGAGGATATTCGTTCCAACATGACGCTGATTGCTCCTGCAGCTGCAGGTGGA
GGTTGGGATACTTTCCAACGTGAGCAGCAGCAGTCTATGCGCGTGAATAAGATCGTGAAC
AATATTCAGGTGGTCAACATCCCTGGAGCTGGTGGAACCATTGCACTTGGCAAACTGTCT
ACCATGACTGCACCGAACACCTTGATGGTGGGTGGAACGGGGCATATCGCAGCACAAATT
CAATTCGATACCCCTGCGAAAATCCAGGATGTCACCCCAATTGCTCGTGTGGTGGAAGAG
TTCGACATCATCACCGTGCCAGCGGATTCTCCATACAACACCCTTGAAGAGCTCATTGAA
GGTTGGAAGGCAGATCCAGCAGGAGTGTCCTGGACCGGTGGTGGTTCCTTTGACCAGCTT
GTTATGACAGAAATTGCACTGTCTGCAGGTATAGATCCTAAGCAAACCACCTTTATTCCT
TCTGATGGTGGTGGCGAAGCGATTCAGGCGCTACTGAACGGAACCGCAAAGGCATCAACT
GGTGGTTTTGCTGAT

>RXA02568
ATCCCGGCAGCACCTAGTGCCCCAGGCAGTGCAATTCCAACACCAGGCACAGCAATCCCT
GTGCCTGGAAGTGCAACTCCTGTCCCAGCACCTGGGGTTAGTGCACCTGGCGCAAGCGTT
CCAAGCATTCCAGTACCAGGATCTGTCACCCCACCTGCACCAGGAATTTCCGCACCTGGC
GGTGCACTTCCGACTCCTGGCAGTGCGCCCCCAACACCTGGCGGTGCCCTTCCGACTCCA
GGTGAGGCACTTCCCGTTCCCGGAGCACCTGGTGCACCCGGAGCATCCGGAATCCCAAGT
CCTGGCCTTCCAACCCCAGGTGTCCCAACTCCCGGAGCTTCCTTACCAGTCCCAGGAGCA
CCAGACGCACCTGGAACCCCAAGCATTCCCGCAGCTCCCGGCATTCAAGCACCAGGAATT
CCAGCAGCACCAGGAGCCCCTGCCCAAGCTGCTGCTCACGCAAAGCCAGTATTCCAAGAT
GCAGAGAAACGACCTCGCACAGATGAAGCTGGAAATGCGAAGAAGGAACTGCCGCTGAGA
GTTCGGTTGGCGCAGCCAATTACACGTAAGCAGTGGGCAATGACTCTTGGTGTCCTGGTT
CTCGGAGCAATTGTCGTGGCTGCAATCGCGGTGGTCCTTGCCAAATGGGCGTTTACCACG
GAGTGGTTGCAGGACTTCGTCGAGAAGTATCCGGGTAAATATGACAACCCCGAAGGTGCG
CCAGTAGGAATTCCAACGTGGCTGAGTTGGCAGCACTTCTTCAACATGTTCTTCATGGTG
TTGATTATCAAGACGGGCATTGAGATCAATAGAACCCGCAGGCCAAAGGGTTATTGGACG
CCGAAAAAGGGTGGCAAGAAGATCTCCTTGACGTTGTGGATCCACCTGGTTTTGGATTTG
TTGTGGATCATCAACGGTGCGGTGTTCATCATTTTGTTGTTCGCGACGGGTCAGTGGATG
CGCATTGTTCCAACCAGTTGGGATGTGTTCCCGAACGCGCTGAGTGCTGGTTTGCAGTAT
GTGTCGTTGGATTGGCCGACTGAGAATGGTTGGGCGAATTACAACAGTTTGCAGGAGCTG
ACGTACTTCTTCACTGTCTTTATTGCGGCACCGTTGTCGATTGTGTCTGGTTTCCGGATG
TCGAGTTACTGGCCTAAGAACAATGCGACGATGAATAAGTTGATCCCCATCGGGTTTGCT
CGTGCGCTGCACATGCCAGTGATGGTGTATTACATCGTGTTCATTTGTATCCACGTGTTC
TTGGTGTTGGCGACCGGCGCGTTGCGCAATTTCAACCATATGTATGCAGGTCAAGACGTT
GTGAACTGGGTTGGTTTTGGTTGGTTCGTGGCGTCGTTG

>RXA02569-upstream
AATCTTCAAATCGTTCCCGCAAGCAAAAGGTGACATACTGCTGGCTTGTTTTTGCATTCG
ACGATCTGCATGGGGATTACT

>RXA02569
ATGTCACGCTCATCTAAAATTTCGGTCGCGTTTGGTGGCCTACTCATCGCTGCTACCTGG
CTGTATTTGGTCTTGGTCAGGCCTACCGATTGGGAATCAGTGGGTGGTTCCACGGAAGCG
TTGATCACGTTGGTGGGCTATGTTGCCGGCACGATCGCGTTGTTGGTTGGTGTGCTGCCT
ACGCTTCCAGCCAGGACCATTGCGATCATTCCTGTGGCTTTGGTGCTCAATATTTTGTTA
GGCCAAGTCACTGGTTCTTTTGTCATTCCGCTGTATTTAGATGCGGTGGGCACAGTGCTG
GTCGCAGCTCTTGCTGGTCCTAGTGCTGGTTTGGCAACAGGTGCTTTAAGTTCTGTGGTG
TGGGCGTTGTTCAATCCGCTGGCTTTGCCGTTTGCTGCAGGTTCCGCGCTGACTGGTTGG
TTGACCGGTGTGGTGATTAAAAAGGGTGCGTTTAAGAATATCTTCGCCACCATCATCTCT
GGTGCGGTCATTGGTTTGATCACGGGTGCTGTCGCTGCCCCGGTTGCGGCGTTTGTTTAT
GGCGGAACCGCCGGTGTGGGAACTGGTGCGGTGGTTAGCCTCTTCCGCGAAATGGGTAAC

TCTTTGCTCGCATCGGTAACCTGGCAGTCGTTTATTTCCGATCCTTTGGATAAGGCCATT
GTTATGCTCATTGTGTTTGTGGTGGTCAAGTCGCTACCCAAGCGCACCACTAGGGCATTG
GTTCCGCAGCGGGTTCCGGAGGACGTCGCT

>RXA02569-downstream
TAAACATGAATCCTTTGACATGG

>RXA02570-upstream
CCATTGTTATGCTCATTGTGTTTGTGGTGGTCAAGTCGCTACCCAAGCGCACCACTAGGG
CATTGGTTCCGCAGCGGGTTCCGGAGGACGTCGCTTAAAC

>RXA02570
ATGAATCCTTTGACATGGATCATTGGCGCATTCAGCATGTGGATCGTGGTGCTGGGCGTT
AATAAGCTTGGTTTAAGCATCGCAGTGATCATCATCGCGCAGGTCGTGGCGATGATTCGG
GTGCGCAATGTATCTGTGTTGGCTTCAACAGCATTGTTATCGGTTCCTGCATTGGCCTCG
ATGGCGCTGATTCACATGCCGTATTCTTCCGACGGCTGGTTGATTGCTCTTACCTTGACG
GCTCGTTTTAGTGCGTTGATGTCTATTTTCCTCCTTGCAGCAACAGCGATTACTATTCCT
GAGCTGGTGAAATCCCTATATCGTTGGCCCAAGCTGGCGTATATCGTGGGTTCTGCATTG
CAGATGATTCCGCAGGGTAAACAGACCTTGGCGTTGGTTCGTGATGCCAATGCTTTGCGC
GGGCGCAGCGTTAAAGGTCCCGTGCGCGCGGTGAAATATGTGGGTTTGCCCCTGATTACA
CATTTACTTAGTGCAGGTGCCGCGCGAGCGATTCCCTTGGAGGTCGCAGGCCTGGACAGG
CCGGGGCCGCGTACGGTGTTGGTTGAGGTGGTGGAGGGGCGCGTCGAAAAGCATTGTCGC
TGGTTGTTGCCGCTTTTGGCAGTCGGGATGGCGTGGTGGCTC

>RXA02570-downstream
TAACTCAAATCGTCGGACCGTCC

>RXA02573-upstream
CTTCCACACGGCTCTAACTATAGGAAAAGACGGCAGCAAAGCATTAATCGTCGGTAGGCT
GAAGTGAAGTACTTTCCGAAAGATTCACAGGGAGCATGCA

>RXA02573
ATGACGAACAAAACCATGCTGGTTGCTTTTGATGGCTCACCGGAATCCCGGCGCGCTTTG
GAATATGCGGCGAAATTGTTGCAGCCGCGCACCGTGGAAATTTTAACTGCGTGGGAGCCA
TTGCATCGGCAAGCTGCGCGCTCGGTTTCGTTGATCACCTTGGGGGGTGGAACCCGAAGAC
CCCGCCCATTCCGCTGCACTAAAAACCTGCCAGGAAGGCGTAGAGCTAGCCCAATCTCTA
GGTCTGGAAGCGCGAGCCCACATGGTGGAATCCGCAACGGCCGTGTGGAGCGCCATCGTT
GATGCTGCTGACGAGCTCCGCCCCGACGTGATTGTCACCGGCACCCGCGGGATCTCCGGA
TGGAAATCCCTGTGGCAATCCTCCACCTCAGACAGCGTGCTCCACCACGCCGACGTACCA
GTTTTTGTCGTTCCACCCCTGGAC

>RXA02573-downstream
TAAAACCGAGACGAGAACCAAGA

>RXA02575-upstream
CCAATTGCTCTACATCACACGTCTCGAACAAAAGTGAAGTTACCAGTCCGTAACCCCTTC
TGAGTAGGAATTTCGCATCAGTGCAACTAGCCTTTCAGGT

>RXA02575
GTGAAGAACTCTGGGAAAAATTCGGCAAAGAATCGGACCAAAGGGATCCTAATCGGGGTT
CTCGTTGGTCTGATTGCCATTTTTGCAGGCATCTATGCGGTCGATGTTTTCCTCAACAAG
GACAACATCCCTCGTGGAACAACCGTCGGTGGCGTCAGTATTTCCAACCTCAGTGCACAA
GAAGCCCGCACAAAGTTGGAAACCGAACTGGCCAATGATGTGGTGCAGCCCGTCACCGTG
ACGGCAGGGGAGCAGAGCACCACTTTTGATCCAGTTGCCTCCGGCGTCGGCATCGATTGG
GACGCAACCATCGAAGGCACCGGCGAGCAGTCTTGGAACCCCATTACCCGCTTCGTGGCG
CTGTTCAAAGAATCCGAATCTCCCATCGTGAGCACCGTCGATCCCGCAGCCTTCGGCCCG
ACCCTTGATCGCATGGTCGGCGAACTCTATCGAGATCCCATTTCCGGAAACCTGCATATC
GACGCCGGCACCCTCGTGGTCAACGACACCATCGACGGACAAGCCGTAGACCGCACCATT

TTGGAACAAGCAGTCACAGAAAACTGGCTCAACCCAGAGGGCGTAAAAGCCGAGCCATAC
GTTGTTCCCGCTGCGATCAGCCAAGACACCATCGATAAACTTGCAGAAGGCGCCGGAGCT
AAAGCAGTATCTAGCCCTTTCGTCGTCCGAGGCGATGACGGAATTGAAGGCACCATCCCC
GTCGAGCGCATGGGTGAAGTGGTGAGTTTCCCAGAAGAAAACGGCACCATCCGCGTCGAC
ATCAATGCAGAAGCAGCAACAGCAATGCTGGCCGAAGGTCTCAAAGAAACAGAGATCGAG
CCCACCAACGCTCAAATCAGTTTCTCCTCAGGCTCCCGCGTAGTCACCCCAGAAGTCACC
GGACACGGAATCAACTGGGAAGAAACCCTGGCCGATCTGCCCAACAACCTCACCGGCGAT
GGCCCCCGCACCATCGACGCAATCTACGAGGACACCCCAGCAACATTCACCGCCACCGAC
GCCCAAAACGCTACCTTCAATGAGGTCATGGGCGAGTTCACCACCGGCGGCTTCTCTGCT
GCCTCCGGAACAAACATCCGCCTCACCGCGCAAATGGTCGACGGCGCAGTCGTTTCACCT
GGCGATACATTCTCCCTC

>RXA02576-upstream
CTTAGGCCTGTCGTTGCTTGCGATTGGTGTGTTCCTCACGGGAATTTTCAAGCGCGGCCA
GCTGATGAGCACTGTGAATAAACTCAGGAGTTAAATCCTT

>RXA02576
ATGACCCCGACCCGCCGTATCCTGCTGTGGGCATGGACGACTGTGCTTTTGGGTTCTTTG
CTGTGGCCGTTGGCTGCGCCTGGCGAGTTGTTGTTGCGGGATATGTCGGTGGTGGACCAT
CCTGCGTTGTCGTTGAATGCGTTGGGTTTTGGTGATTTGCCGTCGCGGAACGCCCCGCAG
GATGGTGTGCTGGCGTTGCTTGGCTTTTTGCCGGTGAGTTGGATCGTTCGAACCATGCTG
CTTGTGGCGGGTTTCGCGGGCGCGTGGGGTGCGATGCGCCTTGGGCCTTCCAAGTTTTTG
GCCGTTACCGTGGCGATTTACAATCCCTTCGTGGTGGAGCGTCTGCTGCAGGGCCATTGG
TCGTTGGTGATGGCGGTGTGGCTGTTCCCGCTGGTTGTGGCGCTGCGCAGGCATCCGCGT
TGGCAGGTTGTGGCGATCTGGGCGGCGTCGTTGACGCCCACGGGTGCGGTGGTTGCGGCG
GTCACGGGCGTGGCGAGTTCTAAAAGAAAACGCTTTACGACGCTATGTTCCTTCCTTTCG
TGGCTTCCTTGGCTAATACCTGCGCTTCTTGCCACCCCCACTTCGGGAGGTGCGCTGACC
TTCGCCATTCGTTCTGAAACATATGCAGGAACGTTGGGAACTGCGCTGGGCCTGGGTGGA
ATTTGGAACGCGGGGGCCGTGCCGGCCTCACGCGAACTGGGTTTCGCGGTTGCTGGAATT
TTGTTATTTGCGATTCTGCTGGCGGGTTTCAAAAACTGTCCGTGGGTTCTCGCACTGCTG
GCGGTCGTAGGTTTTATGGGGGCGATCGGTCCGTGGCTGATGCCGAATCTGTTCACGTGG
ACCATCGCATATGTTCCAGGCGCCGCGCTGTTTAGGGATTCTCAAAAACTCCTCATGCTG
GCTATCCCTGCCTATGTGTGTTTGGCCGCCGGGGTGAAAAGCCCACTGTCGTGGGTGGCT
ACCGGTTTGGCGTTGCTCCAGATTCCTGATGCACCACGTGAGGTTTCCGTGATACGCCCA
AGTTCAGCGCATGTGGAATCAGTGGAAGCACTGGCAGAAATCGCTGATGGCCGCGACATC
TTAATCATCGGCCAAGGCCCCTTGGTGACCCGCGAGGATGGGATCCCGGTTGTCGATCCC
AAAACCAAAGCCCTCTCCGTGGTGGAATCCGGCGAACTGCGTGTGGACGGAATCATCACC
GACGCGCCCTCACAGCGGTGGACCGAAGCAACGCAGGCATGGGCGGCCGGGGATATCGAG
CGCCTTGAAGAACTTGGCGTTGGTGTCGTGGTGGATGGAGATACGATCACAGAAACTGGC
GCACCACCGCAGCATGGCTGGAAATACTACCTCGGTGTGGGCCTGACCGTGCTGTGGATG
GCGTTGCCGCTGGGACTACTTTTTCGACGCAAGACCAAGAAG

>RXA02576-downstream
TAGTTCCTCGAACTGCGCTCCCG

>RXA02577-upstream
GGGGTCGACGGAGGTTTGGAATGCAACGTGGGTCGCCAAGACTCCCAGGGAGGCGATTGC
GCGTAGTCCCTCGAGTGAGCTGATGAATCCGCGATGGCGG

>RXA02577
ATGGGTGCATATGATTGGGTAGACATTATTTCAACATGCGAGTTTAGCGGAAAGGTGTGG
GCTGTTTTTATGAAGCGATCTGCAACGGTCCTCATTATTGCGGGCGTGCTGTTCCTCATT
TTTGCCTTCACGGTACCGCCGTATGTGACTGGTCAGGCGCGGACGATTCCGAAGGATTTG
GATCTGACGTTGGTGAGCGAAAGTCCGCAGGGGTTTGTGCGCACTGAACATATTGTGACT
GCTCCGACGGAAAAGGTCGATGAGATCGCGACGCATGTGGATCAGACAGTTACGGATGTG
CAGGGGAAAACTGTTGCGGAAATTTCGGATGATGTGGTGTTGATTGGACACTCTCGTTAT
CCGGTGATTAAGCCGACTGCCACCATTTCGGGTTCGCCGGCGGATAGTAGCAATGTGGTG
CGGGAGGGGTTGCATTACTTCTTCCCGGCTAATACGTTGCGGAATTCTTATCCCTATTAT
GACATCGTATTGGGTGAGGATTCCCCGGTGGATTATGTCTCGCGCGAGGGCAATACTTAT

ACCTTCTACCAGCATCTTCGTTATGTTCCATTGGATGATTCTCACACCTATTCGGTGGAG
CGGACCCTGAAAGTGGATCGTTTTTCCGGCATCATTGTGGCTAAAGATGAGGCGATGACG
TTTCATGGCCCAGACGGCGATGACACAGTAGAATTCACTTATACTGCGGATACGTTGAAG
CTTCTGCAGGATCATGCGCATGATATTGATCAGCGGTTGTCGTGGGCTAAGGGGTTTGAT
TTCTTTTCTAAATTCTTAGGCCTGTCGTTGCTTGCGATTGGTGTGTTCCTCACGGGAATT
TTCAAGCGCGGCCAGCTGATGAGCACTGTGAATAAACTCAGGAGT

>RXA02577-downstream
TAAATCCTTATGACCCCGACCCG

>RXA02584-upstream
GACTCAAGGCCAATGAATCCCTGGATGTGGAACAGGATACGATTAACTCAGACTCTAACC
GACAGTCCGCAATTGAAAGGCCAGATACGTGAACCGCTGG

>RXA02584
ATGTCCTTGCTGTGTGATTCCATCGCCATCGGTCTCTTCGCACTCTTCGCCCGCGTCGCC
CACCAAAGCGCCGACATGCCACTAAATGTGCAGGGCTGGTTTTTCACATGGCTGCCATTC
CTCGCAGGTGTGTTCATCGCCTACCTGGTGGCAATCCTCCCTGCGAAGCTTCCCAGCGAA
CGCATCCGCCCCGCTGGCCTGACCGTGTGGATACTCGCGGTAATTGTGGGACTTGTGATT
TGGGGCTTCAACAATGGTGGGGTTCCACACTGGTCCTTCATGATTGTCGCAACGACCGCC
TCCGCCATTTTGGTTCTCGGCTGGCGAGCGTTGTTTAAGGTGACAATGCGC

>RXA02584-downstream
TAAGTGCTTTTAAAAAATGGGAG

>RXA02585-upstream
GCGAGGATTTTTCAGCAACCCCTGGATTCGTTGGGCTTTGTCCCTGGCGTTTCTAGGGGT
GATCCTATTTTTCCTGAGGGATCAGCTGGATTTCCTCAAA

>RXA02585
ATGGGCATCCAACAAATCCGCCACGTCAGCCCCGTAGGCGTTGCCCTCACCATGGTGGCG
TTGGTGTTGTCATTCGTTGCGATGGCCAGAGTCATGCAGATCATGTTGAAAGCCGGAGGT
AGTCCTGCGACTCTCAAAGCCACCACGGCTTTAACTTTTGCGGCTAACTCCTGGTCCGCG
ACCCTTCCTGGCGGCCCGGCGTTTTCCGCGATTCTCACCTATAAAGTGCAGCGCAGCTGG
GGTGCCAGCGCCGTGCTGTGTTCGTGGTTTTTCCTGCTCTCCAGTGCCCTATCGACCGTC
TGGTTGGTTGCTCTCGGTGTCATCGCCGTGTTTTATATGGGCGCATCGCTGAACTTATGG
TCACTGATCGCCACATTCATCGCCATGGTCGGGCTGTCTGGCGCCGTTTATTGGGCAGCC
AACAACCCCGACTCCTTGGCTCGGTGGGTGCGAAAATTGACGAAAAACAGGGAGTGGGGC
TTCGTCGAAAAGCTTCTTGGAAGCATTGAGCAGCTGCGCTCGGTCTCGCTCACCGGGCCG
CAATTCGCGGCCAGCACCGCGTGGTCTTTAGGCAATAGGCTTTTCGACGCCATCTCCCTC
TGGATTTGCATCTGGGCGGTCACCGGCACTGCCCCGATGTTTGAACCAGAACCCAACAAC
ACCACCATCGCAGGCGTACTGTTGGCGTACACCACCGCAAAAATCGCAGGCTCAATCCAA
GCCACCCCAGGCGGAATCGGCCCCATCGAAGCCGCCTACATCGCAGCCCTCGTAGCCACC
GGTATGACCGCAGTGGAAGCCGCCGGAGCTGTCATAATCTACCGTTTATGCTCATTTATC
ATCATGGCGATTGTCGGATGGGTCATCTATTTTATCTATTTCACCCCCCAGGGACTCAAG
GCCAATGAATCCCTGGATGTGGAACAGGATACGATTAACTCAGACTCTAACCGACAGTCC
GCAATTGAAAGGCCAGATACG

>RXA02585-downstream
TGAACCGCTGGATGTCCTTGCTG

>RXA02588-upstream
CTCAGCTGACTGACCGTCAGGTCATCACCAAGTTTGAAGGCAAAGGCTTGGAAAAAGATC
ACGTGATCAATGAGTACTTGTGGCAGAAGGTGCAAAACTA

>RXA02588
ATGTCTGATGTGCATGAGGTCATTCATAGCTACAATCCCACTGACAAAGAAGGCCCTGAA
AGTGTCCTTCTAGTGTGGGACGCTCCCAACCTAGATATGGGTTTGGGCGCTATTTTGGGT
GGTCGCCCAACCGCTGCGTACCGACCTCGCTTTGATGCCATCGGTCGGTGGTTGCTTGCT

CGCGCAGGTCGCAGGGCACATGAGTTGGGCCGCCACATTGAGCCTGAGGCAACGGTGTTT
GCCAACATCACCCCAGGTGGCTCTGATGTTGTTCGACCTTGGGTGGAAGCGCTGCGTAAC
GTTGGTTTCGCGGTCTTCGCTAAGCCTAAGATCGGCGAGGATTCCGATGTCGATCCGGAC
ATGATTGATCACATTCGCAGGCGCTATGAAGAAGGCGTGCTGCGGGGTGTCATCGTGGCC
AGTGCAGATGGTCAGAACTTCCGTGAGACTCTCGAGGAGCTCGTTGCAGAGGGCATTCCT
GCCACGGTCATTGGTTTCCACGAGCACGCGTCATGGGCTGTAGCTCATGACACCATCGAG
TTTGTTGATCTGGAGGAAATCCCCGGCGTCTTCCGTGAGCCGCTTCCTCGCGTCAGCCTG
GATAACCTGCCAGACGGTGGCGCATGGCTGCAGCCGTTCCGCCCTCTGACTGCCTTGTTA
TCCAACCGCCACAATTCCCAGGAG

>RXA02588-downstream
TAATCCACCCGTGTTTTCTAAAT

>RXA02591-upstream
ATGTGTCCGTTGTCTCACCTAAAGTTTTAACTAGTTCTGTATCTGAAAGCTACGCTAGGG
GGCGAGAACTCTGTCGAATGACACAAAATCTGGAGAAGTA

>RXA02591
ATGACTACTGCTGCAATCAGGGGCCTTCAGGGCGAGGCGCCGACCAAGAATAAGGAACTG
CTGAACTGGATCGCAGACGCCGTCGAGCTCTTCCAGCCTGAGGCTGTTGTGTTCGTTGAT
GGATCCCAGGCTGAGTGGGATCGCATGGCGGAGGATCTTGTTGAAGCCGGTACCCTCATC
AAGCTCAACGAGGAAAAGCGTCCGAACAGCTACCTAGCTCGTTCCAACCCATCTGACGTT
GCGCGCGTTGAGTCCCGCACCTTCATCTGCTCCGAGAAGGAAGAAGATGCTGGCCCAACC
AACAACTGGGCTCCACCACAGGCAATGAAGGACGAAATGTCCAAGCATTACGCTGGTTCC
ATGAAGGGGCGCACCATGTACGTCGTGCCTTTCTGCATGGGTCCAATCAGCGATCCGGAC
CCTAAGCTTGGTGTGCAGCTCACTGACTCCGAGTACGTTGTCATGTCCATGCGCATCATG
ACCCGCATGGGTATTGAAGCGCTGGACAAGATCGGCGCGAACGGCAGCTTCGTCAGGTGC
CTCCACTCCGTTGGTGCTCCTTTGGAGCCAGGCCAGGAAGACGTTGCATGGCCTTGCAAC
GACACCAAGTACATCACCCAGTTCCCAGAGACCAAGGAAATTTGGTCCTACGGTTCCGGC
TACGGCGGAAACGCAATCCTGGCAAAGAAGTGCTACGCACTGCGTATCGCATCTGTCATG
GCTCGCGAAGAAGGATGGATGGCTGAGCACATGCTCATCCTGAAGCTGATCAACCCAGAG
GGCAAGGCGTACCACATCGCAGCAGCATTCCCATCTGCTTGTGGCAAGACCAACCTCGCC
ATGATCACTCCAACCATCCCAGGCTGGACCGCTCAGGTTGTTGGCGACGACATCGCTTGG
CTGAAGCTGCGCGAGGACGGCCTCTACGCAGTTAACCCAGAAAATGGTTTCTTCGGTGTT
GCTCCAGGCACCAACTACGCATCCAACCCAATCGCGATGAAGACCATGGAACCAGGCAAC
ACCCTGTTCACCAACGTGGCACTCACCGACGACGGCGACATCTGGTGGGAAGGCATGGAC
GGCGACGCCCCAGCTCACCTCATTGACTGGATGGGCAACGACTGGACCCCAGAGTCCGAC
GAAAACGCTGCTCACCCTAACTCCCGTTACTGCGTAGCAATCGACCAGTCCCCAGCAGCA
GCACCTGAGTTCAACGACTGGGAAGGCGTCAAGATCGACGCAATCCTCTTCGGTGGACGT
CGCGCAGACACCGTCCCACTGGTTACCCAGACCTACGACTGGGAGCACGGCACCATGGTT
GGTGCACTGCTCGCATCCGGTCAGACCGCAGCTTCCGCAGAAGCAAAGGTCGGCACACTC
CGCCACGACCCAATGGCAATGCTCCCATTCATTGGCTACAACGCTGGTGAATACCTGCAG
AACTGGATTGACATGGGTAACAAGGGTGGCGACAAGATGCCATCCATCTTCCTGGTCAAC
TGGTTCCGCCGTGGCGAAGATGGACGCTTCCTGTGGCCTGGCTTCGGCGACAACTCTCGC
GTTCTGAAGTGGGTCATCGACCGCATCGAAGGCCACGTTGGCGCAGACGAGACCGTTGTT
GGACACACCGCTAAGGCCGAAGACCTCGACCTCGACGGCCTCGACACCCCAATTGAGGAT
GTCAAGGAAGCACTGACCGCTCCTGCAGAGCAGTGGGCAAACGACGTTGAAGACAACGCC
GAGTACCTCACTTTCCTCGGACCACGTGTTCCTGCAGAGGTTCACAGCCAGTTCGATGCT
CTGAAGGCCCGCATTTCAGCAGCTCACGCT

>RXA02591-downstream
TAAAGTTCACGCTTAAGAACTGC

>RXA02593-upstream
TGACGATGACGCCCGCATCGGCGCCTCCCGCCTTGGACTCTAGCACCAGTTGAACGTCAT
TGCCGGGGGCTCTGGAGATTCCGGGGATTCCGGGGATTAT

>RXA02593
TTGAAGATTGCACACTTCGACCTAGACAACCCCGCCGACGAGTCCTCCTACATCTTCGCG

CGCAGCCTCGCAGAAGTAGACGGCTGGACCCTAGAATTCGGCGTCGCAGGAGTAAAAAAC
ACCACCATTGTTTCCTCCATCGACGATGCCATCACCACCATTTTGCGATGGATGAACGGC
GAAGACATCCGCGACCTCAACTGGACCCGCGCA

>RXA02593-downstream
TAAATGGCCTCATTTCCGGAGCT

>RXA02594-upstream
GCGTTCACTTCCGCCACCTTGAGGATGAGTGGTATCACGCCAGCACAACAAAAGGATCTT
CATAGGGTTATTCAGTCTAGCTGCTTTTAAACAAGCCATA

>RXA02594
ATGGAAGCCATGGCCACAACGATCACCGTTTTCTCTCCCACCCACTCCCCCGCACAAATC
CGCGAAACCATCCTCAGCGCCGCGAAAGAAGACGACGTGGACTTCCTCGGAGTCCCCTTT
ACCCACCCCAGAAACGTCACCATCGAAGTCGACGACGAACTGATCAACGACTGCTTAGGC
TGGCTCGACGACGTGGCACTCGCCTCCGGCCTGGGCATCCAATACAACGACGAAGTGCTC
CGCTACGGCGACGAAGACATTTCCTTTACCGTCCAAACCAAAAATGACGATGACGCCCGC
ATCGGCGCCTCCCGCCTTGGACTC

>RXA02594-downstream
TAGCACCAGTTGAACGTCATTGC

>RXA02598-upstream
CTTTGGGAAAGTACCCCCTATGACGGAAAACTGGATGGATCCTGTGGTTGAACCACAGTC
AACGGGAGAGGGGAAATCGGACACTATATGGTTGGAGATC

>RXA02598
GTGACAACTGACCAAAACAAAAGAAGTCTCAGTGAGCTTGCGGCCAGAATCGTTAGTGAA
ATCTGTGCACCGTGGGTACTCAACATCGGATTTTTCCTCATCCTGGGCGGCGTAACAGGC
GCCTGGACGCTAGGAATTGTGGCGGCAATCGGAACCGGAATCGTTCCGATGATCTTAATT
TTGGGCTTGATGAAGCTCGGCAGGGTAGGAAACCACCATGTGACGACCCGAAATCAGCGC
GGCCTTGTGTTTGTGGGCATCATTGTTTGTGTCATCATTTTGATTTTTATCCTCAGAGCC
CTTGAAGCACCTCAGCTGATTTGGGATGGCATGTTCTCAGCACTGATTTTCTTAGTTCTG
TTTGCACAAGTGACGTTGAAAATTAAAGCCTCAGTTCATGTTGGGCTGTGGGTGTGTTTA
GTGATGTTCCTCGGTCTGACGGTTTCTTCGTGGTGGTTACTCGGGTTGCTGTTTACCCCA
GTCACCGCGTGGGCACGTATGCGGATCAAGCATCATACGATGTCGGAGATTGTGGCGGGC
GTTGTTACAGGAGCAGTTGCAACCGGCATTTGTTATGCACTCCTACTTGCG

>RXA02598-downstream
TAAAGGAGAATTATGGATCAGCT

>RXA02600-upstream
GATTTTGCTTTTCGACGCACCGTTCGGCCGTTATCTAGATCTGGTCACAATGTCGGTTTT
TCATGGATTCATGTCCTTTATCGGACGTACTGTGGGGAGT

>RXA02600
ATGCAACCTTTTCCACTGTCCTTAACCAACAGCTCCGTCGCTGGTATTGCAGCGGGAGCG
TTGCTGTTTCTCTCCGTCCCTTTCGCATCGCCTGTTCACGCGCAAACCATACTGCAAGAC
ACCCTTGAAGTGACTGTGTTGGATAATGCCGACGAGCTCGCTCCAGAGGATGAGGATTTC
CTCAGCACGGAAACACCCAAGATTGATTTCCCTGACTCAGTTACCGCAGTCCGGTACATC
ACGCTCACGGACAACACTGACAAAATCAATGATGACGTTGAAAATTACCTGCGCGCCGAA
CACCCCGAGTGGATCCAAACAAACTCTTTCGCCCCTGGTGAAGTGATCATCGCAGTCGGT
TTCGACCCCAACACCATGGGTGCCTACGCGGGTAACGATGTGGCCGCAGAGACTGGGATC
GCAGAACAAGACCGCATCGACGGCACCACCGATGCGATGCGCCCATTACTCCAAGACGGT
CGCATTGCCCTAGGCATGTTGGAGGGTGCAAAATCGGTTGCTGATACCTCTGTCGTTCGG
GAAAGCTCAGCTCCAAGTGGTGGAGTAATCGCCGCTATTTTGGGTGGCATCGCTGCTCTC
GTGGCAATTATTGTCGCGTGGGCTACGAGTTACGCGAATAAGAAGAAGGCAGAAAAGGCT
CGTGAGCAGTTTGATTATGCATCACGCCATTATGGTGAGGTCGCCCAGCAACTCGACGGT

ATCAACGTGCGAGCGCACTCGCTAACTTCCCCACTGGCTGATGATGAGCTCCGCAGGCAA
TGGGACGATGTAAATTCTCGTTTTCTTGAAGTCAATGATATTTTTGGCAGGCTCGAAGGT
TTGACCTCGACCTCAGAAAACAAGGCATTTCGAAAAGCCTTGCCAGATATTGAAAAAGCT
CATACTGCCGTGACTCAAATGGAGATCGCACAGAAAAACATTGACACGCTCTACGATATG
GAGCACGGCCATGAAGACACCCGTCGCAGGGAATTAACTAGGCTGCGTGCCGATATGCAG
GAAGCCCGTCAAGATATCAACGATAAAGATGCAGTTGTTGACGATATTCTCCGCACGCTG
ATCCAGCGCACGGAAACTATCGCACCGTCCGCACCTGATTTCATGGACCAATACGCCCGC
TTGATCCGTGATTATGCCGTGGCGCTTCAAGGTGTGGAAAAGAACCTCGAGCAGGTTAAA
CAGACCACCGAGCGCAATGCTCCAGCCATCTACGACGACAATTGGCGCGTGGGCACTGGC
TACAACTCGTGGGTCCCGTACTACATGATCAGTTCTTGGCACGCAGCTGATGTCAGTGCT
GCATCGTCAGCTTCTTCCAGTTCAGCAAATACCACTTTCAGCAGTGGTTTCAGCGGCGCT
GGAGGAGGTTCCAGCTGG

>RXA02600-downstream
TAAACACCACCACTGAAGTCAAC

>RXA02601-upstream
CTCATACAATTGCCAGGATCTTCCATGGCGGATACGGCGCGTAAGTTCTGTGAATGCGGG
GTCCGGATACTACGCTTAGGCAAGATAAATTGTGAGTTCA

>RXA02601
ATGAAGGGTGAAGATACGTCAATGAGCGCAACAAACCTGGCGGTTGAGCAGCTACAGCGA
GTGCTCCTGCCGAGGCGCGGCGAGCCAGCAGATGTCAGGTCGTTGTACCTGTTGGAAGCA
GAAAGTAATAAGGAACGCCTGGAATGGGAAGATCGTTTTAGCGTTTCCGTCCCCGCTGGC
GCCGAGGTGTCTTTTCAGACCTACTTCAATGCATTTCCTGCAAGCTACTGGCGTCGCTGG
TCACAGCTAGATTCTGTCGTACTGAAACTGAAAGTTTCCGGCGAAGCGCGCGTCGACCTC
TACCGATCCAAGATCGATGGAGCACGCATCGGAATTACCGGTTCCGTAGTCAAAGATGAC
TTCATCGAATTTGAAGTTTCATTAGCCCCATTCGAAGACGGCGGCTGGATCTGGTTCGAC
CTCACCGCTGAAACCGACGCAACCGTCGAAGAAGCAGGCTGGTACGCTCCACACGCGCCA
AAAGCCCAGATCATGCCAGATGGATCTGAAGTCGGCCCATTTGAAGCCCGTGCAACCGTC
GGAATCCCGACCTTCAACCGCCCAGCTGATGCAGTTGCAGCACTGGAAGCACTTGCCTCC
GACCCAGCAGTTGACGCCGTCATTGATACCGTCATCATGCCTGATCAAGGCAACAAGCAC
CCTGCCGACGAGCCAGGTTACAAGGCAGCTGTTGAGCACTTCGGCGACCGCTTCTTCGAA
TTCCGCCAGGGCAACCTCGGCGGATCCGGCGGTTACTCCCGCATCATGTTCGAAGCCCTT
GGCGGAGTCGACGGCAAGGGCGAAGCAGGCGCTGCCAAGAGCCCATACATCCTGTACATG
GATGACGACATTGCTATTGAGCCAGACTCAGTGCTGCGTGCGCTTCAGGTAGCCCGCTAC
GCAAAATCCCCCATCCTCGTTGGCGGACAAATGCTCAACCTGCAAGAGCGCAGCCACCTT
CACACCATGGGCGAAGTAGTTGGCGGACACGACTTCATGTGGACCGCCGCACCACACGTG
CACTACGACCACGACTTCTCTGCACACCCACTACATGATCGCGGTAAATTCGACGACAAG
CCAGACGCACCAAACTCCCGCGACCTGCACCGCCGCATCGACGTTGACTTCAACGGCTGG
TGGATGTGCATGATCCCACGCGTTGTCGCCGAACAGATCGGCCAACCACTCCCACTCTTT
ATCAAGTGGGACGACGCCGAATACGGTCTACGCGCACGCAAAGCTGGATTCCCCACAGCA
ACCTGGCCAGGAATCGCAATCTGGCACATGGCCTGGTCCGACAAAGACGACGCCATCGAC
TGGCAGGCCTACTTCCACCTCCGCAACCGCCTCGTGGTTGCCGCGATGTACCACCAAGGC
AGCGTCGACGGCATTGTCCGATCGATGCAAAAAGCCACCTTCAAGCACCTGCTGTGCCTG
GAATACTCCACCGTGGCAATCCAAAACGAAGCAATGAAGGACTTCCTTGCAGGACCAGAT
CAGCTCTTCTCGATCCTGGACACCTCACTACCTCGAATTGCAGCGATTCGCAAAACCTAT
CCAGACGCCGTTGTGCTGCCAAGCGCCACCGAACTGCCACGAGCAACCGGCGCGCCGGGT
GTCCCAACCAAGGACATCGGTGGACGCCTGGCCCCAATCAAGAAGGCAATGTGGCTGGCT
AAGGGCCTGAAGCACTCCCTGTCTAAGGAAGATGCCTCCCACCACGAGGTGCCACAGGCC
AACTTCGCACCAATCGAAGCACGTTGGTTCAGCCTGTCCCGAGTCGATGGCGCAACAGTT
ACCACCGCGGATGGCCGCGGCGTGGTCTACCGCAAGCGCGACCGCGACAAAGCTAAAGAA
CTTGGCAAAGAAGCACGCGCACTGCAAAAGCAAGTAGCAGAGCGTTTCGACGAACTCAGT
CGCGCCTACCGCAACGCTCATCCTGAGCTTGTGAGCCGTGAAGCCTGGGGAAAGGTCTTC
GATGAGCAA

>RXA02601-downstream
TAAGGAAGTACAGATTCTGGTAG

>RXA02602-upstream
CTGCAAAAGCAAGTAGCAGAGCGTTTCGACGAACTCAGTCGCGCCTACCGCAACGCTCAT
CCTGAGCTTGTGAGCCGTGAAGCCTGGGGAAAGGTCTTCG

>RXA02602
ATGAGCAATAAGGAAGTACAGATTCTGGTAGCAATCCAGGATCAACTCATGGATGCCCCA
GGAGTACTGCCCACCGCACGAGGACTCAGCCTGCTCGGCGAACATGCTGCAGGCTGGCTG
GCACTCGGCGCTGGCGGTGCTGTTGTGGACAAAAAACGTCGCCGCTCCTGGGCTGGACTC
TTCATCGCTGCACTGGGAAGCCACGCAGCATCAGTGATCATCAAACGAGTTGTCCGCCGC
GCTCGGCCACATGACCCAGCCATCAGGATTGGTGTGGGCACCCCCTCAAAGCTAAGCTTT
CCTTCTTCACATGCGACCTCGACAACCGCAACTATGGTTTATCTTGCGCGCATCACCAAG
TCACCAGTGCCACTGCTAGGAATCCCCATCATGGTGCTATCACGCATGGTGCTTGGCGTG
CATTACCCAACCGATGTGCTAGCCGGCGCGTTGTTGGGAGCAGCGACCGCAGAGGCCGTC
CATAAGATCGAAAGGGCTACGAAG

>RXA02602-downstream
TGAGCGAACACGCCGCTGAACAT

>RXA02604-upstream
TCTGCATCGTGATGGCTGTGTACATCATGCCGATGTTTTGAATATTTACCAATGAACATG
CTCTGACCAGCATGTCCATTAACGTTTGAGGCCACATGCG

>RXA02604
GTGCTAGCATGTGGCCTCATGACGTTTAGCCCCCAGCGTCCGGAGTTTGAGACCGGTAAG
CAGCCAGATCCAGAAACTGAACACGCAGGTGACTTCTTTGAAGAAACCTCAAGCAGTGCT
CCTCGCGCCGCATCTAACGGTTCTTCTGGTCCGAACTACACCCTCATTACAACGTTTCTA
GCGGCCCTTACTGCTGGCATCTTTGCTTTCTGGGCAGGCTGGACCCGCAAATGGATCAGC
GACGACGGACTGATCGTCCTACGCACCGTCCGAAACCTCCTGGCTGGAAACGGGCCAGTA
TTCAACGCTGGCGAACGCGTCGAAGCCAACACATCTACTCTGTGGCAATACTGCATCTAT
CTGGTTGCCTTAGTAACTGACTATCGCCTCGAAGATATTGCTCTGTGGCTTGCGCTGCTG
TTCACCACCGCAGCGTCCATCATCGGTGTCCTGGGTACCGCGCATCTCCACCGCAAACGC
ATTGCCGTATTGCTTCCTGCAGGCGTGATCGGCTACTTCAGCCTTTCCCCGGCGCGAGAC
TTTGCCACTTCCGGATTGGAGTGGGGCCTATCTTTGATGTGGATTTCCATCCAATGGCTG
CTGCTGGTGTTGTGGGCGACTTCGGGCAAGACCTCGGGCAAGAAGGCTTCGGGCGCAAAA
ACTTCAAATCCTATCGTTAATGCCGGTGCAATAACCTATGCTTTGGCCTTTTGGTCAGGC
TTGAGCTGGCTGGTTCGCCCAGAACTGGCGATGTATGGCGGTTTGACTGGAGTGTTGCTG
CTGCTTACTGCGCCACGATGGCGGGTAGTTTTGGGGATCCTGGTGGCGGCTTTGCCTCTT
CCAGCTGCGTACCAAATCTTCCGCATGGGTTATTACGGGCTGATGGTGCCGCACACGGCT
GTAGCGAAATCAGCCTCAGATGCGGTGTGGGGGACTGGTTGGGAATATGTTGAGGATTTC
ACGGGGCCTTACAACCTGTGGCTCGGTTTGGCCTTGCTGTTGGCCGCAGGCGCGTTGACA
GTGTGGAAAACTGACAAGCACTTAGCGATACCGAAGGGGCGGCTGGGGCTGCGCACTCCG
GGTATGGCTATAGCGTTGCTGGTTATCTGTGCGCTCGTCCACTTCCTTTACGTTATCCGT
GTTGGTGGCGACTTCATGCATGGACGCATGCTGCTCCTTCCACTTTTTGCCATTCTGCTG
CCTGTTTCTGTCATTCCGGTCAATGTTGTTGATCGAGGTTGGCAGGATTTGGTTGCGCTG
GTTCTCGTTTTCTCTACGTGGGTGTGGTCCACTGTGGTTTTTGTGCAGGGGCACCAATGG
GAAAATACCGGCCAGCATGTGGTTGATGAGCGTGATTTTTGGATTGATTTCACCAACCGA
GATGAAGATCATCCTCCGCTTTATGCAGAGGATTTCCTCACTGTTGATTCCATGAATGAT
TACGCAGAGGTTATGCGCGATCAGACGTTGGTTAATCCAACAGGCCAGCAACTCAATATT
CTGGCCAGCAGTGACCCGACCACTTATTCGTGGATCACCACACCTCGCGTGGAGGGGGTT
GAAGCCGGTGATTTGGCTAACCTCTCGCCAACTGTTTTCCATGTGAACCTCGGCATGACC
TCCATGAACGCACCGCTCAACGTGCGTGTGACAGACCTGATTGGTTTGGCAACGCCACTG
GCAGCCCGCCAGCCACGCATTGAAGGTGGTCGAATCGGCCACGATAAATTGATGGACTTG
GAATGGCAGGTCGCGGAATCCGCCACTCCGCTGGCGTACACACCGGGTTGGTTGGATACT
CAAAAGACTTATGAGGCCCGCCAGGCGCTACGCCACCCAGAATTGGTTCACCTTTTCCAG
ACTTACCGTGAGCCAATGTCCTACCACCGGTTTGTGGACAATATTAAATACGCACTCACT
ACCGGAAGAACACTGGAAATTTCAGATAATCCTGAAGATCTTTTGAAAGAATTTAACCCG
ACCCCTGCAGAGATTCAGGACGGGTTAGAAACTATTGCTTGGCCTGGGGAAATTAAACTT
GATGAACCTCGCGGAGAACCTTTATATAGCTCTCAG

>RXA02604-downstream

TAAACACTTATTCGCAAATCATT

> >RXA02606-upstream
AGGGCGCGGATCACTTCGGATCTGTGGATAACTTTTAAGGCCCTTGTTTTCCCCTTGAAG
CTTCGGTTGTGTGGAAAACAGAAAAGGAGGGGAAAACAAA

>RXA02606
ATGCAAGAAATCCACACCATCATGAAACACATGGACGCGCTCATCGCCGACCCGTCCGCC
GCCGCATTCAAAGCAACACTCCCCTTCGCCGAACTCCTCGAAAAGCTCCACAACAAAAAA
GCGCTTTTCGACGCCGCCCTCGCCAAATCCGCCGAGCGCGCCGATGCCGGACGCATCATC
GGAAAAACCTCCCACATCGATGCCCTCGCGTACCTTCTCGACATCTCCAAATCCGAAGCA
TTCCGACGCACAAAACGCGCCGAAGAACACTACGGCAACCCAAGCCCGGAACCCAGTTCA
GAAGAACTCGCGAAAGAAACCCCCGAAGAGAAGCTAGCCAGAGAAGAAAAAGAGAAACAA
GACCTAGCCGAACAAGCAGAAGCCAACCGCATCGCCCGCGAACACGGCATCTCCGCCGAA
AAACAAGACACCATCCGCTACGAACTAGAAAAACTCAACGACAACACATCCCTATCCCGA
GCCTCACTCCGCAAACTAGCAATGCAGGAAGCCACCAGCCGAACCCCCGAAGACCTACGC
AACTGGACCCGCAACAAAGTTATCCGCATAAACCCCACCGCCAAAGACCCACTCGCCGCA
GTAAAGAAACGCTCCTTAAGCATCGGACGCCAAGACCACGACGGCGGAGCCAAAGCATCC
CTCTATTTAGATGCCAAAGGTCTAGCCCTGCTCAAATCACTGATGTCTAAAGCCAAGCCG
GGGCATTTGCTTGAAGACTCTTTGGCGGAGGATAAACGTACGAAACCGCAACGCCAATAC
GATGCCTTCGCCGACATCCTCCACCGCGCACACAGCGATCTCCTCCCCGCACGATCCGGA
GTGGGCACCATCCTCGTCTCCCTCTCCGCCAAAGACGTAACAAACCTCAAAGCATCGGGC
CCCGACCACCGCTACCCCACCAGCACCGGCATAAAACTCACACCGCTTGAGATCCTGCGA
CTCGGTGCAGCCAAATATGACTTCGTGACCGTCCTCGACTCCGAATCCGGCCGTCCGCTG
CACCTGGCACGCACTCAACGCACCGCCAGCCTGTATCAACGCCTAGCCCTCTTCGCCTCC
GAACTCGTCTGCACCCGCGAAGGCTGCGACTCCCCCTTCGAAGACAACGAAATACACCAC
ATCAGATCCTGGCTAGACGGCGGCCCCACAGACATAGAAAACATCACCAACATCTGCCCC
CACGACCACGGAAACAACAACGACCAACGCGACGGCAAAGACAACATGGGGCACATGAAC
ATAGATCCCACAACCGGGCGCGTCGGATATCAACCCGCCGACCGCCGAAAACCCATGCGG
TTTAACAACACCGCAGCCGCAGCAGAATCAGGAGGAGCACAGGCCAGGACC

>RXA02606-downstream
TAAGTTTTTAGCGCGCCAAAAAG

>RXA02609-upstream
GACCGAACGCAGCAGTCAGGCGTCGCAAAGCAATGGAAGCGGCGGAAGCACAGCCCGGGA
CGGGGCAGCCGAGGAAATCGACGGCCTGCCCGAGGTGACC

>RXA02609
GTGGAACGCAGCGCTGAGGCGCAAGCGTTCCTGGATGCGCTGAAAGATGAAAAAATCGAC
ATCTCCGGCGTGGAGGACCAGTTGATTGCGACTGCGCGAAATTACTGCAGTTCGGAAAAC
AAGGACCAAAACGTCACTGTCGATGCGGTTGCAGGCCAGCTCATCGTGCAGGGACGCACC
AGCGTGAAGGAAGATCAAGCAGCGGAAATTTCTACGCTGCTGAAGGAATCTGCGGATCGG
ACGTATTGT

>RXA02609-downstream
TAACCGATGAGGAAAACCATCAC

>RXA02610-upstream
CCAGCTCATCGTGCAGGGACGCACCAGCGTGAAGGAAGATCAAGCAGCGGAAATTTCTAC
GCTGCTGAAGGAATCTGCGGATCGGACGTATTGTTAACCG

>RXA02610
ATGAGGAAAACCATCACCGTTATTGCTGTATTGATCGTCCTCGCCTTAATCGGCGTGGGC
ATCGTGCAGTATGTGAACACATCCGATGACTCAGATTTCATTGGCCAGCCTGGCGAGCCA
ACCGGTACCGAAACCACGGAACCACCGGTTCAACCTGATTGGTGCCCTGCGGTAGAAGTC
ATTGCCGCGCCGGGTACGTGGGAGTCGGCTGCTAATGATGATCCGATCAACCCGACCGCT
AATCCGCTGTCATTCATGTTGAGCATCACTCAGCCACTGCAGGAGCGTTATTCTGCGGAT

GACGTCAAGGTGTGGACGCTGCCGTACACTGCGCAGTTCCGCAACATCAACTCGCAAAAT
GAGATGTCCTATGATGATTCGCGCAATGAAGGCACCGCGAAGATGAATGAGGAACTGATC
AACACTCACAATGAGTGCCCTGCCACGGAGTTCATCATCGTTGGTTTCTCCCAGGGTGCG
GTCATTGCGGGCGATGTGGCTGCTCAGATCGGTTCAGAGCAAGGTGTTATTCCAGCTGAC
AGCGTCAGGGGTGTCGCCCTGATCGCTGACGGTCGCCGGGAGCCTGGTGTGGGCCAGTTC
CCAGGCACGTTTGTGGATGGCATCGGCGCGGAGGTTACTCTGCAGCCTTTGAACTTGCTG
GTGCAGCCGATTGTTCCGGGCGCAACCATGCGTGGCGGGCGCGCGGGCGGTTTCGGTGTG
CTCAACGACCGGGTGCAGGATATTTGTGCTCCAAATGATGCGATCTGTGATGCTCCGGTG
AATGTCGGCAACGCCCTTGATCGTGCGTTGGCCATGGTCTCCGCCAACGGTGTGCACGCG
CTCTACGCCACCAATCCGGATGTTTTCCCAGGCACAACCACCAATGCGTGGGTTGTGGAT
TGGGCGACCAACCTCATCGACAACGGA

>RXA02610-downstream
TAAAGCTTTTTCGCTTTTCGACG

>RXA02617-upstream
CTCTTTAATTAACTTTTGGGCGACCCTTTACGGTCGTCCTCTTGCGTTCCCAAAACATAC
CCAGTAAGTTACTGGGTATCCAACTCTTGATTGGGGAACA

>RXA02617
ATGTCCATAAAACATGCACTCTTGGTGCTCATGCTCGACGAACCAACCTCGGCAAGTCAG
CTGCAAACCAAGTTTGAAGAAACAATGGGGATCTGGCAGCTCAATATCGGCCAAGTCACC
CAAACCATCCAGCGGCTACAGCGCGACGGCCTGGCGGAAACCGCAGGCACCACCGTCAGT
TCCAACGGCCGCACCGTAGATACTTTCCAGCCCACGGACTTAGGTCGCGAACTTGTCGCG
CAGTGGTTCGAAAGTCCCGTCACCGTCACACTGTCCGAACGCGATGAATTAGTCACCAAA
ATCGCCATCGCAGAATCACGTGGCCTCAATTTGATTCCACTTTTAGACATTCAACGCAAC
ACAGTCATGGCGGAACTACGCGCACTCAACAAATCCAGCCGCGATCTCGCCGAAACCAGA
AACACCCAGCGGCTCCTCGTCGAAAAGCGAATCTTTGAACTAGAAGCCCAGGCACGTTGG
CTCGACCGAATTGAAGCATTGGAGCAG

>RXA02617-downstream
TAAATGACAAACACGCCTTTCCC

>RXA02619-upstream
AGCGACTTCTCAAAGAACCACCCCACTCATTTCGAGTGCGGGTGGTTTTTTCTATGCCTA
ATTCTATGCCTAATTCTATGTCTGATTCTATTGGTGTCGC

>RXA02619
ATGCGCAGTGTAGTTTTAGAACTACTAGAGAACTGGAAGGAATCACTCGTGCTTCACCCC
TCATTGACTGAGCTAGCGGATGCTGCCCCACTTGCACAGGATTTTGCCACCGTCCGCGGT
GTGCTGAAGGAATCGCTGGATTTGTTGGGCAATGCACTGAACCACGGTGAAGAGCCCGCG
GAGCTTGCAGGGTGGCTGTCACAAGTTATTACTGATGTTTTGCACTCCCCTGGCTTGGAT
GCCCACGTGGTGCTCACCGGCCCCGTGGGGCGTGGAGACGCACTGCCTACCTCGCCCGTG
AGGTGGCTGGCGGTCGTCGATAGCCAAGAAGATCCGAATGAAAAGATTTCAGCGCTGTTA
ACTGAGGTGGGCTTCATTGCGGAGCCGATCGGTGCGGCAACTCGTGAGGAGTGGGAGCAG
CGTGCGCGCGCTGGTGAGGATCCAGAGGTCTATTTGGATGCTGGCACGTGGGTCGCGGCG
ATCGCTGAAGTAGATGACAAAGCACTGTTGCAGGATGCGTTGTCATCTAGGCCGCCTGCG
GTGGAAACTTATGAGGGTCTTCCTTCGTTGGACATGGTGGTAAACATTCGTGAGAACCTC
ATGATTCCCACGGTGAAGATCGCTCGCTGGGCAGCACACAAGGCTGGTTCTTTGGCGCCT
ACGACTGCGCAGCGCCTCGTGGATGCCCGTGGTGTGCTCACCAATGATGAAGTCGACGCG
CTGACACAGGTGTGGACTTCCGCACTGAGCTTGCAGTCGAAACGTTGGATGGATCACATC
CATGATCAAGAAACCACCGCTTGGGAGCTTCCCGCGCTGCAACGTGCCACTTTTGGCGCA
TCGGCTCGGTTGCTTTCTGAGGTGTTGCGGTCCGTTGAAGCCCGTGAAATCGATACCAAA

>RXA02619-downstream
TAGGAACTCTGCACAATTACTGG

>RXA02620-upstream

ATCGATACCAAATAGGAACTCTGCACAATTACTGGCTACAATCTCTTGAGATCAATAGGC
CAAAACTTTAAGGAAGTAGAATTACGCTATGGCAGGAGCA

>RXA02620
GTGGGACGCCCCCGGAGATCAGCTCCGCGACGGGCAGGCAAGAATCCTCGCGAGGAGATT
CTTGACGCCTCTGCTGAGCTTTTCACCCGTCAAGGCTTCGCAACAACCTCCACGCATCAA
ATCGCTGATGCCGTGGGAATCCGCCAAGCCTCGCTGTATTATCACTTCCCGTCCAAGACG
GAAATCTTCCTCACCCTGCTGAAATCTACTGTCGAGCCGTCCACTGTGCTCGCCGAAGAC
TTAAGCACCCTGGACGCCGGACCTGAGATGCGCCTCTGGGCAATCGTTGCCTCCGAAGTG
CGTCTGCTGCTGTCCACCAAGTGGAACGTCGGTCGCCTGTACCAACTCCCCATCGTTGGT
TCTGAAGAGTTCGCCGAGTACCACAGCCAGCGCGAAGCCCTCACCAACGTCTTCCGCGAC
CTCGCCACCGAAATCGTCGGTGACGACCCCCGCGCAGAACTCCCCTTCCACATCACCATG
TCGGTGATCGAAATGCGTCGCAACGACGGCAAGATTCCAAGCCCGCTTTCCGCAGACAGC
CTCCCGGAGACCGCAATTATGCTTGCCGACGCCTCCCTCGCCGTCCTCGGCGCGCCGCTG
CCCGCCGACCGGGTCGAAAAAACGCTTGAACTAATCAAGCAGGCTGACGCGAAA

>RXA02620-downstream
TAACCATCCGCGCCTGCGAAATC

>RXA02624
CAGGGCTACGACGACTCCGCCTCTGTTGTGGCCTTGATCGTCCTGAGCATTCTGTATCTG
CCCAACATGATGATCTTTGCGATGGGCAATCTGATCGGCTCACCCCTTTACTTCGGTGAC
GCCTCCATCAGCGTCTTCAGCGTGCATTCCGTTCCATTGCCACCGCTTCCCATCCTCGCA
GCTCTCCCCAGCGAAGCCCTCTCATGGGCAGTGGCCTTACTGGTCATCCCTGCAATTATT
GCCACCTGGGTCTGCGTGAGAAACCCCATGCGCCTTGCCGTGAACACAACAGCAGCAGTC
ATTTCAGCACTGTGTTTCCTCGTCCTGGCAGTTTTCGCCGGCGGAACCTTGGGCGTATAC
AACTACGTCGGACTCAACCTCCTGGCGTCAGTTGGCCTAGTTTTCGTCTATTTCGCCCTC
GTTGGACTCCTCATCGCCGGAATCGACAAGCTGCGCAACCCTGTAGAAGTTAAGTCTGTT
AAGGCTGTGGCTGTTGTGGAGCCCGAGCCTGAAGAAGTTGAAGAGGACGAAGAGGAGCAT
GTTGAAGAAGAAGTAGATGAGGAGGAAGAGGAAGTTGAGGAAGGGGTAGAAGAGGTCGAA
GAAGACGACGCAGAGGATCCTGAAGAGAATCCTGAAGAGGAAGAATCCGACGAAGAAATT
GAGACAGAAACTGAGGCTGAAGAAACCAATGATGGTTCCGAGGCCGAAGACCGT

>RXA02624-downstream
TAACATATCTGTTGTGAATTCTG

>RXA02639-upstream
CGAAAATGTTGGAAATCGCCGAACGGGAACGTCGACAAGCAAAACGCGCGGCAAAGGTCG
CCAAGAAACGCACCACCTTTATAAGGAAAATCTTTAAAAA

>RXA02639
ATGATTGCACTGGGTTCAGCGCCCAAGCTGGTTGCCTCCGATGTTGATGGCACCCTCATC
AATAGTTCTGAGCGCGTGCCGCAACGCCTGCGCGATGTGATCACGCGGATGACCAATCAG
GGCGTGACCCTGGCGCTGTCCACGGGCCGCCCGCCGCGCTGGATTCATTATGTGCTGGAT
CAGCTGAGCGTGAAGCCGATTTGCGTCTGCGCGAATGGCGCGGTGCTGTACGATTCCGCT
GCCGATGAGATTCTTGCAGCTCAGACGCTTAGTCCGGAGGTTATGGCGAGTGCCGTCATG
GCTGCGCGTGCCGCTTTGGAAGAGCATGGCGGGGTCAGTATTGCTGTCGAGCGCGCTGGA
AAATCCGCTTACGATCCAGCCGATGAGCTGTTTTTGGTCACCCCGGAATACAGCCACGCG
TGGCCCTCAAATGATCACGGCACCTTCGAGGAAGCCGAAGTGCTTTCCGAACCAGCCACC
AAATTGTTGATGCGCAGCGATTACCTCGATTCCAAGCAGCTTTTTGATATCGTCCGCGCC
TCCGTTCCCGAGGATCAAGTCCACGTCACCTTCTCCATGTCCGGCGGACTCATTGAGATC
GCAGCGCCCGGCGTGACCAAGGCACTGGGCGTATCGATGCTGGCAGAGCGCCTAAAGATT
GCGCAAAAGGACGTTATAACGTTCGGCGACATGCCCAACGATATTGAAATGCTCCAGTGG
GCCGGCCGGGGAGTGGCGATGGGCAACGCCCGACCAGAGGTCAAAGCCGTGTCAGACCAC
ATCACCCGCACCAACGACGACGCCGGTGTAGCAGATGTATTGGAGTGGTGGTTC

>RXA02639-downstream
TAATAGGTGGTGTTAAAACACTG

>RXA02647-upstream
ATCTTCTATCTTGTTTCCATAGTAAATCCGCATATTTATTGCCAGGAGAAAAGTTTTGTC
TTTGCGTCGAAGTACTTTGACCCTTGTTACAGCAAGCGCT

>RXA02647
GTGGCATTGTCCGTGTTCACTCCAGTTGCCCAGGCTCAGTCCTCTGACGCACTGACACAG
CTCTCAGACAACATCACCTCATCACAGATCCTTGATGATGATGGAAATCCAGTCGATGGA
AACGAAACCTGGCCAGGCAGCTCTGAAGGCAGCTCAATGCTCAGCAATGGCGACATTCCT
GCGGCCCCAAGCTTGAGCTCCTCCGGCAAAGACACCAGCGATGATGACGATGAAATCAGC
GAAGAGCAGCAAGCACTGATCGATCGGTTGTCCGAAATGCCAGTGATTGGTTCCATTGTC
TCCCCACCAGAATGGCTTGCCATTCCTTTTGCGGTACTGCAGGGATTGCTCGCAATCACC
ACTCTTGCTTCCACCGCAGCATCCTTCATGGTGACCGTCGACCCATCGTTCAAGCAGACT
CTGCGTGACATGCTCACCCAGTTTGGCATCAACGTCGACGCT

>RXA02647-downstream
TAAAAGCACACTGACATAAAATG

>RXA02649-upstream
TTTTACACAGTTGCAGCAAAAATTCGGCCATTCCGATTGCTTTTGACAGCTAAACTTTGC
ATTTGTTCTTTTTGGCGCCGATGCCGATAGGTTTAAAGGC

>RXA02649
GTGCTAAAACGATTCTCTCACCACTCCAGCCCGCAAGTTCTTTCACGGAAAGTTGTCGCG
TCCGCATTAGCTTTAACAACCGCGCTGGCTTTAGCCGCGTGTAGTTCCTCAGCCGAGCCG
GACTCCCCTGAAGTTGAGCAGGCGGTGGGTCTTGCGGTGGATACGCCACGTGTGGTGGTT
GTGGATCCAGGCACTGGCGATTTGCAGCGCTTGCAATACAAAGACATCGCCCCTGATGCC
ACACAGGAACAGACCATCAATATTGCTGAAGGTTTTGCCCAATCGGTGGTGAATGCGGAC
AGCGTGGATCCGCAGGCACCAGCCGGTGGCGATGTCACCACATTCCACCTTCCTGTTAAA
GCCACCACCGAGGAAGCGGAGTTCAGCGATCAGGAAATGGTGAGCGCGACTCGCGATATC
TCTCTACTTTTCGGTAAACCTACCTACACCGATCTTTCCCAAGTTGAAGATGTGAATTCC
ACCGAGGGATTCACGCTGGGAATCCGCGCAACAGATAGTGGACAGCACACCACCTTAAGT
TTCGCAGCCCCTGTTGATTCCACTGAAACTGGTCGCATGCTCATGGAGCAATACTTACTC
ACGTTTACGTCCCTTCCCATTGTGTTCCCCTCTGACGATATTGGCGTGGGCGCGAAGTGG
ACTGTGGATAGCCGTGTGACAGGCGAATCAACGCTGCTACAAACCGTGACCTACACGATC
ACAGGGATCGACGGCGACAAAGTAAACCTCGATGTGGAAGTCTCTCAGCGCCCCAGCATG
GGTGCGTTGGAGATCACCGATGAAGAATCGGACGAGACCACCGGGCAGCTCACTGTCCTT
AATTCCAACACCACCTCCGTGGGCACCTTGGAAGTCGATCTGACTCAGCCTTTACCCACG
TCAGGACAGGTTTCTTGGACCACTCGCGTGATTTACGGCGGTTCCAATGAGCAGGTGCGT
GTGGTGCAGGATTCCACCTCTTCGGTGAGCTTCGGAGACCAG

>RXA02649-downstream
TAATTTACCAATTAGGGTTGCCA

>RXA02652-upstream
CGCTTGGATTCAACCACCCAGCAGATGGCCGATGGATGGAAATCGTCTCCCCATATCCAA
CTGATCTCCAACACGCTTTAGACGTTCTCCGCGAGCAATA

>RXA02652
ATGGATGGTGTCGATAAAGGGCGACGCATCGTCGCCCTCCTAGCAATTCTCGCATTGGTT
GTCGTGGTTGCGATCTTGAGTTTCAGCGACCGCACCGCGAAACCCATGCAGCTCAACGGT
GACATGCTCGGCCAAGACAACACGGAAACTTCCGTCGAGTACCGTCAGCGGGCATCGGAA
TCATTGGAAAATGCCGCGGTCGGCGAAGAAGCCTATTCACTGGTGACGTTCACACAGCCG
CTTTCGCCTTCCGAGGCCTCTAACCTTCTTAAAGGAGTCGGTCGCGTCAATGCCATGGTT
ATGCTCTCGGCTCCTGCCATGGATCTACCCGAACCCATCGCAGGCGAGACCCGTGAAGAT
GTTTTTAACCGTCAAATAAAGCTTGTCGACGCCCAGTTATCCGGTATCGGCAACGTCCGC
GCGCCGGGCGAACTCAACGGGGTAGTGGTTTGGGATATTCCTCAGAAAGTTCGTGTGTTG
TCCGAGAGCTCGCTGGTTTATAGTGTCGAAACCCTGCCACCTGACGCGGCGTGGGGCAGT
TTCGGTATTCGACCAGTCGATACTTCGGGTACTAATTTT

>RXA02652-downstream
TAGAAGAAAATTCCAGATGCCCC

>RXA02655-upstream
AATTCGATGGAGAAGAAAAAGTCATGGGGGTCAGGCTAGGAGAAAATGATCTCATGATGG
CTTTGGAACGGTACCTCGCTCACGAGTTTGGTGAAATTAG

>RXA02655
ATGAGTCCAGAAGCCAAAGAAGCCCAAGATTCTAGGCGCAACGAGATGCCCGAGAAAAAG
CGAGCGGTGCTACGTAAAGCGATTAAGTTGGAATGGGCAACGATCGCATGGGTTCTTTTT
TCGATCGTTTTGGTAGGTGTTGTCGCTGGTCAATCGCAGGCCATGCGTAGTGCATGGATT
GAAGACATGCTTTCTTTGGTACCACCTATCGCTTTTCTTTTAGCCTCCCGAATCAGCAAA
GCTGTGGCAACCAGAAAACATCCATACGGCAAGCACCGGTCGATTGCTATCGGGCACCAA
GCTGCAGCACTGGCCCTGCTTATCATGGGAAGCCTTTTAATTTATGAAGCGGTATCTGCA
CTGATCAAGGGAGAAAGGCCTCCGATAGGTTTAGCTATTTTATTTGGCCATGACGTGTGG
TCAGGTTGGTTAATGATCGGGGTTATGATTTCAGTGTCGATCCCGATGGTGATTGTAGGG
CGAGTAAAAATAAACTTAGCTAAAGATCTCCACGATAAACTCCTCTATGCAGACGCGGAT
ATGGCCAAGGCTGACTGGGGCACAGCAGTCGCTAGCACAGTAGGCGTGCTCGGAATAGGA
CTGGGTTTTTGGTGGGCGGATGCAGTTGCAGCTCTAGTAATATCAGCTTCAATTCTCAGA
GATGGCGTGATAAATATGAAAGCTGCTATATCTGACTTAGGTGATGGACGAGCCATGACT
TATGACAATTCCGCCCCTCACCCATTAAATGATGATGTGGAAAAGGCTGCCCTAGAGATG
CATTGGGTCAAACACGCCCGCGCTAGGATACGCGACCAAGGCCGCTGTTTCCACACAGAG
TTATTTGTCGAACCAGTAGAAGGATACACACCTGCTCCGGAAGAAATAACTTCTCTAGTT
AAGCGAATCCAAAACCTTGACTGGAAGCTGCAAGATGTCGTAGCTTCCGTCGTCGAAAAA
ATCGACCGGTTTCAGGCCCCTTCG

>RXA02655-downstream
TAAAACTTAACTGAGAAAGTGAT

>RXA02662-upstream
CCAAGGTGTCACCCTCACCGTTGCCATCGCCTTCATCATCGTCAATATCGCCGTGGACCT
GCTCTACGTCCTGGTCAATCCACGTATTAGGAGCATCTAG

>RXA02662
ATGCGCCGTAAACTAACCACCACATTAGAAAACAAGCCCGGTGCACGACTTGGTGGCTTC
CGCGCACTTGCACCAACTTCAAAAATCGCGCTGGTTTTCCTTCTCCTGATCTTCCTCCTC
GCGATCTTTGCCCCACTGATTGCTAAATACGATCCACTGGCCTCCGGAACTCCAGTCCAG
CCTCCAAGCGGTGAGCACTGGTTTGGTACCGACGCCATCGGCCGCGATATTTTCTCCCGC
GTAGCCACGGCGCCAGAGCCTCCC

>RXA02662-downstream
TGATCATTGGTCTTTTCGCTACG

>RXA02665-upstream
CAAGGCGACCCAATGGCGTTTAAAGTAACAACCCCCATTGATATGATGCTGGCACAACGC
ATCACCGACGAAGCCGAACCCACAATATTTGAGGTACCAG

>RXA02665
GTGACTAACCCAATCATCCCCCGCGTAGGAATCGCCACAGACGCCCACCAAATCGAAGCG
GGAAAACCCTGCTGGATCGCCTGCCTCCTCTTTGAAGGCGTCGACGGCTGCGAAGGCCAC
TCCGACGGTGATGTTGTAGCTCATGCAATTGTGGATGCTCTCCTTTCTGCCTCTGGTCTG
GGGGATTTGGGCTCTTTCGTTGGTGTGGGGAGACCTGAATACGATGGTGTTTCTGGTACA
CAGTTGTTGAAGGAAGTTCGGGAGCTGCTTTCGGCACACGGGTACGTCATTGGAAATGTC
GCCGCCCAACTGGTTGGCCAAACCCCCAAATTTGGACCCCGCCGCGAAGAAGCACAACAA
GTCATCTCCGAAATCATCGGCGCACCATGCTCACTGTCTGCCACCACCACTGATCACATG
GGATTCACTGGTCGCAGCGAGGGTCGTGCATCGGTAGCAACGGCAGTGGTGTGGAAGGCT

>RXA02665-downstream
TAAGTTTTCTGTAGGGATTGGGC

>RXA02670-upstream
CCGTTTAATCAACCGACTGTGTGAATGCGCTTAAACGGACTAGGGTTGTGAGCAGCATAT
CCAGATTTTTCTGGATAAATCCTGGAATTTCTTAAAACCA

>RXA02670
ATGGAGGACGAATCCGTGAAGTCCCTGAACTTGGCTGCCCGTCGTGGCGCGCTCGTGACC
GTGGCTGCTGCGTCAGCTCTTGCGCTTGCATCCTGCAGTGCCGGACAGATCACCCAGACC
TCAAGCCAGGTTGCAGCAGTTGATGGCAACCAGGCAGGCTCCGCGAACGACCCAGTTCTG
GTGCGTGATGTAACCGTGCACCTCACCACCGACGGCGAAGCTGGAGTAAAGTTCACCGCC
ATCAACCAGGACACCTCTCACACTTCTCACACCCTTGAGTCCGTCACCGTTGACGGCGAA
GAGGTTGAGCTTGATGATGCAGAGCCAATCGAGCGCAACTGCTCCCTCGTTGCAGACATC
CAGTCCGAACTGGATCTGATCGAGGAGCCAGAAGTTGGCTGCATCCAGCACGTAGCAACT
TCTCTGGAGAACCCAGGTTTCGCATACGGCGGAGTCGTGCCAGTTGAGTTCGTCTTCGAC
ACCGGTGCGATCACCATCGATGCCACCGTTTCCGCACCTGTCCTCGAGTCAGGCGTAGAA
AACCGCGAGGTCGGCGGAGACACTGCAGAGGCAAGCCACCAC

>RXA02670-downstream
TAAGCCTCTCAAAGCTGCTTGAA

>RXA02672-upstream
AGCAGTCATCCCCGGAGGCTCAGGCATCAAACAAACAAGCCTGAGAGTCATCGAAGCTTC
AACACTTGCCGAAGCACTTGCAGCAGTAAGCTTATAAAGC

>RXA02672
ATGACACCAACAACCACTCCTGTATCAAACCCAGATGCCCTTTCCACTGGAACTCAGGAT
GTGCACACCCTCAAAGGAACGTTGCAGCGCCTCGCCCCAGGCACACCACTTCGCGATGGC
TTAGACCGCATCGTCCGAGGACACACCGGCGCGTTAATCGTCATTGGTGATGATGAAAAC
GTCTCCTCGATCTGCGACGGCGGCTTTGAATTCGACGTTTCGTTTGCTGCAACCCGACTC
CGCGAGCTGTGCAAGATGGATGGCGCTGTCATCTTGTCTTCCGACCTTGAGCGTATCAAA
CGCGCCAATGTTCAGCTGCTGCCTTCACCAACCTGGCCAACCCAGGAGTCCGGCACCCGC
CACCGTTCTGCAGAACGCACCGCGCTTCACACCGGTGTGCCAGTGATTGCGGTATCCGAA
TCACAAAACACCATCACTCTCTACGTCGAGGGCAAATCCCACATGTTGGAGCAGCCAGCT
GCCCTGCTTAACCGCGCCAACCAAGCTTTGGGAACAATGGAGCGCTACCGCGATCGTCTC
GATCAGGTCAATAACCGCCTTCACCTGGCTGAACTCCACAGCTATGTCACCGTGATTGAT
GTTGTTTCTGTCATTCAGCGCGAGGAAATGCTGCGCCGAGTGGGTGAAATCATTGATGGC
GATGTTCTTGAACTAGGCAAAGACGCCAAGGAGATTCAGATCCAGCTCAGCGAATTACGT
GGCGATAATGACCGAGAACGTGAATCAATCATTGCTGATTACCTTGTCACCGACGGTATT
CCTGCAGATGAGGAAATCCACGCAGCCCTCGAAGCGATCTCACATTTAGATGATAAGGCT
CTGCTGAATCCTGCGAACATCGCGCGTGTTCTTGGACTGCCACCGACCGAGGAAGCACTT
GATGAGCCAGTCACTCCTCGCGGCTACCGCACGCTCAACAGAATTCCTCGAGTGCAAAAA
TTCCTCATGGATAAACTCATCGTGGAATTCGGCAACTTGGATGCACTGCTCAATGCGTCA
GTAGAGGATCTAAGTGCAGTCGATGGTGTGGGCTCACTGTGGGCACGCCACATCACCGAC
GGACTTGGCCGTTTAAGT

>RXA02672-downstream
TAGGTTAAAGGTCACCGCTGGTG

>RXA02673-upstream
ACGCCCAAAACGCTAATCCGCTGAACAGGCCGATGAAAGTAATAGAGTGTTCTGTGTGGG
AACGCCGAGACATAATGAAGTCATTTACAAGCGCCGCCGC

>RXA02673
ATGGCAGCGCTCCTAGTTCTGCTCGTCGTGATTGCCTTGATTATCTGGGCAGTCGTCGCG
CTTCGAGGTGGATCATCGGAGCCTGAGGAAGAGCAGCCAAATAATGCTGTAGTGACCTCC
TCAATGGAATCTTCCGCGACGTCTAGTTCTTCTTCTAAAGAATCCACGACTGAAGCCACC

ACAGAAGAAGAGACTTCCAGTGCTGAACCAACCGCAACATCCTCCGTTGCAGCAGATGCA
AAAAAGACCTGTGAGCTTAGTGACTTGGTGATTTCCGCAAGCACTAATCAGCCGACTTTC
TCAGGTTCTGCGCAGCCAGAATTATTTATGGCTGTGCATAATCCGACTGCTGTTGATTGC
GAAATTGACCTCGAGGAGAACAAACTCCGTTTCGAGGTATACAATCTCGCGACCAACGCA
CGAATCTGGTCTGATGTCGACTGCAACCCTGCAGTTGAAGACGGCACGAGCGTGTTCCCT
GCCGGCGAGGATCGCTACTTCCAGGCAACATGGTCTCGTACCACTTCAGCGCCAAACCAG
TGCAACAACCGCACTGATGTCCCCGCCGGTGGCTACTACTTGCACACTGTGGTCGGTAAT
AACCCTTCACCAGCGGTGACCTTTAACCTAACT

>RXA02673-downstream
TAAACGGCCAAGTCCGTCGGTGA

>RXA02678-upstream
CTGTGGGCGCGCGAACAGGGCGTCGACATGCTCGCCACCAATTATCCGGACCGTGCGGCG
GAGCTTTTGAACGCACATCCCAAGCCCGCCATGTACGCTA

>RXA02678
ATGCGCATGGCAAAGAAGACTAAGAAGAATGAACAGCTGCCGGAGGGCATGAGCCGTCGT
CAGGCAAAACTTGCAGCCCGCGCGGCTGAACGTGCAGCACTTGAGCGTGAACCTCGCCCA
TTCGAGGGCCTGGCAATGGAGTCACAGCTCGTTGCACTGCAGGAATTCATTCCATCTGCA
ACCGCACCCATCACCGTTGCAGGCACCGATCGCAAGATCACCCTCTGTACCGTGCTTCCA
GGCGCAGCTGCGGCACTTGTCCGCGAAGAAGCATTCGGCGGCGAAGCGTTTGTTGCAATG
CAGCAGGCCATCCGCTCCAACAACCCAAGCAAGGACCTCGCGTTCGCGCTGAACTGGGTC
ATCAACGCAAAAGCCGGCGAGTCACTGGCCACCGCCACAGCGGACGGCACCCAGCCAGAG
CTAAAGAGCTTGCTTAACGACGCCGACACCCTCGAAATCACCACTCACCAGGACTTCAAC
TGGTGGCTGGCGGAAAACGACAACCTCTCCCCAGAAGTTGCGCAGCACATGCAGGCAGCC
AATGACTCCATCCTGCCTTCACACGAAGTCGAAGCAGACGTCCCAGGCGCTGTTTGGTGG
GTCAACCCAGGCGGAAAAGCGCACATCCGTTGGGTCCGCACCGAAAACGAAACCGCACTG
TTCAACGCTTTGGCACGCATCGCAGCACGTGGCGAGCTGAATCTCGGCGAAGAAACTAAG
TTCGCTGGTGCTTTCCGCACCCACGGCATCGTCGTCCCAGTGTGGGATCTCGATCCTGAG
CGTCCATCCACCGATTACGCCGATGTTTTGGTTGCACTCAACGAGAAGATCGTCGCTGAA
CTGGATAACGATGCACAGCTCAACGCCGACGAGCGCCGTCAGCTGGAGAACATCAAGTCC
CGCCAGGTGACCATCCGC

>RXA02678-downstream
TAAAATCTCTTAAAAACACTTCA

>RXA02679-upstream
CACCATTACCACCAGGGCCGCCGCCCATCATTCCGCTGGCTGCTTCCTGAGTTACGGAGT
TAGCGTAGTCATTGGTTGGGTCGCGGTAGATGGTGTGAAT

>RXA02679
GTGGCCCCATCCAGCGGTGATGACACCGTCGATGTCGGCACCTGCAGAACCTTGCTGGTT
AGCGAACTCAATGTAGACCTTTGGGCCACTGATCTGGAAGTAGATGCCGTCGCCGGTGGA
GGTGTCGTACTCGGTGGCGCCGGACCAGTTGATGTAGGTGTCATCCAGGGTTTCGCGGAT
GGCATCGAGTTCAGTTTCGGTGGTTTCCTCATCGGCGAGGCCAACCCAGTTTGCGATGAC
ATCGATGAGCAATTCTTTTTGCTCATCGGTGAGGTCAGAGCCTTTCAAGCCGGTGCCGGT
TGGGTAGTCGCACGTGCTGCCCGGTGCGCACACCATGGAATCCAACTCTTCACCCTGGTA
GAGCTGTGCTTGCTGCTCTTCGGCGAGGCTGTCGTAGAAGGCGAAGGCGGTTTCGTACAT
GTTGCT

>RXA02679-downstream
TAGTGCTGCAACGGTTTCGCCGT

>RXA02680-upstream
AATACCAGGTCAACACACACAGGAACCGTTCAGAAACCTTCCAGATTGCTCACTTTTTAA
TTTCACTTTTTTGAGAAGTTTTACTTTTATATTAGTTCTC

>RXA02680
ATGCGCCTCAACAAACGACTCCCAGCGGCACTCTCCGGACTGCTGCTCTCTGCTGCCCTT
CTTGCCGGATGCTCCACTTCTGGAACCGCCGAGACCACGACAACAACCGTTTCATCTGCT
GCGGCATCAACAACCACTTCCACCTCCTCTGCTTCGTCTTCCTCTTCCTCCTCCTCTTCC
TCCTCTTCCTCCGACTCAAGCACCACCGCCGAAACCATCTCCAACACCGCGGAAGCTGCC
CAAGCTTTCTTGTCCACCCTGTCCACCGAAGAACAAGACGCCGTACTCTACGACTACGAC
GCCGAAGAAAAGTCCACCGGCTGGTCTAACTTCCCAGTCACCTTCGTGCAGCGTTCCGGC
GTGAACCTCACCGACCTCACTGAGGAACAGCAAGCAGCTGCCCTCAACGTGCTGAAGAAC
CTGCTCAACGACGACGCCTACCAAATGATCGAAGACATCATGGCTAGCGATCAGTACCTC
AACGACGAAAGCAACACCACCGAGGATTCCCTCGGCCAGTACTACATCGCATTCTTCGGC
GATCCAAGCAGCGACTCCGACTGGTCCATCCAATTCGGCGGACACCACATCGGCATCAAC
ACCACCTTCTCCGACGGTGCCATCACCTTCGCCCCAACCCACCTTGGCACCCAGCCTTCC
GAGTGGACCAACGAGGACGGCGAAACCGTTGCAGCACTAAGCAACATGTACGAAACCGCC
TTCGCCTTCTACGACAGCCTCGCCGAAGAGCAGCAAGCACAGCTCTACCAGGGTGAAGAG
TTGGATTCCATGGTGTGCGCACCGGGCAGCACGTGCGACTACCCAACCGGCACCGGCTTG
AAAGGCTCTGACCTCACCGATGAGCAAAAAGAATTGCTCATCGATGTCATCGCAAACTGG
GTTGGCCTCGCCGATGAGGAAACCACCGAAACTGAACTCGATGCCATCCGCGAAACCCTG
GATGACACCTACATCAACTGGTCCGGCGCCACCGAGTACGACACCTCCACCGGCGACGGC
ATCTACTTCCAGATCAGTGGCCCAAAGGTCTACATTGAGTTCGCTAACCAGCAAGGTTCT
GCAGGTGCCGACATCGACGGTGTCATCACCGCTGGATGGGGCCACATTCACACCATCTAC
CGCGACCCAACCAATGACTACGCTAACTCCGTAACTCAGGAAGCAGCCAGCGGAATGATG
GGCGGCGGCCCTGGTGGTAATGGTGGCGAGATGCCTAGCGGTGACATGCCTACTGGTGAG
ATGCCTTCTGGCGCTCCATCAAAC

>RXA02680-downstream
TAACGCCATTTAAGAGGCCGAAC

>RXA02681-upstream
CGAGGCTGTCGTAGAAGGCGAAGGCGGTTTCGTACATGTTGCTTAGTGCTGCAACGGTTT
CGCCGTCCTCGTTGGTCCACTCGGAAGGCTGGGTGCCAAG

>RXA02681
GTGGGTTGGGGCGAAGGTGATGGCACCGTCGGAGAAGGTGGTGTTGATGCCGATGTGGTG
TCCGCCGAATTGGATGGACCAGTCGGAGTCGCTGCTTGGATCGCCGAAGAATGCGATGTA
GTACTGGCCGAGGGAATCCTCGGTGGTGTTGCTTTCGTCGTTGAGGTACTGATCGCTAGC
CATGATGTCTTCGATCATTTGGTAGGCGTCGTCGTTGAGCAGGTTCTTCAGCACGTTGAG
GGCAGCTGCTTGCTGTTCCTCAGTGAGGTCGGTGAGGTTCACGCCGGAACGCTGCACGAA
GGTGACTGGGAAGTTAGACCAGCCGGTGGACTTTTCTTCGGCGTCGTAGTCGTAGAGTAC
GGCGTCTTGTTCTTCGGTGGACAGGGTGGACAAGAAAGCTTGGGCAGCTTCCGCGGTGTT
GGAGATGGTTTCGGCGGTGGTGCT

>RXA02681-downstream
TGAGTCGGAGGAAGAGGAGGAAG

>RXA02683-upstream
GACGGTTTCTTCTGTCATGACGGAAACTCCTACTTATACCTCTTCATCTAGGTCGGTGGA
ATCTACCGCGGGGACGATCGCTGCCTCGGAGGAAGCCACG

>RXA02683
ATGACGCTACTGGAGAATAGTTCGGGGGATCCGGGATCTGATTCTGGGGGTGCACGCTAT
AGCCTCAATTCGCTCAAAGTTTCTGAGCAGGCCGCGGCTAACGCCGTCTTAAAGGCCGTG
CTTAACGACGTCTCCTACCAAGAGTTCGCAGACTCCTCCTACTTAGAAATCACAGGAACG
CCCTCCGCCGACGGAACATGGGGCATCTCATTTGGCGGACCTTCCGAATCGGCCTCCGTG
GAATTCTCCGACGGCAGCATCAGCTTCTCCCCTGTTGACATGACAGTGCCCGCAACACGA
TTGCCTCAGATGGGCGCATTTTATGAAACCCTGACCGAAGAACAATTAGGCATGCTGGAG
ACTGGCCTCGCGGTTTCCACCGTGGATTCGAGCCAACAGGAAATGCTTCTGGACTTGGTC
TCCAACTCGATCGGCCTGGCAGATACTGAAACCACTGCGACTGCAATTAGTAAAATCCGA
GCAACGCTTTCCGAGACCTACCTGTTCGGAACCCCCGACGGATTAACCTTGGCGCTTAGT
GGCCCACACGTTGATTTCGAAGTCTCCCACCAGGGCAGCACCGCGAAAATTACTTACCGC

GATCCAAGCACCGACACCTTAACCGCCGAAGATCGGGTAGATACCGCAAGTGTGGCTGCT
GCTCCGCCGGAGGTTGTT

>RXA02683-downstream
TAGGCGTTTGCCGAGAAATTTTC

>RXA02685-upstream
TAGCAGCATTTGTGGAAAGAGCTGTGGCATGAGTAGTTCAGTAATGTCACCGCGTCGAAT
AAAGGCGGAAATACTTATCGTTTTAGCCATCACCTTTGGC

>RXA02685
ATGAGCGGCCTGCGATCAATCCTGCGCCTCATCGACGATCTCCTCGCACCGGTTGCGCTC
AACGACCAGCAAGTTGCACTGAATGCCTCAATGGCAAACTCCGCATGGCTGGATCTCACC
TTGCAATTGTGTTCCGCCGGAGTGCTGTTTTCCTGGGGAGCACTAGCGATCTACCTGCTA
GGTGAACGTTTTCAGTGGATTAAACCCAAAGACTGGGCATGGGGTGCAGGCCTTGCAGCA
CTCATTGGTATTCCAGGGTTAATCTTCTACGCCAGTGCTGTTCATTTGGGGCTGTCCAAA
CAGGTTGTGCCCACCACGTTGGAAACCTGGTGGGAAATCCCAGTACTTCTTATCTGGTCA
GCTGCCAACGCCTTTGGTGAAGAGATCGTGGTAGTCATGTGGTTTTTCACCAGGCTGCGC
CAGCTGAAGTGGAGTGTGCCTGCAGTTATCGTGACATCTTCAGTACTACGCGGTTCCTAT
CACCTCTACCAGGGAATCTCTGCAGGCTTGGGCAACATCATCATGGGAGTAGCGTTCGCG
TACTTCTATCACCGCACGGGCAAAATCTGGCCACTGGTAATCGCTCACTTCTTGATTGAT
GCGGTGGCTTTTGTGGGCTACTCCGCAATTGGCGGGAATTTAAGTTGGTTAGGGCTT

>RXA02685-downstream
TAAACTGAAGTTCCTATTTTATT

>RXA02688-upstream
GTGCGGAAGACAGCACGCCCCAAACCGACCAACTAGCTAAGCTACACAAGGCGGACGAAT
GGGTTCGCGCAGCAAGCGAAGGAAGGAAACTTAACTAGCC

>RXA02688
ATGGCCGGCCGGATTATTTTGCTACGACACGGGCAGACTCACAACAACGTCAAACACCTC
CTGGACACCCGCCCACCAGGAGCTGAACTCACCGACCTGGGCCGTAAACAAGCCCTTGAA
GTTGGCCACGAACTAGCCACCTACTCCGGTGAGCGCCTCGCCCATGTGTACAGCTCCATC
GTGTTGCGCGCCCAACAAACCGCCGTGCTTGCCACCTCTACCTTTGAAAAAGCTCGCGAC
ATGCAGTCCGGTGCGATTCCACTCGACGTTGTGGAAGGCATTCAGGAAATCAACGTCGGC
GACTTTGAAATGCGCGGCGATGAAGAAGCCCACATGAATTACTCCCGCGCACTCAACGGC
TGGCTTCACGGGGATCCTGCCGCTGGTCTTCCCGGCGGTGAGACCTACAAAGACGTGCTG
AACCGCTACCAGCCGACTCTTGATCGAATCATGGACAGCCACGACCTTGACGACGACCGC
GACGTTGCCGTTGTCAGCCACGGCGCCGTCATCCGCATCGTGGCAACACACGCAACTGGT
GTGGATCCCAACTTTGCGTTCAACACCTACCTGGGCAACTGCCGCTTCGTGGTGCTGGAG
CCAAACGGTAAGAAATTCAGCCAATGGGATGTTGTGCGCTGGACTGACAGCCCACTGCCA
TGGCAGGAG

>RXA02688-downstream
TAATTGAGACCAAAGGCTCGGAT

>RXA02689-upstream
GTGAAGTTCCCCCACCTCAGCCAGAGCGCGATCCGCTCCGTGACACTGCAGGAACGACAG
CATCCGCGGAGGTCGGAGTACCTGTAGAGGAGAACGCTCC

>RXA02689
ATGATTGAAGTCAGCGACGAACGCTTCGAGGAACTGGTCGAACTAGCCTTCGACCAAGTT
CCCCAGCAATTCCTGGATCATATGCGCAACGTGGTTTTACTCATTGAGGATTTCAACCCA
GATTCGCCTTATATCTTGGGTTTATACCACGGCGTTGCTCTCACAGAGCGCACATTCAAC
CACGGTGGCCTGCCGGATTCCATCACCATTTATAAAGGTGCGTTGCAAAATTACTGCAAT
TCAGAGGAACAACTAGTGGAGCAGGTGCGGGTGACCGTGCTGCATGAGATTGGGCATTAT
TTTGGCCTCGGCGAAGAGGACCTGCACAGGCTCGGATACGCC

>RXA02689-downstream
TAAAACGCCTCATTAGGTGCACA

>RXA02690-upstream
TTTCCTTGTACCGAACCGACCGATATTCTTTAAAAACATTGGTTACACGCTCCGAAGATC
TCTGACGTGAACCCATTTTGGTGGCATGATGGTGTCAATT

>RXA02690
ATGAGTACAAACTTTGACACTTCGACGTCTCCAGAGGGTGAAACCAAGAAGAACTCTTCT
TTCCGCACTGCGGCCTCTGTGCAGACCATGCTTGTTGCAGCTTTGGCAGCAACGGCTGCT
GTTGGCGTGTACTCCTACAACACGGACAATTCAGCAAACGGCGGCGAATCCCCCACAGGA
CCTGAGCAAAGTACAGTGTCCACCACCGCAACTATTGCCTCATTTACCACTGCTGACGTG
GGCCAATGTGCAACCTGGGATGTTAACAATGAAGGTCTAGTGTCTGGTTTTGAACAAACC
AGCTGCGATCAAGAGCACCGCTTTGAAATTTCTGCTCGGGAAAACTTGGCAACTTACCCA
AGTTCGGAATTCGGTCCGGACGCAGCTCCACCAAACCTCACCCGTCAGGCGCAGCTGCGT
GAAGAGCTCTGCCAATCTCCTACCTTGGCGTATTTGAATAACCGTTTCGATCCATCGGGG
CGCTACACCATCGCCCCGATCCTGCCACCTGCGGAAGCGTGGGCTGCGGGAGATCGCACC
ATGCTCTGTGGACTTCAGGCAACCGACGCTTCAGGCACTCCACAACTCACCGTCGGACCG
ATAGCAGCCAATGACCAGGCACGCGTTTTTGAAACCGGCGCCTGCGTGAAGGTGGAATCC
TCCGCAGAGTTCCGCCAAGTTGATTGCACGGAAGATCACCACCTCGAATCAATTTTGACA
GTCAACCTTGGTGTCCCCTTCCCACAGGGCGCGCCCAGCACGGATGAGCAGAACAATTTC
CTCGGAAACACCTGCACCCAAGCATCCATTGATTACCTAGGCTCCGAAGAAAACGTCTAC
CAATCCACCCTGCAGACCTTCTGGCCAACGATTACCTCCAACTCCTGGTTGGGCGGTTCA
CACAGCGTGAACTGCTTCCTCATGTCACCATCCACCGAGGGTGCTGCAACATTTAACACC
CTCAACGGTTCAGCGACTGGCACATTCACCATCAACGGTGAAGTTCCCCCACCTCAGCCA
GAGCGCGATCCGCTCCGTGACACTGCAGGAACGACAGCATCCGCGGAGGTCGGAGTACCT
GTAGAGGAGAACGCTCCA

>RXA02690-downstream
TGATTGAAGTCAGCGACGAACGC

>RXA02693-upstream
CAGACCAAGTGTTATTTTTGTTGAAAAAATCACATTGTAAATCGAGCAAAACCAACCTAT
GCCCTGCAGAATTGTGCATGCTCTGCCAAGATGACTCAAT

>RXA02693
ATGGTTTCGCTCCCCAGACTAGCGTCTCTGCTCACCACTCGCCTGGCAACGCTTAAACCC
GCACTAAAACCTGCCACCCACCTCGCCTCCCTCGGCGCGCAGGTCATTGCAGAGCTAGTT
CCGGGGATCCGAATGTCGCCAAACCGCAGGCGAATCCTCCCTGCAAATATGGGCGCTGGC
TTTATCGGAGCGGAAATCGCAATGTGGTGGGCTCTCTCGCCGTCATTGTTGCCGAAACCG
TGGTGGGTTACGGCTGCTAACCTGGCTGTTTTACAAGCGGTGGGGCATGCGGCAGCGACG
GGAATCCACTCGATCCTCCCCAGAACCAACCGGCGGGTATCCAGGAAAATTTACAACGCC
ACCCACATCGCAACTGGTGCCATCACGTTGACCACCACGGTTGTGGGATTGATCAGGCAT
CGCACCCAAATCCGGCTGATTGGGCAGAAGAATTTTGGACCGAAGGAGACGATCGCGGGC
ATTAGTGTCGGCACCTTGGGGTACGGCGCGCTGCTGATCACCGGCGAATTAACCCAGCAC
AGTATTAATGAGGTCAAGCTCCTAATTGAGAGGTTTTTACCGCCGTGGATAAGTTTCATC
GCAGCGGTTTCGGTCATTACATTGACCACTTTGACCTTGGCCGATCGCGTTTTGTTGCGG
CGCATCTTGCATAATTCTGCAATTCAAGCAGCGCACCTTAATCGCATGGTGTTCCCAGGA
ACTGAGCAGCCGTGGGAGCCGGAGCGTTCGGGTAGCCCGTGGTCGTATGAAAAATGGGGT
GCGGTGGGTTCGCAGGGCCGTGCAGTGTTGTCGGGAGGCCCACGCAAAGATGACATCATC
ACGGTAACCAGGCTTTCTGACACGGAAACACATGAACCGATTCGTATTTTTATCGGTATG
GTTCCGGGACGATCCTTAAGCGATCAGGTGGATCTTGTCATTCATGAAATGCGCCGCACG
GGAGCCCTGCGCCGCGACCACATCGTGATCAACAATTCCACGGGCACCGGCTGGATCACC
GATTGGTCCGCCCACACCTTTGAGTTCCTCACCGGCGGAAACTGCGTGACAATTTCCATG
CAATATTCTTATCTTCCCAGTGCACTGAGCTGGTACAAGGACAACGACGGCCCCATTAAT
GCGGCGAGAATGCTTATCGACGCCGTCCTCCACGAGCTAGACCAGCTTCCCACCGGGAGT
CGCCCAAAGCTGTTCCTCGCGGGAGAGTCACTGGGGGCGTATGGGTTGGCTGAGGTGTGG
GGAGACGTCGAAAAGCTTCTTGGAACCGCTGACGGCGTGCTGCTCAGTGGGGCGCCGCGT

TTTTCGGACGCCATGAATGCGTTGCGCACCCGGCGCGATGCGAGCAGCTCCGAGCGGCTG
CCCGTGATTGATAGCGGGCGGCACATCCGTTTTGCGGGCGAGCCTGAGCACCTTGATATG
CCGGCTACCTGGCAGTTTCCGCGCATGATCGTGGCGCAGCACGCCTCTGATCCAATTGTG
TGGTGGAACGCGGAGCTGTTTATTCGGCGGCCGGAATGGTTGAAAACTCCCAAGCAAGAC
CACCAAGATGTCTTTAACCGCTTGCGATGGATGCCGTTTGTTGCCGGCTGGCAGGTGGCT
TTGGATTTGTTCACTTCAACCTCCGTT

>RXA02696-upstream
NGCTTNAAGAAATAAAGCCCTNCCCAGTTAANGGTGNGNATGGGTACCAGCCCTGTGGAC
GCTGTACATNTAAGTCATTNCTGGTTNAGGTGANCTGCC

>RXA02696
ATGTCCATGCTCAAGAAGACTAAAGAATTCTTCGGACTCGCTCCATACGAAGCGGAGCAC
GAGGATGCTTACTATGCAGATGAACCACGTTACGAGGGCACCGCTGCGTACGCACCTGAA
TACCGTGAGCGTGACTACGGCTATGCACCAGAGGCACCAGCCCCTGTTGCTCCATCGCCA
GCACCTCGCTCTTACCAGTCCACCATCGTTCCAGTAGAGCTTCATTCCTTTGAAGACGCT
CAGGTTATTGGTGGAGCATTTCGCGACGGCGACGCAGTTGTTTTCGACATGAGCTTGCTT
TCCCGTGAGGAAGCACGCCGCATTGTGGACTTCGCTGCAGGCCTGTGCTTCGCATTGCGT
GGCAAGATGCAGAAGATTGACAGCGTCACCTTCGCTGTCGTTCCAGAGCTGTCCAACATC
AGCACTTCCGAGCTCGAGCGCGCCGCACGCATCCGC

>RXA02696-downstream
TAAACACACCCTCGTGGTGTGGA

>RXA02697
CCTTTTGTGGTGTGGATCGGCATGCATCATTTCGCAGGATTCTTAGCCACCAAAAAGGGC
AAAGACTCCCCTACCCTTAAGCAACAGGTCCCCGCGTTCTTTGCCACTGGAGCTGCAGGT
GTTGCTGTCACTGGTGTTGTTGTCAGTGCGATCACTTGGGCGTCTGGCGCTTCGTGGGGC
TGGATCAGTGAGATCAGTGGCAACAGCAAGGTAATCAACCCGCTGGCTTTCCCTTCTTTG
GTGGCCAGTGTGATCACCATGGTGGCTGAAGTGTTCGTTGACGATTTCGACTACAACGCA
GTGGTTAATGTTGTGCGCTCAATCTCCATGCTGATCATGCTTGGCGGGTTGGTCGTATGT
TGGTGGCTGTTCCGCCAGAACGAACGCAGGGCGGTCACTGGTACAGCGGCGGCTTATGCC
GTGGCTTTTGTGTTCAATTCTGTGACCTTGCCGTGGTACTACGCCAGCTTGATCTCTTTG
CTCGGCACATTTAAACCACCGATGTGGTTGATTCGCTTCGCAGCGGGTGCTTCGGTGTTT
ATCGCGCTGATGTTTACCGGAAGTGGAAACCACCAGCTGTACAACATCGTTACGGTGATC
ATCGCAGCAATTATCGCGTGGCTTGCCACCGTGGTGATCTTTGATGACACTGACCCTGCA
ACAACGGCCACGGAGAAACCCTCCCCGCATACCGTTTCC

>RXA02697-downstream
TAGTTGCATAAGGTAAACCGCCA

>RXA02700-upstream
TGACAACTGATGCGGACGACAACGATCGAATTTATAGTCAAACCCCTCGTGCACGCAGCG
AAGTCTCGGTAGGGGGAGAAGTTACAGTAAGGGCGTTTTA

>RXA02700
GTGGTTCCCTCGTTGCAGCAATGGCGAAAACCTGCTCTCATCCTGGCCATTTTGACGGTG
CTAGGCGTACTCCTGACCCATTGGTTCGCCTGGCCACTCACCTGGCCGCTGGGGCTGCGT
CTTCCCGTTGATGTAGAGGTGTACTGGCAGGGTGCGCGCGAGTTTTGGCTCGCCGATGAT
CTCTACGACATCAGGTATGACACCACTTTCGACAACTTGCCGTTCACCTATCCCCCTTTC
GGTGCGTTGGTGTTCACCCCATTGTGGTGGATTCATGACCTCTTTGGTCTTCTCGTCACC
GAACGTGTCTTCGCGCTAATCACGCTGCTCACCACCTACGCTGTGGCAGTTTTCCTGCTC
CGCCTGGCCGGCGTGCGCGATCGTGTGTGGGAATTCGTCGCATTCGCAGCCCTGCTCGTG
TCCGCGCCGGTGTATTTCACACTCAATATTGGGCAAATAAACGTCATGCTCATGGCTTTA
ACGCTTTTCGACGTCGCCCTCCCCCGCAGCACGCGCCATTCAGGCGTGCTCAAATACGTG
CCACTCGGCGTACTCACCGGCATTGCCGCTGCGATCAAACTAACCCCACTAGTGTTCGGG
CTGTATTTCCTCATCCTGTGGGTCGTGACTAAATCACCACGCGGACTGTTTGGAATGATT
GGTGGCTTCCTCGGGGCATCCGGGCTTGCAATTATTTTCCGACCATCCATTAGCATCCAA

TATTTCACCGACGTGCTGTTTACCGCAGAACGCATCGGCGACCTCCACTTCGCACGCAAT
GTCTCCATCCGTGCGGTTTTGGAACGACTCCCCGAACTTGGTTCCGCAGCATCTATCATG
TGGCTTGTTGCTGTGGCGCTAGTGATCATCGCAGTCGCAGTTGCTGCTTACCGAATCCTG
CGGACGGATCTCTCCGCGCACAATCGTCTGCTGGCTGTTTCCCTCGTGTCGCTCGTTGCA
CTGTTGTGCTCCCCCGTCAGTTGGTACCACCACTGGGTGTGGCTTGGTCCGTTAATCGTC
GCTCTCTGGCTAACTCAACACCGCTGGCTGGCTCTATGGGGCGCATTCGCCGTGACATTC
GGATCATTCCACAATTTCCTACCCTCAGAAAACAATATGGAGCTCACCTGGCCGTGGTGG
ATGCATGTCCTCGCAGCACATTATTTGATCTTCTCCGCAGTGGTTACTGCCGTATTTAGT
TGTGGGAAAATGCCCCAAAAAACAGAGCTTTCCCAC

>RXA02700-downstream
TAATCGATCAGGAGTATCACATC

>RXA02701-upstream
CCCACTAATCGATCAGGAGTATCACATCTCCATGATTTAAGATTAAAACTTTGTCTAAAC
ACGAACGGTGTTTTCATGTTTAAGAAAAGGACTCCTGGTT

>RXA02701
TTGACGAACCCCCAGACAGCACATGCTGCCGCGTCTGACTCCGCATCCCAGAAGGAGGCT
CCTAATCCTTCACTCTCCATCACTGTAGGTATTAAAGATCTGCTGGGGCTGCTTTCAGTT
CTTGGCATTGCAGCGGGGCTGATAGCCAACAAGATTCTCATCGAACGCTACAACTGGCGC
ATCGATGCCGCAGTTTACCGCGAAGGCGCGTTAGCGCTGGTCAACGGGGAATCACTGTAC
GCGCAGCCGTTTGATATGGGTGATATTTCACTACCCTTTATCTACCCACCGATTGGTGCC
ATCCTGTTTGCGCCTTGGGGGTACTTTGATTTCATCACAGTTGAACTTGCGGGAAACCTT
GTTGTCATAGGCTCATCCCTGCTGTTATTACTGTGCCTGTATCTTGTCACCAACGCTGTT
CTTAGCGGTCGAGACAAGCTGTTGGCCTTCACCATCGCTGCGATTTCCTGGCCGATCGCT
CTCTTTGCAGAGCCAGTGTTTTTGAACGCTGACTTGGGCCAAATCAACATTTTGATCATG
GCTTTGGTTGTCATGGACCTGCTTCCGATTAAGCGCAGAATCCCCCGAGGTGTCCTGATT
GGCCTTGCAGCCGCCATCAAAATCACTCCGCTGGCCATGCTGTTGTATTTCCTGGTGAAG
AAGGATTTCCGCGGAATCATCAATGCGGTGATCTCACTACTTGCCTTCACTGCTATCGGT
GCTGTGCTCGCATGGGAAAACACCAAAGAGTTCTTCTCTTCAACCCTTCTCAACTTAAGT
GCTGAAGGCGATTCAGGCGTAGACACCACGTTCCAATCCAACAGCTCGATTCAGGCCATG
CTGTATCGCTGGTGGACCTCAAAGGCAGATGCCGAAGCATCCTCACTGCCCACCATCTTG
TGGATCGTACTGTCCCTGATTGCTGTGGCGGCCGTTGCCTACCTAATGCACCAACTCTTC
TCCAGAGGATTGCACGTTGAGGCAGTCATGGTTAACGCCATGCTCATGCTACTTATCTCC
CCCATCTCATGGTCTCACCACTGGGTGTGGCTACCGCTGTGGGCTGTGGTGTTCTTCGTT
CGATACCGCCAGCACCGCTCTCACCCGAAGTTCTTGTTGTGGAGCGGAGTTATCTTGAGC
GTCATGCTGCTGATGCTGCCACCAAAATGGTGGTTTGGCCGCGATGGCGTCAACGTCTTC
GAACTGAATTTCTGGGAGAAACTACTCATCTCTGACTGGACGTGGCTCTCCATCGGGCTC
ATGATCACCTTGGGTCTTGGGCTGAAAGCATTTCCCAAAATATCCAAA

>RXA02701-downstream
TAGATAAAGGTGTGG

>RXA02712-upstream
CTGAAACGGCTTCGGAAGCTGAAATTGAAGAAAACCCACGTGCCGCACCTGTGAAGGTGC
GCGCAATCGAAAGAATCGGCAACAACTCAGGAGACCTCTC

>RXA02712
ATGACCATGACAAATGGCTCCCGCACAGAGTCGGGAAAGATTCGCGATCGACGTGTCGCT
GACGCTGATCCACGGTATGGCCGTCGCGTCTCGGTGAGTAGGGATTTCTCCACAGCGGAA
GCTTCGGGGAGGGGCGCGTCGATAAGCACGCAACCTCGTCGTGACATGGCGCCGGAAAGG
CGCCACACAACCCGGGCCCTAGTGAACCCTGGCGTGCAACCAACGCGTAAGCGTTTGATG
CAGCACAAGCTGGGCTCTCAGCAGGTTATGTCGGTGCGTGGTCGCCGCGTTGAGGCAAAA
CGTGCTGATCCTAAGGTGATCCAGCTGTCTGTGCTGGTGGTTATCCTGCTGTGCGTTGGT
GTTGGCGCGACCATGGGTCTGTCCGGAACGTCTACACAGCAGACTTTCCAGTTGCAGGAA
CTTCAGGCAACTGAAACGGATTTGAGCAATCGCATTGAGTCGCTCAACCGAGATGTGGAA
GATGCTCGCTCAGCAGCAACCTTGGCAGCGAATGCTACGGAGATGGGCTTGGTATCCCCA
GTGGAACCTGGCGTGCTCGCAGTGCAGGAAAACGGTGATGTTGTGGAGGAGCGCGAAGCA

AATCCAGAGACACGCCCTATAGTTGACATCAATGGACAACAGACCCGACCAAATCGGGCA
TCAAGCAACCCTGACGAGACTAACGCAGTGACTGAAAACCTCCAGGCGATTCCACAAGAA
GCAGCAGCTCCGCCGTATCAGACCAACACTGTTCCTTATGCTGCAACCACCGGACAAGCA
GGTGGCGCAGGGCAG

>RXA02712-downstream
TGACTTTCCCCAGCAATGGCAGA

>RXA02714-upstream
CGCGGTGGTCTTGCATGAGAGGCCACTACGCACCCTCAGAGACAAACTGAATGGTTGGTT
CTGTTTATGCCACTGAGTTGCTGGGAAGGGGACTTCAAGG

>RXA02714
ATGTTCCTTGGTACCTATACCCCGAAACTCGATGACAAAGGCAGGCTGACTCTTCCAGCA
AAGTTCCGTGAGGACCTTGCGGGGGGATTGATGGTCACTAAAGGTCAAGACCACAGTCTC
GCGGTTTATCCGAAGGAAGAATTTGCAGCAAGGGCTCGCAAGGCAGCTGCAGTTTCTAGG
ACAAACCCTGAGGCTCGTGCGTTTATCCGAAACCTTGCAGCAAGCGCGGATGAACAACGA
CCCGACGGCCAGGGGCGCATCACCCTTTCGGCAGCGCACCGCACATATGCGGGGCTGACA
AAAGAGTGTGTCGTTATCGGTTCGGTGGATTTTCTGGAGATTTGGGACGCTCAAGCCTGG
GCCGCGTATCAGGAAGAGACGGAGGCTGCCTTCTCAGCAGCTGAAGATGACGTCCTTGGA
GGATTGCTC

>RXA02714-downstream
TGATAGTTGGGCAATGCTTCGAA

>RXA02715-upstream
GTTTTTGTCGTTATTGGCATAACGGGGAACATTCTGGATATTCTGGGCGTTAATAAGGCA
TAGAAGAAAAAATGTCTCTACTAACCACCGGGAGGACATC

>RXA02715
GTGTCGCTTTCAGAGCAGGAGCAACGCGCACTGCGCGAAATTGAGCAAGCGCTCATGGCA
GATGATCCGAAATTTGGAAAAGCGGTTGCAAGTAACAATGGCCTAGCAGGCGGTGGGTTT
ACCCTTCGGGGAATCGCACTTTTCGTACTCGGACTTGTCCTTCTTGTTGCCGGCGTCGCA
TTAAGCCAGCAAACATTGTGGTTCGTTGCGCTCGGAATTATCGGATTCTTAGTCATGTTC
GGATCGGGAGTGTGGATGCTGCGCGGGGGCGGCTCCAACAAAATCTCCGTCACATCCCGC
ACTTCCAATGCGAAGAATCGCCAACAGGGCAATTCCACCATTGGGGACAAAATGGAAGAA
AACTTCCGTCGACGATTCGAGGGCAATAAG

>RXA02715-downstream
TAAGAAGTAACTGAATAAGTCTT

>RXA02719-upstream
TTTGGCTCACCTCGATGATGTAGACATCCCCGATGAGGTGCGCGCACAGTTGCGGGCACT
GGCTATCCGCTCAACCGAACGTCGGATGTAGTAGACGCGT

>RXA02719
ATGACACTTTTTCAACGTTTAACCAACCCTGTAGTGCTCGGCGGCCTAGCAGGTGTTTTG
CTTCTGCTCGGCTCTTTCGGTGGCGGTGCCATTCGGTACCGTGGCGGAGTGCTCGATGCG
TTGGGGCTTAACTTCCTTGCTTTTGGCCACGCGCAGGGTATTTCCAATACCGTGTTGTGG
GTTGGGCAGCTGCTGCTGATTGGCGCGTGGGTTCACCTTGGACGTCGGTTGTTCAAGAAA
AAAGTCGCTGATGACACCGCAGACGCTGCTGACTTAGGTCTTGTAAAGCGCACGTTGTAT
GCCATGGTGGTGCCCCTCATTTTTGCGGCACCAATGATGTCGCGTGATGTTTATTCCTAT
CTCATGCAGGGCGCGATGCTGCGTGATGGCTTCGATCCCTACACTGAGGGCGCTGCGGTA
AACCCTGGCCCCATGTTGCTTGAGGTCTCTCATGATTGGCGCAACACCACGACGCCGTAT
GGTCCACTACACCTGTGGATTGGAGACATGATCACCACGGTTGTGGGCGATAATGTCACC
TTGGGCGTCGTCGCTTACAAGATCTTGTCGATCATTGGCCTTGCTGTGACAGGCTGGAGC
ATTGTCCGCATTGCACAACATTTTGGAGCCAACCCAGCAATTGCATTG

>RXA02720-upstream
CCACGCTGCACCATCGAAGACGAAGATCTGTTTTCTTACCGCCGCGAAGGCACGACAGGC
CGCCAGGCCGGCGTGGTGTGGCTGCCAAAGGAGGCATAAA

>RXA02720
TTGGAGCGCCGCGAAGAGCTGCAGGTACGACTGCAGCAGGTGCAAGCGCGTATCGACGCG
ACCCTCAACGAACACAACCGCCCCGAGGGCAGTGTACGTCTGTTGCCGGTCACCAAATTC
CACCCCGTGGAAGACATCAAGATCTTACAAGAGTTTGGTGTCACCGCAGTGGGAGAGAAC
CGCGAACAAGAAGCACGCGCCAAAGCACTCGAACTTCCCGACATGGACTTTCATATGATT
GGCCAAATCCAATCAAAGAAAGCCAACTCGATCGCCAGGTGGGCAGCTGCAGTGCACTCC
GTTGATAGCGAGAAAATCGCCGAAGCATTGGGCAGGGGAGTAGCCCTTGCATTGGATAGA
GGCGACCGCACCAGTGACGAGCTTCCGTGTTTTATTCAACTGAGTTTGGATGGTGACCCG
AGCCGAGGTGGAACTCCATTGAGCCAGGTCACACAACTTGCCGATTGCATCAGTGACACC
ACACATCTGCGTTTTGAGGGCCTCATGTGCGTCCCACCGCTTGGTTGGGGCCCTGAAAAA
GCTTTTTCCCAGGCAAGAGACGTACTTTCAGGTTTAGAGGAACACTTTGACAGGTCTTTG
GAATTTTCGGCAGGTATGTCTGGAGAC

>RXA02721-upstream
CCGTGATGATCGTCGTGACGATCGCCGCGATGACCGCGGAGACGACCTGGATGTACCCAG
CTTCCTCCAGTAATTAAGAAGGAGAATAGACTTATCCACT

>RXA02721
ATGGATAGTCTTGACCCCCGCAACCGCCCCGTCCGCAAGGTCTTCACGACCCGTGCCGGC
GGGGTTTCGCAGTCCCCGTATGCTTCCTTCAACCTTGGTGATCACGTCGGCGACGATCCT
CAAGCTGTGGCATCCAACCGCAATCGCTTGGCTGACATCATCGGTTTGTCCCCAGACAAG
GTGGTGTACATGGAGCAAATTCATTCCAATACCGTCACAGTCATTGATGAAGCCCCAGCG
GATGGCCAGGCTGTAGAGGCCACCGATGCGCTAGTGACCACGCAACGAGGGCTAGCGCTG
GCCGTTTTGGTTGCTGATTGCGTGCCAGTGCTGCTGTCAGACACCGACGCTGGCGTGATT
GCGGCAGTGCATGCAGGCCGCATGGGAGCCCGCAATGGCATCGTAGCTAAAACCATTGCG
AAGATGGAGGAGCTCGGCGCGAAACCCAGCCGCATTCATGCGCTCATGGGTGCAGCGGCA
TCGGGTGCGAACTACGAGGTCCCAGAGGCCATGGCGCGCGATGTGGAAGCCAAACTTCCA
GGTTCCATTGCGCGTACGACAAAAGGCACCACAGGACTGGACATCCGCGCAGGGCTGCTG
CGTCAAATGCTCAGCCTGGGTGTGCAAATGATTGATTCTGATCCACGCTGCACCATCGAA
GACGAAGATCTGTTTTCTTACCGCCGCGAAGGCACGACAGGCCGCCAGGCCGGCGTGGTG
TGGCTGCCAAAGGAGGCA

>RXA02721-downstream
TAAATTGGAGCGCCGCGAAGAGC

>RXA02725-upstream
GAAAGCCCGCTGCACATCGGTGTGGCGGGTTTTCTCATGCCCAGATATTGACCTTGTCAC
TGTGTCAAGGCATTGAATAAGTGCCATGAACATAAGTGCC

>RXA02725
ATGGACAACTTCGAACATTCAAATGCATCTATCCGTTTACAAGCAGCGTTGGCCGCAGGA
ACTGCTGAGGACACCACTGCGATCGATATTCTTTTGTACCGCAGTGGGGTAGAAGAAGAC
TTCTTTGTGCGCGACATGATAACGTGGGCGCTCACCCGCATGCCAGTTGATGACGTGTTT
ACCTCACTGGTCGCTGATTTGGATTCTGAGGTACCTGATCGACCATTCGGTGCAAGTCAA
GCACTCCACACACTCTCCAAGTTAAGGGTCGCGCAGTCGTGGCAGGAATTGCAAGCACGG
CCTTGGCTTTTGCACCGGGAGGACACCGCCCAAACTGCGTGGCGAACCTTTGTGGGACTG
GTCCCAGATGATCAGACCGCATGGTTGGCGCACCAATTGCTCCAAGAATTGGATAAAGGA
ACGCCTGAAATTCAGCGGAGTTTAAGTCGGGCGATGGCGGAATTGGAGGGGAGGGAGGCG
TCGATAAGCGTGCTTCTAGGCGCTTTAACGAGCGCGCACGCGGTGGCCACCGCCAAGCTC
ATTGCGGATCCGGACTCCGATTTCATGGCTGATCTGGAGGAAGCGCGGCGCGTGGATAAT
ATGGGTGCATGC

>RXA02725-downstream
TGATCGGTGAGGTGTCCAAGCTC

>RXA02727-upstream
GATCAGTTCCTAGATCTCGTTGAGGACGCCCTCGTTCAGTTCCAAGAGGAAAACGAAGAC
CTAAAGCAGCAGGTCGAAGAGCTAGAGGCGCAGGTTGCCG

>RXA02727
GTGGTCCTTCTTCCGCTGCTAGTTCCTCAACTGCAGGTGCAGCCACAGTTGCAGCTTCCA
AGTCTGTTGACGAGGCAGCGCTGCGCAAGGAAATCAAAGAGAAGCTGCGCTCCGAATACG
GCATCCAAGCTCGATGATGCCTCCAAGGCCGCTCAGAAGGCTCAAAACGATGCGAAGTCC
GCTCAAGATCAGCTACAGCGTGCACAAGCTGACGCAAAGGCAGCTCGCGACGAAGCTGAA
AAGGCCAAGGCTGAAGCTAAGTCAGCAGCATCCTCCAGCACCACTAAGGCAGCAGCGGTT
GGCGCTGTCGGCGCTGGCACCGGAGCAGCAGTTGCTACAGGTGCTGCAAATGTGGACACC
CACATGCAGGCAGCGAAGGTTCTGGGACTCGCACAGGAAATGGCAGACCGCCTGACCTCA
GAGGCTCGCTCCGAATCCAAGTCCATGCTGGACGAGGCTCGCGAAGCAGCAGAGAAGCAG
ATCGAGGAAGCAAACAGCACCTCCAACCGCACTCTGGAAGATGCTCGCGCAAACGCTGAG
AAGCAGATCGCTGAAGCGCAGAACCGCGCTGACACTCTGGTCAACGAAGCTGACGCTAAG
GCTAAGAACCTGGTTTCCGAAGCCGAGAAGAAGTCCGCAGCCACCCTGGCCGCATCCACC
TCTCGTGCAGAAGCTCAGATCCGTCAAGCCGAGGACAAGGCAAACGCCCTCCAGGCAGAC
GCAGAGCGCAAGCACACCGAAACCATGGCTGCAGTCAAGGAACAGCAGAATGCTCTGGAG
ACCCGCATCGCGGAACTGCAGACCTTCGAGCGTGAGTACCGCACCCGTCTGAAGTCCCTC
CTCGAGGGCCAGCTGGAAGAACTCCACGCACGTGGCTCCTCTGCACCAACCAACAACAAG
CCATCTGGTGAG

>RXA02727-downstream
TAAAAAGAAAGATTAGTTATCTT

>RXA02734-upstream
AATCCTATCCCTAAAAAGTTTCTAACAAAAGTATTGCACTTACTTTTTGATAGTGCTATC
TTCAGTTGTGTACTTGAAACACACACGAATGGAGCAAGAA

>RXA02734
ATGCGTATTGCAGTAACTGGAGCAACGGGATCTTTGGGTGGACATGTTGTGGATAGTCTT
CTAAACAAGGGCGTCGCAGCATCAGACATCGTTGCCATTGTTCGAAATGAAGAAAAGGCA
GCAGACCTCAAAGCCCGTGGAATCGCTCTTGGTGTGGCTACTTTTGAAGACGAAACGGCA
CTGACTGCAGCTCTTGAAGGTGTGGATCGCCTTGTGTTTATCTCTGGCAGCGAAGTGGGG
CAGCGCGTTGCGCAACACACCAATGTCATCAATGCCGCTAAAGCAACTGGCGTGACATTC
ATTGCATACACCAGCTTGCTCAACCTTGGTCCTCAAAGCTTGCACTTGCTCCAGAGCACA
TTGCAACCGGAAAAGCTCCTGGCA

>RXA02735-upstream
GAGGAGCTTCGCCACATGGATCCAGATTTGGGCTACCAGCACGCACTATCCGGCTTGTCC
AGCGTCAAGCTGGAAACCGTCTAAGGAGAAATACAACACT

>RXA02735
ATGGTTGATGTAGTACGCGCACGCGATACTGAAGATTTGGTTGCACAGGCTGCCTCCAAA
TTCATTGAGGTTGTTGAAGCAGCAACTGCCAATAATGGCACCGCACAGGTAGTGCTCACC
GGTGGTGGCGCCGGCATCAAGTTGCTGGAAAAGCTCAGCGTTGATGCGGCTGACCTTGCC
TGGGATCGCATTCATGTGTTCTTCGGCGATGAGCGCAATGTCCCTGTCAGTGATTCTGAG
TCCAATGAGGGCCAGGCTCGTGAGGCACTGTTGTCCAAGGTTTCTATCCCTGAAGCCAAC
ATTCACGGATATGGTCTCGGCGACGTAGATCTTGCAGAGGCAGCCCGCGCTTACGAAGCT
GTGTTGGATGAATTCGCACCAAACGGCTTTGATCTTCACCTGCTCGGCATGGGTGGCGAA
GGCCATATCAACTCCCTGTTCCCTCACACCGATGCAGTCAAGGAATCCTCCGCAAAGGTC
ATCGCGGTGTTTGATTCCCCTAAGCCTCCTTCAGAGCGTGCAACTCTAACCCTTCCTGCG
GTTCACTCCGCAAAGCGCGTGTGGTTGCTGGTTTCTGGTGCGGAGAAGGCTGAGGCAGCT
GCGGCGATCGTCAACGGTGAGCCTGCTGTTGAGTGGCCTGCTGCTGGAGCTACCGGATCT
GAGGAAACGGTATTGTTCTTGGCTGATGATGCTGCAGGAAATCTC

>RXA02735-downstream
TAAGCAGCGCCAGCTCTAACAAG

>RXA02736-upstream
CAGAGGATTACCCAGCGGGTACGTGGGGTCCAAAGAGCGCTGATGAAATGCTTTCCCGCA
ACGGTCACACCTGGCGCAGGCCATAATTTAGGGGCAAAAA

>RXA02736
ATGATCTTTGAACTTCCGGATACCACCACCCAGCAAATTTCCAAGACCCTAACTCGACTG
CGTGAATCGGGCACCCAGGTCACCACCGGCCGAGTGCTCACCCTCATCGTGGTCACTGAC
TCCGAAAGCGATGTCGCTGCAGTTACCGAGTCCACCAATGAAGCCTCGCGCGAGCACCCA
TCTCGCGTGATCATTTTGGTGGTTGGCGATAAAACTGCAGAAAACAAAGTTGACGCAGAA
GTCCGTATCGGTGGCGACGCTGGTGCTTCCGAGATGATCATCATGCATCTCAACGGACCT
GTCGCTGACAAGCTCCAGTATGTCGTCACACCACTGTTGCTTCCTGACACCCCCATCGTT
GCTTGGTGGCCAGGTGAATCACCAAAGAATCCTTCCCAGGACCCAATTGGACGCATCGCA
CAACGACGCATCACTGATGCTTTGTACGACCGTGATGACGCACTAGAAGATCGTGTTGAG
AACTATCACCCAGGTGATACCGACATGACGTGGGCGCGCCTTACCCAGTGGCGGGGACTT
GTTGCCTCCTCATTGGATCACCCACCACACAGCGAAATCACTTCCGTGAGGCTGACCGGT
GCAAGCGGCAGTACCTCGGTGGATTTGGCTGCAGGCTGGTTGGCGCGGAGGCTGAAAGTG
CCTGTGATCCGCGAGGTGACAGATGCTCCCACCGTGCCAACCGATGAGTTTGGTACTCCA
CTGCTGGCTATCCAGCGCCTGGAGATCGTTCGCACCACCGGCTCGATCATCATCACCATC
TATGACGCTCATACCCTTCAGGTAGAGATGCCGGAATCCGGCAATGCCCCATCGCTGGTG
GCTATTGGTCGTCGAAGTGAGTCCGACTGCTTGTCTGAGGAGCTTCGCCACATGGATCCA
GATTTGGGCTACCAGCACGCACTATCCGGCTTGTCCAGCGTCAAGCTGGAAACCGTC

>RXA02736-downstream
TAAGGAGAAATACAACACTATGG

>RXA02744-upstream
GCCAAAACGTCATGATTCGCTCTTTGGATACGGGACACCGCTCATTGGAAGATGTCTTCC
TGGACATCACCGGAAAAGAACTGAGGAGTTAACGCACACC

>RXA02744
ATGTCTAAACCTTTTGAAAACTCTGCGCTCCGCGGTTCTTCTCGATTCCCAGCTGGAACG
TTCACCCCTGCTCCCAAACGAGCCACCCCGGCAAAAATGTTGGCTGCTCAGGGCAAGATG
GAATCCCTGCTGTTTCTTCGCCACGGCGAACAGCAACTGCTCAGCATCATCATTCCCTTG
GTCGCGCTCATCGCACTAGCGAATTTTGATTTCATCCCTGGTGAGAACTCCCTCGACAAG
ACTTTCCCCTTCGCGCTGGCCACAGCAGCCATGAGCGCTGGTTTTACAGGTCAAGCCATC
AGCCTAGCTTTTGACCGCCGCTATGGTGCCCTCAAGCGCACCGGCGCCAGCGGTGTTCCC
GCCTGGACGATTATTTTTGGCAAAGTCATCGCAGTCATTGCAGTCACCATTGTGCAGATC
ATCTTTCTCGGTGTGACTGCACTGCTGTTGGGCTGGTCCGCACCTGTCGGTGGTGTGCTC
TTTGGCATCGTGACCCTATTTGTGGGTGTTTCCAGCTTCACCGCGCTCGGCATGCTGATG
GGCGGAACGTTGTCCTCCGAATTGGTATTGGCACTGGCTAACTTGATTTGGATTGTACTG
TCCGGCCTTGCAGCATGGGCGGTCTTTTCCCCTTCCGTCAACGCTGAAGGAGTGCTGTCC
ATCATCCCATCCGTTGCGCTGTCCCAAGGTATGGTTGACGCATTCAACGGCGAACTTCCG
TGGCTCCAGCTAGGAATTTTGGTGGGCTGGCTAATTATCACCGGCGTGGCCGCAAACAAG
CTATTTAACTTCTCTGCGAGCCGC

>RXA02744-downstream
TAGATATACCCTTAGTCGGAAAA

>RXA02751-upstream
GGTGTCTTCTTGTCAAATAACCACTGTTTATAGGGCAATTCTTTGGCAATGTACCCAACT
CATTACCCACCTGCTGATTCAAAGAGTAGATTTAAATAGT

>RXA02751
GTGCTTCCGATTGCCTCCGGTAACGATGACCGGAATTTAATCCGTTATGTCGACGGTGGT
CGATTTGATGAAATCATGCTCACCGGAGACCTCACTGGCCTGAGCAGTTTTCTTACCAAC
GCTGGCCCGAACGCCCGGGATGATTTTGATCTCACGGTGCTCATGCGCGCTGCCGAGGCA
GGCAACCTCATGGTTGTTGCCCGCTTGTTAGATTTAGGTGCCAATCCCCGACTCACCAAT

CCTCGTGGTGTCACGGCCCTACATATCGCAGCGATCGCCGGGGACGATGGCATTGTGGAA
TGCCTCATTGATGCAGGCGCTGAAGTCGATGCTGTAGATGATCAAGGTCGCACTCCCCTA
TGGAACGCAGCGGCTCATCATCTGCCTGATTCTGCGGTGGTGGATGTGCTGCTTCGCGCA
GGTGCGAATGTGAATCTGCGCGATTGCAATGGAGTCAGCCCAGAAGACATGCTG

>RXA02751-downstream
TAGAAGCATTCTTTAGCAGGATT

>RXA02753-upstream
AACTCAATATTAAAGTCGCGTAATTAGTGTTATATTAATTACGCGACTTTAATAGTTTTC
GAATACGTAGATTCTCGAAATACAGCAGAAAGCAGGGGTT

>RXA02753
ATGCTCGATTCATTGAAAAATCGCTTCACCAAAGCGAAAGGTTCTCATGGAGTGGGGGAG
GGGGCTGTTTCTGGCGATGCAGCAGTAAAGCCACTGCGCAAAGAAGAACGACTCGCCTCA
GTCATTCAGGAAACCGAACCAGGTGCTGCAGTCGAGGTCATGCGTCGCAATGACGCATTC
GCTTTGCCAGGTGAGACCGGTTGGGTAGTCATGCTGTTGCCAACTCACGATTCACAATTC
GGTGGGCTCAACGCTAAGGAAAAGAACCGCGAGGATAAAGGCACGATCATCAACCTGGTG
GTCAACGATGATATTCATTCCGTTGTCACTCCAGAACTTCTTGACAGCGATGTGCTTGGT
GTCATTCCTGATGCAGATTCTTTCGATCGCATGGATGAGTTTGATTTACTGCGTAACAAA
GCACGCTGGCACTACGGAGTGGCTGCAATTGAACCTGACACGGGTGAGCTGGTGGTGTTT
AAGGTGCCCGCGAAAAATAGCGCTTCGGCACGCGGTGACATTTTTTCCGAGGTCGGCGAT
GTGCTTAGCGGTGCTGCTGACCTCGAAGACGTGGTTGATTTTGAGGTCATTGCCACCTTC
CTAGAGGTGCTGAATGAGACCTCTGAGGTGGATATTGATGACGAAGATGGCGACGTGCCT
TATGGTCTTGAGGGTGTCAATGCAGCGGGAGTTATCACGGATGACCTCATTCGCGAGAAG
CTTGATGTGGATTCCTATCCGAGCAGTGCAGAGATCATTGACAATATTGTGCATGTGTTC
ACCAAGTTGCAGGGCAAGCATCATGTGGCACCACAGCCGGTGCTTCACAGCGCAGACGTA
GTGGATGTTGATGCACAGGAGTCCCATGACACAGTGGTTATTGAGAGCCCTGATGATGTC
GCACTAGCAGAACAGGTGGATGTACCGGATTTCAGTGATGGATTTGGTATTGACGATGCC
GAGGTTACTGAGCCAGAGGATGAGGAGGTTGTCGAAGCAACAGCTGATGCAGATCCTTTT
GGTGATGTAGCAGAAGACGATCCTTTCGGCAGTGATGATGAACCAGATTTTGGTGCATCC
GATGTTGTTGCTGCACCGGCACCTGTAGCCGGCATGTCCGATGAGCAGATCCAGGCGCTG
ATTCGTGGTGTGTCTGAGTCCGTGCAAGCAAAGACTGGTTCAGAACTTAATGCTTTGCGA
GAAGAACTTGCACAAGCACTGGCTTACAATCCGGTTCAGGATTCACAGGCAGCATTGGCA
CAGGTGCACGCAGCTGATGCCCGCAGCTTTGATGCCGATCAAGTGGGTGATGCTGTCACC
AAACGTTATGTTAATGACGACTTGGGGCTGTATGTCGATGAGGCAAACTTCAATAATGCT
TTGACCAGGGCACCGTTCCAGGTGGCGATGCCGCAATTCCAGGAGACTACACCGTGGTTA
GGTGATCAGCTTCGTACATTGGTGGCTGTGTTTAATGGTCAGCTGCTTGATCAGCATCAG
CGTGACTACGAAGAAGTGCGCGCGATGTACATTGCGCTTAATGATCGCTCTAATCTTGAG
ATCGCTCGTGATCTTGGACTGGATAATAAGGATTCCGAATTCTACGAGGTTTACCGTGCC
ATTGAGCGTGACCGCGATGTTATGGCTGGTGATCAACAGCGTGTGGAGTCAGAGCGTCGT
CAGCAATTGCAGCAGGAGTATGAGGCGAACCGTGAAGAATATGTCATGGCAAAGATCGCG
GAGCAGCGCGTGGAGTATGATCGCCGTCATATGCCTCGCCATACCGCATCACTAGAAGCG
GTAGGTCGAGAGCTGACGAGCCTGCGGGATCGCACCATTGAGGATTACACCGCACGCATG
AACACGCTGCGTCGTGCACGTGCTGGTGAACGGGCTAACGCTGCAGAATCTCGCATTATT
GACGAATTGCGCCCGATTGTGGAGCGCCAGGCAGAACTGCAACGAGCAGCTTTCGATGGT
TTCATTGTTGATCTTGACAAGTTTATTGCTGATCACCGCGAAGATGACCTGCGTTTGGCA
TCGGTGAATGAGCAGAAGCTTGCTGCAGATAATCGTGTGGCACAGTTGACCAAGGAAGCC
GAAGAGCGCATCGAGGGTATCCGCGTCGAGACCGATAAGATGATCGCCTCCCAGCGCAAG
GCACTTGAGCGTCAGGAAGCGGAATTCGCAGCAGAGCTTAAGCGTCGCGACACTATTGTC
GCTGCATCGGAGGAACGTGCTGAGCGGGAAATTACCACAGCACGTCTTGATGCTGAGGCG
GCGCTCAAGCGCATGGAAGAGCAAATTCGTGTAAATAATGAGGCGCATGAGGCGGAGATT
GTTATTGAGCGCGATCGAGCCACCCAAGCAGAGGCGAACTCCATGACGTTTGTTGAGTCA
GTCAAGCAGCAGGATCGCAGCAACAACATCATTTTGATTGCCGTCCTCATTGTGGGGCTG
ATTGCCGGCATGGTCGCTGGCGCAGCCTTCTTC

>RXA02753-downstream
TAAAAGATCGTTGCGCGGGCTGT

>RXA02756-upstream
CGTGACGGTTGTTGCAATTCCATAACTAAACGAGCTTTGATTAACAAGTCCTTGTATTGT
GTAAATCGCTTATTGCACACAATTGAAAAAGGACATTGTT

>RXA02756
ATGACAAGCCCTTATGGATCCCAATACCCAGGCGACGACAACAATAATTGGAACTCCCAG
TTCGGCAACCCTTCCGGCGAGCAGAACTACGGTCAGCCCTACGGTGCGCCATATGGACAG
CCTTACGGGCAGCCATTTGATCAAGGATTCAACGCCTACAGTTCTCCCATCCCACCTGAG
GTCCCACAGCCTTCCATGCAGGAGGCTCAGTGGCGCTCCTTTGACCTTGGAACTGTTTTT
GGTCAGGCATGGAAGGGCTTTACCGCAACGTGGCAGGCATGGGTGCTGTCTGCACTGATC
TACTTCGCGGTGTTGCTTGTGCTGATGTTTGCGTGGATCCTCCCGATGGTTAGTGTGCTC
GCAGCGACCTCATCTGGTTCTGATTCCGCAGCTATTGCAGCGACGGGTGGCACCAGCTTC
TTCGGGTTCATGCTGATGATCGTCCTGGCATTCATCAGTTTTGTGTACTCCCTTAACTGC
TACCGCAACGCGGCTCGAGTTGTGCGCGGTGAGCAGATCACCATTCAGAGTTTCTTCAAG
ATGAAGGGTCTTGGTAAGGCGCTCGGTATTTACATCTTGATCAATATCGTCATCTTCATC
GGAATGATCTTGCTGCTCATTCCTGGAATTATCGCTGCCGTGGTGCTGATCTTTGCTGTT
CCTGTGGCATTCCAGCTGCGCGACGCCTCGATCGGTGATGCGTTTTCCGCAAGCTGGAAG
GCAGTGTCCAAAAACGTTGGTCAGGTCATTCTCTTAGAACTGGCTATCTTCGCGTTGAGC
TTCTTGGGCAGCGCAGTGATCATCGGTATGTTGGTGACCACTCCGCTTACATTCCTGCTG
TATGCCTACGCATTCCAGACCGCCAGCGGTGGTCCCATCATGCAGCGTCAG

>RXA02756-downstream
TAGCAGTTAGTTTTACTTAGTCA

>RXA02757-upstream
TTCGGATCCTTCGACCGTTCAGGCAATGCAGATCGCGTTGCACATTCCGAAACAGAATCC
GCCCCGGCGGACAGATGTGTTGGAAGCGGCGGCGAGGAGT

>RXA02757
GTGGTCAAGCTTTGCCTCGACGAACGAGTATCCACCGATCCTGATTTTCGGGCGGCCTTG
GAACGTTGGTACGGACACTTGATTCGGAAGGTGTCACGTCGCGCTCGTAATGCGGCGTGG
GATCGGGTGCAAGATTTACCCGGCGTGACTGTGGAAGATGATGCTGCAAAGGTTCGGGCA
TTTTTGCCCAGCGCAGTGGTGGATGTGCCTGCAGATATCAAAAAGCTGCAGATTTCCGGT
ACGGAATTGCCTCTCGATGAGCCGAATCCGATCAACGATGAATACCCCGTTATCTACATT
GATGAATCGTTGAAGATGACGCTGGGAAAGGCCGCTGCGCAGGTAGGACACGCATCCATG
TTGCTTGCCGCGCACCAACCGTTTGAGTGGGTGGAGCAGTGGGAAGCAGCGGATTTTGCG
CTGCACGTCAGGGAGATTCCCTCGGAGGAGTTCCTGCGCCTTATCGAGTCTCCTGGTGCT
GTTCCAGTTCGCGATGGCGGCTTTACTGAGGTTGCCCCCAACACCGTGACGGTTGTTGCA
ATTCCA

>RXA02757-downstream
TAACTAAACGAGCTTTGATTAAC

>RXA02765-upstream
TCTGAACTTTTCCGCATCGACCCAGATGAGGTTTACCCCGACGACGACGCCACCTGCGAA
TTCAACCCATGGCCGTATCCTCGCGGATTTTAGGAGATAA

>RXA02765
ATGTCTAATCAATTACCCGATCACGTCCGCGACGCCTTCCAAGTAGGTGCGGGACCTGCC
GAACAACTCGGTCAAGCTTGGGACTTCGGATTCCGCGTCGGCAACACTGTGTTCGCCAAA
GTGACGGCGCCGGAAGTGTCGGGCTGGTCGTCGAAAACCCGCGAAACCCTGAAACCAGAA
GGCGTGCGCGTCGTACGACCGATCCGCTCCACCGACGGCCGATTTGTGGTTGCGGGGTGG
CGCGCATCGGTGTTCTCTACGGGAACGATCAGCAAGCGAGTCGATGAGACGGTCGTTGCG
GGTCTTCGTTTGGCAGATGCATTAGTGGATACGCATGCACCGGAACCTGTGGACAATGTG
TTTAACCGTGCTGATGTGCAGGCCTGGGAAGAGCAGCCCGGTCGAATCGGTGAATTGTTG
GAGCCGATTAATCGCGTGAACCAGGTTGGTCATGCGGATATGTTGGCGACAACGCTGTAT
GCGGGAACTCAGCCACCTGCAGTGACGGATTTGGTGCCAGTGCTGCGTCCGCATGGTTTC
ACTGCGGCATTGGTGATCGTTGATGGGTTGCTGCTGGGTGCGGTTGATGAGGGAATTCTG
CGGAGGTTTTCGCATTTGCCGGAAATTGAGCAGCTGGTTTTGAGGGCATTTTTGTTCCGT

CGAAACTTGCAGGAGTTCTCTGAGAACAACGATCCGAATGTTATTTCGAACCTAAACAGG
GTGGAATCGACACTCGTGTCGTATGTTTCTGACAAGATT

>RXA02765-downstream
TGAGGTATGTCGGAATACAAACC

>RXA02766-upstream
ATTTCTCGCCGCGCCGCACGGTGACGCCGGCCATGTTGAGTGCTAGTTCGCGCATGGGTA
ACACCTTACTGGCGTAAGGCCAGGGCTTAGACTGGTACCC

>RXA02766
ATGACAACCTCAGAAAATTTTTATGATTCTGTGGGCGGCGAGGAAACGTTTTCCCTCATC
GTCCACCGTTTTTATGAACAGGTCCCCAACGACGATATTTTAGGCCCGATGTATCCGCCG
GATGATTTTGAGGGCGCCGAGCAGCGTCTAAAGATGTTCCTCAGCCAGTACTGGGGCGGC
CCGAAGGATTATCAGGAGCAGCGTGGACACCCTCGTCTGCGCATGCGTCACGTCAATTAC
CCCATCGGCGTCACCGCAGCGGAGCGTTGGCTGCAGCTCATGTCCAATGCACTCGACGGC
GTGGATTTGACCGCGGAGCAGCGTGAAGCGATTTGGGAGCATATGGTGCGCGCGGCCGAT
ATGCTGATCAATTCCAACCCCGATCCGCACGCT

>RXA02766-downstream
TAACTTCTGCCAAAAAGTCGTTT

>RXA02770
GGTATTAACCGCCAGGTGATTTACACTATCAATGAAGATGCCACCTACTCAGATGGTCAG
CCTGTGGTGTGTGATGATTTTCTGCTCTCTGCGACAGCTGGGCAGATGCCGGAACTGTTC
CAGTCCCATGTGCCATTGACCTCGCAGATTGAGCGAGTGGACTGTGTATCTGGTTCTAAA
GTAGCCACCGTGGTGTTCAAGGAAGACCTCGGTGAGCGTTGGCGTTATCTTTTTGAGCAG
GGCGATTTGTTGCCAGCCCATGCCGTTGCTTCCAAAGCAGGTATGACCTTGGAGGAGCTT
AATCAGGCGTTGAAGGATAAGGATCCTGAAGCGTTGACTGAACCTGCTCGTGTGTGGAGC
GAAGGTTTCCAGCTGTCCCAGTTTGATCCAGAGCTGCAGACGGCTTTTGGCCCGTACAAG
GTGGATTCTGTGGGTGAATTCGGCGAAGTCAAGCTGGTACGCAATGAGTTTTACAGTGGC
GACCAGGCGGTTGAAGCAGAAATCACGATGTGGCCTAAAGGCTCGGATCTCAGCGCCATT
GCGGATAATGGAAACCTTCAGATCGCACATGTTGTGGCGTGGGAGAGCGAGCCGTGGGTA
AATCGCGATGACCCATTGAATCCTTATGACATTAAGGAAGAGGTCGGTGTTTTGACTGAG
CAGCTCACCTTGGCCAGTGCCGGTGTGTTTTACGCTGCGGAGGCCCGGCAGGCGTTTGCG
GCCTGCGTTGACCAGGAAGCGGTGGCTGCGGCGTCGTCAAGCATCTCTGGAATCGATGTG
CCTGCCGTAGGTGTGCACTCGGTGCGTCACCAAAATCCGGTCGTGCACCAAATCGGTGAT
CTGCCAGCACAGCACATGGCGGTGGATATTAATGCCGCATCAGCGTTGGCGGGTCAATCC
ATCCGCATTGGCTACGACGGACCCGATGAGCGCAAGGCTGCAATGGTGGAGGCGATTCGC
CAAAGTTGTGAGCCTGCCGGTATCACCGTTATCGATGCGTCGCAGGAGGCTGTTAGTCTT
AATGATCTCAGTCGAACCGAAGTCAGTGAATGGGGCTATGAGCAGTACTTCGAAGGGACA
CTTGACGCTGTTCTGCGTACAGTGGATCCACATCGGGAGTATGAAAATGCCAATACCATT
GGAACTGATGCGGAGTCGACGAGGCGCACTGAAGAACAATTGTGGGCTGAAGTCCCATCA
ATTCCACTAGCAGCGCAACCCCGAGTGTTTGTGATAGATCGCACAGTCGGTAACGTTGTT
GTTAATACAGACCTAGCCGGTATCGGATGGAACATGGACCGTTGGTCCAGAAGTGAGGAA

>RXA02770-downstream
TAAGTAGTGAGCGAACAAGCTCT

>RXA02774
CCCTGCCCACCAACACAGAAGCTGCTCTATGCACAGATGCGTGAAATTGCAGCCGAACTT
ACAGCCTGTGACGCTACTCGCGGACTCCATGCCGAAGTGGCTGCCGAATGGCTTAGTGAC
GCCATAACCGGCGAACCCACCTCTATCGAGATTGACCCCCACCGCAACCTGTTCTACGCA
CTTAATGTTGAGCACCCGCGACTCCATGAACTCTTTGCCGGTTACGCTACACGCCTTGAT
GAACTCGACCGCGCACCGCAGCAGTGTGAGTCGCGTCAATATTTTCTTGATTATGTCTGT
GCTGACAACCCTTTTGGCTCAGACAAACCAGAGGGCATTATCGTGCTGCTCGCTGATCAC
GTGCTGGCAGCAGATCCAGTGACAAACAAGCCGGCACTCAAATCAGAGGCATTCCCTACT
GTCACAGACTATTGCCGCACTCACTCTGCTAAACCAACAGACATTCTCATT

>RXA02774-downstream
TAAGGATTTTAGTCACCATGACG

>RXA02775-upstream
GCCCCCACCATCTTTGGCACTGAGATTGTGTTCGATTAACTACCACTGCTGCACACACAC
ATACAACACCTCTCACACACAAACAAGAAAGGGTCACCCC

>RXA02775
ATGACCACCGTTCAAGTATCCACCCGCACTGTGCGCGAACACCGTTTTACTGTGCCAGTG
GACTACGCTGTCGGCGCCACCATTTCAGAAATCTATGCTGCCTGTGCCATGGCCGAAAAG
AAAGCCAACAACCTTGGGCTTAACACTACTAAGGACGATTGGGCACGAGTCACTGTCACT
GATAATGCTGTTGTGTTCATTGTCGAGAATGTTATCGGGAATACT

>RXA02775-downstream
TAGAATTGTGTGCTCCTTAACGG

>RXA02776-upstream
GCAGCACCTAGCAATGCAGCCGAGGCAGCCCCTTCAGGTTTTGAGCCAGGTACGGCTATT
CAAGTTGTATAATCCTTCATTCGATGATCAAACACCTTCG

>RXA02776
GTGCTCTATCCTGTTGAAGCAGGAACGGTGTCTCTCGTTGATGTAAAGAAAGCGGCTAGC
CGTGCCTTTGAACAGTGGGAAAAGCACAACGAGTCCGCTGGTGATGTCGGTGATGATCTT
TCACTGCAGAGTATCGTAGATCTCATTGAGCGTGACACTTTCCCCACCGACGATGAGCAA
GAGCTCAATAATGTGGCTTTGCTTATCGGCGAACTCCTGGTGAGGGAGGCCGGTGGAGAG
TGGACGTCGTACATCTCAAAGAAAAATGATGAAGATGAATCGCTGGAGATTTTCGGGGTT
TTTGGCACCGGTGGCACTGAAGGATTATCTGTAGTGGGTAAT

>RXA02776-downstream
TGAGTTCGCATGGTTAGTGAAAA

>RXA02777-upstream
GGTCGCACCACACCAACTACTGTTTCTTCTGTAATTTGCACTGAAACTATCGCCTACACT
GTCACTGCTACCATCACAATCGGTTGCTAGTAGGCTACAA

>RXA02777
ATGAACCGCCCCCTTCAAAGTCAAAATTTTTCAATAACCAGCGAATGGGCAAATGCCACG
TTCAACGATATCGAAGACTCTTTGGAGGGGTCTTTTGACATCGAACCAGGCCAATACATT
GGACGCGGAGAATACTTCGTAGCTACTTCTGGAACGGGTTCCAAAAAGTTTATCAAGGTG
GTTTTGGGTGACGGTATCGATAGCGAACTAAATCGTCGCATCGAAGGTGAAATTCTTGCA
AGTAGTCTCCATCTTCCATCCACAGACCTAATCTCTCCTGTCGTAATTCAGTATGTGAAA
GAGTCTTCTAATTTTCCCGGTGACTTCTACATCGTGTCCGACTTCAAAGACGACACAGAA
ACTTTAGAGCTATCTAAGGCTTCTCTACCCCTCACTGACTTAGCCAAGATCGGAGCGTTT
CTCTTTCGTTTGGAATCTGTAACAGTTCCCCCTCAAAATCCTGCAAGGCGAGCAATGGAT
GTTTTGGATGGACTTTCTCTTCTTGCAAATAAAGGCAACATTGAAACAGGCGCACAATTA
ACAAAAGGAACTATACAAGCTCTTGAAATCATTAATCAAGAAGCGACCAACATCGAGAAT
GCACTTGAAAAAGTAACTAAAGTAGGATCACGGAAGTTTTTCTCGCATGGAGATCTTAAA
TTTTCTCAGTTCTTAATTAATGGTGAAACCGGAAAGATTTTCCTATGTGACTGGGAAGAA
TGCGGTAGTGCACATTTCGCAAATGACCTATGTTTTCTCGCAGGTGATTTGTTCTATAGC
ACAATTCGGGAACTGGTGGATACCAACATCAAAAACATTAAAGGCTCCTCGATCATTCAG
GAAGCCTACGATAATGCAACGCTTGAGGCTGTATCAAAAGTAAATGCAATATTAACTGGC
TATTCCTCAGAGAGGGGTTACTCTCTCACCTCGGACGAAAAACGAATCATTAGTATCAGA
ATCGGATTGGCTGGTCTATTTCGACTTTACACTGTGAGCGCTAAATCTAATGAGTTACGC
CCGCGCGAATTAGCCTTAGCCTCCATCGGAATGCAAATTACTTTAGGTCAAGCACCCAAT
CTGGTGTTTACAGATAGCAAGGTGGTT

>RXA02777-downstream

TAAGTGAGGAATTTGCACGAAAC

>RXA02778-upstream
CTCCGATTTCTGAGGTCAGTACGCGCTCCTGTCTAACTTCTACCACCCAGCCCAACCAAT
CGTTTTTCAAGGGTTCACCGAAGCAACTGTTGAGCACCTC

>RXA02778
ATGCAGGTCATTGAGACGCTTGATCCCGATCAGCGCGCAGCGGTGCTCGCTGCAGCGATA
CCGCGCGAGGCTAAGATCCTGGGGCGAAAAGTAACTCTTCGCCCTGGTTGGGGCAATATG
CGCGTACACGTCGTGATTGCAGTTATCTTTATCAAGTTTTTGCAACCGGATCTTCGCCAG
GCGCTGCTAACAACAGGTGATGCCGTACTTGTCGAAGATGATACC

>RXA02778-downstream
TGAGGCGCCTTCTGGGGCGTCGA

>RXA02779-upstream
CTCAAAGGAGACTGCACATCATGTTCCTCACCAAAGATATGCTCGCACGTTTTCCTGCAA
GTTTGAATTTGCCAATGCACAGTGCTCAGAACCAGAAGAA

>RXA02779
ATGGGCGAATACTTCCAGGTCGTTCAAAACATCGCCATGACACTGGGTGCTGGCGAAAGC
GTTGATCTTGTTGTCCGCGAATACATCAACGATGTGGAAGGCAACCCGACCATCTATCAC
GGTATGCCGCTGCGTACTGAATACCGCGCATTCATCGACCTTGATCACTGTGATCCGTCC
GCTGGTGAGCCTGAGCCTCGCTTATTGGGGGTTACTCCCTACTGGCACCCCTCCGTGATG
GAGAAAGCTCTTCGCCTTTGCTTCAAGCGATGTTGGTGC

>RXA02779-downstream
TGAATTCGGTCACATCAACGATG

>RXA02780-upstream
ATGGAGAAAGCTCTTCGCCTTTGCTTCAAGCGATGTTGGTGCTGAATTCGGTCACATCAA
CGATGATTACCGCACCTACCGTGCCCACAAAGACAGCCTC

>RXA02780
ATGTCCAAGTTCCATACACACCGTGATGATGTCATTTCACGTATCACTGCACTACTACCC
CAGCTTCGTGCACAAGAGCTGCAAGGTCAATGGTCTGTGGACATCATGAAAAACGGGGAG
GATTTCTACCTCATTGACATGGCTCTCATGTGCGAGTCCGCACTGTCTGAACTACTCACT
GTTACAGATGAGTACGCCACAGTCGAGCCGAGTGTCATCAATGACTTCGCCAACCAGCTG
GTCATTGATTATGACGAGCACGATATGGGCTTTGATCGAGACTTTCCAGCAGGTGTGTAT
AACACCCGACAAGCAAGTGCTATCAAC

>RXA02780-downstream
TAAAAAATACACACATCCACACC

>RXA02781-upstream
CTCCGAGAGTTTCCGCATCCGCGGTTCGATCCCGGACGTTCCCCGGGAGACGCGGTGGGA
CCGGCTGTGGCGGCCCTTCTGGGCGATACCGGCTGCCAGC

>RXA02781
GTGGTCGCGGCCCTGGTTTTCGGTTTCCTGCTTCCCACGTGGGAACGTGGGTTGTCCGAC
GCCGCGCTCAAATTCGTTTTTGAGGGTGGGCCTGATGCCGCCCGCGAGGTGCTGGGCACC
ATCGCCGCCTCCACGATCTCAGTGACCGGTCTCATCTTCTCCATCACTCTCGTTGTTCTG
CAGCTGGTGAGCAGCCAGTTCAGCCCGCGAATGCTCAACGGCTTTCTGCGCAACCGCATC
GTGCAGGCCACCCTGGCGATGTTCCTGGGGACGTTCGTGTTCTCCCTGACGGTCATCCGG
TACGTGTGGAGCGAGGACGAGGACATCACCGGATTCGTCCCCCGTGCTTCAGTGTCGGTT
GCCTTCCTGCTGGTGCTCGGGTGTCTGGGACTGTTCCTGGCGTTCATCCGGCTCATCACC
TTCTCGATGCGGGTGGCCAACGCCATCTCCGAGATCGGGGAGGAGACGATGGCTCTGGCC

GCACGTATCTATCCCGTGCAGAGCGACGACGCAGGCCCAGTCCAGGGGCCGGGCTGGTCA
CCGCGGCCCGGTGACCCCCGGGAAGAAATCCGGGTGGGCAACCATGGTTCGCTGGTGTGG
ATCGACTACCGGAAGCTGGTGTCCTGGTCGACGGAACACCAGGCGGTGATCACGGTCGAC
CGGCCGGTGGGGGACTTCCTCGTCGAGGGCCAGCCGCTGCTGCGGGTCTGGTGGGACGGG
GAACTCAGCGACCGGGACCGACGCGTTCTGCACTCGGCCATCGAGGTGCGGACCGAGCGG
GAACTTCACCAGGATGTGGCGTTCGGACTGCGTCAACTGGTCGACATTGCCGATCGTGCG
TTGTCCCCGGGCATCAATGATCCGGCCACGGCGGCCCAGTGTGTCCAGGAGATCCACCGG
ATCTTCCGCTATTTGGTCACCGTCATCGAGCCCAGCCCCTACATCGCCGATGACGACGGT
CGGGTCCGTGTGGTGCACCAGCCGCAACGTATCGCGGACATGCTCTATGAGGTGATCCGT
GAGATCCATCTCTACGGGGCGGATTCTGCGATGATTCCGAGGCTGCTGCGCACCATGGTC
GAGGACCTGGTGACGGCCGCTGCCGATCATTCCCTGCCTGCCGTCGAGCGTGCCCGCGGC
ATCCTGGACGATGAGACGGACGAGGACCGCGACAGTGACACCGCGAACGTC

>RXA02781-downstream
TGATCCGGGATCAGGTGGCGGTG

>RXA02782-upstream
GTGGATCTGTTGCAAGCATGAACCACCATTTATCTGGAAAACCTCACCAATTTTGCGTGT
ACGACAGAACACCCAGTGCCCTGTGTGCTCAGAGCGAACT

>RXA02782
GTGGCGCCGGCGCTTAATGATCTTGCAACCACTCACCCTAAACTTGCCGAGCAAATTGCA
GATCCTCAACCAAGTGGTGTGAGCGCCGCGGCCATTATCCCCACCATTAGCAGGGGTTCC
CATACGCAATTAACATGGCAATGTTCTAAAAATCATGACCACCAATGGGTCGCCACAGTA
AAGGATCGTGTTCGCGGAACAGACTGCCCCACCTGCGCAAATACAGGAACTTCACGCAAA
GAGGCTGAACTTATTGAGGTCATCCGTGCATTATTCCCAAACACTGATGTCCAGCAAGGT
GCGCTCATTAATGGACGTACCGGTAATCAAGGTGCATCGCCGTCAACCGATGTACTCATA
CCGTCCAAAAATCTCGCTATCGAGTTCAACGGCCTGTACTGGCACTCTGAGCTTTTCATC
AAAGATAAGCATTATCATGCGAACAAATCAGCTCTCGCAGAACAAGCCGGTGTGCAGCTC
ATTCATGTGTGGGAGGACGACTGGAATCTTCGCCGCGACATTGTGATCCGCATGATCGCA
CACAAGCTTCATGCAACCCATAACCTCAGTGCTGTTTTGCCTACCGAAACTACTGACTCA
CGTGTGGCAACCACCGCTTTCGCCGTACACTCACACTGTCGGTGGTCTCTGGTTCACGCG
CTGCTGCATTCT

>RXA02782-downstream
TGAACAGCAACCATATTCAGGGT

>RXA02783-upstream
ACAAGCTTCATGCAACCCATAACCTCAGTGCTGTTTTGCCTACCGAAACTACTGACTCAC
GTGTGGCAACCACCGCTTTCGCCGTACACTCACACTGTCG

>RXA02783
GTGGTCTCTGGTTCACGCGCTGCTGCATTCTTGAACAGCAACCATATTCAGGGTGCTGTC
TCGGCCACTAAGCACTTTGCCCTGTGCGACAACAACGACGATATTCGAGCACTCCTGTCG
GTGCGCTCACCAAAAAACAATGCCCGCATGTATCGCAAAAAAGGCACATGGGAAATCCAG
CGCTATGCGACACTCGGTAACGTCCCTGGCGGTTTTACTAGGCTGCTGAAGTTTGCCGAG
CACACACTCAACGAACACAGCACAGTACTCAAGCAATGGATCTCATTTTCTGCTGCTGAT
GTCTCTGACGGCAGCCTGTATCGAACTGCCGGTTTTACCGCCGAGCAACAGCTTGCACCG
GATTATCGCTATGTCGGTGGCGCAACAGGTTGGCGCCGAACACCCAAAGAAAGCTTCCAG
CGCAAACGCTTTAGAGACGACCCAGCGTTGCTATGGAACGAATCTTGGACAGAGCACGAA
GCAGCGCTCAACAACGAGCTCTACAGAATCTACGATGCCGGCAAAACCCGGTGGGTTAAA
AATGTTGCT

>RXA02783-downstream
TGATTCTGCAGATTAGTTACTGA

>RXA02784-upstream
AGCTGCAACTCAGGTAGAAGAAACAACAGTCGCCCGAGTTGAACACGATACTTACGACAC

TATTGCTAACCAGCTACAAGATGCCGGTGTCTATGACGAT

>RXA02784
GTGGCCTTTGCCGAAGGCTACTACCAGGAAATGGCTGAGGTTGTATGTGAAGCACGCGAA
GAGGGTATCACCCACGAGGACACCCTGCATATGCTCAATGACATGATGGCAATGAAACGA
TCTGGCGAAGTACTCAATACGCTCGCTGATGTTCTCTATGCAAATGAATGCCCTGAATAT
CGAATC

>RXA02784-downstream
TAAATTGTTGGTCACTCTGCATA

>RXA02786
ATCCTGCGCAACCTCGGCCAATCGCTGGGCAGCCTGCACGCCGCCACCGCAGACCGCGAA
GAAGACTTCAACATTCTGCTCAACCGTATGCTGGCCAAATACCCAGCCACAGCTGAGATG
CAGAAAAACCGCGATAGGTTGCTGCCCGCAGCAATTGAGGTGGGTAAAAAGATACTTGTC
GACGCCGGGGTCACCGTTCCAGAAGTCGTCGAGGAGTTTGCCCGCGTAGCTCGGCGACGC
CTGATTTCCGGACGCCACCGTGCCTTCACACCTTTTGACTTGTCACCCGACAACATCATC
GTGGCTGAACGCACCCACTTCCTGGACTACGAAGTTGCCGGTTTCAGGGATGCCACCTTT
GATGTTGCTTGTGTGATCGCAGGTTTCCCGCAATTCGTGTTCAGCCGCCCCATCTCTGAT
GATGAGGTAGACGAACTCATTGAATCCTGGGTCCAAGAAGTCCGTGGAATCTGGCCCAAT
GTGAACAATGAAGAGCGCCTCCAAGCACGTATCGTGACCGCTCTCATCGGCTGGGCACTA
TCGAGTGTTGCCTTCATGAAGCTCGGCTCCATCAGCGGCATGCTTAACCTGCTGCACGTC
ACCGAAGATGGAAACACCACTTTGGATGTCTCCAACCTTGATGAACTGTTGATTCCACGA
TCTGCCGAAGATGACGAGCTGGTCCAGCAAGACCTCCACGACACGTTCTCCGCGCTTCAG
CGATTTGCAGCGCGCGGGCTGGATTCCAGGTTCCCTGAGGTGGCACGATTCGCAGACGAC
GTGGTGCGTTTGTTCCTCAAAAATGAC

>RXA02786-downstream
TAGCTGAAGAGCACCGGTTGCTT

>RXA02789-upstream
TTCTTCCGTACGGCTATGCTTAAAAGCTAAATTTGTCTTTGTGCCTTGCAACACATTAAT
TTCTTAACACTAAACAATGGAAAGGTAAGCGGGTTTTTCT

>RXA02789
ATGAAGGTTTCCGCCGATACACCCGGTCACGATGATCCAGGCCCAGGCCGGCGCCTTGGC
TTAGATGTCGGCACCGTGCGCATCGGAGTGGCAGCCTCTGACCGCGATGCCAAGCTTGCC
ATGCCTGTGGAAACCGTTCCGCGGGAAACTGGATTCAAAGGGCCAGACCTGGCCGATATT
GATCGGTTGGTCGCCATCGTTGAGGAATACAACGCCGTGGAAGTCATTGTTGGTCTACCC
ACAGATCTGCAGGGAAATGGCTCCGCCAGTGTGAAGCATGCAAAGGAAATTGCTTTCCGC
GTCCGTCGGCGCCTCACCAATGCTGGAAAGAACATTCCGGTACGGCTTGGCGACGAACGC
CTCACCACCGTCGTGGCCACCCAAGCCTTGCGGGCCTCAGGAGTCAGCGAAAAAGCGGGA
CGTAAAGTTATTGATCAAGCTGCCGCAGTAGAAATCCTTCAAACCTGGTTGGATGCTCGC
ACCCGAGCCCTTGAACCACAATCCACAGACACCCAAGATTTCGACGAGAAGGGAAATTTC
CCAGGA

>RXA02789-downstream
TGAACCAAATCCGAAACCGCCGG

>RXA02793-upstream
TGCATGCTCCTCTAGTGATGTGGTGGAAAGTCAAGGGATAACCGTTGAAAACTGTGGCTC
GGTGGTGAATTTTGATAGTCCACCATCACACATCGCCTTG

>RXA02793
ATGAAAAGCGCCGCCGTACCCACGCTTGATGCTTTAGGTGTTTTGGATCGCGTGGTGACC
AAAGCTGGTGCCTTCCCAGCTGGGTATTACGACGCCGATTTATCGGAAAGAGTCACGGAC
ATCCCAACGCTGTCCAACAAGATCGACGCCAGCGGACACGTGTTGATCTCGAAAGAAGTC
GTTGTTGCCGCCAACCCAGACATTGTTTTCGGCGAAACTGACACCATCAACCGCGCATCC

ATGGCATCCTCGAACATCCCGGTCGTGGAGGAACCAGCATTCTGTGGCAGCATCGACGGC
GACGTGAGTTTTGATGATGTCTGGTCACAAATCTCCACCTATGGCACCATTTTTGATCGC
TCGACAGAAGCAGACGCATACATTGCAACGTTGAAGGAACGTGTTTCTGAAGTATCCTCG
CGGGTTACTGACTCCGGAAAAACTGTGGCGGTGCTCTACCCCACCATCGGCGGCGGAGTC
ACCTACGCATACGGCCGCGGATCCATGGCCAACCCACTTGTTGCCGAAGCAGGCCTGACC
AACGTTTTCGCAGACCAATCCGAACGCGTCTTTGAGGTCACGGCAGAAGAACTGATCTCC
GAAACCCCGACTCATCATCGTTTTACACAGCGACGGTTCCCCTTCAGACATCGTCGCAGA
GGTGGGCAATCTCCAAGGGTCCAGCGCACTCACTGCTCTGAG

>RXA02793-downstream
TGAGAACAAAGTGCTGCCCATAC

>RXA02796-upstream
GATTATTCATGGAACATCCTTAGCGGAGTTATGCAAACGTTTTCATAAGGGGTTATTCCA
TTCTACGTCGATCTTTGTAGAAGGTGGTTATTATGGCTTC

>RXA02796
ATGAGACTGTTCGCGTCTATCACTCCGCCGATTGAAGTCACCGAGCATCTGATCAACGCG
CTTCGTCCCTACAAGGATGATCTGCGGTGGTCTGATCCAGACAATTGGCACATCACGTTG
GCGTTCTATGGAGAATTACCTGATGGGGCAGTCGAAGATCTCATTGAGCATCTGACAAGT
GCAGCCCGAATCAATGAAGAATTCACCATCAGAATCAAAGGCGCAGGCTCATTTAATCGG
AAGAATTTGTGGATGGGTGTTGGTGGTGACACCAAAGATCTGCGGCGACTGATGGCTGAT
TGTCTGATTGATCCTGAGGAACGCCGACGCCAGCGTGCACACCTGACCGTGGCGAAACCA
ACGCAGCGACAGCGCAGCCGCGATTGGGATCCTGTCATCCCCGATCTGGTCCACGCTCTC
TCTATATACGAAGGCCCCGAATGGCCAGTCGATGAGATTGAACTGGTGTCTTCTGAACCT
GGAAAAGGCAGAAGCGGTGGGCCACTGTATACAACCGTGGCCACCATTGCGTTGTCATCT
GCGCTGGTT

>RXA02796-downstream
TAAAGGCTCAACCGCGGAACGGC

>RXA02798-upstream
GCATCAAAATCATGTGCATTCATCATTGCTGATCATCATAGACCTGTTGGCAAATGAATT
CACCAATTCTTTAAAGCTCTCACCCTCTTTAGGGAACTGA

>RXA02798
ATGCGGTCTGTACTCGACTACTGGATCATGACTCTTGCACCTTCCACCAATGCGGTTTCG
CAGCAAACAAGAAGGAACCCTTCCCAAGCGCCGCGACTTCTTCATCGACTTCACTTCTTT
GCCGGCATTATCTGCGCACCGTTGATTTTCATCGCTGCGCTCACCGGACTGGTGTATGCG
TTCTCCCCCACCATTGAAAGCATCTCTAATCAGGAAATGCTCACGGTCTCCAAGTCGGCT
AGCGACACAGCTCTTCCGGTGCGTGAACAAGTGAGCATCGCCCAAGAACTCCACCCCGAT
TTAGATCTCTCAGGTGTCCGGCTTGGCGATGATTCCTCCACCACCCGCGTCCTCTTCGCC
GACGAGACGCTTGCTGAATCCACAGTCCGCGCCGTGTTTGTTGATCCCTACACCGGCGAG
ATCACCGGTGATACCACCCAATACGGAAGCTCAGCTGCACTGCCGTTTCGGCAATGGGTC
TCGCAAGGTCACCGCATGTTGTGGCTTGGTGAACCTGGACGTATTTATTCCGAACTTGCG
GCAAGTTGGCTCGGAGTTTTAGCCGTAGGCGGTTTCGCATTATTGTGGTTGCGCAACAAA
AAGCCCGGCCGCTTGAGAAAGATGGTGCGAACTGGTGGCCGTGGTCGAGTGAAAACGTAT
CGCCGACATGCAGCATTGGGCACCGTAGCGGGCTTGGGTTTTGTGTTCCTCACCTTTACT
GGCCTGACCTGGTCAACTTATGCGGGATCCAACATCACGGATTTACGCACCCAACTCAAT
TGGACGCAGCCTTCCGTTAACGCTTCTCTAACAGCTGCCCCACAAGTGGACATGCATGAT
GAACACGCAGGTCATCACATGCATATGGAGTCGGCAACCTCAGGCTCAGGTTCTATAGAT
CTGGTAGCGGCCACGGCTATCTCCGAATTACGCACTCCCCTCACCATTACTCCCCCAGCA
CAAGATGGCCTCGCGTGGACTGCCACAGAAAACCGCGACGCCTACCGATTCACCACTGAC
ACCATCGCTGTTGATGGCGACACCGGAATGCTGACCAACCGTTTGAATTCCACTGATTGG
CCATTAGCTGCTCAAGCGAGTGCATGGCTCATCCAGCTTCACATGGGCACCCTGTTTGGC
CTTCCCAACCAGGTTGTACTTGGGCTGTTGGCTGCCTCAATAATCGTGATGATCGGCCTT
GGGTATTGGATGCTGTGGCAGCATCGGCCACGGGAAGGTTGGCCTAGCGCTCCCAAGCGT
GCAGGATTTGAAAAACCCACCTGGGGAACTATCGCGTTGGGTGTTGTGGTGATCGCGTAT
GGGCTTCTCGCGCCACTTTTTGCAGTTTCACTGCTCGTGTTTATTGGATTAAGCCTTGGA

GTGCGGTTTATTTCTCGTATGTCCGGGCGCGCGGACACGTCCAAC

>RXA02798-downstream
TAAGAACACCAAACCACACCGCC

>RXA02799-upstream
TCGCGCGCAAGTGTTCAGTAATATGGACTCCCAGTAACGGGTTTTCATGACGCGTTAAAT
TTTTTAGTTGATCACAGATACACCAATCAGGAGTAGCGCA

>RXA02799
GTGGCACGCAACATTGAAGACATCCAGCGCGATATTGAGCGCACCCGCCGTCAGTTGGCT
TCCACCCTCGACGAGCTGGCAGACCGCAGCAAGCCTTCCAACTTGGTCGATGACGCCAAG
AACCAGGCAACCGCGAAGCTGCAGGAATCAAACGTACAGAAGGTGCTCCTGGGCGTCGCT
GCTGTCGTCGTCGGTGCTGTTGTATTCAGCGTTGTGCGTGGCCGTAAGAAGGCAAACGAT
CTGAAGGAAATCCAGCGCCTGCTCTCCGAGCGT

>RXA02799-downstream
TAAATTGCTTTTCGACGGGGCGT

>RXA02812
GCTTCAGGCACCGACGCCTCAACAATCACCCTTGACCAGGTAGCTCTTCCCGTTGCCACT
AACTCCGGAGCATCCGCAGCCGTAGCGCTGGCGCTGGCTGAAACCCCAGAAGCTGCCGCT
GCTGCGCTCAACCGTGACGCCGATGTCACCGCAACTGGAGCTGCCGACTCCCCTGCGTTT
GCCACCGTTGAAGGAGCAGAACTTCCAGAGGGCTACACCTTTGAAGCAGTAGACAGCGCA
GAAGTACCTGTGTGGGCTGTTGCCATCAACGCTGGAAACGGTATCTCTGAAGACCAAGCC
CGCGCCGCCTCTGATTTCAGTAGCTTCAGCTTCGACACCGGCAACGCCGATAACTCCGCG
CTTGAAAGTGTTCTCACCCAAGCTTCAAGCGAATCCGCGGCAGAAACTACTGAGGCGCAA
CCAAGCGAGACCCCGGTCGAGCCCGCCGCTGCTTCCCCATCCGATACCATCATCAACCTG
GATACCTCATCCAACATGGATCGAGTTGTTGACGGCAGCCAGGAAACCTACCACACGGTT
ACTTCCCGGACTCTGGCCAACCTCGCC

>RXA02815
TGGCTGCGCAGTACCAAAGAGTTCGAAGACCAGCCCGTGATTCCGGCATTCGAAGTAATC
GCAACGGTTGCCTCTGAATTCGCAGGCGACGACGGCAACTACTCCAACGAATTCCCCGTG
GAAGATCTAGTCGGATACGTTGACGCCATCACCGAAGCCGGCGGATACGCAGTCCTGGAT
CTTCAACCCGGACGCGCCAACTTCCTCGACCAAGCCAAAATGTATGAAGAACTCCTCAAA
CGACCAAACGTTGGATTGGCGCTAGATCCCGAGTGGAAAATCGGACCCGATGAGCAACCC
ATGACACGAGTGGGCTCTGCAGATGCCGCCGAAATCAACGAAGTATCCCAGTGGCTCGCC
GACCTGACCGCCGAGAACGATCTTCCACAAAAGGCATTTGTACTGCACCAATTCCAATTG
GAAATGCTCACCAATCGGGATCAAATCAATACCGATCACCTGGAACTGGCTGTCGTGTTG
CACGCAGATGGACACGGAAACGCAGGGGATAAGTACGCAACTTGGAACATGCTTCGCGAG
GGACTGAGCCCG

>RXA02817-upstream
AAAATTCCCACCCCCAAAACTCCCCCACTTCGGTTAAGGAATCAGGATTCTCACAAAGTT
CAGGCAGGCTCCCGCTACTTTTCAGCGCTAATCTTGGCTC

>RXA02817
ATGATTTTAGGCGTACCCATTCAATATTTGCTCTATTCATTGTGGAATTGGATTGTCGAT
ACCGGTTTTGATGTAGCAATTATCCTGGTCTTGGCGTTTTTGATTCCACGTATCGGCCGA
CTGGCCATGCGTATTATCAAGCGCCGAGTGGAGTCTGCAGCCGATGCGGACACCACTAAG
AACCAGCTCGCGTTCGCCGGCGTTGGCGTTTATATCGCGCAAATTGTGGCGTTTTTCATG
CTTGCCGTCTCCGCGATGCAGGCTTTTGGTTTCTCTCTCGCGGGCGCTGCGATTCCGGCA
ACCATTGCGTCAGCTGCCATTGGCCTTGGTGCGCAGTCGATTGTTGCGGACTTCTTGGCC
GGATTTTTCATCCTGACGGAAAAGCAATTCGGCGTGGGT

>RXA02818
TCCTATTCCCGGAAGTTTTTGACCCAGGTGTGGATTCGAGACAATGTCGGCGATTATAAA

GGCCTTACCGATACGGCGTTCCGTAAGAAGCTGCAGCGCGATCTTGCCTACCTGCGCAGA
GTTGGCGTTCCGATTGAGCAGTTCACGGTCACCTCAGGCATAGCTGAAGGCCAGCAGGCG
TACCGTCTGGCCCAGGATTCTTATAAGCTCCCCGAGGTCGAATTCACCCCAGATGAGGCC
GCCGTGCTGGGCATGGCAGGGGAGATGGGCCATAATCAGGAACTCGGCGCCTTCGCGCGT
TCGGGGTGGACCAAATTGGCGGCCGGCGGCGCGCAGCGTGATCTGTCCACGTCCACAGCC
TTGACCAATGCGGGCGATTTAGGTTCCTTGTCTGCAAAAACCCTCGATGCGATCATCAAA
GCCCGCCAATTGGGCAAGCAAATCAGCTTCGAATACCGGCGCGCCCCCAAAGACGCCCCC
TCGCTTCGACACATGGATCCTTGGGGTCTGGTCCCTGAGCGCGACCGCATCTACCTGGTC
GGATTCGACCTCGACCGCCAAGAAGCACGCACCTTCCGCATCACCCGCGTCCGCAACATC
AAACTC

>RXA02823-upstream
TTATGTNTNTAAACAGCCAGTTGGGGGTCATGGGGGAGCGCCCCGTGACTGGTTAATGCC
CCGATCTGGGACGTACAGTAACAACGACACTGGAGGTGCC

>RXA02823
ATGACTGTTAGAAATCCCGACCGTGAGGCAATCCGTCACGGAAAAATTACGACGGAGGCG
CTGCGTGAGCGTCCCGCATACCCGACCTGGGCAATGAAGCTGACCATGGCCATCACTGGC
CTAATGTTTGGTGGCTTCGTTCTTGTTCACATGATCGGAAACCTGAAAATCTTCATGCCG
GACTACGCAGCCGATTCTGCGCATCCGGGTGAAGCACAAGTAGATGTCTACGGCGAGTTC
CTGCGTGAGATCGGATCCCCGATCCTCCCA

>RXA02824
TTCTACGAAACCGGCGAAGCCCTCGACCCGACCGGCGACAGCCTGACCATTTCCTCCACC
ACCACCGCGCCATCGACCAGCACGACCTCCACCTCTGCCTCAACTTCCGGTGGAACCGCC
GACTGTTCCTCCGGCGCATTGGGTGTTGTCACCACCGGAACCAACGACGGCATGCTGGGC
ACCATCCAGGAAGTAAACAACACCTTCGCGATTTGGAACAACCTCATCGTCAACACCGAG
CGCATGTTCTGCAACATTGATACCCTCAAGGCGCGCTTCGACACGGATGATTCCAGCGAT
TCAGCGACCTCTGCGACTTCTGGGACTACTGCGTCCACCGGCACCACCGCTGCAACTACC
GCGGGAACCACGGGTACCACTGGAACTGCCAGCACCGCTTCCGGAACTTCCGGAACTTCC
GGAACCTCCGGCACCGCAGCAACTGTCGCTGGCACCACCCCAACTGACAATGGCGTTTGC
ACCGCTTCCGGATCTTTGGGCGTGACCCAAGCATCTGCGCAGTGGGGT

>RXA02825
AATGTTTCTGCAACGGAAGCTTCCGGTTCCGCTTCGGTGTCCCTGTCACAGTCGGGTTCG
CAGGCGTTCGCTGATTTCTACACCCCAGGCACCCAGTTGGATCCGATCAGTTTCAGCGCA
ACTTTGGGCGGCGACGCCAGCTGCGCCACCGGATCCACCTCGACCACAGGCGCTGCTGCC
ACCGCGAACACTGACAACACCGAAGGTGTTGCCGGCGAGGAATCCACCACCCCCGCTAAC
CAAAACAGCCAGTTCCAAATCCGCCAGGCCGCTGCAGATTCCACCGGACTGGATACCACC
ACCACAATGTTGCTCATCCTCGCGGCGTTCGTTGTCGCAGGTGGCTCCATGACTCGCTTC
ACCGTCGGCAACCCGACTGGAAAA

>RXA02825-downstream
TAAGGCTTCACATGAATAACGCT

>RXA02827-upstream
CGGTTTACTTTTATTTATCGAATGAATCATGTACATAGAATAATAAGCATTAAAGGGGGG
GCGGGTAGGAAGAAGCAGCCGTGTCGCATATGCTTACTTT

>RXA02827
ATGTATGAGCAGCAGAAGATCCTTAACGAAGTCAGTGAAAAACGTCTTCAGGCAATCAAA
GATTTTACAGAACTGGGATCTGGATTCAAGATTGCGATGCGGGATCTTTCCATTCGCGGT
GCAGGTAATCTCTTAGGTGCTCAGCAGCATGGATTTATTGATGCAGTCGGTTTCGATATG
TATTCTCAAATGCTAAGCGAAGCTGTTTNTCGTAAACAAGGAAAGAATAGTCAAGTGGAG
AAGNCCNCTGTTGAGATCGACCNCGGTGTCGATGCGTATCTACCTGAAACATACGTGGCA
GATCANCGGCAGAAAATCGAGATCTATAAACGAATTCGTGAACTTGATTCGCAAGAAATG
CTAGATGAACTAGAAGATGATCTGCTCGACCGTTTTGGAGAACANCCAGAAGAAGTAGCA

CAT

>RXA02838
ACCGTGCCGCTGGGCGACGGGCAGGGGCGGTATATCGCGAAGATCCCCTCGACCGCGTTT
GTGGGGGTGTCGGAGAACAAATTTGCCAATCTGGCTTTGGCCGAGGCGATCGGGATGGAG
GTGCCCGCGCGCGAGTTGGTGGGGCGTGCGCAGTTTGAAGGCGTGCCCCCCGAGTTTGAG
GCCATGACCGACGGGTTGGTTTTGCTGGTGCGGCGGTTTGATCGCGCGGGCGATGGCGTG
CGCGTGCATATGGAGGATTTCGCACAGGTGTTCGGCCTATACCCCGCGCGCAAGTATGAT
GGGGCGGCCAGTCACGATATTGCGGCGGTGCTGGGCAGTGCGGTGTCGATCGCGGCGGGG
TTGGAGTTCGTGCGGCGGCTGGCGCTCTCTGTTGTGATGGGCAACGGCGATATGCATTTG
AAGAACTGGTCGCTGATCTATCACGGGCGGGGCGATGTGCCG

>RXA02840-upstream
AAGTGAAATCAATCGGCTTTTCCAGCAGCAGCACTGGTCGCGCCAGCGTGGGTGTTATGG
TGAAGGCGAATACACCTTCAGCACCGCTGAGCCGGAAGAG

>RXA02840
ATGACGGTAATCAGTGGCGCGCTGAATGTGTTACTGCCTGACGCGACCGACTGGCAGGTG
TATGAAGCCGGTTCGGTGTTTAATGTTCCCGGTCACAGTGAGTTTCATCTGCAAGTTGCC
GAACCCACCTCTTATCTGTGCCGCTATCTG

>RXA02840-downstream
TAATTCCTCGCCTTCCCCTTGAA

>RXA02841-upstream
ACCACC

>RXA02841
ATGTTCGCAGCTTTTAAAAGCAATCTTCCGACCATTAAAAAGCTGGTTTATGAGGTCATT
AATGGCGTCGATGCAGCGCTCAACGAACTAGAGCGACACGTCACTAATGAATCAGTCCGT
GCTCGCGAACTCCCTAATGTCCAGTACAAAGCCACTGCGGGGCGCAACTTCGCCATATCC
AAGCTGGTCCAAAATTTGCGTCGCATCAACAAGGCACAAAACAATCCACGTGGTGTGCCC
ACTCATGCCACCGTGATTCTGCTTAAGGGAGACGGCAGC

>RXA02842
GATGCGGGATTTGTGTACTTCGGTGAAATCGATGATGCTGGCCATATTTTCGGCCTGGCA
GGCGACGAATACCGAGGGGGGATTCGCAGGGTCGACACCCACGTGAAGAAAGTTCTTTCT
GAAGTGTCACGACGCTCCGACGAGCTCGGGGAGGACTGGCTGGTAGTGATCACAACTGAT
CATGGTCACCTTGATGAGGGCGGGCACGGCGGCACCACCGATCGGGAGCGAGAATCCTGG
ATCATCACGTGGAGCCCGCACCGGGAACTGCCACAGTGGCCTGAAGAAATTGCGCCGCNT
GAGCTGGCAGAACTGATGCTTGTGGAGCGCCGAACCTTGAGG

>RXA02842-downstream
TGATTGTCACTAAA

>RXA02845
GAGGATCACACCTCAATGCTCACCCACTTTTCCGCAGCTGTCGGCATGCATGACCGCGAT
CCGGCTCGCTTCCCAGGCCAGGGCGACGGTTCCTACCCGGATCTTTTTTGGCTGTACAAA
AACGCCCTCAACCTGGTCATTAGCTCAGTGTTGTTCACCCGTGAGCAGATGGACAACATG
CTCGATCAGATGGATGAACACTTCACGCGCGCGGGTATCCCGCGCATCGCGATTAATATT
GAGCGCCGCGACGACGCCCTGATGAACGGCTCCCTCGAGCGTGCGCTAGAGCTGCAAGAG
CTTATCGACGCCTCCCAGCACGACGATCCCTTCGACGACTGCCCAACCTGCCAAATTGCA
GGAAAAGCGGCACTCGCAATGGCAGCAGATGATTACGACGAAACCCAAAACCTCGTCTCC
CAAATCATCAGCTACGGATCCATCGGCTGCGTCATGGAACCAGAGACCACCCTCGCTGCG
TTCATGCTGCGTGTGCTTAAGTCCGGCGATGCTGATTATGCCCGCTACCTGCAAGATGTC
AGTGCGAAGGCAAACCCAGAATTCCAGTCCCTTGATTCCGTTGGACGCCACCTAGAATTC
CTCGGCATCACTGGA

>RXA02846
GTGAATGGTCTGTCCATCATCAACGCGGTGAATAATGCGTGGTCGGTGCGCAAACGCACT
GACTGGGCCAAATTCCGAATTCTTGCCGGCGCTTTGGTGCTTGGTTCTGTTCCTGCTGTT
GCAGTGGTGTATTTCCTTAACGGACCATGGCTGTTGATTTTCGTTGGTGCGATGGTGCTG
CTCGCGTTGGGTGTTTCCCTGTTCCCAACAGAGAAATTCGCACTCAAGCAAGAAGCTAAA
CTGCCTATGGTCATCTTCGGCATGATTGGTGGATTCATGTCCACTGTTGCAGGCATCGCA
GGGCCATCCCTGACTGTTTATGCGCGCCTGAGCCGCTGGGATTACCGAGACTTTGTGGCC
ACCTTGCACCCAGTTCTACTCGTGGCCAACACCGTATCGTTCCTGCTCAAGGTTATCTTG
ATCGGTGGACTCGATTTCGGTGGCGCACCCGCATGGCTCTGGATCGGTGCCGTAGCGATG
ATCTTTGTCGGTGCTTGGTTGGGTGAAATCGTCAACGCTAAGGTGTCCACCCCAATGGCC
AAGCGCATCGCTACGCTCCTGGCAGCAGCTGGT

>RXA02847-upstream
CCAGCCTCTTCTATGTCCAAAAACTGGGAGCTCGCATCCCAAGGGTGCTGCCTACGGAGC
AGCCTCTGCAGAAGTCAGTCCTTTCCAGCACTTGTGGTCC

>RXA02847
ATGGCTGTGCAAGGGCAGTTCTACCTCTTTGCCATCTTGTTGAGCATGGCGATCATCCTG
ATTCGTCGATACCGCCCCGAATACTCCGCAGTGCGACTAGCGACTCCTGTGCTGGCAGTG
CTCACATCCGTATCATTTTTCAGTGCAATCCTGTGGCATTTCATTGATCAATCAGTCAAC
TACTATTCCACCTTCACCAGGTTCTGGGAGCTCGGCCTTGGTGCACTATTGGTGCTGCAT
GCGCCTCGAATTTTGATTTCTGCGAAGACTAAATCAATACTCGCAGCCGTCGGTTTGTTT
ATGGTGCTATCCACTGGATTCTTCATGGATGGCGCAGAGACTTTCCCTGGATTCCCCGCG
CTGTATCCCATCTTGGGTGCTTGCTTAGTCATCCTTGGCGACGGTAAAATCTCGGTCTTT
CTCTCCCGAAAATGGATGCTTTGGCTCGGCGATATCGCCTACCCGCTCTACTTGTGGCAC
TGGCCTCTGCTGATCATTTTCACCGCTTTGTTCAACCAAGAAGAGCCATCCATCTGGCTG
GGTATCGCCGTGATTATGCTGTCCCTTGGCTTGGCGCAGCTGACTAACAAATAC

>RXA02848-upstream
AGCAAGGACCGCAACAACTGGGGCAACCTGGATGAGCGTCTGTCTCGCCCGAACACGTTT
AACCCCAGCGCGTTTCAGAATGTGAATTTCTTCTAGTTAC

>RXA02848
ATGCAGATCGTTCTGGCTTCGCAGTCCCCGTCCCGCCGAAGAATCCTCAATTCGGCGGGC
GTCGAGCCCCTCATCCACCCAGCTGATGTTGATGAGGACGCGCTCCTTCACTCCCTCAAC
GGCTCTGCGCCGGAGGAGATCGTCCGCCAGCTTGCGCTGGCTAAAGCACAGGTGGTTGCG
CCGTCCTATCCGGGCGACGTCGTCATCGGTGGCGATTCCATGCTGCTTATCGACGCCACC
CTCCAAGGCAAGCCGCACACCCGCGAAGCCACCATCGAAAGATGGAAACAACAACGCGGC
AACAAGGCCACACTGATCACCGGCCACGCCATCATCTTTGGCGATGAAGTGATCGTGGAG
TCCTCCTCCACCAACATTCATTTCGCCGAGGCCAGCGAT

>RXA02849
TCCCCATACCCCGTCATGATCAGCACCTCTGCCGACGCCTCAAACGTGACCGTGCGCATC
ATGGGTGTGGACACCACCTCCGTGGAATCCATCAACAACGGACGTTGGTCCACCACCCAG
CCCAACACAGTTCGAGTATCGGGTTCAGATTGTGTGCCATCAACCGGTGCACCAGGATTT
ACCACCTCAGACACCCGAATCATCAGCGATCTTTCTGGCAACGAAATCACCAGAGAACCC
GTCACCACGGTTTACGATCCTTCACCAAACGTGGTCTGCTCC

>RXA02849-downstream
TAAAACAAAATGCCCCACCAGAT

>RXA02856-upstream
GTTAAATCATTGCCGCCCAGAAGAAGACCGCGCGGGCGAATTTGGGCTTGGAGGGAACCA
AACGGCCACTTTTCCAGTCCAACAAAGTATGAGGATTAAT

>RXA02856

TTGCCCCACGCCAAAGAGCTCGCCCACGAGCTGTGTTTGTTGCCCACCCCTGCTGTGCCC
GCGCTTCCCACTGATTCTGGCGCGCAGTTTGATATCCACCAGGCACTATCCGCCTCCCTT
GCCACCTATGCCCGCAACCTCACCTTGCTGTCCCACACCGCCGAGAATTTAGGAAACCGC
GCGCTGACGGGCCTCGCTGAAATCGAAGACACCGACGACCAACTCGCACACGCATTGGAG
CGCCTGACA

>RXA02856-downstream
TGATCGGTCTGATCAGCGCCCTT

>RXA02858
CCAGAGTGGAAGAAATTCAACTCCGGCGACGCAGCCCGCGTTGTCCCAGACGCCAACGCA
GAGCTCGACATCATCGGCGCACCAGCACTTCTTGCCGATCGCCCCTCCTACGCAAACGTC
AAAACCCTCTCCCGCATCTTCGCTGTCATGCGCAGCCTCGGCCACGTCACCGCTGCCTCC
CCAGTCACCGTGTTCTTCTCCTCCCACTCCGTGCTCAGCAACGTTGACCGCGGATCCGAG
CACTACTCCGGACCCAACGGCCTGGGCGAATGGACCTCCGTTGGTCGCGCAGTAGCCACC
AACTGGAACGGCGTTGTCGACGCCCTCGACGAAGCCATCACCGTCAAGGAAGTAAACAGC
CTCTTTACCGAAGACGCCGCAACCCGCATTCAAGAAGCACAAGCAGCTGTTCAGGCAGCT
CGCGAGGCTGAAGAGCAAATCGCCAAGGAAGAAGCCGAAAAGGTCGACCCTTACGACAAC
TCCCCATGGGCTGCAGCAGGCATCGACCCCATCAAGGTCTCCATCGACGGACGCACCATC
TACACCCTGCGCACCTACCTCGGCGGACAGCCAGTATTCCTCGGAAAATTCGGCGAAATC
TTCACCTTCAACAGCCAAAAATCCCTCCTGCGCTGGCTCGTCGAACACGATGACCACGAC
CTCGCCCGCGCCTCCACCTGGAGCGACCTCATGCTCGGCATCAACGCCGGTGAAACCGAA
CTCCTCGTCCACAGCGACAACGTCTACTCCTTCAACGGCCTGGTCAAAGACATCAACACC
TCCGTCGACGCCGTAGACACCCAACAAATGGCCCGCGCCTACGAACTCATGGCAGACACC
GCCGACTGGGCCGACGACGACTCCATGAATTCCTACTTCCTGGCCAACCCACGCATGCAG
GACTACATCTCCTACATGCTCGGCGGCAGCGACACCTCCGGATATGTCCCTCACGCACCA
TTCAACGACCACTCTGAGAGCTGGCGCGAGCTGGAGGAGATGCTGATCAAGCGATTCAGC
AAGTTC

>RXA02858-downstream
TAGGTCGCCTATTTGGGGTTCGT

>RXA02862-upstream
GCCGCGACTGCGGGTGCTTTTGCGCTGTTGCGTAAAAAATAGTTTTTATTAAGGGCATTC
CCTGATTCCCAGGTGGTGCCACATTGTTTATGGTGGAGAT

>RXA02862
ATGAACACGAACTTGCCGAACCTATACACCGCATTTGACCTTGATCGAAGTGAATCCTCC
GAAGCTTTAGGTGTTTCCCTTTCTGCCCGCGATCTTCGCTTAGAACAAATGGGAATTGCC
CAGGACGATCCTCGACGTGCCCAAACCGTCCAAGCTTTCGCAGTGCTTGCAGACCCAGCA
AAACGCGCCACCTACGATGCTCAATTAGAAGCTGGAGTTCCACTCACCTGGGCGCAGATT
CAGCATTTAGGAAACTTCGGCACCTTGCCTTCCACCCCTACTGCGCAGCCGTTTGCGGCA
CCTCAGCCGGAGCCGTCGCCGGAACCGCAACAGCAGTGGAATAGCGGACAAAACTATGCG
TATGGCAATCCGACCATGGATTACCAAACTCAGCAGAGCTACAACCCGATGCAGGACCAA
ACCCAAGCGTCGATGTATGCGCAACCTTTCGCGAACACCCCTGCACCGATGTACAACAGC
AATCAGGTTTTTAACAGGCCTACTGCGGGTACGCGTTTGTGGATGGCGATCCTCGACAGT
ATTTTTGCCGGCATCGCTGGTGGAATTGTCTCCGGTATTTTCGGCTTTGGATCTGAATTC
CTCACCAGTGTCATCATGATTTTGGTGCTGATCGTC

>RXA02867-upstream
TTCAGCACAGATCACCCTTTGCCAGCTACCGACTTAGTTTCGTAACACGTATAGTGGGAG
GCGTTTTGCCAGACGCCAAAGAAAGATAATTGGATTACCT

>RXA02867
ATGAGCGCCACCAACCCTGATGCCCTAGACGTGCAGCACGTCTATCCCATCAAGACGAAA
AAGACTCCACTTGCGGTGATTTTCAACATCATTAGCGGTGGTTTGATTGGAATGGCGGAG
TTGGTGCCAGGAATTTCCGGCGGAACTGTCGCTTTGGTTCTTGGAATTTATGAGCGCGCA
CTGCACAACGGTGATCTCCTCATTGATCTGATCAAGGTGTTGATCAAGGACCGCTCGAAG

GTTAAGGAAGCTGCGGCGAAAATCGACTGGTGGTTCCTCGGCGCTATCGGCGTTGGCATG
GTCGTGATGGTCTTCTCGATGTCATCGATTTTGCATACAGTTGTTGAGGACTACCCAGAG
ATCACTCGCGGTCTGTTCCTTGGAATGGTTGCCGTGTCTATCCTTGTTCCGTTGGGAATG
ATGGATATGCGGGATGCCAAGAAGCGCCTCGCAATCGTCATCCCGCTATTTATAATCTGC
GCCATGCTGGGATTCTTTGGAACATCCTTCACTAGTGCGCCTCGCACCGATCCTTCACTG
ATCTTTGTCTTCATCTGTGCTGCGATCGCTGTGTGTGCTCTTGTTCTTCCTGGTGTTCAG
GATCAC

>RXA02874
ACCGAACTCAACCGCGACACCCATCACCTGTGGGTCGTCTTAACCACCGACTCCGACGAC
TTCGACGCAGACTCCTTTACCACCGAAGTCATCCGGATCACCGGCTACTCCCGCCACGAA
GTCAACAACGGCCTTAACGCCATGGCCGCGATGACCAACCTCCCACACCTGCGCGCCATC
CAAGAACGCTACTACTTCCTGAGCATCCGCTACCTCGCCTCCATCATGATCGCCGTGGCC
AAAGCAGACCCCACCCTGTGGGAAGAACTCGACCTGCGCATCACCGACGCCTTAACACCA
GTCACCGCAGGGGAAGTCATGATCCAATCCTCCACCCTGTCCAAACNGCATCGCCNGCCT
GGATCAAAGAACTCGACCCCGAACCCACACCAGAGCCCACACCGAAAGAGGACTATGTTC
ACGTCCACACCACTGATGAGGCGACCTATGTCCGCATCAAAATCAGCGGCCCCAACCGCC

>RXA02874-downstream
TGATCCTCAATGACATCATCACC

>RXA02876-upstream
AACTGTTGGCATGGCGAAGTACAATGTTCGTGCAACTGGTCACGTGGAGCGCATCGTCCG
CGAAATCACCGCGGCGTAATAGCACCAGCTTAAAAACCTT

>RXA02876
ATGACATCAGACAAAGACACTGAACAATTGGAAGCGGCAGGCACTGAAATTTTAATGCCT
CGCCGCCGTCCGGCACAGCAGCGCAGTCGTGAACGATTCAATCGAATCCTCACCGCTGCG
CGTTCAGTGCTTGTCGATCTAGGTTTTGAATCGTTCACGTTTGATGAAGTCGCTAAGCGT
GCAGAGGTACCGATCGGCACGCTGTACCAATTCTTTGCCAATAAGTATGTATTGATCTGC
GAATTGGATCGTGTGGATACCGCAGAAGCTGTCGCGGAGTTGAAGAAATTCTCCGATCAG
GTTCCTGCGTTGCAGTGGCCGGATATCCTTGATGAATTCATTGAGCACTTGGCTAGGCTC
TGGCGCGATGATCCGTCTCGGCGGGCCGTGTGGCATGCCATCCAGTCCACGCCGGCAACT
CGTGCGACAGCTGCGGCGACGGAAAAAGAGATGCTGGAAATCATCGCGGAAGTTATGCGC
CCGCTTGCCCGCGGTGCCGGCTACGAGGAGCGCATGTCACTGGCGGGATTGCTGGTGCAC
ACGGTAAGTTCCCTGCTTAACTATGCCGTGCGTGATGTCAATAGTTCCGAAGAGGATTTC
GACAGCATCGTGGAAGAAATCAAACGAATGCTGATTTCTTACCTCTTCTCCGTGGCTACT
GGA

>RXA02876-downstream
TAGTCAACACGCACGTCGCCACC

>RXA02881-upstream
CTGCCCGATTTCATGTTTTCCGACGGCACCATCTGCAAAGAACGAGTGTGACCGGTAGCT
TTATGGGCTGAACAATTCTAAGGAGAATTATCC

>RXA02881
GTGAAAAAGAAGCTTATGTTGCCTTTGATTGTTGCAGCTTTGGGGTTAAGTGCCTGCAGC
TCCGAACCTGCAGCAGCCCCACTCGAAGCAGAGCCATTACATAACCTGCTCATTGATGGT
TCAGAGTCCGGCTTGGACAATGCCACTGAAGGAAACGACACCTCATTAAGTGGCCAACCC
ATCAATCTTACAGTGGTCAACGGTGCCTTAGATATCGATGGCTCCTGCGGAAAAGCCCTC
CAAGCTGTAGAGGACGTCAATCTGGACAGCGTAGCTAGCGCATCCAGGGCACTGGCATCC
GGCGACAAACAAGTAGGCATCGCCATGTACTCAACCGCCGAAGACAACGACATCTCACCA
ATGGACCTCTACGCAGACATCGCGAATGCTTGCGAAGACCCCGTCGTCGATTCTTCCGAC
ACCACCTACACCTTCGGCAAACTCGATGATGCTCCCGACGGCGCCGTTGGATTCACCCTC
GACATTGAAGTCACCCCTGACAATCAAGGCTCCACCGTGATGATGATCCAAGAATTAGGA
AACCACCACATCATCGTCGCAGGACTTGAAACCACCCCAGAAGAAACCGCCACTGTCTTC
GAAGCACAACGCACCAAACTCGAAGAAGGCTTGCAGCTTAAACAGAATTGGCAGCTTGGG
TGGGTT

>RXA02881-downstream
TAAATGCGCCCAACCTAAGAAAA

>RXA02884-upstream
GCGATGCTCGAACGCGCAGAACGCTCCTGGGTAGACAAAGCCGCTGCATACGATTTGCGC
TGGTCAGATCACTCACCACTGAACGTGATCTACTCCTAAA

>RXA02884
ATGCTGCTGACAATTCTATGGGCCATCGGCATCACCGCCGAAGGCATGACAGGCGCGCTG
GCCGCAGGCCGACAAAAAATGGATCTCTTCGGAGTATCCGTCATCGCATGCGTTACCGCG
ATCGGCGGCGGATCCATCCGCGACATGCTGCTGGGACATTACCCGCTGGTGTGGGTGGAA
AAGCCACTGTATCTACTGCTGATCATTGGCGCAGCCATTTTGACAGTGTCCATTTCCTTC
CTGATGGAGCACTTCCGTGTGTTGTTCCTCGTGCTCGACGCCGTGGGTCTTTCTGCATTC
GCTGTGATCGGCACACAAATCGCACTGGAAATGGGCTACGGATTCATCATCGCAGTAGTG
GCATCAGTGCTCACAGGTGTATTCGGCGGCGTCATGCGTGACCTTTTGTGTGACCGCATC
CCACTGGTATTTCAAAAAGAGCTCTACGCATCAATCGCATTC

>RXA02885
CGAGGTAAAGGATTCCACTTCACCTCGACTGAGTTTGCCGGTTCTTATTCTTTGGTCACC
AATGGTCTTAACGATGTTGCTGGCGAATACGTCGGTGTCATGCGTGGCGATGTCAACAAC
TCCGCTGTGCTTTTTGATGTGGATCGCTGGTCGGGACATGTCGTATGCGCAGATAGCTCG
ATTAATACATCACCACTACTTAAGCGTCCCCGTGTCGTTGACATGTGGGGGTCGAAGATT
TCTCAGGCAGCGCTACTGAATAACCGTCGCGTAGTGCACCTGGTGCTCAATGGTGCCAAG
CTCGATGAAATGGGACCAAAGCTAGAATCCATGACCGCTCATGTGGATATGACTAGCGGA
GATCTCAACATGTTCGAGCTGTTTGGTAAGCAAGAAGATGAGCTGTCGCTGTATTCCACA
CACATGGACAAAATCGTGTTTATGACCGAGCAGGCATTGGGCGATAAGACCTCTGAGCTG
GCGCTATTGCGCGGAAAGCTCAAAGAAATTATTACAGCCTTTTATGTGGATATGAAAATG
TGGGCTCTTAATGCCGGTGAAAACCGTGACAAGCTGCGTCTTGTTGGTGTGCCTCATGAG
CAGATCCCGTTGCTCTCTGTCTTCGTGTCCTATTTGGATCAAGAATATGAGCGCCAGAAA
TATGAGGGAACCAAAGACCCTGAAATGTTTCGTGCCATTTCTGTGCTGCGACTGACCTAT
AAGGATTTGCTCGATACTCATGGCGATCTGTTTAATCAGCACACGGCAGATGGCATTGAT
TCTGTGAACTCTGCACGCCGCGTGATCTATGATTTTTCTGGAGTGCTGCGACGTGGCGCA
GGTGTCGCGATGGCACAGCTGGTTAACGTGATTGGTTTTGCTGTGGAGACGCTTGGTCAA
GGCGATGTGGTCATCATTCACGGTGCTGATGGCATTGTCGATGTTGATGTTCAGGATTAT
TTGGCTAATCAGTTCGCATATATGGCTGAGCGTGGTGGGCGAGTGGCGTATCTCTACAGC
TCGATGGACGCGATGCTTGGCACTGTTGGCTTCAATCAATTCCAACGTGCTGCGTACACC
ATTTTGGGCCCGATGAACGTTGACTCGGTGGATACTTATCAATCTCTGATTAATAGTCAG
ATCCCGATGGACTTGGCACGGTTGGTGACAACGCAGAATTCTGGTGCGAGCTATTTGCGC
CGAGGATCTACCAATGTGGTGTTTGAAACCAACCTTGCGTTGGGCGTTAATCCTTATATG
GAGCAGCGTCGCAAGATTGAAGCACAGCGAGGTCAGCGACGATCCAAGCGAGACAAGCAC
TACGGTGGTGGCACGACGATGGTGGGCACAGCGGATCTTGATGTTGTCGCAATTCAGGCG
AAGGCCGAGCACCGCGAAGAGCGCTTTGATGAGAAATCTGCGCGCAAGATGAAGGAGCTT
GATGATGTAGAAGCGAAAGAACTAGCTTTGAAAACTGGGCCGAAGAATCTTGATGATGCG
CTTGCACAGGTGGAGAAGAAGCGCCTGGCGAAGCGG

>RXA02885-downstream
TAGTTGTTGGCTGTGGTGAATAA

>RXA02888-upstream
AAGGTCAGCCGTATTTCGGTCAGTCAGCAACTAATTACGCTTATCTTCCGTGTACGATAG
ACCGTAGTTAACATAAGGAATGGAATAGGAGAATTGCGGC

>RXA02888
ATGTATTCCGACAAGCTGATTCTCTTGTTCCTTTCTGAGCAGGATTCAAGCTATGAATGC
TGCGTAGGTTTATTAGATGGCTCAGATGGACGTGATTATATTGAAAAGCTTCTGAAGGGT
AGGAAGCTGAAGAACCATTTTCTTGAATGGGAAGATATTAACAAGGCTGATGTTGCTCGT
GAAGAAATATATAAAGGGCAATTGGTGCATCTGGTGTTTGTGACGGCTCTTTCCACGCCT
GGTGAAATTTCTTTTGTTTTTCCAGGTCAATCTCTTATGAGTGCAACACTCGAAGAAGAC

TTTGCTGCGCTTGTGCTCGAAGAGGAGCGCACATCATTTAGACCTGAACTGTCTCACCTG
TGGTCACTCCCCGTAGGGTGGGTAGCTCCGGGGCTTGAGGGTTTCGTGGAGCGTAATTCC
GAGGCAGCT

>RXA02888-downstream
TGAACCACCGCTTTCTGAGCCGG

>RXA02892-upstream
ACCGAGGAACTGAAGGAAAATGTAGGTGTCGGGGCTTAGAGAAACAAAAAAGGCTGCTAC
GCGGACAGCATTGTCACGTGCTGCTGCGGAGATCGCCTTG

>RXA02892
ATGGAAGGCCCTGAGGCGTTCACGGTTGCGGCCATTGCAGCTGCAGCCGGGGTCTCCCCC
AGGACTTTTCATAACTACTTCCCTTCTCGGGAAGACGCATTGGTGCAATTTGTGGTCATT
CGCGTTCAGGAACTCACGGATCAGCTATACGAGTTTCCTACAAGCGTGCCCCCACGAGAT
GCCATTGAACAATTGGTGATAAACCAATTGCGGGATGGCGATGACGCTATGGATTCTTTC
AGCGCAATGTTTCGAATCGGTGAGATCCTTGAAAATCTTGACCCCATCAAGTGTGTTATC
GATAAGGAGCGACTCATTGCTCCGTTGCTTGAGTTCATGGTTGAACGTGACAAAGACCTT
GACAAGTTCGATGCGGCAACTCTGATCCATTTGCATGCAGCGGCAATTGCAACCTCGCTG
CATACGTTTTACCAAGCTTCCGAGCCCCGGGACATAGAAGATGGAGTCGCATTGATCCGT
CGGGCATGCGCCTGGATTAAGAAA

>RXA02892-downstream
TAAAAATTGTGGCGTGTGAACCT

>RXA02898-upstream
CACCTGAATTGGCTGAGGGAGAGGCACCGACTGGCACCGAAGAGGTGCTTGCCTCGAAGG
CGGGCGCTGAGGCGAATGGCCTGGAGTAGGGGACCAGATC

>RXA02898
TTGGTCGTGGACTCCAGTGGCCGCTACAACGTCACCATCACAGGCCTGACCACCACTGAG
ACGGATTCGGCCACCGCGCTGAACCTGCAGATGTCGGAAGCTGGCTACCTGGAGCGTTAC
ACCGACGGGGCTACCGTCCCCAGCGTCATGCTGTCGGCTGCAGATGGCACCACGCCTCAA
GAGCTTGTCGACGCCCTCGCTGCCGAACTTGGATCGAACTTTGATGTAGAAACCGGCGAA
GCGCTAGTCGAGCAGGCTACAGGAATGATCACGCAGGCCTTGAGCTTCGTGCAGTACTTC
CTCGTTGCCTTCGGTCTCATTGCACTGCTGGTTGGTACCTTCATCATCGCGAATACCTTC
TCCATGATTGTGGCTCAGCGCATGCGTGAGTTCGCTCTCCTGCGAGCCCTGGGTGCGGCG
CCAGGACAGATCACTCGCTCTGTGGTGCTGGAAGCAACCATCGTTGGCCTCTTCGGCTCT
GCTCTTGGTGTGCTGGGTGGTATGGGCCTCGTAGCGATCATTTCAGCTGTCCTCAATAAC
CTGGGCATGCCGATGGGATCCAGCGTTGGCTTGACTCCTTCTGCAGTGGTTACCGCGCTC
GTATTGGGCACCGTTGTCACCATTGTGAGCGCGTGGGCTCCGGCTCGTCGTGCAGGTGAG
GTTAAGCCTGTTGAAGCGATGCGCAACATGGAAACCACCACTATGCGTTCCATGATGGGG
CGCACGATCACCGGTGGCATCGTTCTAGCACTCGGCATCATCTTTGCGATTGCCGGTGCG
ATGATGACTGATTCTTCCACCGCTACTCGTTCCATCCTGGTGGGCATTGGTGCACTGTTT
GTCATCGTGGGTACGTTCCTCTTCTCACCAGCGCTCTCCATGCCTGTGGTGGGTGGCCTG
GGCAAGGTTATCGGTGCACCGTTTGGCAGCGTTGGAAGCCTTGCTGCGACCAACTCCAAG
CGAAACCCTCGCCGTACCGCAACTACAGCGTTCGCACTGACGTTGGGCATTGCCTTAGTG
ACTGCAATTGGCATGCTTTCTGCAACCATGAAGGACGCAGTCTCCGACATGATGGCGGAG
CAGTACACCGCAGATTACATCCTGCAGGGACCAACCAACGGTTCCATCACCATGCCGAAG
GAATCTGTCAATGATGTTCGCGATGCTGAGGGCGTTGCCGATGTCGTGCTCGTTTCCATG
AACTCTGCCTCGGTGAACGGTCAGGCTTCATACAGCCAGCTGGGCCAGTCTGTAACCTTT
GTCGCTGACGGCGACCTGAGCAAGGTCATCAGCACAGAAAGCATTGATGGCTCCCTCGAC
TTGAGCAACCCAGGTGTTGTGACTAACCAGACGTTTGCTGATGAAAACGGCTGGGCAGTA
GGCGATACTCTGCAGCTTGAATCAATGGGGCAGACCATCGGCGATATCGAGTTGATCGGT
ACCTTCACCGGAAACGACGCCATCGGAAATATGATCATCTCCGAAAGTTCCTTGGCTGAT
ACACCAGCGGCAGACACTGCTGTTCCTCAGATGATGCTGGTGGTAGGCGAAGAAGGCTTT
GATAAGGAACAACTGCGCACCAACTTGGAAGACGCAGTCGCTGATTACATTGTCATCTCT
GTGAAA

>RXA02899-upstream
GTGTCATTTTCTTGGCGGACGGTCGTATCGTGAACCAGTTGTTTGATCCCACCATCGAGG
AAATCTTGGCCACGATGAACGGAATTGAGGATATTGCCTA

>RXA02899
ATGAATTCCGGTTCCACAATGCGCAGAATCAGTCTGCGCAATATTGGCGCGCACAAGGTC
AGGCTGTTTTTGACAGTTCTGGCAGTGGTGCTCGGCACGTCTTTTGTTTCCGGCGCGATG
ATGTTTACCAACGCGCTGTCCTCCACTTTTGATGAGGCTATTGCCAGCAGCTTTGACGGC
GTGGATGTGGTGGTTTCACCAAACGGTGCATCAGAGGTGCAGGGTGTTCCTGTTGAGACG
GTTGAATCTTTGCGTGAGGATTCCCGCATCAACCATCTCAACATCAACGGTTCCCAGACT
GTCGTTCTGGCGGATGCTGATTCCAAGGCAATTCAAACGACTGGGGGATCGTCGTTAAGC
ATTTATTACAGCGCGGACGACGCGGTTGCCCAGGCACCTGAATTGGCTGAGGGAGAGGCA
CCGACTGGCACCGAAGAGGTGCTTGCCTCGAAGGCGGGCGCTGAGGCGAATGGCCTGGAG

>RXA02899-downstream
TAGGGGACCAGATCTTGGTCGTG

>RXA02905-upstream
CGAAACATCTAGGCAACCCGACTTTTATGTCCCTGCTTGAGTTGAAAACTGCTGTCGATC
AAAGGTGCCCCAATTGTTTCATGCCGTGAGTTTTGCATTA

>RXA02905
ATGGACTCCGTAAATGTCCTGCTCATTGGCATAATCGTCGCGATTGCTGCTTTGCTGCCT
CGCAAGGGTAAATATGGGCCAATCGCCACGCTACTGGTTGCCGGCGATTGGCTTGGCGTT
TTCCTCCTCAGTATTTTGGTGATGCTCGTTTTTGATGGACTAGAGGATTTAGTTCAGGGC
TTTTTGGATTCAATCTGGTTCGGAGTCATCCTTCTTGTAACTGGCATCGTTTCCTTCGTT
GCGACACTGGTTTCTAAAACCGACAGCACTAGAAAGCTTGATGGATTCCTAGCGCCAGTA
AAAACTCCTAGTTGGAAAACTGTTGGAGCCGGATTGATCCTTGGAATCGTTCAGTCAGCG
ACATCTGTACCTTTTTATGCAGGGCTTGGATATTTGAGCGTTGGCAATTTCAGTCCAGAA
ATTAGGTATGGCGGACTTGTGGTCTATGCGACCTTGGCTCTGAGTCTGCCGATT

>RXN00022-upstream
AGGACTGCTCCGCAAACCTCTAACAACACCTGCTACTCCCCCTGCAGCGCCGGTCAACCC
CACACCACCCACCCCTTAACAACCACAAGAAAGATTTATC

>RXN00022
ATGTCCGCTCCAACCATCTACCCCGGCACCAAAACATCTATTGATCCGATCACCATGGAT
GACGCTCGCATCATCTTTTTCGATATTGAGTCGCTCCACAATATTTTCACGGTAGCAACC
TACGATTCTCTGTCCCACCACGTCGATGTCTTTTACCTGCTCGATCACACAACCAGCCCT
CAGATCACGGTGCTGCCGCACTCAATGGATTATTTCGATCAAACGCGCAGCGATGCTGTT
ATGGCTGCCATCATTGAGCAAAACCCTGCGTTCGCAGAAATTAAAGGCTCACCCATTACA
ACCGCAGATGTAGCCCTCCACAATCTCGGTGACACCAACGCCAACCGACGCTGGCAGTCT
AACGTGCTGCTTGCCCGGCTACTCGGGGGTATTAGTGTGCGCGGAGAGGTACCTGAGCAC
CAGAGCCACAACCATCTCGCCAAGCAGTTTGCCGAGGCAACCTTGGTCACCAGGGACTTC
GATGTGAATTATGATCCAACAAGCGCTCACCCTTTTACTGCTGGCTTCAACTCGATCAAC
TATGACACCACCTTGCTCAGCCTGTACTTCGCAATGTTGACCTCAAATATCGGAAGTACA
CCGACGTATTTCCCGGTGATCACCGCACAGGAACTTCGTGCGCATAACGACAAGCTCTTT
AGCCCTGAGTTCATCAAAAACATGCCAAAGTATCTCTGGGATCGCGACAGCGGTGCTGGA
CTCAGAGCTGCATCGGGTTTCCGCAACGCCATGCTCAAATCGGGTCGCCACATTGATATT
CAACGCCTCAATGAAAAACAGCTCTTTGTTGGACTCAAGCGCCTGCTTGGTCTCCTCGGT
CACCAGATTCTCGAATCTGATCGTCTCTCTGGTGATGATGCCCATGTTGATACTAACGAG
GATGTACTTGATCTCATTGCCTACAACGTCTCAGACGTGGTGGGCACCAGACTGCTCGCT
GAGGACCCGGTGTACTCCGGCTCTTTCGATCTGCGGGCAGGTCTACTGAGCACCTACCCA
GAGACTGTTTTTGATCATGATGGTACTTTCCGTCAGCCATCCACGCAGATGCGTAAAGAT
CGCCTAACGATTAATACCTCATCAGCTCAGTTCGCAGCGCGTATTTTGGCGCCATATCGC
CCACTCCGCGATGTCCCTGATGCGATTGGCGACATGCCGGTGGTGTCTTACTTGTACCCG
GATGCAGCAGTCGCCGAAGCAACAGGTCAAAAACAAGTCAACGTGCTTGATGAGTCAAAG
AAGTTCTTCTATGACAACATCACCGACCCGGAAGCACGTGCTGCCTTTGATGAGGTCTTT
GCTTTTTACGCTGATATTGAGGGTCGCAACTTCAACAGTCACAATGAGGCTATTGATACC
CAGATTAACCAATTACGTGCTTATCTCAACCAGGTTGTCGCATTCGATGCAGCTGGGTAT

GCGCTCTATGATGTACGTACACGTTTTGAGCAGATCTTCCCCAAGGATCGCAGCTACATC
AACGATGCTACGGATATGACCCCTCGCGCAGTATCGAGCTTTGACGATCTGGTTGCACTC
TGTGATGATATTCGCGGTGTACTTGATCGAGGTTTAGAGATCTCATCTCCGAATCATCAT
GAGATGGTGGATGCTATGCGCAAGCAGCTGCACTATATTCAGGCATTTTACCGTGCCTGG
GACCCATCAACGCCGCTTCAA

>RXN00022-downstream
TGACGCTGACCCAGCGGTGACCC

>RXN00027-upstream
TTAGGCAACGACTCCGAAACCTTCAAGAACGTGTGGCACTAACAATTGCGGACTATCCTT
GGGAACTGTTTTAGATTTTATTCAGGGTAGGGAGATTGTT

>RXN00027
GTGGATGAACGAAGCCGGTTTGCGCGCAGCGTTTTCCCGGACGGTGAAGAACCAGATCCA
CGTTTCACTTTGGCCAATGAGCGCACGTTTCTAGCATGGACGCGTACGTCTTTGGCGTTT
CTTGCCGGTGGTATTGCTTTTGAGGCGTTCCAGATCAGTGGACTATCGGATACTGTCCGT
ACAACAATCGCGGTTTTTATCATTGCGGTTGGCATGATCATTGCCGCTGGTGCTGCGGTG
AGGTGGATGAATGTGGAGCGTGCAATGCGTAAACAGAAGCCACTTCCCGTACCTGCGATT
ATTCCGTTTCTGTCTATTGCGGCTTTGGTGGCCTCTGCGGCTGTCTTGGTTCTGATTATT
GTTCAG

>RXN00027-downstream
TAGCTATGCGCATTCATGAGGAT

>RXN00028-upstream
AAAAGTCCTGGCCAGAAAACTCTCTATACTGTGCAGCATGGCACCAACGATCACCGACAT
CCATGTTCTGCTTCGTCGCGGTGAGCGACAATCAGTGATC

>RXN00028
ATGACCCTCACTGCCTCTTCCTTGGAGGCCGGGAAAATGTCTTTTAGTGGCGGGTATATC
GTGGGCGAGACGATGATCTTCCTCGTCGATCCCGATGAAGTCGAGATACGACGCAGCCCT
AACAGCCTCCACGTCCTGCGTAACGGTAGCGATATTCTGCGCCGCAACGAGCATCATTGC
TGGGTATTTGAGAATTTCAATAAACCCATTGACCCACCTGTTCGATTGGGTCCTCGGGAT
ATCATCTGCCCGAGCGCCTTGGCCTGGGTTCTTCAACAGCATTCCATCTCCCGGTCCTTA
TCCCACCACCTTCACGCGGATAAGATCACTGCGGGAGAGATTGCTGGACGCCCCACCTGG
ATCCTCCGTGAGGAACCTACTTCAGGAGGGCAGGACCCAAGTCGATTGGTCAGTCTTGAA
ATCGACCAGGAACACGGTGTCATCCTTGCAGTGGAGACTGGACAAGAACGACTCGAAGCC
ACGGAGATTTCTTTTCCTGACACTCTTCCTAATCCTTCCTGGGACGGAGCCTGGGAACCA
TTCCATTATCCAGATTCGACACCACACACTGCCCCTGATGTTGCTGAAATACCCGGTTAC
ATTCAGTCACTGCCGCCGCAGTCTGAAGATCCTCGCAGACTACGAGTCTTCGTCAATGAG
ATAGCACTCGAAGGTGATTTCCCTGACTACCGTCAAGGACAATCTGTGCGACTTACTTTG
GGAATTAGCTCCTCCCCTGTGCCACTCGAAGGAATGACAACCAGACGCCGGGGCCGGGTA
CGCAACCTTGGGGAAGAAGCTAGTCCAGGCGATGACGGTATGCCCCAGTGGCCAATCCTG
CTCACTGGTGATGGGTGGACGGCGCTGGCCTACACTCCCATCCCAAAACGTGGAGATGCA
GAGATCCAGGGGTGGTTTTATTATTCCGCCTACGGAATTGTTGATGTTCCCACAGATCTA
CGGGTAGAGCGTATTTTCGCTGGTATCGGCACAAGTGGCACCAACGAGCGTTTGTGGCAG
GAGATAGACAATACTTCTTCGGCTTATCACTCGGAAGATTGGTGGATCCGCGATGTCGTT
TTAGACGTCACGTTGGATGGAGCTGTTCCGCCTCCGCTTAGACGTGACGTCTTCACTGCT
GTCGATCCTATTGTGGCGGGTGACAAATTGTGGCTGTGTGACGTGCACTTTCCGGTAGCC
CGCTGCTGGGAGACCACGACCGGCCGATACTTGGGGCAGACTTTAGTCCCAGCACCACTG
CGAGATCGATCGTACGTCCTTGAGCTGCACAGCGACCAACAATTAGGAGCCGTAGCGGCA
AGTGGGAAGAGTGGTTGGATTCTCACACCTGGTCAAGCAGTAGCCACTAAAGCTCCTGAT
TGGACTCCTCCCACCCGGGCAACCGATCTGCCTCAGGTCCCCTCCCCCTGGGAGATCGTC
GCTGTCCGTGGCCAAGGTCTGTTTGAGCTGCAGGTGGAAACTAGTAGACGCACCGCCCTC
GGTCGAGTTAATGCGACCGGTGGCGTCGACATCGGTGAACTCCCGCCCAACGGCTATACC
ATCAGTTCTGTGGTTCAGATCGGTGATGAATACATCGTGGGCAGGTGGGTAGAGGAATAC
CGGCTCAACTCCAAACTGGAGGTCATTTCTACCAAAGAGCTAGATATCTCCGCATCCGGA
TGGAAGAGCAAGGGGACGGTTGCTTATCTGTCGGAAGACACTCACATATGTTTCTTCGAC
CAGGTCAGCGGGGCCGAGCTTCCCAGCCTGGGTATCGCCGAGGGACACCAGGGCGAGGTT
ATGTCAGCAACTTCTTCAGAGAGCATCGTGCTTATCTACCGGCGCAACCCGAACAATTCA

ATGTCGATTGTCCCGACTTCCGTTGCCACCTATGACAATGGCACCTGGACGACTATGCCG
CTACAGGAAGCTCCAGCGGAACTGTCC

>RXN00028-downstream
TAAACTGCTCATAGACTGCTGAG

>RXN00033-upstream
ACACGGATTTAACGTGACGGTTTCTCAGTGTTTTTAGCTTCTGGCTTTTGGCTTCTGATG
CTTTAGCGCTGGACTCAACATTTAAAACAAAGGTGAACAC

>RXN00033
ATGTCAGTACAGCAAAGCGGGTTGCTCGAACGTCTCGGCATTCCCCGACCCTTGATTTTC
GGATTTATCGGCCTCACCATCTTCATGATCGGTGACGGTGTCGAAACCAACATTTTGGAA
CCTTTCCTCAGTTCCGAACATGGTTTCAGCGTTTCCCTCGCGGGAACCCTGGTGACTGTT
TACGGTGTTGCCGTGGCGATCGCAGCATTCTTCGCGGCGGCACTTTCGGACCTGTGGGGT
CCACGAAAAGTGATGATCCTCGGTGCTTCAATCTGGATCGTCTTTGAGCTGATCTTCCTC
ACCGTGGCACTGACCACCGACCATACTTGGTTGATCTTCCTTGCTTATGGTCTCCGCGGC
TTTGGTTATCCATTCTTCGCCTACGGATTCTTGGTGTGGATCACCGCAACTGCCTCACCT
AAGCAATTGGGTACCGGTGTGGGTTGGTTCTACGTTGCCTTCTCTGCAGGTCTTCCTACC
TTGGGTGCGCTGGTTGCCACCATTTCCATGCAGTACGTGAACTTGACCTTCTATGAAACG
TTGTGGGTTTCCCTCGTGCTGGTGGTCATCGGATCGCTCATCGCACTGCTGGGAGTGAAG
GAACGTCGCGGACGCCACCCACTGGTTGCCAACCCCGACGATGTGAAGCAAACACTTGGC
CAGGGCTTCAAACTTCTGCGCAATGATCGACGTGCACGTTTTGTCACCTACATCCGCACC
ATCAACTCCATTCCGACCTACGCGATGGCTGTGTTCTTCCCATCATTTTTCACTGACGAT
CTGAAGTGGCAGCTAAGCTGGTTCCTCATCCTCACCACTGTAATTTACGCAGTCAACCTG
CCGTTCAATCCTTTCTTCGGTAGCTTCGGCGACCGCCACGGTTGGGCACGAACTGTGTTC
TGGGGCGGATCAATCGGTGGCGCAGTCACCCTCGCGTTGGTTTACTTCATTCCGATGTTC
GGCGTTCAGGCTGGCATGTCCAACGGTGTCGTTTTCGGAATCACCATCGCAGCCGGCGCA
CTCTTTGGTGTGTCCCTCGCGGGCTTCGTGCCACTTTCCGCAATCGCTGTCTCCCTTGAT
CCCAAGCACCCCGGCGCAGCGATGGCCACATACAACCTCGGCGTTGGTGGCGCTGTAGCT
GTGGGACCGCTCCTGGTTGCAGTCTTCCACCCACTGATTGGTCCAACCGGATTGATCCTG
GTCATGATCGCCCTCTACCTGCTCTCCGGTTGGATGACTCTTCAACTTCGCGGCACCCAA
CCAGGATTCGACGGAGTGCCAGCACTTGCTGAAGACGCCCACATCGAAGACCTTGCAGAT
GTAAACGCAAACGCC

>RXN00033-downstream
TAACTGTTTTTCGAGCTAAACCC

>RXN00056-upstream
ATATGAATTTAATAATAGATTCCGAACGAAATCGGTGTTAGCGTCTGTGCTGAAACAATC
TAATCGCGTTTCAGGACACCTACATGATCAGGAGCTCTTT

>RXN00056
TTGTTAAACAGAGTCAGTCGTATTGCAGGCGCTTCTGCAATCACACTATGCATCGGCTTA
ACCACAATACTAAGCCCTACTTCCACTGCACAAAGCCTCGAACAGATCACCCCTTTACCT
GAATCTGCAATCGACCTCAACGCCGAGATTCACGTAAACACAAGCGACATTTCAGCTGAA
CAGATCCTTGGTGCTCAAGATGAAATCACAACTATGTACGATTCTCATGACCCCTACGAG
TACTTCGATACCCTCACCGACATCGAACAGCGTTCAATAATAGCAGCGCTTAAACGGGAT
CCGAGTTCACTCCAACAACGCCAAGAAACCCGTCTCGCGGCACAGTCCGACCCCTACAAA
ATTTACATATCAGGCCTCGAAATGCTTTCATGCATCAATCTAGTTGATGTTGTATCATGC
GGGATTGCAAACCAAGCAGCAACCAAAGCAAATAATGAGGCTGTCGCACGATACCCAGGC
GATTCCCTTCGCAACGGCAAAGGCGATGCATTTCGGCATTGCTCATGGAACGCTCTGATG
ACGATACGAATCGGGAGCAATGGAGCTGAAAGAATTGCAACAAACCACGAGACAATCGGG
GACGGTCCGGCCGATGAAAATGCAATGGACCTATTCAATAATGCACAAGGCCGACAGATC
GGAGCCGGATTCATTAATAGTAAGGATGAAACTAGCGCGCTCGCGATATGCGCGCTGTGG
ACAAATCTCGGTAGACTAAAAACTCTAAAA

>RXN00056-downstream
TAAGCAAGGTGCCCTCTGATGCT

>RXN00067-upstream
GGAATCCCGCATGTTGGGCTCCAGTTGGGGACTGACTCTGTTTTTGATCATTTTGACGCC
AATCATTATTTTCCTCACTTTCAGCTAAAAGGACCATGCA

>RXN00067
ATGGTAGACGCTCAGCGCCCCAAAGCAGGCATCTTCGGTAGCCACACAGAAGAAACATGG
GTGTGGCTCGGTAATGAACTTTTCGACGAGTCCGGCGAGGTCATCGCCGACGTTCGCTCC
GACGTCCTCTACGTGGATCGCGAACGACTACTCATCGAATCCACCCCCGGCACCATGCGT
TTTCGTTGCCGCGCAACACTGTCCGGGGGGTGAGGTCTATACGATGACTCAGAATTCTTTC
ACTGTGGGGGATCTCACTGCGGTGTGCGGGCGCCGGACGTATTCACTAAAAAGGGTGTCG
CCGTGGCGTAAAGAACGCCTGATCACCAACAATGGGGGTGGAAGTGGCGCGGCTTCGCCCG
ATGACCAGCGGTAAAGTCGAATTCATTGTGGGCACCGCGGGCAGCGAGGCGTTGCCGTTC
GTCGACGCAGTATTTTTGAGCTGGGCGTGCGTCCTGGTGGATTCGGCCGTGCGCCGGCCG
AAAATT

>RXN00067-downstream
TAAAAGCTTTTTGCTTATCGACG

>RXN00077-upstream
CTAAATTGTTTTAACGCGTGAAGCAGTCCCCGCCCGATTTATTCGAGGCGGGGACTTTCG
CTTTCCGGGATAAAAATTGCAACGCACTACACTGAGCAGT

>RXN00077
ATGAATGATGAGAATATTCAAAGCTCCAACTATCAGCCATTCCCGAGTTTTGACGATTGG
AAACAGATCGAGGTGTCGCTCTTAGATGTCATCGAATCCTCACGCCATTTTTCTGATTTG
AAAGATAGCACTGATCGTTCTGCGTTAGATGCTGCGCTAGAGAGAGCAAAAAGAGCTGCC
GCAGTTGATACCAATGCCATAGAAGGAATCTTCCAAACTGATCGCGGTTTTACCCATACA
GTTGCAACGCAGGTAGGGGCTTGGGAGCAACAAATGGCGATGAAAGGCAAACATGTTAAG
CCTGCGTTTGACGATACTCTAGAAGGCTTTGAGTATGTTCTCGATGCAGTAACTGGTAGA
ACTCCAATCTCTCAGCAATGGATTAGAAATTTGCACGCCGTCATTCTGCGGAGCCAAGAA
AGCCACGAGGTTTTTACAGCCGTTGGAGTCCAAAATCAGGCGCTTCAGAAAGGCGAGTAT
AAAACTCAGCCAAATAGTCCACAGCGCTCAGATGGATCTGTACATGCATACGCCCCAGTT
GAAGATACTCCTGCTGAAATGGCTAGATTTATTTCAGAACTTGAATCTAAGGAATTCTTA
GCAGCCGAGAAGGTTATTCAAGCTGCCTATGCCCACTATGCTTTCGTATGTATTCATCCT
TTTGCAGATGGGAATGGACGAGTTGCACGAGCCTTGGCTAGTGTTTTTCTATACAAAGAT
CCTGGTGTCCCTCTCGTAATCTACCAAGATCAACGCAGAGATTACATCCATGCTCTAGAA
GCAGCGGACAAGAATAACCCGCTCCTGCTGATTAGATTCTTTGCTGAACGAGTGACCGAT
ACTATTAACTCTATTATCGTTGATCTCACTACCCCGATCGCGGGTAAATCTGGTTCGGCT
AAGCTTTCGGATGCGCTACGCCCCACTCGCGTATTACCAGAATTACATGATGCTGCACAT
AGGCTCCAAGAAAGTTTATTTACAGAAATCCGATCTCGATTGGATGAAGAAGGAAAAAGG
AATGGGTTGGAGTTTCTACTTCAACGGATTTTTATCGGTTCCCCATTCAATCTGCCAGAG
GGCTATAACGCTTTCCCTGATAGCTATTGTCTGACCTTAGCTTTCAATAGCAACTCTCCA
AAACAAATCTTCCACCCGCTATCCATAGTAATAGCAGCTCGAGATGGGAAAAGAGCGAGC
AGCGACCTCGTGGCAGCTACTTCTATTGGATACAACTTTCACGCTTACGGACGTGAAGTC
GAGCCTGTTGTTACTGAAAGCTTTCGAGAACGTGTGAAAATTTACGCCGACGGGATTGTA
GATCACTTCTTAACCGAACTGGCTAAAAAGTTTCAACAGAAT

>RXN00077-downstream
TAATTAGCCTATCTCGGCTTTCG

>RXN00080-upstream
ATGTTCTTGTTTCCCTCATGATGAGCTCCGTGGTCTACCTCGCATTCGATGTGGGCTTGG
GACTTAATCTTCCTTCCGGACTTTTGGGTGGTGGCTTTTA

>RXN00080
ATGGATATTTTGTCCCTCTTGATGGAAGGTTTCGCCGGCGCGCTAACGCCGATGAACCTC
CTCTGGGTGATTGTCGGCTGTTTGCTCGGCACCGCGGTTGGCGTCATGCCTGGTCTTGGA
TCCTCCATGGCTGTGGCGCTGCTGCTGCCAATGACCTTCGCGCTTGATCCAACTGCCGCG
TTCATTATGTTCTCTGGCGTATATTTCGGTGGTCTCTTCGGTGACTCCACGATGGCAATT
TTGATGAACACCCCAGGTCAGGCATCGGCAATCGCCTCAACATTCGAGGGCCACCGCATG

GCTCTTAACGGCCGTGCGCCACAGGCTCTGGCTACCGCAGCGATCGGTGCCTTCATCGGC
GGTATCGTCTCCTCCTTCATCGTGGTCTTCCTCGCACCAACCCTGGCGGAACTGTCCACC
GCATTCGGCCCCGCCGAGTACTTCGCACTGGCACTCTTCGCGTTCGTCGCCACCTCCTCC
GTGGTGTCCGACTCCGTGTTTAAGGGACTTGCGTCCCTCATTTTCGGCCTCGGCATTGCG
ACCATCGGCATCGATTCGGTCACCGGCATCGAGCGCTTCACGCTCGGGGCACCGCAGCTT
TTCGACGGAATTTCCCTCGTTACTGTTACCGTCGCGATTTTGGCACTGGGAGAAGTGTTT
TACATTGCAGCCCGCGCACGCCGTGACAAAGCAAATCTGGAGACGCGCTCTGCAGGCCGT
CCGTGGCTTACCGGAACGGAATTCAAAGAAGCCGCTCCAGCCTGGGCACGCGGAACCATC
ATTGGTCTGCCTTTCGGTGTGATCCCTGTTGGTGGATCTGAAGTTCCAACCTTCTTGGCT
TACTCCACCGAGCGCGCATTGGATAAACGACGCAAAGATCCGCAGTTCGGCGATAAAGGT
GCAATCCGAGGACTCGCTGCTCCTGAAGCTGCAGGTAACGCCACCACAGGCATGGCGATG
GGCGCTCTTCTTGCCCTGGGTCTCCCAGTCTCTGCAACTGCGGCCATCATGTTGGCAGCG
TTCCGCCAGTACGGAATCCAGCCCGGACCACTACTCTTCGATCGCAACCCTGAACTTGTC
TGGGCACTTCTTGCCAGCTTCTTCATCGCGATGATCGTCCTGCTGTTCATCAACCTGCCG
TTCGCACAGCTGTGGGCAAAGCTCCTGCTCATTCCAAACCACTACCTCTACTCCGGCATC
GCATTGTTCTGTGGCCTGGGCATTTACGCCACCTCCGGCGCAGTGTTCGACCTGCTCATG
CTGCTCGGCATCGGTGTCGTGGCTTTGATCATGCGTCGCTACGGTTACCCGCTGGCACCG
CTGATGATCGGTATGGTTCTTGGACCTTTGGCTGAAACCTCCCTCCGCGACGCACTACTG
TCCTCGGTTGGCGATTTCTCCATCCTCGTCTCCAGCCCCATCACCTGGTCTCTCTACGCA
GTGCTCGCCATCTTCATCGCGGTCAGTGTCATCACTGCAATCCGCGGTCGTCGCAAGCAC
CTGACTTCTCAGCTCGAAACCATCGACGCT

>RXN00080-downstream
TAAAGTCCCCGTATAGAAACAGG

>RXN00087-upstream
TCGTCAGTCAACAAACGTTTTCCCACCCGGAGGTCTCCCCGTGTCTACCGAAATCCACAA
CGCCCCACCCAAGGCCCCAACTTGGCTTGGCTGGGTGCTC

>RXN00087
ATGATCGGCGGAATAATCGGCCTCATTTTGTCGGTGATCATCATGGCCGAAAAACTTGCC
ATCCTCGAGGATCCCGGTCACATCACCAGCTGCGATTTCAATGCAGTCCTAGCTTGTGGC
GATGTCATGCGTTCCGGCCAAGCTAACGCGTTCGGCATCCCGAATCCGCTCATCGGCATC
GCCGGTTTCGCCGCTGTCGCCATCATCGGCGCCGGCATCCTCGCGGGCGGCGGGTTCCGC
GGTTGGTTCTGGTTCGGCGCCCAGGCCGGACTCACTTTTGCCATGATGTTCTGCCACTGG
CTCGCCTACCAATCCATGTCCGTCATCCGCGCGCTCTGCCCTTACTGCATGGGCGTGTGG
ACCGTATCGATCATCATGTTCGTGCTGGTCACTGCATGGAATGTGAAAACTTTCAGCGGC
TCCGACAGCACGTTCGTCAACGCACTGTACAAATACAAGTGGGTCATCGCGATCGTCTGG
CTGCTGCTCATCGCAGCCGCAGCTGTGTGGTCATTCCGCTACATGTTC

>RXN00087-downstream
TAGGCATTTAAGGCTTTCAGGCC

>RXN00096-upstream
GGGGAACCTGGGGTAAAAGGAGAAGTATTCATTACCCCAATAACCTACTAGGTGGGGTGG
ACACGCATAGTCGACAGCCAGACGTGGCAGAATAGTGTGC

>RXN00096
ATGACTAATGCAGGTGACAACTTCGAGATCAGGATGCCTTCTGGCACGGATGACCCATTG
TCCGATGCGGAGATCCAAAAGTATCGCGAGGAGATCAACCGCTTGGACCGCGAAATCCTC
GATGCGGTGAAACGCCGCACGAAGATTTCCCAAACCATCGGAAAAACACGCATGAGCTCG
GGCGGAACACGTCTCGTGCACACCCGAGAAGTAGCAATCATCAACCAATTCCGTGAAGAG
ATCGGCGAGGAAGGCCCTGCCCTCGCTGGAATTTTGCTGCGCATGGGACGCGGAAAACTC
GGA

>RXN00096-downstream
TAAGTTATCCACAGGTAGAAAAA

>RXN00097-upstream
TCAGGGTTTTAGCCGTTGATGGGCAGAGTTATCCACAGGTTTTTAGCGAGCTGGTTTCCG
ACGAAGAAAATAGTGGATAGGTTACAGGGCAGAATCCCGA

>RXN00097
ATGGAGGTGCCTTCCTTGTTTACCAACTTCTTCGCAGTCAACAACCCAGACAGTCCGCCC
GCACGACAAAAAACCAAACTCAGAGAACTGGAACACCGCTTCTGGCAAGAACACCTGCCA
GGCGACGACGATGACCATTCCACCGCAATCTCCAGCCTCGCCATCGTCACAGGTCTAACA
AAAGCGCAGGTCTCCCGCATATCCATCGCGTTTGCCACGCTCGCCGACTTGCCCGAACTC
AAAGCCCTGCAACAAAAGCTGTACCACCTCGACCTCTCCCGACTGATCACCATTAGCAAC
GAACTCGCCGGCATCAACCCCGACAACCTCGCCGGCGCCGACGCAATCCTCACCGAATAC
CTCACCGCCACCAGCCCCAACCAGATTCTGCCAAGCCCGGCGTCCATAGGACGCAAGATA
AAAGAAATAAGAGATTTGCTTGACGACGCAAGAGCCACCGGTTCGCGCGGTACCCAAGAC
GACAGCTCTTTCGGAGTGACCTTCTCCCCAGACGGAACCGCCGAAATCGGAGCCTCCGTC
GATGCTGTGGACGGGCACATCATCAACGACGCCGTCACCCAACACGCGAAGAAAAACGAC
CTCACCTACGGCGAAGCTTTCAGCGACATCCTTCGGAACAATATCCAAGTCAAGGTAGTC
CTCAACTTGTACACCGCCAAAGACCTCGCCAACGCCCCAGTGTGGGCCAGCGGAATCGGC
TGGTTGGATGCCAAGACTGGAACATTCTGGTCAGAGAAAGCCAACAAAGAACAAGACATG
GATGCGGCTGCCAAAATCAGCACCGACAAACACGATCCTCCACCAGCGTTGCGTGACGCA
CTCATTGGTCGTGATGGCACCTGCCGATTCCCTGGCTGTTCAGTCCCAGCGCTCAAAACC
CAAGCCGACCACCGCATCCCCTACGAAGAAGGCGGAGAAACTTGCCTAGGCGGAATCGGC
TGCCTCTGTCAACACCACCACAACATGAAAACCGACGGCCGAGTCACCTACCTTCTCGAT
CCCTTCTCCGGCATCATCGTCTGGCTCATGGGAGACGGAACATGGGCAGTGTCAGAACCC
AACGGGCCGCTCAATCCCAAAAATGCGAGATGGGCGCAAACAGTCGCCCAACACCGGGCA
CGCCACCACAAGCGTTGGGTTAAGGAGGACGCCAAG

>RXN00097-downstream
TAGCCGGATGGCCACGTCGAAAA

>RXN00114-upstream
TGCATTCCCTAACGGGAATGCAGCTTTTTGTGTTCCTAGTGCAAATCGAAATCTCATGTG
ATTTACTTAAAACCTAATTAAATCTACTATCGGAGATCTC

>RXN00114
ATGAAACTTCTCAAGTTTGCTGCAGCAGGAACCTTCGCACTAGCCCTGGCTGGCTGCACA
CAGACTGAGTCTCTCGTAGCAACAATCGAATCTGCAACCTCTGCAGCACAGGCATCCGGA
AACGACGTAGAAGGAGACCAAACCTCCGCGTTCGAACTCTCCGTTGGCGAATGCTTCAAC
GACACCTACGAAGAAGAAATCTCCGAAGTACCCATCGTCGACTGCGCAGAACCTCACGAC
AACGAGATCTACTACCTCTACGACATCGAAGGCGACGACTTCCCAACCGACATCACCACC
ACAGGCTACGAAGGCTGCCTCCCAACATTTGAAGGCTTCGTAGGAGCTCCTTACGAAACC
TCCATCTACGAGGTCTACCCAATGACCCCAACCTTTGGCTCCTGGACAAACGGCGACCGC
GAGGTAGTGTGCTCCGTGTACTTGGCCACCGGTGAGCAGATGACCGGAACCGCAGCAGGA
ACCGCGCAG

>RXN00114-downstream
TAGATTTTGGATAGGGAATTTTG

>RXN00120-upstream
ACAAACTCTTAATTTAATGAGACGTAAGTAGTTGATAGTTAGGGGAAATACTCCCAAATC
CTCACAGGAAACGCTCTGAATTCTTTCAAAAAAATGTTTC

>RXN00120
ATGCTTATTGGCATGAGCAATCAAACAGTCAATCAAGCAGTGTCGTCAGGGGTGAAAGCA
TCCCCGCACAGGTTCAATCGTTTTGAAATCAAATACTTGATTACAGAGCAAGATGTACCT
GCACTCCGCGAGCAGTTGGCAACGAGGATGAGCACGGATCCGCTTTCCCCACCCGGAGGC
TACCGAGTGGAATCCCTTTACTTCGATTCAGCCGATTTACGGTGCTACACCGAAAAGATC
GAGGGTCTGAAATTCCGAAGGAAACTACGGATCCGTACCTACGGTGATGGAGTGCTCACT
CCAGAATCCACCGTGTCGGTAGAGATCAAGCAGCGGGTTAACAAAGTAACTCAAAAGCGT
CGGCTGGATTTGCCCTTTATATATGCGCTCGCCCTGGGCGATAGCACGGGCGCCGCGGTA
GGCGAGCAGGTGGACGTCGAGAAGCTTCTTGAAATCTCTCCGGAAAACCAGCACGCTTTG
ATTCACGAAATGGCGTCGTTTGCTAAAAATTATCGGCTGCGACCCATCGCCACCACGAAG
TATCACCGCGAGGCATTCGTCGGCGCTGATGCGGAGGAAAGTTCGCGAGTCACCATTGAC
CACGGTGTTTCAGGCCGTGATCGTGATTTTCTGCTTGGCCAAGACCTTGAAGACCGCCCA
ACGGTGGCGCAAGGATTGGCAGTCGTGGAAATCAAATGCGATGAACGCGTGCCGTTTTGG

CTCACTGATATGACTGCTCAACTGGAAATGTCCGTGATTCGGATGTCCAAATACTGCGAA
ACCATCGAAGCGTTTCACAACCGTCCGGCATCAGCTTTCGGCGCTGTCGACCCCATCTTC

>RXN00120-downstream
TAAACAAGAAAGGCCCCTCCAAT

>RXN00128-upstream
CCATTTTCCGTTTGGTCTTGCCTAAAGAACCGCATGGAAATTATCGTGAAGCACCGATCC
CGTTGATCGCTCCAGAGACACCGTGGGAAGGGGAGCAGCA

>RXN00128
GTGAGTAAAATTTCGACGAAACTGAAGGCCCTCACCGCGGTGCTGTCTGTGACCACTCTG
GTGGCTGGGTGTTCCACGCTTCCGCAGAACACGGATCCGCAAGTGCTGCGCTCATTTTCC
GGGTCCCAAAGCACACAAGAGATAGCAGGGCCGACCCCGAATCAAGATCCGGATTTGTTG
ATCCGCGGCTTCTTCAGCGCAGGTGCGTATCCGACTCAGCAGTATGAAGCGGCGAAGGCG
TATCTGACGGAAGGGACGCGCAGCACGTGGAATCCGGCTGCGTCGACTCGTATTTTGGAT
CGCATTGATCTGAACACTCTGCCAGGTTCGACGAATGCGGAACGAACGATTGCGATCCGT
GGAACGCAGGTCGGAACGTTGCTCAGCGGTGGCGTGTATCAGCCGGAGAATGCGGAGTTT
GAAGCTGAGATCACGATGCGTCGGGAAGATGGGGAGTGGCGTATCGATGCTTTGCCGGAC
GGGATTTTATTAGAGAGAAACGATCTGCGGAACCATTACACTCCGCACGATGTGTATTTC
TTTGATCCTTCTGGCCAGGTGTTGGTGGGGGATCGGCGTTGGTTGTTCAATGAGTCGCAG
TCGATGTCCACGGTGCTGATGGCCCTTCTGGTTAATGGTCCTTCGCCGGCAATTTCTCCT
GGTGTGGTCAATCAGCTGTCCACGGATGCGTCGTTCGTGGGGTTCAATGATGGGGAGTAT
CAGTTCACTGGTTTGGGAAATTTGGATGATGATGCGCGTTTGCGTTTCGCCGCCCAGGCC
GTGTGGACGTTGGCGCATGCTGATGTCGCAGGCCCCTACACTTTGGTCGCTGACGGCGCG
CCGTTGCTGTCGGAGTTCCCAACGCTCACCACCGATGACCTCGCCGAATACAACCCAGAG
GCTTACACCAACACGGTGTCCACGTTGTTTGCGTTGCAGGATGGATCGTTGTCGAGGGTC
AGTTCCGGCAATGTGAGTCCACTACAGGGCATTTGGAGCGGTGGAGATATCGATTCTGCA
GCGATTTCCTCCTCCGCCAATGTGGTGGCAGCGGTACGCCACGAAAACAACGAGGCAGTG
CTTACTGTTGGCTCCATGGAAGGCGTGACTTCAGATGCGTTGAGGAGTGAAACGATCACT
CGTCCCACCTTTGAATACGCGTCGAGTGGGTTGTGGGCTGTGGTGGATGGGGAGACGCCT
GTCCGAGTCGCACGATCGGCAACAACCGGTGAGCTCGTCCAGACGGAGGCGGAGATTGTG
CTGCCAAGGGATGTGACGGGTCCGATCTCTGAATTCCAACTGTCACGAACTGGGGTCCGG
GCCGCCATGATCATTGAAGGCAAGGTGTACGTGGGCGTCGTAACGCGTCCTGGTCCGGGC
GAGCGGCGCGTGACAAATATCACGGAGGTGGCGCCGAGCTTGGGCGAGGCGGCGCTGTCG
ATCAACTGGCGCCCAGACGGCATTTTGCTTGTGGGCACGTCAATTCCAGAGACGCCGCTG
TGGCGCGTCGAGCAGGACGGATCGGCGATTTCGTCGATGCCGAGCGGGAATCTCAGCGCG
CCGGTGGTGGCGGTGGCAAGTTCCGCGACGACGGTCTACGTCACTGATTCGCATGCGATG
CTTCAGCTGCCGACTGCCGATAATGATATTTGGCGCGAGGTGCCCGGTTTGCTGGGCACG
CGTGCGGCGCCGGTGGTTGCGTAC

>RXN00128-downstream
TGATGGAGCTGTTCTTCCCGCGC

>RXN00154-upstream
TAGCCAGACGGCAGTATTTTGAAGCGGTGAATAAACGTTTGCTCGAATTTCCATAGTGTT
AGGGAAGTGTAGTGCAGTGCTTTGACTAGGGTGGTGAGCT

>RXN00154
ATGAGTTTTTCAGACCCCTATGCAGGCAATATTTTTGGTGGACACTCCCGCAACAAGCAG
CCGGAGTATCCCGATGTGCCCGCAAAACCAGGCCTTGTGGTGGAAGTTCGTGGAGATGGC
TTCGTCGGCGCTGTGACCGGTTTTGAACGCACCTACGATGGTGATTTTGTGCGTCTCGAG
GACCGCCGCGGACGCGATGCGCTGTACAAGCTGCGCAAGGGTGCGTTCATGATTGATGGG
CAGATCGTTAACCTCACCCGTTTCGTGGAAAAACAAGCACCACGTAAATCTAATTCTGGT
TCCAGGCGTGTAGAAAACGCGCAAGCAAAGGTCGCGGCGCCGTCACGCATCTGGGTAGAA
GGCATCCATGACGCCGCCATCGTGGAGAAAGTGTGGGGACACGACCTTCGCGTTGAGGGC
GTCGTGGTGGAGTACCTGGAAGGTCTAGACAACCTGGAGGAACGTCTCGCGGAATTTCAG
CCTGGGCCTGGACGACGCATCGGAGTGCTCGCTGATCACCTTGTTGAGGGATCTAAAGAA
ACTCGGATGACTAAATCACTACCCGCGGATGTCGCTGTCACCGGCCACCCCTACATCGAT
ATTTGGGCTGCTGTGAAACCAGAGCGTTTGGGGCTTAAGGCGTGGCCTGAGGTGCCATAC
GGGGAGGATTGGAAAACCGGCATCTGCAAACGAGTTGGCTGGTCAGACCCCAAAGAAGGC

TGGCACCGTGTGTATAACGCCGTGAATTCCTTCCGCGATTTGGACTACACCCTAATTGGG
GCAGTGGAACGTTTGGTGGATTTTGTGACCAACCTCGATTTGAGTAAAGAGGACGTCCTC
GCC

>RXN00154-downstream
TGATTTTTCGGGTGTGTTTTTGC

>RXN00162-upstream
GGAGACGTCGAAAAGCATAAACCTGGAACTTTTCCGGGCCCGCGCCCGACTGCTTTGCTG
AAGCCCTATCCCGCTATTTTATTTTTGAAGGAAGAGTTGC

>RXN00162
GTGTCTACCACCACCCCAATCCACCCTGAGCGCAAGAAACGCGTTCGTCAGGCCCTCACC
ATGTTCTCCATCGCTGCGTGGGTGACTGGTGTGTTTTTGCTGGCGCTGGTGGCGGAGATG
ATCATGAAGTACATAATTGGCATGGATCTTCCTGAGTGGGCACGATTCGTTCCGATTGCA
CATGGATGGGTTTACATTGTTTTCTTGATGACCACCCTGAACCTGGGTCTGAAGGCGCGT
TGGAATCCGACTCGTTGGGTGACCACCGCTATCGCAGGTGTGGTTCCGCTGCTGTCGTTT
TTTGTTGAGCACAACCGCCGCAAGGAAGTTACTCAGACATTCCAGCTGAACTCA

>RXN00162-downstream
TAGTTAAATACACAAAAACCTCC

>RXN00167-upstream
CCGACAATCCAGTGGAACTTCCCTATCGCTGTGATGCATTTTTACTTTCACGTTCCGGTA
CCCTGGCAGGCAGATCTTCCAATCTTTAGGAGCCCTCGCC

>RXN00167
ATGTACCTGTTGAATCCACCAGTCACTGAACCCGAGATCCTCACTGTCAACGAGATTCCG
ACCGTCGTCGCTGTCTTTGACAACCACCCCATGAACGACATGCCCGCAGCATTCGATCAA
ACCTACCAAGTGCTCTTCCCCACCTTGGGTGCCAAGGGCATCGCGCCAATTGGCCCCGGA
TTTGCTCTGTACACCTCCGAACCAACTGACACCGTCAGCTTTGAAGTGGGCATCCCAGTC
AGCCAACCACTTGAGGGAGATGTTTCAGCCGCCAGCGGCATCGTGCTGAAAAACTCAGTG
GTCCCTGCCGGAAAAATTGCGCGAATCAGCCACATCGGCTCATTCGACGGACTGAGCCAA
GCATGGGGTTCATTCGTGGAAGCTCTTGAATCTGCAGGCCATGAGATCGATATGCCGTGT
TGGGAGGTATATGTCACCGAGCCTTCCCCCGACATGGATCCCGCAACACTCCAAACTGAT
CTATACGTCCTGTTGAAG

>RXN00167-downstream
TAGAGAAGCTTTCTGGTCAAGTT

>RXN00171
AAAGATCAGCAGAAGCAGATTCATAACTTGGCAGCTGAGGTAAAGCGTCTTCGTGAGCGT
GACGATGCACGAGATCAGCAGCTAGGAGTGCTTAATGAAGCCATGTTTTCACTACTAGGA
GATGGACTTGACCGTTTTCGTGAATCTGGCGATGAGGCATCCTTCAATGCTGCATTGAAC
TATCAGGCAGTGGTGGCACCAGAAATGTTTAAGACCGTGTATGGTGTCGATCCGTCTACC
GGAGAGCCTATTCCCACT

>RXN00171-downstream
TAAAGTACAACACAGTCTTTTCA

>RXN00194-upstream
AAATATGAGAACATAGTGAGAGTTAAACCAAGTTCTGTAGGTGCTTGTTGCAGCGGGCGC
GAAGGCGTACCACTGCAACTTGCGAATAAAGGAGTAAAAC

>RXN00194
GTGGCTGGTTCCTCCCACACGATTGAGCCTGAGATCTACCGCGGTGTATCCACCCTTGAT
GAGCCTTCGGCTGCATGGGGATGGCACGGTCTCAAGCGCAACACCATCCAACTCGCTGGC
TGGATTTCCGTTCTGTTCATGCTTGGATACAACTTCGGTAACCACAAGGGCCACGTTGAA
ACCATCTGGCTTCTCGTCATCACCGCCCTTCTGGTCATCGGCCTGCTGATCCACCTGTTC
GAGCCAAAGCTCTTCCAGGTTCGCACCATCACTTCCCGCAACAAGCCTGTCGGCCACGTC

GAGCCAGACTGGACCTACGACCAGGCAACCCTCACCGGCACCTGGGGTAACCTCACTGAC
TCCCAGCTTCGCTCCGTCAACATCGAGCCAAGCCGTGTCGCTCACCTGCGTGCTGCAGAT
TCTGCGAAAGAACTAGACAAC

>RXN00194-downstream
TAGTTTTTTAAAAAGAAAATGCG

>RXN00197-upstream
GTCGATGATATTTTGGCAACCGAATCTGAGGCACGCGCGCGTGCGAATGCTTTGATCAAC
CGGTTGGCAACCAACTTGTAAGCTAAGGAGCTTCCGCCTC

>RXN00197
GTGGCAGCCTATCTTCTTGGTGTCGTATTATTTTTCCTCGGCATCGCAGTAACCATCGCG
CTTCACGAGTGGGGGCACTTCATCACAGCGCGCATTTTCGGAATGAAAGTGCGGCGTTTC
TTCATCGGTTTCGGCCCGACGGTGTTTGCCAAAAGACGCGGCGAAACCGTGTACGGCCTT
AAAGCGATTCCGGTCGGCGGTTTTTGTGACATCGCGGGGATGACTGCCCAAGATGAACTT
GATCCGGAAGACCTGCCGCGCGCCATGTATCTAAAGCCCTGGTGGCAGCGCATAATTGTG
CTTTCCGGCGGCGTGATCATGAATCTGATCGTCGGCTTTTTGGTGCTTTACGGCGTGGCG
GTGAGCTCCGGAATCCCGAATCCGGATGTGGATACCACCGCGACAGTCGACACCGTTCAG
TGCGTGCCGGAAACCCAAATTTCCGCAACTGAACTGTCCTCCTGCGTAGGTTCAGGCCCA
GCGGGCGACGCCGGCATTGAGCACGGCGATAAGATTTTGGCCGTCAACGGCCAAGAGATG
GCAAGCTTCACCGCCATCCGCGATGCGATCCTCGAGCTCCCAGGCGAAACGGCAACGCTG
ACGATTGAACGGGAGGGAACGCTTTTCGACGTCGACCTCCAGGTTGCCTCTGTCACCCGT
CTCGCCTCTGACGGTTCAGAAATTACCGTCGGCGCGGTGGGCATGTCGAGCCTTCCACCG
ACCGATGTGTACAAAAAATACGGCCCAATCGAGGGTGTGGGAGCAACTGCACGTTTCACC
GGCGACATGATCAGCGCCACGTGGGATGGCCTCAAAGCCTTCCCGGCGAAAATCCCAGGG
GTCGTCGCATCCATCTTCGGTGCAGAACGAGATGTAGAAAGCCCCATGAGTGTGGTGGGC
GCCGTACGCATCGGCGGCGAATTTGTCGAACGTTCCATGTGGGACATGTTCATGATGATG
CTGGCCAGCCTGAACTTCTTCCTCGCGCTGTTTAACCTCGTGCCGCTGCCACCACTTGAT
GGCGGACACATTGCCGTGGTGATCTATGAAAAAATCCGCGACTTCTTCCGCAAACTGCGC
GGAAAACCAGCGGGCGGCCCAGCGGATTACACCAAACTAATGCCCGTCACCGTAGCTGTC
GCAGCCTTGCTGATGACAGTGGGAGGCCTGGTCATTGTCGCCGATGTGGTCAATCCCATC
CGACTCTTTGGC

>RXN00197-downstream
TAACGATACGGAATTGAACTGCC

>RXN00216-upstream
GTGTTGCTCGCGGCCAGGCAGCAGTGCTGTACCTGCCTGACGCGGATGGTGACATCGTTC
TTGGATCAGGCACCATCTGCCACACGGAGTCTTAAGAAAA

>RXN00216
TTGGGCGCTTATGGTTTAGGTGAGCTTCCTGGAAAATCCGCCGCGGAAGCCGCCGACATT
ATTCAGGGTGAAACGGGCGATCTTCTCCATATTCCTCAGCTTCCGGCGCGAGGTTTGGGT
GCTGATCTGATCGGTCGAACCGTCGGTCTGCTGGACATGATCAACGTTGATCGCGGGGCC
CGATCTTGGGTGATGAGCACACGCCCCAGCAGATTGACGCACCTGACCGGCGATTTCCTT
GACATGGATTTGGATGCGTGCGAGGAAACCTGGGGAACGGGCGTCGACAAGCTAAAAATC
CAAGTTGCTGGTCCCTGGACTTTAGGTGCGCGCATTGAGTTGGCCAATGGCCATCGCGTT
TTGTCTGATCGCGGTGCGATGCGTGATCTCACGCAGGCGCTGATCGCCGGCATCGATGCG
CATGCACGCAAGGTTGCTGGGCGATTTCGCGCCGAAGTGCAGGTGCAAATTGATGAGCCG
GAGCTGAAATCGCTTATCGACGGCTCCCTCCCTGGCACTTCCACCTTTGACATTATTCCT
GCGGTGAATGTCGCTGATGCCAGTGAACGTTTGCAGCAGGTCTTTAGCTCGATTGAGGGG
CCGACATATCTCAACCTCACCGGCCAGATTCCTACTTGGGATGTGGCTCGGGGTGCGGGC
GCCGATACTGTGCAGATTTCCATGGATCAAGTCCGTGGAAATGAACATTTGGATGGTTTT
GGTGAAACCATCACCAGTGGAATTCGTCTTGGTTTGGGCATTACGACAGGAAAAGATGTC
GTAGATGAACTGCTCGAGCGACCGCGGCAAAAGGCCGTTGAGGTAGCACGCTTTTTTGAT
CGTTTAGGTGTGGGCCGAAACTATCTCGTGGATGCTGTTGATATTCATCCGGGTGAGGAT
TTGGTGCAGGGGACCATCACCGAGGCCGCGCAGGCTTATCGCATGGCCCGGGTGATGTCG
GAGATGTTGTCGAAGGATTCATGCGACCTT

>RXN00216-downstream

TAAGGCTTTACCGGCGCTGGGTG

>RXN00222-upstream
AGGGAAAAACTACCGTCCGCCTGGACAAAGTCATCGATGTACTCCGCGTCCTTGGACTCG
AGCTTTCTGTTGGAATTCACGATCCCCTCAAGGTTAATCA

>RXN00222
ATGACCCCCACTGCCGATATCTGGTTTAAAGATACTTTGGCTGCTCATTTCACACGCGAC
GGCGACCAGACCACATTCTCCTACACAGCTGATTACGCAGGTCCACCGATTGCCACGTCC
CTGCCCATCAATTCTGAACCCGTGATTACGCGCTCTGGAGCGATCCCACCATTTTTCGCG
GGATTACTCCCCGAAGGTCGTCGCTTAAGTTCACTCCGGAGAAACATTAAAGCCTCTGCC
GATGATGAACTTTCACTCCTTCTAGCAGTGGGAGCTGATCCTGTTGGTGCAGTCGCTATC
TTCCCCCATGGTGAAAATACACAACCTGCACCACCCACAGTTGATTTTGACGATGAACTT
GATTTCTCGGCTGCACTAACCGAGTCCGGGATTGCGGATCCCGTTGCACTGGCCGGTGTC
CAAGACAAAGCCTCTGCACGCACCATCGCGGTCCCCGTTGCAAGCGATGCCATCTTGAAA
CTCTCCCCGCCTGAATACCCTTACTTGGTGGAAAACGAAGCAGCTTGTTACCAGTTGCTG
ACCAAAAATAAGCTTCGCATTGAACTGTCCAAAGTAGAAGTTCTCCATGACAAACACGGC
AGGTCCGGACTCTTAGTTCACCGCTTTGACCGCACACCCAAAGGCAAAATCCCCGTCGAG
GATGCAGGACAGGTCTTGGGAATCTGGCCTGCAGATAAATACTTAGTGAGCTACGAGGAC
ATCGCACAAGCCCTCACTAAAGTGTGCGCCTCCCCCATCTTGGCGATGCGCAATCTCGCC
TTCCAAATCGCAGTCGCGTGGCTCAGCGGCAATGGTGATCTTCATGCCAAGAACATCTCC
ATTATCAACAAAGGCCGCGGATTTGAGATCAGCCCCATCTATGACATCCCTGCCACCGCA
GTATATGGCGACACCACGATGGCATTAGAAATCCAGGGATCCAAAAAGGATCTCAGCCAA
AAGAAATTCCTAAAATTCTGTACATCCATCGGACTACCAGAAAAAACAGCCATGTCGGTT
GCGAACGCTGCACTGTTGGCAACAGAAAATGCCGCAGAGACAATTCTTGCTTCGGGAAAT
TTTGATACACGGATGAATCGAGATCTGGCCAGGGTTCTCAAACATCGACGAAGCGCATGG
GGAGCT

>RXN00222-downstream
TAATTCGCCTGTTTAAGAGGTCG

>RXN00232-upstream
GCTGAAAAAACTCCCATTTGGACAATGAACACTTGTCAAAATGGGAGTTTTGGATTTTCG
CACCACCGGCAGCACTCGAAAACGTGTTTATACTTGAACT

>RXN00232
ATGAACGACAGGGCTCACCAACGAATAGGCGACATCGAGCGATCCCAAGCCCTCGACCGA
CTTGGGTCATATTTTGCAGACGGATACCTCGACATCGACGAATTCGATACCCGAACCGGC
GCCGCAGCAATCGCACGCACAGCCGGTGAAATAGATGTCTTGTTCACAGATCTTCCCGAA
CAACAGGCAAGCACCGCCGTGACACCCGTGCAAGACGATACCGAGAAAGAATTAGACCTG
GTCCTACAGCGAGGAAAGAAGCTCAAGCAGATCGACTCCGCCATTTGGGCTGTCGTGATG
GTCTCGTTCTTCCTAGGCTTGTTTGTTTTCAACGTGCCATATTTCTGGGTTGTGTTCATC
CTTGGCGGAGCGGCCTCCGCGGGTGCGCGATTCTTGCTCAAAGTAGATGACGCCGATGAA
AAACTCTTTGAGGAACTCCACAGCAAGGAACAAAGCGAACGCGAAGCACGCCTACGCATT
GCGGCACAACGTCGACGCGAGTTGGAACAA

>RXN00232-downstream
TAGCCACAAAAGCTATCAAGCCC

>RXN00236-upstream
AATGCGAGAGTTCTAAAACGAGCCGGTAACATCGACCCCCATGAGTTCAGGGGTTAGAAA
AGCAATGGGATTTGGATGCGGTTCGGTTTTGGCCGTCATC

>RXN00236
ATGGTGATCTCATTTGTTGGATGGGCGCTCAGCTTCATGGATGGAACGGCACCTATTCGC
CAACTCCAGCAAATCCCTGAAGATGTTCCGCCGGCGCGTGGTGTAGAAGTTCCGCAAATT
GATACAGAGGCAGATGGACGCACATCCAACCATTTGCGTTTTTGGGCGGAACCAATTGCT
CAAGATACTGGTGTGTCCGCTCAAGCGATTGCGGCTTATGGAAACGCAGAGCTCATCGCG
AGTACTGCGTGGCCTGGCTGCAATCTGGGGTGGAATACCTTGGCAGGTATCGGCCAGGTG
GAAACCCGTCACGGTACCTACAACGGCAAAATGTTCGGGGGCAGTTCCCTGGATGAAAAT
GGAGTTGCAACCCCTCCAATCATCGGCGTTCCACTTGATGGTTCACCGGGGTTTGCGGAA

ATTCCCGACACTGATGGTGGGGAATTAGATGGCGATACTGAATATGATCGCGCGGTAGGT
CCCATGCAGTTCATTCCGGAAACGTGGCGACTTATGGGATTGGATGCAAACGGTGATGGG
GTAGCGGACCCCAACCAAATTGATGACGCAGCATTGAGTGCCGCAAACCTGTTGTGTTCC
AACGATCGTGACTTGTCCACTCCTGAAGGATGGACCGCAGCTGTTCATTCTTACAACATG
TCTAATCAGTATTTGATGGACGTTCGAGATGCTGCCGCGTCCTACGCTTTACGACAGCCG
GCGATC

>RXN00236-downstream
TAAAACTTAACAAGCGCAACCCC

>RXN00242-upstream
GGATCACTATCGCTTTAAACACCGAAACCTTCCTGCTAGTTCACCAAGATTTTTAAGTTT
TACCGCAATTTCTTGAGAGCTTTGGGAGGATAATGGCGGT

>RXN00242
GTGAATGAATGGCGAACAGTCTCGCTTGTAGATTCCACGGCGCTGACCGTGATCATCAGT
GTGGCCGTGTTTACTTCTGCTGTGGCTCTGCTCGGAGTTGTGAAAAAGCGCTCTCGGTGG
CGGGTTCTCGGAGCTCTCATCTCCTCAGCAGTTCTCACCAGTGGCGCATGGGTGGTTATT
GAAAAGCTGTGGAAGCCTTTCCCCGACCCCAATCCGTGGACCATCTATCTTTCCGCTGGT
TTGGCGGTTTTTCCTCTGTTGAGCATCTTGTTCCGCACTGGTCGTACAAGAATACTGATG
GCTACACTCACCGTGATTGCACTGGTTAATACGGCCGCAGTCATCAATGTCATCTACCAG
CCATACCCGACGTTGGGTTCTTTCAATCCCGTGCCAACGGCTGTGTCCATGTCGTATGCA
GATTTTGAATCTCAGACCACTGCCCCGACGATGGATGACCGTGAAGTCGGTGCCCTTGTG
CAGGTGCCGCTAGCTGGAACAACAGATGATTCCACCTCCGGCTTTGATGCGCGCGATGCC
TACGCCTATATTCCGCCTGCGTATTGGGATAATCCTTCCCTACAACTGCCAGTTTTGGTT
CTCATGCCCGGAAACCCCGGCCAGCCAGATCAGTGGTTTAGCAGTGGAAATGCCGATCAA
ACAGCAGATAATTTCCAAGCAACCCACGATGGCATCAGCCCCATTGTCATCAGCGTGGAT
GGCACAGGATCATTCAGCGGAAACCCTGCTTGCGTGGATTCTGATGCCCAAAGCGTGATG
ACATATCTATCCCACGATGTCCCCATGTTGATCAAACAGAAATTCCGAGTCAATCAGGAT
CAGCGCACCTGGACAATTGGTGGTTTAAGTTACGGCGGCACCTGTGCTTTGCAGATCATG
ACCAATCACCCCGAAGCGTATGGTTCTTTCCTTGACTTCTCGGGCCAGGAAGAACCAACA
CTTGGCACACGCCAGCAAACTGTTGATCAGCTTTTCGGCGGCGATGAAGACGCATTCAAA
GCCGTTAATCCGGAAGATCTGCTCAATCAAGCAATCAGCTCAGGAGCGCATACCTACAGC
GGGATTTCGGGCAGGTTTATTGCTGGTAGCAACGATAAAAGTGCAGTGAGCGCGCTGTCT
CATCTTGATAATTTGAGCAATCAGGCGGGCATGTCCACCACCTTTGATACCGTGGCCGGT
GGACATTCCTTCCAGGTGTGGCGCGTGGCTTTAGCGAATACTTTTGATTGGGTTGCCAAG
CGCGGCGGATTGCAGGTT

>RXN00242-downstream
TAACAATGAAAGACGCTTCACAG

>RXN00247-upstream
AACCCCTAACTACTGACCTCGCACCACTTGTTGCAGCCCGTTACCACGCTGCATTGAGCG
CACTGCTGGCACATATCTAAGACCGCTAAGGAAATCAGCT

>RXN00247
ATGCAGACATTAATCTTTATCGCCATTGCAGGCGTCGCAGCACAGCTTGTTGATGGCGGC
CTCGGCATGGGGTTCGGCGTCACCTCAACCACCATCCTCATCATGCTCGCAGGTTTAGGC
CCTGCGCAGGCATCCGCCGTCGTGCACACCGCAGAGGTTGGAACCACCTTAGTTTCTGGT
TTAAGCCACTGGAAATTTGGCAACGTGGATTGGAAAGTAGTTGTCCGGCTCGGTATCCCC
GGCGCTATCGGCGCATTTGCTGGCGCTACCTTCTTGTCCAATATTTCCACCGAAGCAGCA
GCACCGATCACCTCCCTGATTCTTGCCCTGATCGGCATGAACCTAGTCTGGCGATTCAGC
AAGGGACGCATCCGCCGCGACTATTCCGATCGCCCGCACAGCAGGGGATTCCTCGGCGGA
CTCGGTATTGTCGGTGGTTTCGTTGACGCATCCGGTGGCGGCGGATGGGGTCCAGTGACC
ACCTCTACGCTGCTGTCTTTGGGACGCACCGAACCCCGCAAAGTAGTCGGCACCGTCAAC
ACCGCAGAATTCTTAGTCTCCCTAGCCGCAACATTGGGCTTCGTCGTGGGACTGTGGGAT
GACCTAGTAGCTAACCTCTCTGCAGTTCTCGCGTTGCTCATCGGCGGCGCAATCGCAGCA
CCAATCGGCGCCTGGATGATCTCTCGCGTTAATGCAACCGTCCTCGGTGGCTTCGTGGGC
ACCCTGATTGTCACACTGAACCTGCCAAAGGTGCTCAACGTGGTTGGCCTTGATTTCATC
CCCACCGGCCTCATCCAGGTCACCGTCCTCCTCATCGGCCTGCCGCTGACGTACCTCGGC
TTCCGCCGCTACCGCAAAAATCTCCTCAACGAGACCATCTCCAGCGAAGTTGTCTCCGAA

CCAAAGGGCCAAAAGATTAAAAGCACT

>RXN00247-downstream
TAAAACACGCTTTTCGACGCCCA

>RXN00256-upstream
AATTAATCAATCAGAAAAACATATTGAATACTTATAAATTTCTGACATACTCATTAATGA
GATATTCGAAGTCTTTATCAAAATGATTAACAAAAGGAGT

>RXN00256
ATGTTTATGTCGCTAAAAACTCGCCGAATATTCGGCGCACTTGCTGTTTCGCTATCAATC
TCTTTCTCAGCCATTGCTACACCTGCAGCATCCGCACAAGAACTAGTGGTGAGCACATCA
GCAGTAAACGAATTTGGTGTAGTTACCAGTGACATCACGGCTGAGCAAATTCTTCAGGCG
CAAGATCTAATCGCTGAGATGAAACAGTCAGAGGACATATATGAGTATTTCGGTGCCTTG
TCTGACGTTGAACAGAGATCCATCATTGCAGCTGTAAAGGAAAATCCATATCTCATTGAG
AACGAATCACCCCGTATGAGAGTCCAAAGTGAAACACCCGACGAGGAAACACCTGATAAG
AAAAAGCCGAGCAAAACCTACAAGCTCTATATGAGCATTCTCGAAATGATGTCATGTATC
AATCTTGTTGATGTTCCGTCATGTGCCCAAGCCCTTAAAGCGGCAAATATAGCTGAACGC
GAGGCCAAGGCCCGTTACCCCGATTCGGTCACTAATGGTAAAGGCGATGCCCTTCGTCAT
TGTGCATGGAGCGCTCTCATGACTATTCGAATCGGAAAAGATGCAGCCGAAAGAATTGGT
AACGCTCATGAAACCGTTGTGAGAGGTGAACCCGAAGAAAGAGAAATGGATCTCATCAAT
AACGCGCTGGGTAGAGACATCGGCGAAAGATTCATCATCAATGGCGATGAAACGGGTGCG
CTCAGTACTTGTGTATCCATGGCTAATATCGGGCTACTTCATACTCTGTTG

>RXN00256-downstream
TAAACAAAGGAAGTTTCTATCAT

>RXN00264-upstream
AAACCGGAAGGGCCCGTTTACTCCCCTACTTGGCGCAGAAATCCACATCAATCCAGGTGA
AGCAGTCATCTTTGATGTTGATCCCACGTTTGAACACGGT

>RXN00264
TTGCTTGTCGATTCCGGCGACGTCCAACTAGAAGGCGTCACCGTCGAGCCCACCCAGCTG
GCCTACACCGGCATCAATGAAACCCAACTCCGAATCCGTAACATCGGCACCACACCGGCG
CGTACTGTACTGCTAGGTGGCGAACCATTTACCGAAGACATCGTGATGTGGTGGAACTTC
ATTGGCCGCAGCCATGAAGAAATTGCCGAGTACCGTAAACAGTGGCAGGCCGAAGCTGAT
CGTTTTGGTATCACCCACGGATATATCAGCCACCACAAAGATGGGCTCACCAGGCTTCCA
GCACCCGAGCTTCCCAACGCTGCTATCAAGGCACGTAAAAACCCAGCACCAACTGCACGA
CCAGAAACGAGAATTGAT

>RXN00264-downstream
TAAATGCGCTCCGCTCACGGCCC

>RXN00267-upstream
GTCGTACTTATCTTTTAAAGTCATGCCTTAAAGGATACGGAGATCACTCCGGCTTGGCTT
GGGTGGCGGTGTTATCAAAGTAGTCGTAGCGTTGAGAACT

>RXN00267
ATGCGAAACTCTAAGTCTGGCCTGGCCTTTTCCGCAGCTGCACTATTTTGTGTCGTCGCG
GTAATCACTCGTATTGCAAGTTCCCCATCATTTATCGCTATTGTGGCGATCATCGTGGCT
GCGATCGCACTTTTTGTGGGTCTGAACAGTCGTGTGGGAACAAAGCTTGTTGATCAGCCA
GTGGTGTTCACCCAGGAACAAATTGATCAATTGAAAGAGTTGAAATCCCGCGACCAGGAG
GCGGCAGCGATCCGTCAGGCGCAGCTGTGGAGTAGGGGATCGTCCAGCGAAGCGGTCGCA
GAGGCTGTGAGGAAGCTC

>RXN00267-downstream
TAAGTCGACTTAAGTGCGCGAAG

>RXN00271-upstream
TAGTTTAAATCATGAGACATTTCACATATGGTTCTTTATCCGAGACATGTGTTGACGCTG

TCTGCCCCTTTTTGAAAATAACACTTTAAGGAGATGTGCC

>RXN00271
ATGTTTTCTTCCCGTTCGAAGGTACTCGCAAGCATCTTTACTGTTGGCGCCTTGGCGTTG
GCTTCGTGCTCAAGCGATTCCAGTGACAGCTCCACCTCCACTGATGCTGCAGGTGGCGAC
TCTTACCGAGTTGGCATCAACCAGCTTGTTCAGCACCCTGCACTTGATGCAGCGACCACT
GGTTTCAAGGAAGCTTTTGAAGAGGCAGGCGTTGACGTCACCTTTGATGAGCAAAACGCT
AACGGCGAGCAGGGCACTGCACTGACTATTTCTCAGCAGTTCGCTTCTGACAATTTGGAT
CTCGTGTTGGCTGTTGCAACTCCAGCAGCACAGGCAACTGCGCAGAATATCACTGATATC
CCAGTCCTGTTCACCGCAGTTACCGATGCAGTGTCGGCAGAGCTGGTGGATTCTAATGAA
GCACCTGGCGGAAACGTCACCGGTACTTCTGATATCGCACCGATTGAGCAGCAGTTGGAG
CTTTTGCAGCAGCTGGTTCCTGACGCAAAGTCCATCGGCATCGTCTACGCGTCTGGTGAG
GTCAACTCTCAGGTGCAGGTCGATGAGGTCACCAAGGCTGCTGAGCCACTGGGGCTGTCC
GTTAATACTCAGACTGTCACTACCGTGAACGAGATTCAGCAGGCTGTTGAAGCTCTCGGC
GATGTTGATGTCATCTACGTTCCAACTGACAACATGGTTGTTTCCGGTATTTCTTCTCTG
GTTCAGGTTGCTGAGCAGAAGCAGATCCCTGTGATCGGCGCTGAGTCCGGCACTGTTGAG
GGTGGCGCACTGGCAACCCTGGGTATCGATTACACCGAGCTTGGCCGCCAGACTGGTGAG
ATGGCTCTGCGTATTCTGCAGGACGGCGAAGACCCAGCAACCATGCCTGTGGAGACTGCA
ACTGAGTTCACCTACGTGATCAACGAAGATGCAGCAGAGCGCCAGGGCGTGGAGATCCCT
CAAGAGATTTTGGATAAGGCCGAACGCGTA

>RXN00271-downstream
TGATCGGCGCTTTTGAGTTCGGA

>RXN00272-upstream
ACCGATGCACCAGCCACCAACGCGTCCAAATCAATATCAGCCTGGCCCACAAGGTGGAAT
TCCAGTGGGTGGCCATCTGCCACAACCAGGTGCAGGGCAC

>RXN00272
ATGCCGGAACCAGAAACCTCCACGATGGGCTCCATCCAAAAGTCCGGTGAATGGCTCGTT
CCTGCATATTCGGCATACAAGCTCAACGGTGCTGACCTTTTCTTAGATATCCGCCATGCC
ACCGCGGCTGCTCCTGTCATTACCTTTGATGTCAACATGACCATGGGTTCTATGACGCTG
ATTGTTCCACCGGGTGTGTATGTGGAAGTGCAGATGGCTTCCAAGAACTGGTCGGATTTC
AAGGTTCAAACAACCAATCCTCTCCCCGGTGCTCCCCGAGTGTTCATCACTGGTGTTGCA
CGCGCATCAGGGTTGAAGGTTTTCACCAAGCATCCTCATGAGCCTTTTGGGTTCTGGCAG
AAAATGTTTGAG

>RXN00272-downstream
TAGCCTCGGGCCACGCCCGAACC

RXN00283-upstream
GCGTTGGCATTGGCGTTTTTAGCGCGCTATGACGCCCTCATCATGGCCTTCGTAGCCATG
TGGACTGTCGGATTTATGACATGGCGCGCACGATACCGCC

>RXN00283
GTGGCTTCCGCGACCGCATCGGATTCGCACTTGTCGACATGCTGCTCCTCGTCTGGCCGA
TCGGCTTCGCCTTCGTCGCCTGGACTGGCGCCAAGCTGGCTCACTACCGGCGAACTCTTT
GCCCAATTCACCTCCACAGACGGCAACGCTGCGATCATCGCAGCATCCGGCGGCGGCGCC
ATAGGGCCCCAAGCGCTTTTCGACGCCTCCGTCCGCACCTTCCTCATCTCCCCAGCTCTC
CTACTCGTCGCAGTAGTTGCAGTCTTTTTTGCTTATCGACGCCGCGACCCCGAACCCATC
ATCCCCTTAGCTCTCATCGGCTCTGTGGTGTTCTTCCAAATCATTACCTACTCACTTGGA
TCTACCTTCGGCCTGCTGCGCTTTTTCCTCACCGCCCTGCCGCTCACCATTATCTTGCTG
TTCCAAATTATCCCGCCCCGCCACCGATTCCCCTCACTGCGACCAGGTGCGTGCTACCGC
GATCGCGTCACCGGCAAGTACGTGCCCAAAACAATCACCGGTGTTTTAGTTCTCGCGATC
TTCGGCGGCACCGGCATCACCCTGTACGGCATGAGCAGTGCTAACTGGGCGCCCCAGGAA
TATGCCATCCAAGAACTAGTTTTCAACATGGGATCGCCATCGCAGGACGCCGTCCACACC
CTGAACACCTTCTCCACTGAAATGGATGTCGCCGATTTCGTCGACTCCCTAAACCTTGGA
GACGGCGAAGTCCTTCTCTCCACCACCTACGGCTTCGCCGTCCTCACCGCATCAAACAAC
CAAAAGCAATTCATCATCCCCTCCGACGAAGACTTCATCACCACCCTCAACGAACCCGCT
GAGCACGGCGTTAAGTACATCCTCGCCCTCCCACGCGAAGGTCGCGGCGCCACCGACCCG
ATCAACCTGCGCTACCCAGACATGTATGAAACCGGCAGCCACATCGCCACGATGGAAATC

GAATTCATCAATCAAGGCCAAGGACAACCAAATTGGCGCCTCTATCGGGTGCTCACCACA
CCTGAACAGTCG

>RXN00283-downstream
TAGACTCTTTGTAACTACCGTTG

>RXN00334-upstream
ATAAGCCCCGCATGGGATATGAGAAAAGGAATGCACGATGAGTATTGAATTTCCGTTAGG
TAATCCAGCGCCTGCACAGTGGTTTTCTGGCGAGGTCCAT

>RXN00334
ATGGCCAAGCTTGATGACAACGTGCAGATTGAGACTGTGAACGTGTCTTTTGAGGCAGGC
GGTCGCACCAATTGGCACACTCACCCAGTCGGTCAAAACATAATTGTGCTGTCGGGCTTG
GGCATTTATGAGGCGGAGGGGGAGCCTGCTCGACTCCTGGAGCCTGGCGATGTTGTTTTC
GCAGCCGCCGGGGTTCGCCACTGGCACGGCGCCGTGTCTGGTGCACCGATGTTCCACGTG
GTGGTTAACCTCAAAGGCATCGACGGCGAGACCGTCGATTGGGAGGAGCCGGTCGACGAG
GAGCACTACCGCAGCGTGAGCGCGGAGCTACAAAGA

>RXN00334-downstream
TAAAAATGCTTTTCGACGTCCAC

>RXN00338-upstream
TCTTAGAAGGCGTAGTCACACCATTAACCTTGCCAGAATTTTTCAAGGCTTGGCTAGACT
TGGGAAACGAACATGCGGTACCAACCAGGGGAGTTAATGC

>RXN00338
GTGAGTGATGTAACCGTTGGCGATATTCGCCGCATTTTGGATGAGGCTTATCCGCCGGCG
TTGGCGGAAAGCTGGGACAAAGTGGGGCTGATCTGCGGTGATCCAACAGAGTCGGTGAAG
CGTGTCGGTTTAGCACTCGATTGCACCCAGGCAGTGGCCGACAAGGCTGTGGACATGGGT
TTGGACATGCTGATCATTCACCACCCATTGCTGCTGCGTGGGGTGACGTCTGTTGCTGCG
GATGAGCCAAAAGGCAAGGTCATTCACACCCTAATTCGCGGCGGGGTGGCACTGTTTTCC
GCGCACACTAATGCGGATTCCGCGCGCCCAGGTGTCAACGATAAACTCGCCGAGCTCGTC
GGCATCACGGCCGGGCGACCCATCGCGACACGGCTTTTAGGCGGCATGGACAAATGGGGC
GTGCACGTTCTGCCCAAGGATGCAGCGTACCTAAAGAAGATGCTTTTCGACGCAGGTGCC
GGTGCGATCGGCGACTACCGAGAGTGTGCCTTTGAGATCGAAGGAACCGGGCAGTTTAGG
CCCGTGGAGGGGGCGAATCCGGCAGAGGGGGACGTCGATAAGCTTTTTAAATCCCTTGAG
CTGCGCATCGAGTTTGTTGCACCGCGCAACCTGCGCGCCCGGCTCACGTCGGTGCTGCGG
GAGGCTCATCCGTATGAGGAGCCTGCCTTCGATATTGTTGAAATGCACAGCGCTGAGAGT
TTAGAAAATGCGACCGGATTGGGTCGTGTGGGTGAATTGCCGGAGCCGATGCGCCTCGCG
GATTTCGTGCAACAAGTGGCCAACAACCTGCCTGTCACCGAATGGGGCGTGCGCGCTACC
GGCGATCCTGAACAAATGGTGTCCCGTGTGGCGGTTTCATCAGGGTCGGGTGACAGTTTC
TTAAACGATGTGATTAAGCTCGGAGTGGACGTTTATGTCACTTCTGATCTGCGCCACCAT
CCAGTTGATGAATATCTCCGAGAAGGTGGCCCTGCAGTAATCGATACTGCACACTGGGCC
AGCGAATTTCCATGGACTTCCCAAGCCCAAGAAATTTTGCAGGACAAAGCCCCACAGGTT
GAAGTTGATGTGATTTCGATCCGCACAGACCCCTGGACCATGTCTGCGCGAGCAGTGAAC

>RXN00338-downstream
TAAATTCTTGAGAACTAAAAAAG

>RXN00342-upstream
CGGTAATGTGCAATTCGGATATATCAATAGCCCCGCGGTTTCATGTTGAATCCATGTAAT
CGAAAAACACATCGGGGCCCACACGAGGAGGATTATTAAA

>RXN00342
GTGGCCGACGCTCCGGGCGCAGTCAAGCAAGGTGCCCAGGATTATGCTCAACTACTCGGC
ATTCAATCGGGTCATATCGTTCAAGAAATTGGATGGGATGAAGATTCCGACACGCTGATC
AGCGAGTCCATCGAAGATGCAATCGGTGAGGAACTACTCGATGAAGAAACCGACGAGCTG
TGCGATGTCGTGCTGCTCTGGTGGCGCGAGGATGACGGCGATCTCGTCGACGGACTTGTG
GATTCCATCCGCTCCCTCGCTGAGAATGGTCGTATCTGGGTGTTGACTCCTGGCATTGGT
AAAGAAGGAGCCCTGGCTCCTGGAGTTATCTCTGAATCAGCTCAACTGGCAGGTCTCGTG
CAGACCAAGGCAGAACGTCTCGGTAATTGGCAAGGTTCTTGCCTCGTCCAGCGTGGAAAC

AAGAAGCCT

>RXN00342-downstream
TAACAATCGCTAATTTCCACGGC

>RXN00344-upstream
CGGCACGGTTGGCGATGTCATGCAGTCCGAAAAACTCAGCGAACTCTACAACGCACCCGT
CACGGTGGCTCGCATCAACGACAGAATCGTGGTGGTTTAA

>RXN00344
GTGGATCTATCCACCTGGCTTTCCGACACCCAATATCTCATCAGCGTCGATTTCGTCCAG
CACGCACTCATCGCCTCCGCGCTGTTGGGCCTGCTCTCCGGTGTGATCGCGCCGCTCATC
GTGGTGCGCCAACAGTCCTTCGCAGTCCACGGCACCGCCGAACTCGCCCTCATGGGAGCC
GCCGCCGCGCTGCTCTTCGGATTGAATGTAGGCGGCGGTGCAGTGATCGGTTCCGTGGTC
GCCGCGATCCTACTGGCATTACTCGGCATGAAACAACAAGATTCCGCCGTCGGTGCCGTG
ATGAGTTTCGGACTCGGTCTGTCCGTGCTGTTCATTCACCTCTACCCCGGCCGAAGCTCC
ACCGCGTTCTCCCTGCTCACAGGGCAAATCGTTGGTGTTTCCTCATCATCGCTGTGGATC
CTTGTGGCAGTCACCGTGATCGTGGTTAGCGCCGTGGTGATTTTCTGGCGCCCGCTGCTT
TTCGCCAGCGCCGATCCGATCATGGCGCAGGCCTCCGGAGTAAACGTCCGATTCATCGCC
GTTGCCTTCGCAGTTCTGGTTGGCCTCACCACGTCCCAGTCCGTGCAGATTGTCGGTGCG
CTGCTGGTCATGGCATTGCTGATCACTCCCGGCGCGGCCGCTGTGGCGGTGACCGCCAAT
CCAGTGAAAGCCGTGGTGCTGGCAGTCATCTTCGCGGAAGTATCGGCTGTCGGTGGCCTG
CTATTGTCGCTAGCGCCTGGTTTGCCGGTGAGTGTTTTTGTCACCACCATCTCTTTTGTG
ATTTACCTGGTCTGCCGCCTGATCGGTTGGCTCCGCGGCCGTGGAGCTCAGCGTGACGAA
GATGCTTATCGACGCCGCCAGCACGATCACCACCCTCAC

>RXN00344-downstream
TAGGCGTTTCGAAGTCCTATTTC

>RXN00353-upstream
CTTTCATCAGGACCGAAAGCGAACGTTTCGTATTGTTGAGCCTTTTGGTTCCACCACGGA
TGCGCTGATCTATTTTCATGGCTCCCAGCAGTCAGGATCT

>RXN00353
GTGGGGCGCAGCTTCACCAACAGGACTTTTGATCCGTTGCCGTTCATGGTGGTTTATCCG
GATGGGGTGGATCAGCATTGGAATGATGCGCGGTTGGGTTTGGATGAAAATACCCGCCAT
TTAGGCATTGATGATGTGGGGTTCTTTGTAAAACTCGCCACGCACTTGGGCAACACGTAT
GGCATCAAGAGGATCTTTATTGTTGGCTATTCCAACGGTGGGCAGATGGTGTTGCGGCTC
ATGCATGAGGTTCCCAAGATGCTCAGTGGCGCTGCAACCATTGCATCCAACATGCCAGTT
GCAGAGAATACGCTGCCGCAGGTGAAAACCTTCAAGACACATCCGGTGCCTTATTTGGCG
ATGGCTGGAACTGCCGATACTTTTTCACCGTATGAGGGTGGCGATGCCGGTATTGGTCGC
GAACACCGCCGTGGCGTGGGCATGTCCGCCTTTGATTCAGCTGCCTATATTGCCGCCCGA
AACGGACTGACCGAACACCGCCACGACGTGATTGATGATGTGGTGTCGATCGATACCTGG
GATGGAGAAAATCCCGTTGAGTTTTGGACACTCAACGGGATCGGCCACTTGGTACCAAGT
GGGAAAACTTATCCAGAATTTCTAGGCCCCTCAACCACATCAGTGATAGCGGCTGAGGAG
ATTGGGAAGTTCTTTGATGGGGTCAGGCGTCGA

>RXN00353-downstream
TAAGCTCAAGCTTTAAAAACGCA

>RXN00354-upstream
GGCTTGTCGGTAAGGCTGCAGGGTAGCGGGAGTTTCCTTCAGATTGGAAGTTCTTTAATT
TTCTCGATTATGTACCTCATTTACGCGTAAAGTTTGGGGC

>RXN00354
ATGGGAAAGTTACTTTTCGTAGACATCGGTGGCACACTGCTGGATTACTCAAATGAAGTT
CCGCGTTCGGCCGTTGACGCGATCCGTAAGGCACGCGCCAAAGGACACCGCGTGTACTTG
AGCTCTGGTCGAAGCAGCGCTGAGGTGACTTCTCAGTTGTGGGATATCGGAGTGGATGGC
CTCATTGGCGCAAATGGTGGATATGTGGAAAGCGCACAGGAGTCTGTGTTCCACCGCCGT

TTGTCGGGTGAGGAGACCCGCCACATTGTGGAGTGGCTCTACAACCGTGGTTTGGAGTTT
TATCTCGAGTCCAACAACGGTTTGTATGCAAGCCGTGGTTTCCGTGAGGCTTCTAAGCCA
GTGCTGTCTCGCCTTTCGGAGAAGACCGACGTGACAGTCGATAGCATGTACCCGGATATG
TTCTGGGGCGCGAGCCTTGATCGTGACGATGTGAACAAGATCAGTTACATCTTCAATTCT
CAGGAAGATTTGGACGCAGCGCGTGAGGCGTTCCCTAACCTGGAGCACACCACGTGGGGT
GGTCAGACGGGTGCGTTGTTCGGCACGATCGGTGTGTCTGTCAACAAGAAGATCGGCGTG
GATCGCCTGCTGAAGTACCTGAACGCAGATCGCGCAAACACCATTGCGTTCGGCGACAGC
GATGAGGATCTCTCCCTATTTGAGGCGAGCGCTTACGGCGTCGCGATGGGCGAGGCCACC
GAATCGCTCAAGGCTGCTGCTGACCTGGTCACGGATGCTGTTGGGCAGGACGGCTTGCGC
AATGCGTTTTTAAAGCTTGAGCTTATCGACGCC

>RXN00354-downstream
TGACCCCATCAAAGAACTTCCCA

>RXN00362-upstream
CACTTTTTGGGTGAAAATTCCACGAAGTTAATGCCGCTTTAAGTCAATTCAATCACATGT
AACATGCTACGGTTTTTTCGGTCACTTAAAGGAGGCGCTT

>RXN00362
ATGGGAATCATTGCTCTGCTCGTTTTTATCGCAATTGCCGTGATATTGAATGTGTTTTTG
AAACGAGATATTTCAGAAGCATTGCTAGTTGGATTAGTAGGAACTGCGCTTGTCGGCGGT
GTAAATGCACCGACATTACTGATTGATGCTGTAGTGGATGCTGCTCAGTCGGAAGTTACT
TTCGCAGGTATGGCCTTTGTTTTCATGGGCATCGTTGTGCAATCAACTGGATTGATTGAT
CGATTAATCGCAATCCTTAACTCGATTTTTGGTCGGCTTCGAGGTGGCGCAGGTTATGTT
TCCACTCTTGGATCTGCGCTCATTGGACTCATCGCTGGATCAACGGCTGGAAACTCCGCG
ACGGTTGGCTCAGTGACGATCCCTTGGATGAAAAAGACGGGATGGACTGCTGAAAGGTCC
GCAACGTTAGTCGCGGGCAACTCTGGCCTTGGTGTTGCGTTGCCTCCCAATTCAACAATG
TTCATCATTTTGGCATTGCCAGCTGCAGCAGCTTCTTCGGCCTCTCAGGTGTACATTGCT
TTGGCTTGTGGTGGTGCGTATGCAGTGCTCTACCGCTTAGCGGTCGTCTTTTACTGGACA
CGTAAAGATAAAATTCCTGCCACCCCTGATGATCAACGGGTGTCATTCGGTGAGGCAATG
AAGACTGGATGGCGTTCACCGTTGATCTTCCTTGGAATTTTGATCCCCGTAATCCTCACA
ATCGGCCCATTGTCTGAATGGTTAAAGACACATGGAGTTGGGGAGTCTGGTGTTAAATCG
ATGTCGATCATCGTGTGGGTGCCAATTCTGATTACGGCAATTGCTCTGATTGAAGGGCGT
AAACGAATTGCTAACAACATGGCACACTTTAGGGTTCAGATCTCCAAGGACTTGCCACAA
TTTGCCACCGTAGGAATTTCGTTGTTTTCTGCGCTTGCAGCAGCGAACATCATGGAAGAA
CTGGGTGTTGGCCCGCAGTTGTCTAACTGGCTTGATTCCATGGACCTACCTAAGTCTGTC
ATGGTGATCATTGTCTGCATCATGTGCATTGTGGTGGCAACGCCACTGTCGTCAACAGCA
ACCGCGGCTGCGATTGGTGCTCCCGCTGTCGCTGCGTTGGCTGCGGTAGGTATTGATCCA
ACTGTGGCGATCGTAGTGATCTTGCTGTGCACTTCCACTGAAGGTGCATCCCCGCCGGTG
GGCGCGCCGATTTACCTTTCTGCTGCGATCGCCGATGCAAACCCAACGAAAATGTTCGTA
CCACTGATTACGTACTTTGTTGTCCCCATGATTCTGCTTGCTTGGCTAGTTGGAATGGGA
TTCTTACCAGTGATTGTTCCTACGGGT

>RXN00362-downstream
TAAAGGGGTAAAAATGAACTCAA

>RXN00373-upstream
CACGTGGCGGATCTGCGCGCTAAGGGCGAGCTGCCGCCGCCGAGGAAGAAACGCAGGCGT
CGAAAAGCGTCTTAAAAGGTTTTTCACTAGGGTGTTGTCC

>RXN00373
ATGGACATCCAGCAGCTAGACGCCGAAACAACAGCATGGAAAGACAGCCTCCTGCGCGCC
GCACAGGAGGCTGGTTTTCATTTTGAGCCACCGAAACTCTTCGAGGATTTTGAGACCATG
GTGGAGCAGTACAAGCAGGCAGCTGCGAGCGACCCGGACATTGATGTCACTGATATTCAG
CAAATGTGGGGCATCGTGGTGGGGGAGTACCTGCGCGAAAAAATGGGCATGGAATGGGTC
GTCATCACCGATGACTACGGCACTGACCTCGCGATTCTAGCCACGGCACCCAACGGGGAC
CACGTATATTCCTGCCCCATCATCGTGGTGGGCAAGCGC

>RXN00390-upstream
GGAAATAGACCGTTAATAGCTGGTCTTTACATTTGCCAGAAAGCTCCGACGAAACCCCAA

TAGTTGACACGGAAACTAATTCATTCTAGCTTTAGTGACC

>RXN00390
ATGTCAACTACCAGGGAAATTGCATTCCTCATCGCACGTATCCTCTTGGGCGTCATCCTC
ATCGCCCACGGCTGGGACAAGTTCGCCATCACAGGACTTGAAGGCGTCACCGGCTTCTTC
GATTCACTCGGCATCCCAGCAGCCGGCATCGCCGCAATAGCTGCTGCAGTCGTCGAGCTC
CTAGGAGGAATCCTTATCATCCTAGGAGTATTTACCCGCATCGTTGCCGCCTTCGTTGCC
ATAGACATGCTCTTCGCAGCACTGTTTGCGCACGTCTCCTCCGGCATCTTTGTCACCAAC
AATGGTTGGGAACTCACCGGCGCAATCGGCGCTGGCGCGCTGCTTCTCATCGCAGTTGGC
GCAAGTGCATGGAGCATCGACGGGGTTCTGGCAAAACGCAAGGCC

>RXN00390-downstream
TAAATCTAGCGCCACAACTCCGA

>RXN00399-upstream
GGACATTGCTATGTCGTGAGTTGTAGTAACCCCAAAGCCCACGGATTAATCAATAGTGAA
ATTCAATGATTTTCTTTTCCCACAGGCCTAAACTTAAATC

>RXN00399
ATGAGCCACAACGACAGCCCAAACTTTGCTCGCCGAGCGCTCAATTGGCTCCGCCAAGGT
TATCCAACCGGTGTTCCGCGGCACGATACTTTCGCTCTGTTTTACGTTTTGGAGCGCGAA
CTTACTGAGGAAGATCTCAATGAGCTCGCAGAGCTTCTCATCGCGGAAGGTGAGAACAAT
GGGCTGCACGATAATCCCATTACGCGTGAAAAAATCGGCAAGCTGATCACGCATGTTCAC
AGTCAGCCACCTGAGGATGAAGACATCGATCGAATTCAGAAAAAGCTGCAGGCTGAGGGC
TTCCCCACCCGCAAT

>RXN00399-downstream
TAATTAATTGGAGTTTTGTTGTT

>RXN00416
CTGGCGTCTTACTTAAGCCCAACTGCGCTGGTGGTTGCGGTGTTGGCTATTCCGCTGTCT
GCGACCCGCCTGTATTTGGACGGAATCAGCGTTGACCAGGGCTTTAGAACTCAGTTTTTA
ACCCGCATGGCTGACGATATCGGCTTGTCGGACATGAACTACATCGATATGCCTACCTTC
TACCCTGCTGGATGGTTCTGGCTCGGTGGTCGCTTGGCCAATCTTTTGGGGCTGCCCGGT
TGGGAAGCTTTCCAGCCATGGGCAATTGTGTCCATGGCAGTTGCTGCTTCTGTGTTAGTT
CCAGTGTGGCAGCGCATCACCGGTTCCCTGCCGGTGGCAACAGGCATTGCGTTGGTGACA
ACCTGCATTATCTTGGCGATGAATTCCGAAGAGCCCTACGCTGCAATCGTTGCGATGGGT
ATTCCAGCGATGCTCGTGCTGGCTTCCCGCATTGCCAAGGGCGATAAGTTTGCGCTTGCC
GGCGGCATTATTTACTTGGGTGTTTCGGCTACTTTCTATACTTTGTTCACCGGTGCTATC
GCGCTTTCTGCGGTCGCGGTGTGCATCGTGGTGGCGGCTATTGTGCAGCGCTCCATCAAA
CCACTGCTGTGGCTTGCAGTGCTGGGTGGTGGATCCATTGTCATTGCGTTGATTTCTTGG
GGTCCTTACCTTCTGGCCTCCATCAACGGAGCGGAGCGCTCTGGCGATTCCGCAACACAC
TACCTGCCTCTTGAAGGCACCCAATTCCCGGTTCCTTTCTTGGCATCAAGCGTTGTGGGA
CTGTTGTGTCTTGTTGGCCTGATCTATTTGGTGGTGCGTTTCCACAACAATGAGGTGCGC
GCGATGTGGGTCGGCATCGCAGTGTTTTATGCCTGGATGGGCATGTCCATGGCGATCACG
CTTTTGGGCAACACGTTGCTTGGATTCCGTCTTGATACGGTGCTGGTGCTTATTTTTGCC
ACGGCTGGAGTGTTGGGCATTGCAGATTTCCGCCTTGCCAGTGTGTATCAGCTCTACCCC
ACCCAAATCACAGAGCGCACGGCCACCCATCTGACCAATCTAATTGTGGTCCTCGTGCTG
CTTGGCGGCCTCTACTACGCGCAAGATCTGCCGCAGAAGAACGCACGAGCTATCGATCTG
GCCTATACCGATACTGATGGCTACGGCGAGCGCGCGGATCTGTATCCGGCCGGAGCTGCA
CGTTATTACAAGGACATCAACGATCATCTGCTTGATCAAGGATTCGAGCCTTCCGAAACT
GTCGTGCTGACAGACGAACTCGATTTCATGTCCTACTACCCTTATCGCGGATACCAAGCT
TTTACTTCCCACTACGCCAACCCGCTTGGTGAGTTCGGAAACAGGAACGCATTCATCGAA
GATCTCGCGATCCGAAGCTGGGATGAGTTGGCTGATCCTCAACAATTCAGCGACGCCTTG
AACACCTCTCCATGGACGATCCCTGAGGTGTTCATCTTCCGTGGCTCCATCGATGATCCT
GACGCCGGTTGGAAATACGACGTGGCTGAAGATCTGTACCCGAACAATCCAAACGTGCGC
TTCCGCGGCGTGTACTTTAACCCGGAGTCATTTGATCAGATGTGGCAGACCAAGCAAGTG
GGACCTTTCGTGGTGGTAACGCACAATGAG

>RXN00416-downstream
TAATTCCTCACCAAACGACCCAA

>RXN00422-upstream
AAGCGCCGGGCGCGGAAGGCGCTGGCTGAGGCCTTCGGCGCGGAGGTCCAGCCACTGCCG
CTTGACACCGAATAGGACAAATGGGTCTATCCTGGGGCGC

>RXN00422
ATGCCCACGAATTATGCACGCGACAACGTCATTTCCTTGGCGTCTGCCCGCGAGCAGCGT
TCCGGGAAACCCGAGCCCAAACCCGAACTAACACTCATCGTCCGCGCCACCAACGTGCAA
GCGGACGGCGAGGTCCACAGGCAAATTGGGTTGAACTCGGCGATGAGCCTGGACGAGCTG
CACAATGTACTCAACATCGTTTTCGGTGTTGGCGGCGAGCAGTCACCCTGGCGTTTCGAA
GACCAATTCCACCAACCCAGCGCCCCCGACACCAACCTCGGCGAACTCCTGCCCGAACCC
GGCGACTTCCTGTTTTACTTCTGGGGCCTGTGGCAATTCAACCTGCAATGCGTGGAAATG
TACCCGCGCGACAACGGCACCCCGCGCGCGCTGTGCATCGGCGGCTCCGGCGGCCTCGGC
GACGACTTCGACCAAGCCACCATCAACGCCGAACTCACCGGCACCGACACCATCCGCGAC
GTCCTCTCCGGCGTGCGCCCCGAAGTCATCGACCTCGTCGACCGCACCGGCGTCTTCGAC
TTCATCCCACTGCTCCAAGCGCTCGACCTCAAAAGAGAACCGCTTATCGACGCCACCCGC
TACCACACCTGCCGCACGCTGCCAGTGGAAAACAGCGCCGAAGCCTCCGACGCATTCTGG
TCCTGCGTACTCGCCCTGTCCTGCCTCGGAAACGACGAACTTTTCATCGAAGTGATCGAA
TCCACAATGAGCACCCTCGGCTGGGTCGCCGACGACGGCTCCCCACTACGTGCACCAGAG
ATCACCAGCGCCTGCGAAGCCTCCCTGAAGATACTCGCGGAACTCGGTGGCTACGGCCCA
GAGCGGCTTGCCCCCGTGGATCGCCTGGACATTTATAGGGAGCTGCTGTGTTTC

>RXN00422-downstream
TAGGTATTGTGTAACCTCGTGTC

>RXN00447-upstream
GAGCACGGCATCGTGATTCGCGCGTTCCCCGAGGGTGCGCGCATTTCGGTGACCAACGCC
GAGGAAACTGACAAGCTGCTGCGCGCGTGGGAGGCCATCA

>RXN00447
ATGCTGGGTAGTCTTTGGCGTTTTGCGGTGCGCACCGCAGCAGGCGCGGTGGCGTTGTGG
GTGGTTATTAAGCTTATCGACGGCATCTCCCTGAGTTTTCCCACCACACCTCTCTATCAG
GACGGTCAGCACGACAATCTGCTGACATTCCTGGCGGTGGCAGCAATCATTGTCGTGTTG
AATGCCACGGTGAAACCCGTCTTGAAGCTGCTTGGTTTGCCGTTGACAATCATCACCTTG
GGTCTGTTCTCGCTGGTCATCAACGCGGTAATCATGCTGCTGGCGGAGTATGTGTCAGAT
TTGATCGGTTTCGGTCTACGCATTGAAACCTTCGGTGCGGCCTTCTGGGGTGCGATTGTG
CTGGCGTTAGTGAACTGGGTTCTTGGCCCCATTACCGGCCTCCTCGGTGCAAAAAAGGAC

>RXN00447-downstream
TAACCATGGCGGATCTGAGCATT

RXN00455-upstream
GAAGTGTCTGGCCGATTGGCTAACAATCTCTAGTTAAATCCCGCCTCATGAAACCACGAT
GAAACCAACATGAGAGTTTTTTCATCCACGTTTTCTGGCT

>RXN00455
ATGGTTGTGGACGTGCAAAATCAATCACACACCCCAGAAACCCAGCCTCAACCTGGGCAG
GGCGCAGCCAAGAAAACCCCCGTTGCGTCCGGAAACTCCACGTTCATTCACATTCAGCCA
AGCTTGTACCCCATTTTGCTGGCGCTGTTTGTTGCAGTCTTTCTAATTTCAAATATCACC
GCAACCAAGGGCGTAGAAATCGGCCCGTTGGTGACAGACGGTGCGTTCTTCCTCTTCCCC
ATCTCATATGTGTTGGGCGATGTTCTAGCCGAATGTTACGGCTTCAAATCCACTCGTCGT
GCCATTCTTACTGGTTTTGGCATCACGATGCTCGCGGCGCTGTCTTTCTACATTTCCATC
TGGCTGCCTGGCGCAAGTTTCTGGGAAGGCCAAGAAGCTTTCGAAGCAACGCTCGGCCTT
GTTCCACAGATCATCGTGGCATCACTGGCGGGCTATATTGTGGGTCAGCTGCTCAACGCC
AAAGTTCTGGTGGCTATCAAAAAGCGCACGGGTGAAAAGTCCCTGTGGGCGCGCCTGATT
GGTTCCACCGTTGTCGGAGAATTTGTCGATACCCTGCTGTTTTGCGCCATCGCAGCGCCA
GTGATCGGTATTGCCACCGCCCCGGATTTCATCAACTACGTTGTGGTGGGCTTCGTGTGG
AAAACCCTTCTAGAGGTCATCCTCATGCCCATCACCTACGCAGTCATTAGGTGGGTGAAA
CGCCGCGAAGGTTATGAAACCTTCGACGCG

>RXN00455-downstream
TAGTACCGGCCTAAGAATTCTTC

>RXN00473-upstream
GGGGCAGCTGTGGATTTTTCACAACCACCCCTTTTCTCACACCAGCCCCGCATGAACAGG
CTGGTTGCACACCGTTGAAAATGAGTGTTTACTGGAACTC

>RXN00473
ATGAGTGGAACAGGTGTTCGAAAGTTGTGGGGAGATGGCACTCCGGTGTCGCTCCCTGAC
CTTTCAGGATTAAGTAGAGCGGAGCGCATTGATGCGTTGCGTTCACGCATGTCCACCATG
GGTGCTGCGGTGCCAAAGTTTGAGCCGTCGGTGGAAGAAAGTGCTGAACAAAAGCAGGAT
TCTCTCGCCGAAAAACAGGACATAGTTGCAGTTCCTTCCGCTTTTTCTGATCTTTTCCCT
GGGGATGGTTTGCCGCGTCGTGCGGTTACTCAATTGGTTGAACAGCCACTTGTGGTGGTG
GACTTCCTGGCTCATATTACTGCCCAGGGTGGACACGCTGCGGTGATTGGGTGGAAGGAT
TTAGCCTACGCCGGGGTGATTGATTCCGGAGGTGTGTGCGAGAACATCATTGCTATTCCA
AATCCTGGTACGGAGCCACTGAATGTGGCAGCGGTGCTGTGTGAGGGGTTGGATGTGGTC
GTGTACAAAGGCCCGGAGATTTCCCTGTCGCCAACCAGAGCGAGGCCGTTGCTGGGAAAG
CTGAGGCAGGGGACTGCTGCCTTGGTGATGGTTGGCACGAAAGTAAGCTCACCGGCGCTG
TCGGTGGATGCAGAGATCACTGATTATGTTGGCATTGGTGCAGGTAGTGGGCGTATTCGT
GGCGTTGAGATGCAGGTGCGGGCTGTGTCGAAAACTCACGGTGTGCGCAGCGGAAAAGTC
CTGATCAGTAGGCCTCAGGATGCAGCATTGCTTGAGCCTGAACAGCCAACAACGTTGCGG
GCGGTCCCA

>RXN00473-downstream
TGACGCGGGTGATGGCATTGTGG

RXN00485-upstream
TCAACTTCGGCGACGAGGTGGGCGCTATTTTTCATTGTTTTTCGCGATTTTCGCTTCGGT
TGCATTGACTGTTAGCGCCACTGCGTTGACAAATTCTTTG

>RXN00485
GTGTCCAGTGTTAATGATCTTTTTGCCAAGCCGTATGAAAACGCTGATCTTGTGGTCACG
GTGTCTGCGAAAAACGAAGATTCCTTTGCAGCTTTTGAGCAACAATTAGCTACGACACCT
GGTGTTGAAGCTCTGGCTTTTGATCAAAATTTTGCAGCCTCTGTAAAGCAATCAGACGGG
ATTTACGCCAGTACTTCAGTCCAGTCAATTTCGGAAGGCCCACTGCAGTGGCGGCCAATC
CTAGAAGGCCGATTGCCCCAAGGACCTGGTGAGATTGCAGTAACAACGGCCCCGGGTGCG
CCTGAAGTTGGTGAGCACGTATCCATTCGCCTGTCCCAAAACACTGAGGACACTGAGGTT
CTTGTGGTTGGCGTGGTGGAGCCAGCGGCGCAGGAAACTTTAGGTGGCGCACCGTTCGTT
GTGGCGTCTCCTGATGCGCTGATGGAGTGGAATTCTTCCGGTGTGCGGGGTGAATTCCGA
GTGGCAACTTCCGATCCTGCCTCGCTAGAGGCTGCAAGCTTTAGCGACGCTACGGTGGTG
GTTGCTTCGGCGGAGGGGCACGTCGATAAGCTTGCTGATTCTTATTTGGGCCAGCGAGAT
CGCTATTTCTTGCTGCTCGCAGCGTTTGTGGCAGTGGCTGCTGCCGTGGCGTTTTTGGTG
GTCTTTTCTGCATATTCGGTGCTCACTGGTGAGCGAGTTCGCGAGTTCGGGCTGATTCGT
TCAGTGGGCGCATCGACGCCGCAGATTTTGGGGTCAGTGATTTTTGAAGCCGGCATCCTC
GGTGTGGTGGCTGCTGGTTTTGGTGCGCCCGCCGGATTGATGGCGGCGCGTTTGTTGGCG
GATAATGCCGCACGTTTTGGCATTCGTGTGCCCATTGATGTGATTGATCTGCCAAGTAGC
ACGATGTGGCTCATCGCTGGCGTCGGCGTGGTGATGTCCGTGATTGCGGCATTACCGGCA
GTGTTCAGTGTGTGCAGAAAATCCGCAGTGGAATCACTGAGTACGCCTGCTATTTCGAGG
ACTTCCCCCTGGTTCGGTGCATTATGGTTGCTGCTCGCGGGCATTGTGGGCGCCGGCGGA
ATGTGGGCGTATGAGGCAACCTCGGACTACCGCGGCATGCGTTCAGTGGCTTTATCCATC
GCCGGTTCAGGCGCTTTGGTGTGTGCGTTGTTGATTGCCACGGCGGTGCTCGTGCCCTGG
TTATTGCACGTATTCTCCAGGATTGTGGGCGGCACCGTCCCAACACTTCAGTTGGGATTG
GCGTTTGCAGCAAAGCAGAAATCTCGTTCGGCGGCGCTGATCGCTGTGATTCTTGCTGGT
TCTGCATTAAGCTCCGCTGTTCTGCATGGCCAGGCACATATCGGCACGCATTTGGTGGCC
GTGGCTAAAGGCATGGGCGGCACAGACATGATGGTTACAGCGCTTGATGGGGAAATCCCC
GCCGGAATGCTGGAGGAAATCTCTAGCATCGACGGCGTGAAAACTGCCATCGCGCCAGCC
ACCACCGCTGTGGAATTGGAAGATTCCGGCAATTTCTCTGTGCTCATGCTCGCTGAAGAA
GACGGAGCCTCCGTGATGCGCGCAGGCGATACTGGTGCACCAGCTGGTGGCCTTGTTTTG
GGCAGAAACTCTCCTGACCAGGATGCTTACCCGGCCGGCCAGGCTGCAAACATCATTGTC
GCGGATACCCCAACGCAGGCGGAAATCTTCCACAGCGACAACTACTTCTCCATGATCGAC

CCAGCACTCGCCACCGGCCCCAGCACCACACGCAACGTACTGATCCTGCTCGACGGCGAC
TCCAACCAGGCCCCCGACAACGCCACGGCGCAGGCGGTACGCAAGACCATTTCGCTTTTC
GACGGACGATACTCCATCACCGAGGGTTTCTCCGCCCGCCAAAACACTTTTGAACTGGTT
TCCCGCATCACCACCATGTCCACACTGCTTGCCATCGTGGCCTTAGCGATCGCTGCCGTT
GGCCTGATCAACACAGTGGCACTCACCATTTCTGAGCGTGCCCGCGATCGTTATTTGCTG
CGCACCATTGGACTGACCTCAACTGGTCAGATTCTGGTGATGGCTATTGAAATGATCGCG
CTCTCATTGCCGGCTGCCATTGTTGGTGCAGTTTCGGGAGGATTCTTAGGCAGATTCGTT
GCCAGTTCTGCCACCAACACCGCTGCGACGGCACCACTTCAAGTAGACATTCTCGGCGGA
ACGGTTCTCGCGATGGTCGCAGGATCTGTACTGTGCGCGCTCATCGTGCTGGCGAACAAA
CGACGTCGGGTGGTT

>RXN00485-downstream
TGATTATAAAATCCAAAAATCGA

>RXN00496-upstream
CTGCAGAGATGGTGGGCAGCACCCCAGGTGCTGTACGAGTTGCCCAACACAGGGCACTCA
CGACACTTCGAAGCACACTTGAGCAGCAGGAGAACAAGTA

>RXN00496
ATGACTCGACGTCTACATGGTGGTGAGCAGGATGGCCAGGAACACGTTAAAGGACAGCTA
AAGCAGCTGTTCGACGACGACGCGTTCTTGACTGACCTGTCCCGCGGCGTTGATCCCTCA
GAGGGCGATGACGCCCTCGCTGGCCTCCTCCTCGATTTAACAAAGGAAGCTCAGGAGCCG
CCGGCAACAATGCCGGATTGGTCTACTTTGCTCCCTGGAATTTTGGATCAGGATCAGGAT
TTGCCAGTGGAATCCACTTCGGACACCACGGTTATGCAGGCATCAAACCCTGCAACCCAA
GAATTCGCACCTGTTTCTATTTCTGATACCCCCAACACTGCAACTAATTCAGCTGATGCA
GATGAGTCCGCAACTGTTGTTCCACTTGCAGCACGCCGTGAGAAGCGTGCCAAGAGCGGA
TCAAGCGGGGTTCATTCACTGGATGCTTCGGCAACCCAGCGCAAATCTCACCCATTCCTT
AGCGGTTTGGTGGGTGCTGCAGCTGCAACTCTAGTCATCGCAGGCGGTGGAGCAGCAGTG
TACAACGCTGATGAAAACTCCCCGTTGTATGGCATGAATCAGCAGCTGTTTGGCAATCAA
GATTCTCCAAGCGTGGTGGAGCTTGCCTCCACGCTGGAAGAAGTTGATAGTCGTACAGCT
AGTGGCGATGTGGAAGGGGCACGTGCTCTACTCGAGCAGGCTCGAGCAATGCTGGATGGC
ATGGCACCTCCTCGAAAGGCGCCGTCGGAGGCAACCCGAACGGTTGAATCTGAACCAGGT
ACTCAGACGTTGACTGCAACGGTTACTGAATCCGCAAGTCCGGAACCACCGGTCACGGAA
ACTCAAACTGTTACCTCCACCGAGGTACAGACAGTGACAACCACTGCGGTTGCTCCACCG
GTCTGGACTCCTAATCCAGAGCCAACAACCACAGCTGCCCCGACTTCTACGCCTTCAACT
GGTGGCGGTGAGGGAACCGGCAATGATGGTGACTCTGGACTTGTGCCACCTCAGACTCCT
GGAAAC

>RXN00496-downstream
TAGGTAAAAATATAAAAACTGCT

>RXN00503-upstream
AATCCACGAAGGTGCCCAAGAATCACCAATTTCGGTCGGAACTGATCCTTCTTTGTCCGT
TGAGACCCCACAGGTGTTTTAAACATTTAGTATTAGTTCC

>RXN00503
ATGAAACCAGTCTTCTCCGTTGACCAAATCCGACGCGCAGAAAACACCCTTTTTGAGCTT
CAGGCAGATCCGGATGAGCTGATGATCTCCGCGGCATCGGCGGTGGCCGATGTCGCGTTG
GCAATGGTGGACGGCCCCGCTCCAGCGGTCTCCAGTGAGGAGTCAATCCTGCTGCTGGTC
GGCCCCGGTGGCAACGGTGGCGACGCCTTGTATGCAGGCGCGTTCCTTGCAGAAGAAGGC
CACCACGTTGATGCTTTGCTGTTGGGAAACGGCAAAGTCCATCAATCAGCATTGGCATAT
TATGAGTCTTTGGGCGGGCAGATCATTTCCGATTTTCCCCCTCACTACCTCTACCGCCTG
GTGATTGATGGTTTGTTTGGCATCGGTGGTCGGGGAGGGCTCACCCCAGAGCTGGCCAGT
TTGGTGGAGTCTTTTTCCGCTTCAGGTATCCCCATTTTGGCGATTGATGTGCCGTCTGGC
GTGCATGCCGATAGTGGTGAACTGCCGCCCGGCGTGATGGTGACGGTGGAAGGATTTGAT
AATGATGCACCGATGGCGCGTCAGAAAATTCCGGCACACATTGACGCTGATGTCACGATC
ACGTTTGGCGGTTTGAGACGCGCCCACGCGGTCAGTCCTGCGTGTGGTGAAGTGCTCTGT
GCTGATATCAACATCGCTGGTGGCGGCGGAAAATCGCTGTCCGCTGAGTTGAGTCAGGTG
CAGGCAGAAGACGCGACCCCGCAGATGTTTGCCTCCAAGGCGTATCAACGGAAAGATTCG
CTTTTTGAGCGCGCGAATCTCAAAGCTACGGCGCCACATATCCATAGGATCGGCCAGCAC
TTTACCGTGTTGAACATGGAGCCTGGCCCGGATCATGATAAATACAGTGGCGGAATTGTC

GGCATTGTTGCAGGTAGTGGCACCTATCCAGGTGCTGCTGTGCTGTCGGTGAAGGCGGCT
GTCAGGGCCACAAGCGCCATGGTTCGATACGTTGGCCCTGCGTTAAATTTTGTCATCCAG
TCGCTGCCGGAGGTCGTCGCAACGCAATCACTTGCCACCGCCGGCCGCGTGCAAGCGTGG
GTGCACGGCCCCGGACGCGGGCTGGAGGCTGAGCAATCAGCCGAGCTTGCGGAGCTTTTG
AGCCGGCCTGAGCCTGTGCTTATCGACGCCGACAGCCTCTCATTACTCCAGCTCTCAGCG
GAGCTTCGGCAGGCGTTGCGCGAGCGAAAAGCACCAACGGTGCTCACTCCGCACAAGGGC
GAATTTGAACGCATCGCAGCAGAATTACGCTCTGAAGGCGTCGAGATTCCCCAAGCGGAC
AAAGATCCCATTGGTGCTGCGCAAGCGTTAGCTAAAGAATTTGATTGTTGCGTACTGCTC
AAGGGGAAATACACCGTCATTGCAGCTCACGACTTTGTGCATGCGATCAACGCTGGGCAT
TCCTGGTTGGCTACACCTGGCTCTGGCGATGTGTTGTCAGGTCTTGTCGGTGCACACTTG
GCTCAAAGCTACGCAGAATTAAACCGCTTGCCGGAGTTTTTCCCCGATGTGACCTTGTCT
GATTCGGCGATTTACACCCAGATTGCACCTGCTGCGACCATCCACGCGGTTGCTGCTGGG
TTGGCCGCACGAACCGAATTTGGGTTTGCGCCGACCTCCGCAAGTTTGATCGCTGATGCC
ATCCCTGCAGCGACCGCCAAGGTGGATTTGAAGCGAATTGTC

>RXN00503-downstream
TAGCTCTGCATGAATTCCGTATG

>RXN00504-upstream
AAGGTGGATTTGAAGCGAATTGTCTAGCTCTGCATGAATTCCGTATGAATTCTTTTCTTT
CAAGTGGCCGAGATGTGAAGCGCACGGTTAATTGAGAGGC

>RXN00504
ATGACCTACGGATTTCTTGTCAACACAGATCTCACCCACCGCGCGATTGACTTTGATTTA
GAAAACGCTGCGAAGTTCCTCGGCGGTGCCGATGATGGCCGCGTCGCTGTCGCTTTCCAA
GAGGATGGCACCTTGTACGCCGCTCTCTACAGCGCCAGCGCAAAAGATGAGGGTGCCGCA
GCAAACCCAGTAGCATCCCTTGGCCGCAACGCCGCTGCTACCGGTGATGGCTCCTTCTTC
TCTGATCCGACCACTGCAATCTGTGGCCCTGTGATCTTCGTGGGGGCCGAAGGCGAAGAC
ATCACGTTGGATGAAATTGAGCGAATTAAGGACGGCATTCGCGCCGCTCGTAACTACCGC
GATGATTATCCAGAGGAATTCAACCTGTGGCGCAACGCTGTATATAACCTGCGTACGGCT

>RXN00504-downstream
TAAAGTTTGGCTGCCATGTGAAT

>RXN00505-upstream
TTGCGGAGCGTTTAGACACCATTAACTATGAGGTAGTGTGCCGACCAACCGGCCGAACTG
TCCGCGCATATGTTTAAGTGAATACGTTTAAGGAGCAGCA

>RXN00505
ATGAAATCTGAGTTTCCGGTATCCGGCACGAGGCGTTTTGAGCATGCCGCAGATACCCAA
AATTTTGGGGAAGAATTAGGCAGGCATCTAGAAGCTGGCGATGTGGTGATTTTGGACGGC
CCGCTGGGTGCTGGAAAAACCACATTTACTCAAGGTATCGCTCGTGGATTGCAGGTGAAG
GGGCGGGTGACATCGCCGACGTTTGTGATCGCGAGGGAACACCGCTCGGAAATCGGTGGG
CCAGATCTGATCCACATGGATGCCTACCGATTGCTGGGCGAAGACAGCGAGGATGCTGAT
CCGATCGGTGCGCTGGACTCTTTGGATTTGGATACCGATTTGGACTTGGCTGTGGTTGTT
GCGGAATGGGGCGGTGGCTTGGTGGAGCAGATCGCTGACTCGTATCTTTTGATTACCATT
GATCGAGAGACCGCTGTGCAGGAAGACCCGGAATCTGAGGCTCGAATTTTCCATTGGGAA
TGGCGCGAAGGCCGC

>RXN00505-downstream
TGAGAAAGTTTTCCACGCTAAAA

>RXN00507-upstream
GTTCATGTTGAACTATTGTGCCACCAACCGCGGACAGAAATACGATTGGTGCCGGGGTTA
GTGCCAGTATTGCCCCACGCTTTCAACTATCCTTAAACAC

>RXN00507
GTGGCTGAGAATCTGAACAAACACCTGTCCAAACTGTCCAAGCGCGGACCGCACCGCGTG
CTGGTAGGCGATATGAACTACGCCGGCATCCCGGGCAAAATCTACACCCCAGCAGAAGGC

GACGGCATCCCAGGTGTAGCTTTCGGCCACGACTGGATGAAATCCATCAAGTACTACCAC
CAAACTTTGCGACACCTCGCGTCCTGGGGCATCGCTGTTGCCGCCCCAGACACCGAAAAT
GGCTTCATGCCAGACCACAAAGGTTTCGCCTCTGACCTCGAATCCTCCATTCAGATTCTC
GGCGGCGTAAAACTCGGCTCCGGAAACGTCACCGTCAACCCAGCCTGCCTCGGTGTAGTA
GGCCACGGCATGGGTGCTGGGGCTGCAGTACTATCCGCAGCAAACCGCGACCTCGTGCGC
GCAGTCGGAGCAATCTACCCAGCGAAAACCTCCCCCTCAGCAATCGACGCCGCCTTCGCT
GTCAAAGCCCCAGGCCTAGTCATCGGATCCTCCAGCCTCGGCCTCTTTGAATCCGGCGAG
CCAGCAAAACTCGCAGCCAACTGGGCCGGCGATGTCTGCTACCGCGAATCAGAAAAAGGC
AACCAACAGGGCTTCTCTGAAGACACCATGTTCAAACTTGTCGCAGGAATCGGCAGCCCA
CAAACCGGAGCTCAAGAAACCGTCCGCGGCCTCCTCACCGGATTCCTTCTCCACCAACTT
GCCGGAGAAAAGAAATACAAAGCATTCTCCGAACCAGACGCTGAAGCTAAGAAAGTTGTC
TCCTACTTCGGCCAGGAGCTGCAGGAACATGCCTTCCCTAAGGACACGTCCCCATTCGCG
TTCCTTAACGAGAAG

>RXN00507-downstream
TAGTTCGCTTTTCTTAGTGGGTG

>RXN00510-upstream
ACGCTTTTACCCAAACAACCCAAGCCGCCGAGGAAGAAGTTAAACGATTCGACAATACCG
ACAAAGTTTTTGGTGCCGGATTTGATGGGATTGATCCGAA

>RXN00510
GTGAATGATCCTTTAGCCGGCTACGGAGCAGTGATCTCCGCACTACAAGGCGCCAGTGGT
GGGATGTATCGCGGACCGGCGAAATCCGAAGGCCAGTTGCGCGAGATGTACCAAACCATC
GAAGGGCTAGACACCAGCTCGTTGCGCGAAGCTGCCGAAGCAGCAGTGGGCGGAACGAAC
GAAGCCAGAATACAAGGGTGGGTCGGCCCGCTCTTGAAATTCTTCGGGACGGTTGGCGGG
GGAATGATCGCCACGGAGATAGCTGAACGGGCAGTCGATTGGTTCAAAAACCGTAATGAT
GTGGAAGAAGTCAGCGAAGCCGCTGATAAAGCCGCCGATGCGATCGACTCCACTGTCACA
GAGTCCGACCAGGGCATGATGCACATTATCCAGCAGCTCTTGGACATTGTGTCTACGTTG
ACGCAGATTCTTGGCAGCATGGATCGGGGGAAATTTCCTCAAGAATTCCGGGACTGTGTC
CAAACTGGAGCTGATCTTATTGACCAGGCAGGGGACATGCTTGAAGGATTGTGCGCTGAT
CGAGATGATGCGATTTCACAGTGTTTCTCCGCGTTGACCGATCATGGAAAACAAGTTTGT
GAAACTGAGCCAAAGCCGTTGTGTAGTGCAGCTTCTGGGGGTTCATCTGGTGGAGCGACT
TCTTCGGCTGCGGCCTCTTCAGGTGGTTCAAGCTCGAGCACTGCTAGCTCTGGGAGTTCT
GGCGGATCGAGCAGTGCTGCGGATAGTTCGACGTCGACCAATGCTGAATCCAGTGTTGAA
AAGGAAAAGACCACACCTGCTGCCGTTGAGAAACCTGACGAGAAACCAGTGGAGAAGCCG
GTTGAAAAGACGCCAGAAAAGCCGGTAGAAAAACCTGTCGAGAAGCAAGAGTGTGAAGAA
AAGCCTGACCCTGACCCGGAAAAATGCAAAACAGAGCCGGTCGAGTGTGAGCCAACACCG
AAACCTGAAACAGAGCCTGAACCAAAACCGACACCCACGCCCACACCCGGAACACCAACA
CCAATACCTGAGCTAGAGACTGAGGATTGTGAACCTGGCAAGGAGACGGGCACAGACTCA
GAATCTGAATCGGAAGAGTGCGCCCCCGAGCTCAATGACGTTCCAGAAGAGTCGGATCTG
ATTGGGCAACTCATCAAGGGAGCAATCGGTATTGGGATTGTTGTTGTAGGCGTTGGGCTG
TTGGTGAATTTCCTGGAGCAGTGCGTCCCTGTGATTGAAGAAGTACCTGTGCCGGAGCCC
GAGCCTATACCTGAACCCGCTCCGCAGCCTGAGCCAACTTCAGTGAAACCACCAGAGTCT
GAACTAGATAAGGTGGCTGAGCCTGCGCCGAAGCCAATTCCACAAGCTAATTACACTGCT
GCTGCAGCAACTAACTATTCCGCTCCCGCGCACGCTCCCGTTGTCCCAATTACGCCGGCA
GCACCTGAAGTTCCGGCAGCACCAGAAGTGCCTGCACCGGCGGTTAATCTTCACAAGGCC
GGCGGGTGG

>RXN00510-downstream
TAGCGGTGGAGTATGCGGAATTT

RXN00515-upstream
GTTGACGCACTGAAGAAGTAAAGTCTCTTCACAAAAAGCGCTGTGCTTCCTCACATGGAA
GCACAGCGCTTTTTTCATATTTTTATTGCCATAATGGGCAC

>RXN00515
ATGCGTTTTTCTCGAGTTCTTCCCGCACTTCTTATCACCACCGCCGTGAGCATCCCAACA
GCATCTGCTGCCACACTCACCGCCGACACCGACAAGGAATTGTGCATCGCCAGCAACACC
GACGATTCCGCGGTGGTTACCTTCTGGAACTCCATTGAAGACTCCGTGCGCGAACAACGC

CTCGACGAACTAGACGCCCAAGATCCAGGAATCAAAGCGGCGATTGAAAGCTACATCGCC
CAAGATGACAACGCCCCAACTGCTGCTGAACTGCAAGTACGCCTCGATGCCATCGAATCC
GGCGAAGGCCTAGCCATGCTCCTCCCAGACGATCCCACGCTGGCAGACCCCAACGCCGAG
GAAAGTTTCAAAACGGAGTACACATACGACGAAGCCAAAGACATCATCAGCGGATTCTCC
AGCGATCCAGCCAGCGATGTACTCAGCCAACTTCAACAAGCCGCCACCACCGGCACCCGC
ACCGCAGAAATCCGCGCCGAAGTATTCGCCGACCGCACCGATGATTACAACGAATCCCAA
ACCGCTCTTAAAGAGGATTTCCAAAACTGCATCGATGCCATCGATGACGCCCGCCCAATC
CCACTGCAGTACATCCTGATTGGAGGCGCCATCGCTTTGGCGGTCATCGTCCTCGGGATC
AGGGCGTGGACTAACTCAAGGAAGCAGTCCAAGCACAGCCAG

>RXN00515-downstream
TAATACGCCAAGCAAAAAATTGC

RXN00527-upstream
TTCCTTGGCCCCGAAGAAATTAATCATTGTGGCCGTGGTCCTGATTTTGATCATTGCGGC
TGCCTCGTTTTATTTTCTGCGTTCATCATCGAATGACCAG

>RXN00527
GTGATTGCCACTTCTGATGTTCGGGAGATTTCCTCCGAGGGAATCGTGGCGCGTGTGTCT
GTCAACGGAAATATTGAAGCTGCGCGAACCACCACCATTTACACCAGTCTGACTGTGCCG
GTCGCGAACTTGCCGGTTGCGGTTGGTGACCGTGTGGCAGCTGATCAGGTGTTGGCTGAG
TTGGATGCCTCTGCCCTGCAACGACAGTTGGATGAAACTGATGCCAACAATGCGCGTGCA
GCCATGGCGAACCGCAATTCCATCGCGCAGTCGCAGCAAGCATATGAGCAGTCCAGGGAA
CTTCTTGATAGTGGTTTGAGCCCGGAGATCAACTCGGCGCGGTCCTCGTTGCGGGCGTCC
TCACAGGCATATCAGGATGCGATCCGCAGTTTTGAAGCGAAGCAGCGAGATGTGGATGGC
GGATTGGATTCCACCATGGTCGCTCAATCGGATGCTCTCAAGGCAGCTCGTGAGCAAGCA
GATGCTGCTGAAATTGAACGACTGCGCGCGGACTTCGGACTGCTCAACAACGATCGCAGC
AACCTCAACGATGTCATTGGTCTGCTCGATGAGAGAGAATCTTTGGCTTCTGCGGAATCC
GAACTAGCTCAAGCCCGCGCTGCAGGTGACCTAGAGGCAGTCGCTGCAGCTGAAGCAAAG
GTTGCAGGCCTGGAACAATCAATTGCTTCCAAAACCTCCACGTGGCCTAGCCAAGATCAG
ACTTACTTGCAGTCCTACACCGCTTTGGAGGAAGCTGAGCGACGCGTCGCATCCACCACT
GAAGCTCTAGAAATAGCCGAGCGGATCTACATTGATTCACTCGGAAAAGTTGACTCAGAA
CTAGCCGCCGCACAGCGCGCCGTTGCCGAAGCCCACTCAGCACAACAAGACGCAGCACTT
GGCCTCGAGACCGCGCAGCTTTCCACCCAACACCAATTGGAAGCCCAATCAAGCGCCATC
GATGCAGCTTTAGGTTTGGCATCAGTAGATAATGAAGCCGCCACCAGATCCACGTCCCAG
CTGCGGATGGATATCAACAACACCACCGTTCGCTCCCCATACTCAGGCATTGTTTCATCC
GTGCAGGCAGCCCAAGGTCAACCAGCAGCCGGCGCACTGTTGAGTGTTGCTGATGATTCC
GAACTGAAGATCACCGCGAATGTAAAAGAAGCGGAGATCAGCAACGTCACCATCGGATCC
CGCGTCACCTTCACTACCCCATCGACCGGAACCAAAGAATTCGCCGGCCGAGTATCCAAA
GTCTCCCCCATTGCAGCTGCCGCCAGTGCCCCAGCTACAGGTGAAGGAGCTGCCGCAGGC
GCCACAACCACCAACACTGACGTCACCTTCCCCATCGAAATTTCCGTCACCGGCGACCGC
GAAGGCCTCAACCTCGGCGGATCCGCTCGAGTACGCATCGTCCATGAAATCGCACCACAC
GTACTGACCGTTCCTTTGGAAGCTGTGTACAAAAATGATGACGGCAAAGACGCTGTTTTG
ATCATCAGCGACGACAACAAAGTAGAAGAAGTAGAAGTAAAAACAGCTGAATCCGATGAC
TTTGATATCGCAGTCAGCGGTGCTGGAATTTCAGAAGACGCTCGAGTGCTCACCCAGCCT
GGAAACTACCGGGGCCTCATCGGAGAAACTGTGAAACTTCACGCAGATACGGTGGAGCAG
GCGGCGGCTCCTTTTAGTCCTGCGGCCCCTTTTGACCCTGCAGCCCCTGCCGTTTCTGCC
AAGCAAACCGTGGGCCAGGTGATT

>RXN00527-downstream
TAGCCTATGAGCCTCATCGAAAT

>RXN00547-upstream
GGTCGTAGCCTAAACGACCTTAAAAAGGAGCCGACCGCCGATGGACCAGAAATTGGACCA
GCAGAAGGTAGACCGCGTATCGCCCGGTGATAGTGAACCG

>RXN00547
GTGGCACGGGATTTTATCAATGCAATCGGCGGTCGGTTTGGTCGTTTTGCGCAGGTGGGC
ACTCAGCGGTTCTGGACTCCCCTGCGTGTTTTGATCACCACTTCCCTGGTGTTTTTGGCC
ATGGGGTTTTTAACAAAAGCCAATTGCATCCAGGGTTCTAGAGGTACTGATGGTGTGGTT
TCTTTGAACTGGTCGGGAAGTCGCCAGTACACCTCAGCCTGTTACAACGACATCGTTCCG

CTCTATGGGGGGCGCGGAATTGATGCGCCAGGTTTCCCTTATGCCTTTTCGTGGCAGGAA
GGTGATCTCACCAGGTACATGGAGTACCCGGTGTTGGGCGGAATTTTCCAGTGGATTTGT
GGCATTATCACGCGGTTTTTGTACCCGGTTGTTGATGTCATTCCGTTTCATACGCTGCCT
GAATCTGGTCTTTATTTCATCGTCACCGCGCTTGCGTTGGCGTTCTTTTGGGTGTTGGTC
ATCCGCATGATGGTGGAGCTCACTGGCAATCGAGTGTGGGATACCGTCCTTGTTGCGGCG
TCTCCCCTGGTTGCTGTGCATGCGTTTACCAACTGGGATACTCCAGCCATTGCGGCGGTG
ATTGGTGCGATGCTTGCGGTGAAACGCGGAAACCCCTTGGTTGCGGGTGTGCTGATCGGC
GCGGGTACGGCGTTCAAATTGTGGCCGCTTTATCTTCTTGGTGCGTATTTGGTGCTGGCG
GTCAAGAATAAGAATCTCAAGCCGTTTATCACCATGGCTGCAGCGGCTGCGGTGACATGG
CTCGTGGTGAATGTGCCAGTGATGATCGCGTACCCCAAGGCGTGGAATGAATTCTTGCGC
CTGAACCGGGAGCGTGGTGCGGAGTGGACCACGATTTACCAGGTCATCGACCGTAATTTG
CCGATCAATTTGAATGATCCAGTGCTGCTTAATGTGCTGAGCTTCGGCTTGTTTGGTGCA
TCGTGTGTGGCCATTTTGATCCTTGGGCTCAAGGTGCAGCGCACTCCCCGAGTCGCTGAG
CTGGCCTTTTTGATTGTCGCGGCGTTTTTGCTGTTTAACAAGGTGTGGAGTCCTCAGTAT
TCACTGTGGCTGGTCCCGTTGGCTGTTCTGGCATTTCCTCAGTGGAAAGTGCTGTTCCCG
TGGATGGTTACAGACGCCATGGTGTGGCCAATTTTGATGTGGCACATGCTCGGCACGGAC
AACAAGGGACTCCCCCATGAAATGTTGGATCTCATCGTGATTTCCCGAGATGCCTTCATT
GTGGTCATGATAGTAGGTGTAATCCGGCAGATGCTCGGACGACGTGCAGATCCGGTGATG
GATGCGCACGCCGGGCGCGATTTGTTGGCCGGGCCCTTCGGCGCAGGCGAGCGTCGAAAA
GCATTGAAGGAAGTAAGT

>RXN00547-downstream
TGAGCACAACAGTTTTGCTGGTC

>RXN00552-upstream
CCGCCAACAAGGCAGCAAAGCTCGATCCAATTGACGCCTTGCGTTATGAGTAAAAGCCTC
GTTTTTAAGGTAGCCACACATCGCACTAGACTGAAGAACT

>RXN00552
GTGGCTACCTCAAAAATTCTTCTTTATTACGCATTCACCCCGCTCTCTGACCCTAAAGCG
GTTCAGCTGTGGCAGCGTGAGCTCTGCGAGTCACTGAATCTTCGTGGCCGCATCCTGATC
TCCACTCACGGCATCAATGGAACCGTGGGCGGAGATATTGATGATTGCAAGGCGTACATT
AAAAAGACCCGCGAGTACCCAGGTTTCAACCGCATGCAGTTTAAGTGGTCCGAGGGTGGC
GCTGAGGATTTCCCAAAGCTCAGTGTCAAAGTCCGCGATGAGATCGTTGCCTTCGGCGCT
CCAGATGAGCTCAAAGTGGATGAAAACGGCGTCGTCGGTGGCGGCGTTCACCTGAAACCA
CAGCAGGTCAATGAGCTTGTGGAAGCCCGTGGCGATGAAGTTGTGTTCTTTGACGGCCGC
AACGCAATGGAAGCCCAGATCGGCAAGTTCAAGGACGCTGTTGTCCCTGACGTAGAAACC
ACTCATGATTTCATCGCAGAAATTGAGTCTGGAAAATACGACGATCTCAAAGACAAGCCT
GTGGTCACCTACTGCACCGGCGGAATTCGTTGTGAGATCCTGAGTTCACTCATGATCAAC
CGTGGTTTCAAAGAGGTCTACCAAATCGATGGCGGCATCGTTCGCTACGGCGAGCAGTTT
GGCAACAAGGGCCTGTGGGAAGGCTCCCTCTACGTTTTCGATAAGCGCATGCATATGGAA
TTCGGCGAGGATTACAAAGAGGTCGGACACTGCATCCATTGCGATACTCCCACCAACAAA
TTTGAGCACTGCCTCAACGAAGATGATTGCCGCGAGCTCGTGTTGATGTGCCCTGATTGC
TTCGCCAATGTTGAGACCCGTCATTGCAAGCGCGAACGCTGTGCAGCAATTGCTGCGGAT
TTCGCTGAGCAAGGAATTGATCCGCTCGTTACTTCT

>RXN00552-downstream
TAAAAAGGGTATGGTGGCTGGGT

>RXN00555-upstream
CCTGGTGGATATCATTACTGAGCTTGCAGAGGTGTACGGTAGCTGGAAAGAGACCGACAG
CGGTTCTTAACAGTTTTCTCCATCTCAACTCCGGAATTTG

>RXN00555
ATGAAACAACCCCTTCGCGTACTTATTTCTTGTCGACCCGAAGAAAATTCGGGTGGCAAA
CGTAGTGAACAAAATGATGCTGTTTTTGAGTTCGCCGCATGGCTAGCTCGTACTTCAGAC
ATCAATGTTCGTGGAATCACAACTTTCATACGCCCTTGGCCGTCTTCCTCCATCAGTAAG
CTCGGAGGAAAATATCATAAGTGGTATAAGAATTTAGATTCTTACTACCGCAGTCGCACG
ATCAAGGGACTCAAAGAGGCCGGAGTTGAGAAGTCCCAATGGGACGATGATGTTTCAGTT
TTTGTAGATGGTCCTTCTGAATCCACGCTGCTCACCCATGCTGCTGAAGAATTCGAAGCG
GACCTCATTCTGCTTGGCTCTGATGCGACCGCACCAAAAGGCCGCTTTCTGGCCAGCTCC

ACCGCAGATGCCCTCCTTCACTCCTCGCCCGTCCCACTAGGACTTGTGCCGCGAGGGGTG
AAGCTTTCCAAAAAGGGTGTCACCCGCGTCAACTACGCTTTCACCAATGAAAGCGATGAC
TTTGAGCAAGGTTTACGCTCTTCCGCGGAGCTCGCCACCAATTGGAACGTTCCTCTTCGG
ATCCTTGCTTTTTCACCCACAGGCATTACTTCCGCACCAACGTCGCGGAGCTTGGATATT
TCCACTGAGCTTTCCTCCGAGTGGCGTGAACTAACGCTCGCCATGCTTGATCGAGCCCGT
GATGGCGTCCTCACAGACCACCCAAACTTGAGCGTGAGCAGTGAAACCGGTTCTGGCTGG
GGTTGGAGCGGTGCAATTGATGCTTTGCGATGGAAGAAAGGTGACCTGCTGTGCATGGGA
AGCCATCGCACAGACACCCTTTCACGTGTCTTTGTCGGTTCGGAAACAATGGAAATTATC
CGAAACTCTCCTGTACCGACCATCATTTATCCCGGTCTT

>RXN00555-downstream
TAGGCTCTCCAACAGCAGAGGAC

>RXN00560-upstream
AAGGACGACTTCTGGGGAGCGGTGTGGATTCTCACGGGGATTCTCATGCGGATTATCAGA
CATATGGACACTTTAACGGTTCGTACTAGGCTGATGCTTC

>RXN00560
ATGAGGATTGATCCGCTGGAAACCCGGCAAGCCGTATTGGCCGTCAAAGACTGGATTGAA
GGGGAGGGAGACGTCAAAAAGCCTGGTCGTGCGGCACTTGCCGCCGCAACTCGCCTGAGC
GTCCGACTGCTCGCGCAACACGCGCCGGGAAACAGCGTGGAGGTGCGGGTACCCCCATTT
GTTGCGGTGCAATGCATAGAGGGGCCAAAACATACACGCGGCACACCACCCAACGTGGTG
GAGACCGACGCCAAGACCTGGTTACGCTTAGCACCTGGGCAAACCACATTTGATGCAGAA
TTTGAAAGCGGAAAAATTAGCGCATCAGGTACCCGAGCCAAAGAGATTGCGGACTGGTTA
CCAGTGGTCAAACTT

>RXN00560-downstream
TAGATTTCCTAATGCTCATTAGT

RXN00574-upstream
AACTGCTGGGCACTACTGAGATTCCCATGTGGGATGTGGACCGGTGGCAACCATCGCTTC
TCAAGCCCGGTGATTCAGTTCGATTTGTGCAGGTGAAGAA

>RXN00574
ATGAGCTTCAAAGTAATTTCCACTGGCCCCCAAGCCATCTTCCAAGACCGAGGTCGCTTC
GGTTTTGCCAGCGCTGGTGTTGGAACCTCAGGATCCTTTGATCGTTTATCCGCTGCTCGC
GCGAATCACGCTTTAGGTAATGATCCCAATGCAACCGTGGTAGAGATTCTGCTCGGTGGC
TTTGAGGTGGAGGCGTTGCACACCACCTCGATCGTGTTCACGGGAACTGAAGCTGAAGTG
ATGGTTCGAACGGCTGGTGGACAATCCAAAAATGCCACCACCAACACCATCATCGATGTT
GCAGCTGGTGAACGTATCCGCGTCGAGCCCGCAACCTATGGCATGCGTGCCTACTTTGCT
GCTCGCGGTGGATTTGCAGTAAAAAAAACTTTGGGATCTGCTTCAACCGATCTGATCTCC
CACATGGGCCCTTGCCCGATCGAGCCCGGGGATGTCATTGACGTAGCAACAGACATTGCA
GATTCTCAGTGGTGGCCAAAACTTCGGCAACTGCCCACCTTATGGAAACGCATGCCAACA
GAAACGCTTACCGTCATCCGAGGTCCACGTGACAAATGGTTCACGCAAGAATCCCTCAAC
AACTTTTTTACTCAGGTGTTTACGGTGAGCAATGACTCCAACCGGATTGGTTTGCGCATG
CACTCAAGCGAGCCGATCCAACATCGTGTGGAAGGCGAGCTGAAAAGTGAAGGAATGGTC
CGGGGGTCCATCCAGATTCCGCCTGGTGGAAACCCCGTGGTGTTTGGTCCCGATCATCCT
GTGACCGGTGGCTATCCAGTAATAGCAGTACTTACATCAAGGTCGTGTGATCGTTCGGCC
CAGCTGTTGCCGGGCGATAAAGTCAGATTTAAATTGCTT

>RXN00574-downstream
TAGGAACTTTGAGCTTGCTCTGG

RXN00589-upstream
CCGTTATCTCCGTAACTGTTGTTTCTGCAGAACCATACAACTCAGCAAAAGCCGCGACAC
TCCGCGGCAAAAACTAACCAAGGATTTAAAAGTCTTCAAA

>RXN00589
ATGACAACTCTTTCACGTAAGTTCTTCGTTTCTGCTACCACAGCCCTGGCGGCAGTCGCA

CTGGTTGCGTGTTCCCCTAATGAGATTGATTCTGAACTGAAGGTGCCAACGGCAACTGGC
GTTTCTTTACCTTCGAAGAACGTTTCCGCGACCTCAACTGCTACTACAGATGAGGATGCG
CCTGGCTACATTGATTGCGTAGCCGCACCAACTCAGCAACCTGCTGAAATCTCACTAAAC
TGTGCAATGGATATTGATCGGCTCACGGATATTTCTTGGAGCGAATGGGATACTGATTCC
GCAACTGGAACCGGTACCCGCATCGTAACCGCTGCAAATGGTCAAGAGACCGAAACCGAA
GATATTGAGGTGAAGCTTTCCTTCCCCACCGAGTCTTCCCAAGGCCTAGTGTTCACTCAG
GTCACCGTCGATGGACAGGTTCTCTTCCTC

>RXN00589-downstream
TAATCCTCCATAATTAGAGAGCG

RXN00616-upstream
AACCGCAACCTCGCGCACTTGGAGTGAAAATTCTCATCTTCATTTCATCTTGGTGCCTAA
CAATGGAATACAGATTGAGTTGATCAAAGGAGAACCCCCA

>RXN00616
ATGAAATCACTCCCCCGTTTCGCCCCACTGATTACGATTCTGGCTCTGCTCGTACTCGTT
GCCATCGGAGGATCTGCACTGGCAAATAATCGTGCTACCCCTAATGTGGAAAGTGAACCC
GCCACGGTCAACCAGCGTTCCACTCCCACAACTTCCGCGTATGAGCCCCCTGCTACAGAA
TCTCCGGAAGAACCAACCACACAAATTCAAGAATCCCCAGTACAACCCCCAGTTCCTGCC
CCCGCTCAAATTCCTCAAGCCCCACAAGTTCCACTCAATTATCAGTACTATGACGATGAC
TGGGACGACGACGATGATGACTTCGACGACGACTGGGACGACGAC

>RXN00616-downstream
TAACTAACCCCTGAGGCACTTTC

>RXN00647-upstream
TGCATTCTTCCCACAATGACATGAGCTTATTGCAACATCGTGGGTAAAGTTGAATCGAGA
AGTCGAGAAATAACCGACCGATGAAAGAGTTGAGACGATA

>RXN00647
ATGGGCATCTTCGAAGCCATCCGAGCCGCACGCGCGAAGACCAAAGCTGAGATCAAAGCA
GCCGAGGCAAAAGTAAAAACTGAGGCGAAAAACAAAGCAAAGCTAGATCTCAAGCGCGAG
AAGCTTCTTGTCCAGCAGGAAAAGAATCTGCTCAAGGTTGAAGAAAAGGGCCTGAAGAAG
CGCAACAAGCATGAGCTGAAGATGGCCAAAAATATCCTTGAGCAAAAGCGCCAAGGACGC
CTAAACAAAGACAAGGTGAAGCGCTGGGCTGGCACCGCACGTGTGCTCACTCCACTACTG
CTGCCTATTATTTATCGACTCTCCACCGAAGCACGCGATCAGGTTGTTAAGGGACGTGCC
CGTCGTGCAGGTGTCACCGCGGAGCAGCTTAGCCAATTCGCAGGTCACGCAGCAGCGCTG
AAGGCTCGTATTCAAGGTGTTCGCGAAACCGCAAAGAACTCCAGCCTCCCTGCTGGCTTT
GTACGCGATGTTGAAGAGCGTCTCAATGAGCTCGAGGCTGCTGCGAATAACTCTGAGTTC
ATGTCTCCACAGCAGAGGAACCGTGCGCACCAGTCGATCAGTCGTGATCTGAACCAGGTG
TCAGATCAGATTCAGGATCGACTACTGGACAAG

>RXN00647-downstream
TAGCTGCTGGTCGAGTCGCTGCC

>RXN00653-upstream
GTTGAGATTCGCCTAACAAAGATTTTGGACGAAAACAGTAACGATGACAGCCACGTTAAG
CGCGGAATCTTCTCGCAATGGTAAAAAGCCGCGGCCTCGA

>RXN00653
GTGAGTGTTTCCCAGGTTGTTGGTGAAATCTTGCTCACCGTAGGCATTTTGGCCTTGTTA
TTCGCATACTATGAGGCCTATTGGACCAACGTGGAATCTGGGAAATTACAAGAATCGGCT
GGTCAAAAGCTTGATGAAGACTGGAATGAAGCTCGGGTGAATCCTCGACAAAAGCTCACC
CCGGAACTTGGTGAGGCATTTGCCCGGATGTATGTTCCAGCTTTCGGCTCTGACTTCAAC
TTCGCAGTGATTGAAGGAACCGATGAGGAAGACCTTCTTGCCGGTCCTGGCCGTTATGTG
GATTCCCAAATGCCTGGTGAAGCCGGAAACTTTGCAGTGGCAGGCCACCGAGTGGGCAAG
GGTGCGCCATTCAATGATCTAGGAAACCTGGAAGTCTGCGATGCGATCGTGGTGGAGACT
TACAATTCCTGGGATGTGTACCGCGTGATGCCGATGTCCACCAACGGTGCAGATCGTGCA
GCAGAAGCTGCGGATTGCTTCAACGAAAACCAGGTCAGCCGCATGGCTGAAGGTGACTAT
GTGAATGTGTCCGGACGAAGCATCACCACTCCGGATCGCATCGATGCCACCTACCCCACA

CCGGGCGTCTTCGACACTGCAGTGCGTGAAGGATCAGAAGCTCTGCTTACCTTGACCACG
TGTCACCCGCAGTTCTCCAACGCTGAGCGCATGATTGTGCACGCAATGTTGGTGGAAGAA
ATCGATAAATCAAGTGGCGAACGCCCTGCAGCTTTGGAGGAAAAC

>RXN00653-downstream
TAAATGTATTCACTTCTGTGGCA

>RXN00662-upstream
CCCTCATCATAGTTTTAAATCTGGGGCAGAGGCGGGAATTTAAACACCTCTGATACAGCG
TTTACTGGCTATAGTGTTGCGCGTGCCAAATCGAGTTCCT

>RXN00662
GTGTCAACCATTCCGCTGAATCGTCTAGCCGTTATCGCTGCCATCATTGGTGTCGGTACC
GGGCTGTTTGTTGCTGCACTGAACTGGTCTGCCATTGGCGTGGAGCGTTTAGTTTATGGC
GCTGACCATTTGCATAATTACAATCCGGTGGCCAATGTGTCGCCACTTCGCCTGTCCATC
ACGGTGATTGTGCTTAGCGTGGTGGCCTCCTGGGCGTGGTTTTTTGTGCACCGCACGGGG
CCGAAAGAGGTTTCGATTGTGGGTGCGATCCGGGGCGAGAAGATGCCGATTTTGGAGACC
ATAGCGTCCGCATTTTTGCAGGTCACCACGGTTGCTGCGGGTGCGCCGGTGGGTGCAGAG
AACGCTCCACGTATTGCTGGAGCCTTGGTGGGAGAGCGGTTTAGTCGGTGGTTGCAGCTC
GATATTGATGCAAAGCGCATCTTGGTGGCCTCTGCCGCGGGAGCTGGTTTGGGAGCAAGC
TTCCACCTTCCCCTAGCAGGCGTGCTGTTTGCCCTTGAGGTCCTACTGGTTGAGGCCTCC
ACTCGGACCGTGGTTATCGCAATTATCACCACGACCGCCGCCGTTGCCACCACTGGATTT
TTCGTGCAAACCCCAGATGTGTTCAGCACTGTCCCGCTGACGGAAAGCCCATGGATGCTG
CTTGCCGCGATGGTCACCGGAGTAGTCGCCGGCATGTGCGGGCACTGGTTTTCAGCGGCG
GCGCACAAAATGGCGCAGGCCTCGCCCAAGGGTGTGAAGATTTTGTGGCAGATGCCGTTG
GGTTTCGTGGTGATCGCTGCGGTGATTTATTTCTTCCCCGAAACCCTGGCGAATCCCCGT
TGGCTTGCCGATTCCATGCTCGGCGATGGCCTGATCCTCAGCACCATTTTATTGGTACTT
GTTCTGCGCACCGCCATGTTTTTGCTCGCCTTCCGCGTGGGCATGGTCGGCGGTAACCTG
ATCCCCGCATTCGCACTCGGATCCATGGTCGGTGGGGTAGTGGGTGCTGTATTGGAACCC
ATCACTAACGTCCCGATCGCCGCTTTTGCGCTGCTTGGCGCCGCCGCATTTTTGTCCACC
ACCATGGCAGCGCCACTGTTCGGGCTCATCGCCGCAGTGGAATTCACCGACATGGAAGCC
CAAGGCTACCTTCCGATTTTCCTCGCAGTAGCCTCCGCGGTCCTCGCCGTGCGCGTGTGG
TCTGTCATCGCCAAGCACGAGCTCCGCGCCATCCCGATCACGTACGCGAGCTGGACGGGC
GAGCTTAAA

>RXN00662-downstream
TAAGCTTGTCGACGCCTCCCTCC

RXN00666-upstream
AGTGGTGAATGCTGGATAAGTTTTTAACATGTCTAGTGTAGTCGGGGAAGGCCCAAAACC
ACGATTGAGCGTGCTTGATCTCGTCGCGCTGAGTGAAGGG

>RXN00666
ATGACGGCCGGCGAGGCCATTGCACACAGTGTTCGCGCTGCGCAGATCGCCGAAGAGCAC
AATTATGCGCGTTTCTGGGTGGCGGAGCACCACAACTCGGAAGGCTTGGCATCTTCCGCG
ACGACGCTGCTCATGGGTCATATTGCAGGCCACACTTCACGCATTCGCGTTGGCTCCGGT
GGCATCATGATGCCCAACCACTCCGCGCTGCACGTCGCCGAAGAACTCGGCACCCTTGAG
GCCATTTACCCCGGCCGCATCGAGGCCGGCCTAGGGCGCGCACCAGGAACCGACCCCATG
ACGGCGCGGGAATTGGGTCGGGCAAGTTCGCTTGTCGACGACGTCCTCTCCACAATCGTC
TCCCTCCAGAATTATTTGGACACCCCCGAAGAACGCCCGAACATCATCGCGCATCCAGGA
ATAAATTCCCGTGTGCCGCTATTCATGCTGGGATCTTCCCTCAACGGCGCTGCGATGGCC
GCTAAATTAGACCTTCCATTCGCCTTCGCCAGCCACTTCGCACCCTTCCAAATGGGGCCC
GCCATCGCCTCCTATCGCGAACTAGCAGCCAATCCTTATGTCATGGCCGCAGCGAATGTC
CTGGTGTGCGACACCGAGGAAGAAGCCGAATTCCAGATCTCCACACTGCACCAAATGTTC
GCCGGAATCGTGACGAACTCCCGCGGCAAACTTGCCCCACCAGTGCGGAATCTGAAAGAC
AAACTCGACCCGATGATCTGGAAACACATCGAAGATTCATTGGAAATGACTTTCATCGGA
ACAGCCGAATCAGTGGTATTACAACTGCAGGAATTCGCTGATCGCTACAAGTTAGATGAG
ATCATTACAGTCACCTACTCCTACGACCCCGAAGTCAGGTTCCGCTCCATAGCTGCACTT
GGCACGGCATGGAAT

>RXN00666-downstream

TAGTGTCAAAAGCCTCAAAAATA

>RXN00704-upstream
TCAAATTCTGCGCACAAAGTGTTCTAAGACGACGTCTGCCCATCGGCGCTCTAATGCACA
TTACAGCGTTTACAGAATTGAAAATGAAAGGTTCAAAGCC

>RXN00704
TTGACCATTACTTTTAGCCGCGTTGCTCTGACCACCCTGGCAGTCACCGCAACCACTTTG
TCCCTGAGCACTGCTGCGAATGCACAGTCTTCCTTGTTGGATAAGACTCTTGATGCCCGT
CAGTGCATCGATGCAGACAACGTCTGGGTCTCAGTTGACTATGGTGCAGATTCCGAAAAA
GAACCAGAGGGCGCATGTGCCACCGAGTTCACTGATGGTGTTGTAGCTCTTGAATCTGCT
GGGTTCAAACTGACCTTTGACGAATCTGAAATGGGCAAATACATGACCGGTATCAACGGA
GTTGTTCCTGATTGGGTTGAAACTGGAACTTACTGGAGTTACTACTCTGGTGAAGTCGCA
GATGATTACAGCGTGGACTACACCTACTACGAGGTTGGTGCATCTAATTCTGAACCTGAA
GGTGGAACTGTTGAGGCTTGGGTTGTTGGCACCGGCGAGGAAACACCAGCACTCGAGACT
CTTCCTGAAACTCCAGCAGCAACCGGATCTTCTGAAGACGGCGGCTGGATTGCAGTCATC
GCAGGTCTTCTCGCACTGATCGGTGGTGGAGTTGCAGCTTTGTACCAGGGCTTGATCACT
ATCCCAGGTCTGGTTCTGCCTAAGTTT

>RXN00704-downstream
TAAGCAACCTAACCTAAAGCTTC

>RXN00712-upstream
TGTTGCGCGTTAATAAGGAACAATATCGGTGTGATTCGCGATATATTAATCAGCTTGTTT
TCCCAGCATAAGTAGTCGCCTAGTTTAGGAGGTACATGGC

>RXN00712
ATGTCCCTACGCAAGAATCTCGCCCTCGGAAGCAGCACAGTACTACTCACAGCCGTGCTA
AGCGGGTGTGTTTCCCTTGATGAGCGCTCCACTGATACATCCACGGAGAATGTCACCACG
GTAACTGCCACACTCACTTCCACCGCCGCAGCAGAACCCACCACTAGAACGACTGTGCAA
AGTGCTACAGAAGCCTCCACTACTGCACCAGTGCAATGCAATTTGGATCCCCGTACCTCG
GATTTTGGGCCATATCTTGCACAATCTCGCACCCCGGTTGGTGAGCTAGCTGGATCTGCA
GATTCCGTCGTGCAGGTTCCTGACTGGTTCTATCACTTCCAAATGGGCGACAACGGCTAC
GATTCCTGTTCCAAGCTCAGCTATGTGGTTCTCAACGGTTCCAATGGAGACGCCGAACGT
TCTACTGGAACGGGTGCTGCGATCGCCGACGTGGTGGTGCTGTTTATCGACGGCCATATG
GTTGCTCGTCCTGCTCCTTTTGAAATGAAGACCGTGGAATCCGTCACCAGAGTGTCAGAT
TCAGAAATCCAAGTTGTTTACGGACATGCCGGCCGATCTACTGCCGAAGGTGTTACGGAC
TATTTCACCTTTAACTTCTTCGTTGACAACGGCGTTCTTTCAGGACGCGGCGATCTCCCA
GAACACATCGATACTCACATGCGTCTATATCTGCTG

>RXN00712-downstream
TAGCCCCATCTAAAAACTCTTGA

>RXN00720-upstream
CTGATCTATACGTCCTGTTGAAGTAGAGAAGCTTTCTGGTCAAGTTCCTTGAGTATGGTG
GTCGAAGACCAGCACTCCAGATTCAAGGAACTTATAAAAC

>RXN00720
ATGGCATCACCGCGCCGCCCACAGGTTGCAGCACCACGCATCAAAGAACTTCGCCTAACA
GGCCTTGACAACGCTGACCCTCAAGACATCGAATCGAATGAGCAGATAGAGTCATGCCGT
TTTAACGAGGCCGAGCTTTCCGAACGCGATCTTTCTGGTGCTGGTTTCATTGAATGTGAA
TTCCTTGGGCTGGAAGCACACGAAACCGAGCTACGCCGGGCTCAATTCGTGGAAACACGC
ATCGAAAGAGCCAATGCTCCATCTTTTAAGGCAGCCCGCTCCATCTGGCGCAACGCAACG
ATTTCCGACTCCCGCTTTGGTGCCGTCGAAATGTATGAAGCAACCGTCCAAGCTTTGAAA
ATCTCTGATTCTAAGCTGTCGTTTGTCAATCTGCGGGGTGCATCGTTACGGGATGTGCTC
TTTGAGAACTGTGTCATCGACGAGCTTGATCTTGGCCAAGCCAGAGCAGAACGCATCGCT
TTTAAAGACTGCACGGTGCATTCGCTCACCTTTGATCATGCCGTGCTCAGCAATGTGGAT
CTTCGCGGTTTAGATATCGAGCGCATCAGTGGCGTGGAGTCCATGTCCGGAACCGTGATC
TCATCCCTGCAGGCTGCTGACCTGTCGGGAGCATTTGCACGGCATTTAGGAATTACTGTA

AACGAT

>RXN00720-downstream
TAGAAATCCGCTCTTTTGAACAA

>RXN00722
GCTGTTCTCCGAGAAGCCGGAGTTGTTGATGCCGGGGGACAGGGCCTAGTTATTCTCCTG
GAGTCCCTGGCCGAACAAATCAACGGAAACCCACCTCACCATCCATCGCACCACAGTGAA
CCAGCCGAAGAACCCTCCTTCCACGGCAAAACCGGCGACCTAGAAGTGATGTTTTACATT
GCATGCGACTCCGCGCAAACACTCGATGCTCTCCACAACGAACTTGAAACACTAGGCGAC
AGCCTGCTCATCGCCCGAGAAACCAATACCCGCGGCACCGTTCACATCCATTCGCGCCGG
GCAGGCGAGGTCATCCAAAAAGCATTTGCCGCAGGAGACGTCAGCGAACTCCGCCTTGAA
ATCCTCCCCGATACTTCCGGCAGCTTCACGGAAGAACCACGCCGGGTCCTCATGGCTGTC
GCACCTGACGGCCTGGTGGCGGAGCTGTACCGCAGCGCTGGAGTGAAGGTGGTGGCCCGC
AACATCGCGCAATCCAAGTCTGATGATGTGGTGGCAAAGATCGTTTCCATCGCGCGCAAG
TCTGGTGCCGATGAGGTGATCTTGCTGCCCAACGGTCTTTTGACCAAGCGTGAGCTGGTT
TCCATTGAGCGTTCCAGCCATGCTTTTGAGCAAAGTGTGGTTATTTTGCCTACTGCCACG
TTGGTTGCAGGTCTTGCAGCGGTGTCCGTTCATGAGCCAGCGCAACCCCTGGCGGTGGAT
TCCTATGCCATGGCAGAGGCCGCCGGTTCCATGCGCACGGCCACGATCCGCGCCGCCACC
AGCGCCGCGCTCACCCAGGCCGGCGCATGCTCCAAGGGTGATCTATTAAGCTTCATCGGC
CCGGAGATAGCTCTGGTCTCCGAGGAGCTCAACGACGCGCTATCGCGCACCGCTTTAAGG
CTTCTCGACGGCTCCAGCGAGCAAATTACCCTTCTCATAGCGCAAGACCGTCAGTCCGCC
TTCGACGAAGATGTTTTCCGCCGTGGCCTGGGAACTCACACGGATGTGGAGATCACGGTC
TATCCTGCTACTGGAATGGAGAATCTGGTAGAGATCGGAGTGGAG

>RXN00722-downstream
TAGCCACATGTTGGGTTGGCATG

RXN00729-upstream
TTCAGCACAGATCACCCTTTGCCAGCTACCGACTTAGTTTCGTAACACGTATAGTGGGAG
GCGTTTTGCCAGACGCCAAAGAAAGATAATTGGATTACCT

>RXN00729
ATGAGCGCCACCAACCCTGATGCCCTAGACGTGCAGCACGTCTATCCCATCAAGACGAAA
AAGACTCCACTTGCGGTGATTTTCAACATCATTAGCGGTGGTTTGATTGGAATGGCGGAG
TTGGTGCCAGGAATTTCCGGCGGAACTGTCGCTTTGGTTCTTGGAATTTATGAGCGCGCA
CTGCACAACGGTGATCTCCTCATTGATCTGATCAAGGTGTTGATCAAGGACCGCTCGAAG
GTTAAGGAAGCTGCGGCGAAAATCGACTGGTGGTTCCTCGGCGCTATCGGCGTTGGCATG
GTCGTGATGGTCTTCTCGATGTCATCGATTTTGCATACAGTTGTTGAGGACTACCCAGAG
ATCACTCGCGGTCTGTTCCTTGGAATGGTTGCCGTGTCTATCCTTGTTCCGTTGGGAATG
ATGGATATGCGGGATGCCAAGAAGCGCCTCGCAATCGTCATCCCGCTATTTATAATCTGC
GCCATGCTGGGATTCTTTGGAACATCCTTCACTAGTGCGCCTCGCACCGATCCTTCACTG
ATCTTTGTCTTCATCTGTGCTGCGATCGCTGTGTGTGCTCTTGTTCTTCCTGGTGTTTCA
GGATCATTCTTCTTGCTGGCGGTCGGTATGTACGCGCCAATCATGGAATCTCTGTCCAAC
CGTGACTTGTCGGTCATCGGCGTGTTCTTGCTTGGCGCGCTCACCGGTGTGATCTTGTTT
GTGAAGGTTTTGTCTTATGTTCTCGAGCACCACCGCACCATCACGCTGACCATCATGGCT
GGTCTCATGCTGGGTTCACTTCGTGCGCTGTGGCCTTGGCAGGACGGTGACGCTAATCTA
CTTGCTCCTGGCGATAACGCCGTGATGATTTTCAGCATCATCATTCTTGGTGGCGCGATT
GTCGCTGCTTTGATGTTTGCTGAGCGTGTGTCTTCCAAGAACATTGATTCTGAGACCGTG
GCAGAAGAGCACCCGCGC

>RXN00729-downstream
TAAATAAGAACTCCACAAAGAAA

>RXN00730-upstream
TGGTGCAATAACCTTAAGTGAGGCTGGATTTTGCGTTGGCAGGCGCTCGGGTTTTGTTTT
ATCCGGCATGGGCTCGGGAGGGACTTTAAAATAAACAGCT

>RXN00730

ATGTCGAGCCAACAAACGATCTTCATCATTTTGCTCTTTGCCGCAGTGATTCTCATTTCC
ATAGTAATGATTACAGCTGCCTTCAAAACCCGGAAAAAGCGCTTTGCCGCGCGGGCTGAA
GGAATGGCCAACCCTACAATTCCTGCGCCAACTGTGCCGTGGCAGCGCTTCGCCGGAGCA
CTTGCAGCCTTGTACGCTAGGCCTGAATGGCACAAGACCCGCGGAGCGAAACGAGTGTAC
TCAGCTGAACAGACTTATTTTGGGTTTGTCTCAGCAATGCCACTGGGGATGGTGCAAAAC
ATGCTGCAAACAGACTGGGGTGTGAAAAAGTCTGAGCATGCAGTTGATCAGCTTTCTAAA
GGAGTGGAAGTGATCGTTGGGGTAGCCGCAGGCAACTGGCGTAAAAACGGAGTATCACCC
GCACAAGTGGAAGAGGCAGGCCAGCGGTTAGCAGCTGAAGGATTGGCTCATCCACACTTT
GTTGTATTCCAAAAGCAGCTTCAACAGGCAGATCCAAATGCAGAATATGATCTCGATGTG
CTCGCATTTGATATCGCACGCGTAGCCAACCTCCTTCGCTGGGCTGCTTATACAGATCTG
TTGCTCCCTGCAGAAGCCCGTTGGTTCCAAGACCAGCTGGGAATTGCGGCTGCTGTGTCC
TTTGGGAGCTGGGAAGAATACGGAGAGCGATACGTCCGTGGACTACAGAAGAACTTCAAG
GGCGGAAACAAGCCATATATCGAAGGAGAACGCTGGCTCAACACTGAGGCTGAAAGTCCA
TGGAAGACCCAAAAGTGGATTAGCGCC

>RXN00730-downstream
TAACTGCTCATGAGCTAAGCGGC

>RXN00731-upstream
TTGATACCGTGGCCGGTGGACATTCCTTCCAGGTGTGGCGCGTGGCTTTAGCGAATACTT
TTGATTGGGTTGCCAAGCGCGGCGGATTGCAGGTTTAACA

>RXN00731
ATGAAAGACGCTTCACAGTCCTACTTATTATTCGGTCTGAGATGGCTGGGCAGGTCCCTG
CGTTTCGCACCGTTAAGCCTGCTCATGATCGTTGTCATGCGGGGTTTGAGGGAAGTGTTT
GGCGCCGAAGATCCCGCAAATAGCTCTTTGGTAGACAACCTTGGGCTCACCCTGCCGTGG
TCTCTTAATGATCCGCATTTTCTCACCGCAGGGTTTAGCGCTTCCACCACCACAGCAGCG
CTCATGTCCACGTTGTGGATCATCGTGTTTGCGGTGCCCTCTGAACGGATTCTGGGCAGC
CTCAAATTCGCGATCACAGCAGCGCTTATCCACATCACTTCCATTCCGCTGGGCATCGGC
ATCGCCCACCTCATCGAAGAAGCCGATCTCAACCGCTGGGGCAACAACATGTTGGCCGAT
GTGCTGCTCACCCCAGATTTCTGGGTCTTCGGCGTCGCCGCTTTCGCATCCGCCTCCATG
CCACTGCTCTGGCGACGGCGCACCCGATTGTTCCTCTTTACTATCACCTTGACGCTGCTG
CTTTATACGGGCACGCTTGCCGACGTCACCATGCTCACCGCGACCATCATCGGCACCGTT
GCCGGCGAGTTGAACAGGCATCGGAAAACCCCAGGTGGCCGCTGGCTTCCCGGTTCCCTC
ACCGTGCGTGAAGCGCGCATTATGACGGCCATTTTGGTCACTGCCGTAGCAGCAGGTCCA
GTGCTTGCTGCGCTTAATCCACTCACCCACGGCCCTTTTTCCAGTGCAACGAAATTGATC
TGGCAGCCCCTTGTCACTGAAGAACACATGCATCACCTCTGCCACACAGACAGCACCTCT
GATGCATGCCAAGGTGCGCTTGATCAGCTCCAACAGCACGGTGTTGGCCCTTCCGTTGCC
AACCTGATTCCACTGATCCTCACCGTGGTCCTTGCGATGGGGCTTAGCCGCGGACGTCGA
CTTGCATGGATTTTGGCGGTTTTGGCCCAGCTCATTTCCATCGCAGTGTTGATGTTCCAG
CTGACCAAACTATCGGCTGATTCCACCGATCTTCTATGGTCAGTCAATGCCTTTAGCGTG
ATCGTTCCTTGGCTGGTGGCGCTCGCCGTCTTGGTGTTTTCCCGCCGTGCATTCCAGGTG
AAGATTGATACCACCCGGATTTCTAAATCCTTAGGCGCTCTCATGGTTACATGGTTGGCA
ACGGCAGCATTGTGGATCCTTGCCACATTGTTCCTGCCACACGCATTCCACCCACATCCA
ACATTGGGGCTGGCTTTCAAAGAACTCCCCTTCCGCTATCTCCCACCAACTATCGAAACG
GTGTTAAGCCATCAACTCTTCCCCAGAAGCCCTGCTGGGTGGGCAGTGTTTGAATGGACT
GGAACGCTATTCTGGCTGGTCGTAGCAGCAACTCTTTATCATCTGCTCATGGGTGTGCCC
AGCAACAAAGCGCACGAGGACCAAGAAAACGCAGCGACTCTCCTGCGCTCTGGCAGCGGC
GATCACTTGTCCTGGATGACCATTTGGGGTGGCAATACGTATTGGTGGGCACCAGAAAAT
GCAGGATATGTGGCCTACCGCGTGAAAAGGGGCATCGCAATTACATTGGGTGAGCCTATT
CTGGGTCCGGATTCATCCGTCTCTAAAGCAGAGCTGGCCGCACAGTTTGAAGAATTTGCC
AGCAACCAAGGCTGGATTGTTGCGTGGTATTCCGTTTGTGAAGAATTCTCAAAGGAACGC
ATCAACGCTGGCCACCACACACTTCGTGTGGCTGAGGAAGCAGTCTTAAGCTCAGCTAAT
GCGGATTTCAAAGGTAAGCACTTCCAAAATGTCCGCACCGCCCGAAACCGCGCGGCCAAA
GAGGGCGTAAGTTCCATCTGGACAACCTGGGCTGATTTGAGTGCCGAAATGCAGCACAAG
ATCATCACGCTGTCGGAAGAATGGGTCTCTGATAAAGCTCTGCCGGAGATGGGCTTCACG
CTTGGCACTGTCAACGAGCTCTCAGATCCAGATACCTATCTTCTTCTCGCGATTGATGAG
GAAGAGCATCTGCACGGTGTGACCAGTTGGTTGCCGGTCTATGAAAAAGGACGCATCGTC
GGCTACACACTTGATGTGATGCGCCGTGATCCGCAAGGCTTTAAATCTGTCATCGAGTTT
CTCATTTCCGAGGCCGTCGTTATCGCAAGGGATCACGATCTGGAATGGATGTCGATGTCC

GGCGCTCCTTTGAGTACGCCCCCAGGTGTGGCCGACGACGGCACCATCGGACAAATTTTG
GAGCTTTTGGGCCGAGCAATGGAGCCGTTCTACGGTTTCCGTTCCCTCGCTGCGTCCAAG
AACAAATTCCACCCAGAACACCACGGTTGGTACTTGTGTTACCGCGATGAATTATCGTTA
CCAAGCATTGGCCTTGCCGTTGCTGCCTGCTACCTCAACGAGTTTCCGCTGCCGAATTGG
CTGAAAAAGACCGCCACTTCCGCCCCAAGCCACAGC

>RXN00731-downstream
TAGAAAAACGCGTAACCTTGGTG

>RXN00738
TGTCAAGAGGAGACGGATGGCTTTTTTGATTTTGGGCGCGATATGCGGCCCGGTGAGCGC
CGGTCGTATGGCACTTTGCTTAACGACGCCACGACGCAGGTGTCGCACATCCTCGGCAAT
GCCTTCACCCGATCTGGGCTCAACGCTGAGTACGCGAATCTTTATGGTCAGGCGTTGGTG
GGCATGGTGTCGATGACGGCGCAATGGTGGTTGGATGAGCGCACTCCGCCGAAGGAAGAA
GTTGCCGCACATATTGTTAATCTTTGTTGGAATGGTTTGACGGGGATGGAAGCCGATCCG
AAGTTAACTCCCATCAGTTCTGCTGAGGGTGCGATTTTTGGTCAAGAAAAGGAGAGTGAA
GCG

>RXN00738-downstream
TGACACCTATGCTCGCGGGGCTG

RXN00750-upstream
TTTAAACAAAAGCGATAACAATGAACCGATGGTGTCTACGACAGAACCGACTCCCCCACC
CACTAACACCCCACCAGAAAATAACACCTCGACCGAACCT

>RXN00750
ATGGACTGGTCGATCATTATTAATGTGCTTGCCGTTGCTACTGTCGTGATACTCACCCTT
ATCATCGCAGCTGCATTATATAGGGGTTTCACACGCAACAAAATAAAAAAACTTGAAGCT
ATACGAGAAGCCCAGCAACACGAACGCGACAATCCCACTATCCGCATTGCTGATCTTCGC
GGCATCATGGATACTCACCACTACATCTACACCGACGTCATGGTTACACGTGCACATGAA
CTCATGATTACTGCACCCGCATTCTTTGATGTCACTCTCCCCGAAGCAGTGCTCTACGAA
GATACTAAACGTGCTGCTCATGATGCCCTTAACGGCTATAAAGACACCACTGTCGCTAGT
GCAGAGAAGATCATGCTTGTAGATGCAGTCACCGCAGCATGGACTCTCTATTCCACAAAA
GCAAACACCGGATCCACG

>RXN00750-downstream
TGATCCGAGAGCCGAGTACCGCT

>RXN00762-upstream
GATGCTGCGATGGTCACAAGTCGTTTTCTGGATTTTTCCACATCTATATCTTTACCCCAC
GTTCCTGCAAGAGATTCAAACTTGGGGCTAACCTGGGGAC

>RXN00762
ATGAATACTTCCGATCGTATTAAAAGCACTCAAATCGCGCTGGATCGTGACCTCCGTGAG
CAGGCACTATTGCTTTTGAAGGAGGTTCGCGCAGTTGATGGCGTGGATGCTTTATCAGAA
CAATTTGTCCGTGGGCTTGCAGAACCCGGACTTGTTCACTCCCATTTAATAGTCACGCTC
AATAGCGAGCTGGTTGGCCTCGCGGCCGCGGATGAGGAAACCACGGAACTGGCTGTCCAC
CCGGCGCACAGGCGTCAGGGAATCGGTAAGGCGCTTATCGACGCCGCCCCCACCTCATCA
ATCTGGGCGCATGGAAATACAGCAGGTGCACAAGCGTTGGCATCCACCCTGCGTATGAAG
AAGACTCGCGAGCTTCTGGTGATGGAGATTTCCGACAGGGCGCTCGATGACTCTGCAGCA
TACAAAGATCCAGATGGAATTACACACAGTAGTTTGGCGAATGCCCCTGTGGAGAAATCA
GTAGCTGAGGCTAAATGGCTTCAATCCAACAACGAAGCATTCGACTGGCATCCCGAGCAG
GGCGGATGGACAACTCATCGGTTGGCGCAGGCTCAGAAAGCCGATTGGTACAAGGACTCT
GACGTGTTATTCCTCTGGGACGGCGAAGAGATCGTTGGCTTCCACTGGGTAAAGCAGCAC
AGTCCAGAATTACAAGAGATTTACGTAGTTGGCCTTTCTTCAGCCTACCGTGGTCGCGGC
TTGGGAGATCCGCTTGTTCGCCTCGGACTGCATCACATGAGGGCTCATGGTGCTCGAAAA
GTGATTCTTTATGTGGAAGCTGGCAACACTCCGGCAGTCGCGGCATACGAAAAACTGGGA
TTCACTGTCGCGGAAAGCCACGTAGTTTACGAAAAG

>RXN00762-downstream
TAAAAAAGAGACTTGCTAAAAAC

>RXN00768-upstream
TCAAGCGCCATAACGCCTGATTATGCACGGTTAAGGCGCATCTCGCTCACTGGTGCTAAC
CACTTGCGCTTTTGGAAGGAATAACCCTTCCTGTCAGATT

>RXN00768
GTGGGTACTATCGAAGACGTGGCTAACGAACAAATCGAGGTCGCGAACAACACTGATCAG
ATTCCTGCAGGATACAAGTCCCCTCTTCTTTCTAGAAGTGGTGCGGCAGAAGCGCAGGGC
GCTGCTGCTCAAGCAGGTACTGAAGGTGTCGCGTGGCATTACGGTTCCCCTCTCGTCGAG
CAACGCATCTTCGAAACTGGCACGGGCTTAGTTGACCGTTCTAATCGCAAGGTGATCAAA
GTCGAAGGGCCTGATGCCCCCACGTTCCTCAATAATATTTTGTCCCAAAAGGTTGATTCC
GTTGAAAACGGCTTTACTGCCGGTGCCCTGGATTTGGATGCGCAGGGTCGTATTCAACAC
ACAATGCAGGTAACTGTCGTCGATGGGGTTTTCTACCTCGACACGTCCGCGGCGGAGTTT
GATACCCTCATCGGTTTCTTGACCAAGATGATTTTCTGGTCGGAAGTCACCGTCCAGGAA
GCCGATCTGGCGATCATCACTCTGCTCGGCCAGGAAATTGCCCTTCCGGACGCGGTCTTT
GCCCGTAGGGTCGATTGGAATGGGCCATCGCGTATCGACGTCGCCATCCGGCGTGAAAAC
CTGGAGGAGGGCGTCGACAAGCTCTTAGAAGCTGGCGCAAAGCTCACCGGTCTCATGGCT
TACACGGCCGAGCGCGTGAAGGCGTTGGAGCCCGCTGCGGGCGTGGATTTGGATGATAAG
ACCATTCCCCATGAAATCCCCCATTGGATTGGCCGTGGCGAACATTTAGGCGCTGTGCAT
TTGACCAAGGGTTGCTACCGCGGGCAGGAAACTGTCGCGCGCGTTGATAATCTTGGGCGT
TCCCCGCGCGTGCTGGTTCTGCTTCATCTTGACGGTTCCGCACCGCTGGATCCTGTGACT
GGCGCTGAAATCAAGGCCGGTGCGCGCACCGTTGGTCGTCTGGGCACCGTTGTCCATGAC
GCCGATTACGGGCCGATCGCTCTCGGGCTGGTTAAGCGCAGCGCTTTGGATAAAGAACTT
CACATCGATGATGTCTCTGTAAACGTCGACCGCGATCTGCTTCCTGCGGAGGAAAGTGAA
CAACGCGGACGCGCAGCGATCAATAAGCTCAAGGGTCTT

>RXN00768-downstream
TAACTAAAACGATTTATAGCGAA

>RXN00769-upstream
GGCTATTGTGTCTATCAGGAATACAGTTAATACATCTTGAAAAGCCCATGGGCCATCCGA
ATTCCCAGGATCGGCCCGCTCACTCCAAGGGGGTCAGGCA

>RXN00769
ATGGGTCGCGGTCGCGCGAAGGCAAAACAGACCAAAGTTGCTCGCCAGTTGAAGTACAGC
TCTCCAGACATGGATCTCGATTCGCTGCAGCGGGAGCTGGCTAACCAGTCTCCTAGGCGT
TCCTACTCCGATACCCCTGATGATGAGGACCAGTACGCAGAGTATGCGGACTGGGATGAG
GACGACACCGACAATCGTGCCTACGGCACAAAC

>RXN00769-downstream
TGATTTCGTGTGTCCTTAACTCT

>RXN00771-upstream
TACCCCTGTTTTGGAGAATGCTCCGAGCCAGGGGTACTTTTCTTTTCCTCACACACAGTA
GCTGCTGAGAAAAATGAAGACCTTTTGTTAGGTTGGGAGT

>RXN00771
ATGACCAACCCATACGAGGCCTTCATACCGCTCAAGCATCGTACGGGGATTGAACCCGAG
CACACCTTTTGGGAATGGGAAAACAAAAGGGTTCACATTGCAAGGAGACGTCGAGAAGCG
CCCGTCCGCGTTATCGTGGTGCATGGGCTAGGCACCCATAGTGGCGCCCTCTGGCCCCTC
GTCGCGGCCATTGAGGGCGCGGACCTCGCCGCGATCGACCTGCCTAAAACTCCGCTTTAC
GACGATTGGCTGCGCCTTTTAGAATCTTTCATCTCGTCCGAAGACGACGGTCGGCCACTC
ATCCTGATCGGTGCAGGCACCGGAGGCTTGCTTTGCGCAGAAGCTGCACACCGCACAGGA
CTGGTCGCACACGTCATTGCCACCTGCCTGCTCAACCCCTCCGACCAGCCGACGCGCCGG
GCACTGTTCAGGTTTTCACCGCTGACTCGGTTGATCCAAGGCCGCTTGCGCAACCGCGAA
ATTCCCGTGACCAGAGTGTTGAACTTCAGCAAAATCAGCCGCAGCCCAGCCCTGAGCAAA

TTGTGCGCGGCCGATGAATTTAGCGGAGCATCCAAAATAACCTGGGGTTTCCTCGCGTCA
TATGTGCAACACAAGGCCAAACTGGGTGCAGTTCCCGTCACTCTGATGCACCCTGACCAC
GACCTTCTGACTCCCGTTGAGCTCAGTCTGCGTACGCTTTCGCGCCTCAAAGCGCCCACT
GACGTGGTTATGCTCAAGGACTGCGGGCATTTTCCCATCGAAGAACCCGGCTTCACCACC
ATGCTCGAAACCGTCACATCAGTTATCGCGCGGAATAGT

>RXN00771-downstream
TAGCGGGCGCATGTGGTTGGGAT

>RXN00785
ATCATCGCTACTCTCGGTGTGACCTTGCTGGTTGAGGCCCGCGGATTATTCTTGACGGTT
GCGTCCATTCCCATTCTGTTTGGTATTTTCACACCACTGACTTCGTGGTTTGTGTCCCAA
CAAGGCGTGGCTGCGAATGTGTCCCCTGGTGTTTCCGTCACGGAAATCCTCACGGCTGTT
TATCCTTTGGCGCAGTTGTTCCCCACCCTGATCATGGTCACTTTGGTGGCGGCATTGATC
GCTGTGGTGCGGATTATTCTGCTGCGCAGGAACCAGGAATCTCGTCAGGTTTCTGGGGAA
CTTACCCGGCGCGCGCAGCGTGAGGCTGAGGAAGCTAATCAGAATGCTGCTCGTCGTGCT
CGCGCACAGAGCACGAGGGTACAAAGTTCTAAAACACGTAACCGTCGCGCGCAACCAACC
GGCGATACCGGTTCACAAGTCACGGTTGATGAGTTGATCAGGCGTAGCCAGGAGCGCCGG
CAAACTGTTGCGCAGCGCCAAACTGAGCGCGGTGTGCCGTTTACTCCAACTCCGGGTCCT
GTGGTGGCCCCCAAGCCGCGCCCGAGCGCCCCTGAGGCGCCGGCTCCTACGGATGTGGGT
GAGCGTCGACAAGCAGCCCCTAAACGCCGCACCTCGCTCGACGATGATCTGTACAGC

>RXN00785-downstream
TAAAAAATCCCCGCTCATGTGGC

RXN00795-upstream
TTTGGATTCTGGACACCCAAAAGGGGGTTTCGTACCAAACTCGTGACATACTAGGCGGGT
GGCTGAGAAACGACCGAAAATTTTTGATGGCAGTCGAGAC

>RXN00795
ATGATTATCTCGTTGGTAGTCTCCGCGATCATCATGTTGGTAGCGGTGGGATTCACGGGA
ATGTGTTCTTTCAATACAGGATCCCCTGAAAATGGGCAGGTACCTGAAGTTGATGCTTCC
ACTTTTATGTCAATGGAAGCGCGCGCAATGACTGATCATGCAACTAGGTTGCCGGAAACT
CCTGAAGGCTGGACCACAAATTCAGCTCGACGCACCATGGTGGATGACACCCCGGCATCT
GTAGTTGGATATGTCACCGCAGATGAGGGCTATATTCAGCTCACTCAAACTGGTGAAACC
GTTGAGGATGCTGTGGCTGGTTATGATACTCGCTGGCGTGATCTTTCTGAGTCTTATGAT
CTTGATGGCCACGACGTGGGAATTTACACCTCACAGGAATCTGATGTGCGTGATCTGCGT
GTGATGGATCTGGGCGATGCCCGCGTCATGGTCTCGGGTGCTGCTACCGATGAAGAATTC
AATGATCTGCTTCGCGCAGTTGCGAATTCGGAGCCACTGCCTACCAAT

>RXN00795-downstream
TAAGAATTGGTCGAACCACCAAA

>RXN00831-upstream
AGCTCCAAGAAAGTCAGTGCTGTGCATGGCTCGGTGCTGCTCATGCTTTTCGGTGTTTAC
ATGATGAGCATGTTCGCCTGATTTAGGTAGCCTGGTGGGA

>RXN00831
ATGAGTGCACTTGAGACATTGCAATGGCAGGACTGGTCAAGCGTCTTAATTGTGGTAGCT
CACCCAGATGATCCGGAGTATGGGCTTTCCGCGGCTGTTAAAGAATGGACAGACGCCGGG
GTGGAGGTGTCTTACCTGCTGCTCACCCACGGGGAGGCAGGTATCCAAGGTTTAGACCCT
AAAGAAACCGGGTCATTGCGCGCAGCGGAACAGCGGGCTGCATGTGATGTGGTAGGAGTT
AGAAATCTCACCATTTTGAATCACCCAGATTCCATGTTGGTGTACAATCTGGTACTGCGC
AAAGATATTGCTCGGGAAATCCGGATCCGTAAACCAAATGCTGTGGTGGTATCCAATTTT
GATGTAGAGGCCTACGGTGGTTTGAACCAGGCGGATCACCGCGTGGCGGGATTAGCCGCA
ATTGATGCGACCCGCGATGCCGCTAATCCGTGGGCGCAGCCAGAGCTGTTGCAGGAGGAT
CTGCAGCCGTGGGGAGCTGAAGTCATCATCATTGCCGGACACCCAGAGCCCACCCACACC
ATGGATCTGGCTAAAGATTCTGTTGATGCCGGAGTTGCATCCCTTCAAGCTCACAAGGAA
TACTTGGCCGCTCTTCCAGATCCCCCGAAGCCGGAGGAGTTCATTCCGGCGTTTCTCGAG
GTAGAGGGCGGTTACGCAGCGGCCTTCCGAGTTTTCGGACGG

>RXN00831-downstream
TAAGCAGGGCGATACGTGATAGG

>RXN00835-upstream
ACTGCACCAGCGCCAACGATCGCAATTTTCATACCTGCTATCTTGCCTGAGCACAGATAA
GATTTGTAAGCACTACCCCTTCTCTCTACAAAGGAGTCATCA

>RXN00835
ATGGCCGGTGGATTGGCAGCACTATTAGACGATGTCGCAGCAATTACTCGAGCGGCTGCA
GCCAGCCTCGATGATGTCACGGCGATGGCTGGAAAAACCAGCGTTAAAGCCGCAGGCGTG
GTTGTAGATGACACGGCAGTTACCCCGCAATATGTTCAAGGTGTCAAACCTGCACGCGAA
CTGCCCATGATTTGGCGGATCGCTAAGGGCTCTTTGGTAAACAAGATCATCATCATTTTG
CCCATCGCGTTGCTTCTTTCCGCGTTTGCTCCGTGGGCTCTCACACCAATTTTGATGCTG
GGCGGCTCCTACCTGTGCTTCGAAGGTGCAGAAAAGATCTGGCACTCCCTCCACAGGCGC
ATCAAAGGTGAACAGCACAGCACCGAACCCAAGTCGCAGGAAAGCCCAAAGTCAGAGGAT
CAGCTGGTCAAAAGTGCCATCACAACTGACCTCATCCTTTCCGCAGAGATCATGGTTATT
TCACTCAATCAGATTGCAGATCAAACTATCTGGATGCAGGCTGCGGTTCTTTTCGTCGTA
GGTATTGGCATCACCGCGCTCGTGTACGGCGTAGTCGGTGTTCTTGTGAAAATGGATGAC
GTCGGACTTACACTTTCAAAGCGTGACTCCGCAGGTATCCAGAAATTTGGCCGCGGCTTG
GTCAAAGCGATGCCCATCGTTCTTCAAGTTATTTCTGTTGTCGGCGTTTTTGCCATGCTG
TGGGTTGGTGGCCACATCATGGTCGTTGGAACTGAAGAGTTAGGATGGGAACTTCCCTAC
CACCTTGTTCACGGACTAGAGTCCTGGGCTAACGGTATCGGAGGCAGTGCTCTGGGATGG
GTTGGCAATACTTTCGGGTCACTTGTGTTCGGCCTCATTTGGGGCGCGATTATCACCGTT
GTGGTCAGTGTGATCAAGAAGTTCATTCCACAGCGTGCGCAAAACTCGTCTCAT

>RXN00835-downstream
TAGTGGAGAGTTGTTCGCTGTAA

>RXN00836-upstream
GGAGAGTTGTTCGCTGTAATTTCGCTGTACAGTTAATATGACTTTTTACTGTCTCAATCA
ATTCACAAGTTTGCACGAAATTTAAGGAAAGGAGTGCCCA

>RXN00836
ATGTATACCCATTCAACAGGCACTCCTCAGCTTGATTTCGACGGTGACATCTATCCCCTT
CACCTCTTCTTCTCTGCACAGACTGCCCAACATTTCGCTCTCGAGCGCGTCAATTGGCAT
GTCTTACGCGCTATTGTGAAACCTGAGCAAGGCGAACTCATCGTCGAAGCGCTTCTCGCA
CCAATAGAATCCGCAACAAAAATCGGTGTTTGGGTTCAAGATGAATTTCTCGGGGTGATT
GCAGAGTCCCAGTTCCTGTTGAATTCTCAATTGTCTCGAATTTTTGCCTCTGGCCACCTG
ATTTCCAGCCAACTACTTCTCACACCGAGTAAAGGATCTCTCGCTTCAGTTCTTCTTCCA
AACCTAAAATTCGGGCTCATCAGCAATGATCCTCCACGAGCTGATTCCCACCTCTTACCG
CTAGGCAGAATGTGGCGCGTTGAGCCCACCGTTCATGCTCTGTTTGAGGATTTCTCACTT
GGCTCCACGATTCTTTTTGGGCTGAGGCTTGATTTAGAAGCCCTAATTGTCTCCTATAAC
GGAATAGAATGTGGCATCTTAAACTTTGATGACGCCTCAGCACTAAGCTCTGCTGTGAAA
TTCTCAAATGCAAATGGTCTCACCCCCACGGTGCTCGGCCACGTAGTCCGGGAGAACGGT
GAAACATCCTTCGAGATTGACGTTCTCCCACTGGAGTTGTGGTCGAAGAAGCAGCATCGC
CTTGAGGTTTTAAAAATCCCTCGGTTGATACCTAAAGAGGCAGATTCCCAAAATTATGTG
AAGGCGACAGCGCTCCTTTCAGACGAGATTCTGCGACCACAAACGCTGTCCAAAAAGGCA
CTGTCTTTGTCGGACACCGCAGTTAAGTACAGCCCTCATGTTGCTTGTGGCGTGGGGATG
TTTAGTCTTTTCGCCGTTATTCCCTTTGACAAGTTGAGTGATCATAGTGCGATGCTGCTC
GCAGTCATTAGCTTGATGCTTTTTGTGCTGGCATTAGTAATTCTTTTCAAGAGAATTCAG
TCAACTAATACTCAGCGTTGGAACTTGGCCTCGTCAGTCGGATTACTCGCGACACTTCCG
ATTATCATATTCCTGGTTGCTGATACATTGATTCCTCAGGGCAGCCTGGAAAACCATGCT
CAACCCGACGTACAGGTAACAACGTTAGCTAACAGGCGGCCAAGTTCACCTACCTCACTG
GACTCACTAGGCGCACTGAATTCACCAAGTTCGCCGAATTCCCCGAGCTCATCAATGCTG
CAAAACTCTGAAATGTTCGCCTCACCACCGATCGCCTCTGGGCAGTCACCGGTTTCGACG
TTCCGCTCATGGCTAGATCGATCCATTCTGCCACTCACACGAGAAAATTCCGCTTCAGAA
AGCGCAGTGACAGCTCTTGGACCGTCGATAGTGCAGCCTGCATCTGAATCGATTACAACT
CCAGCTCAAACGTCGCAAAGTCGCCACGCAATTGACGATGGTGACGACAGTAAAACCTCA

ACGGGAAGACCAGCTCCCACTACTAACTCGCCGATCATTGCTCTTCCCCCAACGTGGATT
ATCGGGCCGGAAGATCCAGAATCCACCGACCCTACAGCACCAACCGAGCCCACCGAGCCA
AGCGAACCTGTCGCAACCGACGAACCCTCAGAGACCTCTGAACAAACTTCACCTCTCTTA
GCTCGCGACACCCCCGAACTGAACCGGAAACAACTG

>RXN00840-upstream
GCGATTAATGTGACAGGAGGAAAAGAAGTTAACTGAAGTTACTAATGTGACTAAAGTTGT
TCCCTCCGCATTGTCTCGTTGAAAGGTAAGTAAAACTCAA

>RXN00840
GTGACAAAGACACTCCCCCGACTGCTTACAGTCGCTGCCGCTCTAGCCATTGCACTCCCG
GCAACCCCGGTAGCATCGGCTGTCACACCAGTTGAACAAGCTTTCAACGCCTCATCGAAT
CTCTCCAGCGGTCTCCCCGTAGACCAATGGGGACGCCCCAACGAGCAGTTCCGCCAACAA
ATCGAACAGGCAGTAAACCAACCGTGGGTCCCGCAGGAAATCAAGAACATCGTTTCTCAG
GCCATGGGTTTTATCACCGGTGACGGCAGCGAAGGTGGGGACATTGAAATCCCCGACAAC
GCACCACGCATCGCGCAGTTCTTCTGGCCCACCCGATCAGAAAACTGCATCAACGGAAAT
TCTGCAGCCGTAGGATCTGCCTTCGCAGTTCCAGGACCAGCAGATCTCCCCCTCCCCGGC
GCAGGTGTCGGCCAAACCTCCTTCGTGTTCACCGCACTGGGAACTGGCCCCCTCGCAGAA
CAGCAAAGCACCGCAATGACTGTTCAATGGGCAAACTTAAGCAACTTCACCCATGGCACC
ACGACGTTGAGCAACACCGGAATCAACCCCGATGGCCCCTCAACGATTTCCGGTGTGGCA
GACACAGGACGCGGCATCATCGTCGCCTCCATGTCAGGCGGCCTCACCACATCCACCGAA
AACGGTTCAGCGAACTGTAATTTCATCCCGACTGCCGTCGTATTCGATGTGAGG

>RXN00840-downstream
TAAGAAAACAATGACTGATCTTC

>RXN00841-upstream
GCCTCCATGTCAGGCGGCCTCACCACATCCACCGAAAACGGTTCAGCGAACTGTAATTTC
ATCCCGACTGCCGTCGTATTCGATGTGAGGTAAGAAAACA

>RXN00841
ATGACTGATCTTCATCCCGTAAAGCAGGAAATTTTCAACACTGCTGAATCCATAAACACA
GATCCCAAGGGGTTTCTCCGCGAGGTAGACACCTTCAAAGTAACCGACTTCGGCCTGTAC
ATGGCTCGTGGTGCAAACCACCCCAAGTTCGGATACTTGGAAAGCTGGCTCCTCCCAGAA
CTTGGATTGCGTGCCAACATTTTCCACTTCCGCAAAGGCGTGGATGAACGTCAGGATTAC
TACATCGATGTCGCTGAAATTCGCGTCGAAGACAACATCTGGACCACCCGCGACCTCTAC
GTGGATCTCATCTCTGTCTGCGGAGAACCAGTAACAGTCATGGACATCGACGAACTAGCT
GCAGCAACCTCAGCAGGGCTTATCACTGCAGATGACGCTGAGCGCGCAATTGATGCCACC
TTGAATGCTGTTGAAGGAATCACCCGCCACGGCGACGATCCTATGCAGTGGCTGCGCTCC
AAGGGAATCGAACTCACCTGGGCTGACGCCAGCCAGGTAGAGCTCGTCCCTGCAGAG

>RXN00841-downstream
TAACTACTTCCTAACCGCTGCTT

RXN00846-upstream
CTGCGGGAGACTCGGGTAGAAGCGAAAAATAACGGTATCCTCGGGGCTGCGGATGGCTGG
CCTGGGGGGAATTTCAAGTGCTGCAAGTTGGAGGAAAAACG

>RXN00846
ATGTTGAAGAATGATCTGTCTGGTGCTCGAGTTGTAGCTGTGCATGCGCACCCTGACGAT
GAGGCGATTACCACCGGTGGTGTGCTTGCGGATCTTGCTGCTCGTGGCGCCGATGTCACG
GTAATTACCTGCACGTTGGGCGAGCAGGGTGAGGTTATCGGTGAGACATTCGCGCAGCTA
GTCAACGGTGATGCGGATCAGCTTGGCGGGTTTAGGATCCATGAGCTTTACGCCTCGCTG
GAGATTCTGGGCGTGCGTGGCATTCATCTGGGTGGCGCTGGCTGCTGGAGGGATTCCGGT
ATGGTTGGTGATCCTGCAAATGAGCATCCGCGTGCGTTTATTCACTCTGGTGACCGTGCA
GTGGAGCAATTGAAAGAACTTCTTGCGGAATTGAAGCCACATCTTTTGATCACCTATGGC
CCTGACGGCGGCTATGGGCACCCCGATCACATTCGTGCGCATGAAATCACCCACGCAGCA
GCCGGCGAGCAACGCATTCTGTGGGCTGTGAGCGACCGTGAGGAGCTCGAGGACGGTCTA

AAGGCAATCACTGGGCTTCCTGAAGGTTGGGGCAGGGGAGAGCTCTCTGCGGTCGATTCC
GTGGACCTCTCTGTTGAGCTGAACGATGAAGTGTATGCCACCAAGGTGGAATCCATGCGC
GCGCATGCGACACAATTGTGGATCGCTGACGGTTCCGTATCTCGCACCAACCCGGTTGCC
GCACACGCAGTGACACAGCAGGACAATGTGAAGGTGTGGGCGCTATCTAATTTGATTGCA
CAACCCATCATGCGCCACGAGCACTACCAACTCGGCGCCGGAACACCACTGCCTGAAGGT
GCAACTGGAGTGCTTGACGGACTGGAGTTC

>RXN00846-downstream
TGACACGGTTATGGCAGAATCTA

RXN00850-upstream
GGCAGTTGTGCCGGTATACGTGGCGTCATGGATAATGATCGCATAAATGAATACAGCGAA
ATTACCTGTTTCAGATATTTAGGAAGGCTCACTTTTCAAC

>RXN00850
ATGGCTAATCCATTCTCCAAGGCATGGAAGTACCTCATGGCGTTGTTCGACTCCAAGATT
GAGGAGAACGCGGATCCTAAGGTACAGATCCAGCAAGCCATCGAAGATGCTCAGCGCCAG
CATCAGGAGCTCTCCCAGCAGGCAGCAGCTGTTATTGGTAACCAGCGTCAGCTTGAAATG
CAGCTGAACCGCCGTCTGGCTGAAATTGAGAAGCTGCAGGGCAACACCCGCCAGGCTATC
CAGCTGGCTGACAAGGCTCGCGCTGACGGTGATGTCAAGAAGGCTACTGAGTACGAAAAC
GCCGCTGAGGCTTTCGCTGCACAGCTGGTTACTGCTGAGCAGTCCGTTGAAGATACCAAG
CAGCTCCACGACCAGGCTCTGCAGCAGGCTGATCAGGCTAAGAAGGCTGTGGAGCGTAAC
TCCATGGCTTTGCAGCAGAAGGTTGCTGAGCGCACCAAGCTTCTGAGCCAGCTGGAGCAG
GCGAAGATGCAGGAAAAGGTTTCCGAGTCCCTGAAGTCCATGGATTCTTTGACCTCCGGC
AGCACTCCTAACCTGGATCAAGTTCGTGAGAAGATTGAGCGTCGTTACGCTAACGCGCTT
GGCCAGGCTGAGCTTGCGTCCAACTCTGTTGAGGGCCGCATGGCTGAGGTTGAGCAGGCT
GGCGTTCAGATGGCTGGACACTCCCGCCTTGAGCAGATCCGCGCTGAGATGGCTGGTGGT
TCCCTGACCGCTGGTAACAAGCAGGAGTCCATTGAGGCTCCTGCAGCGGGCAACAACGTC
ACTGATGACGCAGTTGCACAGCGCATGCGTGAGCTGCGCGGCGAGGCT

>RXN00850-downstream
TAAACCTGCCACAGCAGACTAAA

>RXN00854-upstream
TTCATCCGCCCTGGAAGACGGTCATGACGGGGACCCTTCTTAGGGTCGCTGTCGGAGATT
GGACACGTAACTTCTGTGCTTGCGCTGTATTATCGTCCCC

>RXN00854
ATGCGTTTATCGGAGTTTCGGCAACTCATTGAAGATGAATTCGGAGAAGCCAAAGGGGAG
TGGATTGCACACTCGCATGTGATTGGTGCCCTCGGCGTCACTGCAGATGTTGCAGTAGAT
ACCGGGGTTGATCTGCGCGATGTATGGGAACAACTGTGCATTGATTTCAGTGTTCCCGAA
GAGCGACGACTTGGTAAAGATGAACCAGGGTTC

>RXN00854-downstream
TAGCTTGTTCGAGGGGGTTCGCA

>RXN00855-upstream
TAAAAACCTCTCGACGGACGAAGCGCCACAAAAGCAAGAGAAGAATATAAGTGAACCAAA
TTCCGTTTAGTGTACGTCTAGACGCCTAAACTTACCTGTT

>RXN00855
ATGACTTATTTTGCCGTGCTTTACACATACAACCCAGACAGCGAGAAAGTCGCTGAAGTT
CGTACCGTCCACCGCGAGTTCATTGCCAACCTTCATGCGGAGGGCAAAATCGTTGGCTCC
GGTCCTTTCGTGGACGGCGACGGTGGCGCGCTGATTGTCATCAAGTTGGAAGAAGGCTCC
AACCTTGTTGATGCTGAAACCCTGATGAACAATGATCCATTCCACGTAGAAAACGTGCTG
GACAACCGCGTCATCCGTAGCTGGAACCCTGTGACCAAAGATTTC

>RXN00855-downstream

TAGGCAACTTTTTCTTTAACAAT

>RXN00869-upstream
GCCAACACCGCGGGTGCGCTTGTGGCGTCCCGTCTTGAATGCTCCACCGCAATGCCTACT
ACCGATGAGGTGGAAGCCTCCCTCAACCAGAAAGTCTGAT

>RXN00869
ATGACTCCTCCGATTATCTCCCCAGAGAGCTTTGAAGCCCTAAGGCGGATGCGTGCGGCT
GAACCCACGATGGTGGCGGAACGTTTCAAGCAGCGCCGTAAGCGTGAACTGCTCGGTGAG
GACGGCAAGCTGTTTATCGTGGCTGCCGACCACCCAGCGCGCGGCGCACTTGCTGTTGGC
GACAATGAAACCGCCATGGCTAACCGCTATGAACTGCTCGAACGCATGGCTATCGCACTG
TCTCGCCCGGGTGTGGATGGTGTGCTGGGAACTCCAGACATCATTGATGATCTGGCGGCG
CTCGGACTGCTCGATGACAAGATCGTGGTTGGCTCCATGAACCGTGGTGGCCTGCGTGGC
GCTTCCTTTGAAATGGATGATCGCTACACCGGCTACAACGTGTCCTCCATGGTTGATCGT
GGCGTGGATTTCGCGAAAACCCTAGTGCGCATCAACTTGAGCGACGCCGGAACCGCCCCG
ACCTTGGAAGCCACCGCGCATGCAGTCAATGAGGCTGCAGCAGCACAGCTGCCCATCATG
CTCGAGCCGTTCATGAGTAACTGGGTAAACGGCAAGGTGGTCAATGATCTTTCCACCGAT
GCAGTTATCCAATCTGTCGCCATTGCTGCTGGTCTGGGCAATGATTCTTCCTATACCTGG
ATGAAGCTTCCAGTGGTGGAGGAGATGGAGCGCGTCATGGAATCCACCACCATGCCAACC
CTGTTGTTGGGCGGCGAAGGCGGCAACGATCCAGATGCCACCTTCGCATCCTGGGAGCAT
GCACTCACCCTGCCGGGTGTGCGTGGCCTGACCGTGGGACGCACTCTGCTGTATCCGCAA
GACGGCGATGTCGCCGCCGCTGTTGATACCGCAGCGCGACTTGTTCACACAGATATTCAA
CAATTCACTTCGCAGAGCATT

>RXN00869-downstream
TAAGGAATTTACACACATGTCTG

RXN00915-upstream
CTTGGCTGCAGGTCCACCATCAGCACAGGTCTTTGACATGAACGTAGCTCGCCGCGACGT
TTCTTCAGGACCTTCTCTACCTGGTGAGGGTGAGTTCTAA

>RXN00915
ATGTCCGCCGCCTATTCGCAGGACACCATTTTGACGGTGTTTCTGGGGAGGGGTCTGACC
GCTGAAGGGATCCGACAGACCCTAGAAGACTTCGCAGAAACCGGCCTAGTCCGCAACCTG
GTGTGGATTGATGCCGATAGTTTCCACGAGTCTTCATCTGAAGTCACCCACTTGGCAACC
AACCAAGACGGTCTTCCGGAGCTTCAGCGACGACCTTTCAATGAGTTGGTGTCCCGGTCA
CGAACCACCAAGCTTCACATCGGTGTCATCAACGTCATTGATGGCAGCGAAGGCATGCTT
CATGCAGAAGAACTCAACCCATTGGTTGGGATCATCGACAGTGTCTGTTCACACCACCAA
ATTCACCGATCCAACGTGATGATCGGTGCGGTGGCTGCCACACTTGATGAGGAACTTCCA
ATTCTTCGTGGTTATGTGAACCTGATGCTGGCACCTGAAGATAGCCACAGCCCAGGCACC
GCAACAGTGACCTACCGTCATGGTTTCAGCGATCACCGTTTACCCTGCACTGCGTGGCTA
ATATCGCCAGCTTGTACGGACTGTGGGAAGGCAGCACATCCACACCAATCGAACAGCTCG
TACCTGCGAAAGGTTCCAGCTTTCGTTTGG

>RXN00915-downstream
TGAGGTCTTTTTACAGGCGAATT

>RXN00917-upstream
TGCCGTGGAAGAAAGCGCTCTTTACTGCGACAGCCGTCCTATTGGTGTTTGCTGTTGTGT
GGTCGGCCTTGGATATTGCCCTGTGGGTAGGAAAGCAGTC

>RXN00917
ATGGTGAACACGTTGAACTCTAAAACCGTGAATGTACCCCGTTTTGCCAGAGGCGTTGTT
GCTGCAGCCACAGCGCTATTTTTTGGCGCTTTGGTAAGCCTCGCGCCTAGTGCGTTGGCG
CAGGAACCACCTGCAGTTGAGGCCGGAGCGTCAGGTTCTTTGAGCAACCTGGGTGCCTGC
ATCGCTGATAAAGGCACTCTTGATGTCATCATCATGATCGATGAGACAGAATCCTTGATC
CATGAAGCTCGTGACGGCGTGGTCAACGCCAATGAACCAGGCGCGGACGCACAGCACCAC
CGTGTTCCTGCAGCACAGAGCTTTGTGGATGAGCTTCTAGCCAAGCAAAGCGATGGTGAT
CTGAACACCCGCATCCGTGTTGCTGGTTTCGGCCAGACGTACAAATCTGGTGCCACTGAT
CCAGACAATTACGGAGCATGGACGCAACTAGATGCCTCCACCGTTGGCGGAGTACAAGAT

GAAATCTCCCGCTTCGCTGACCGCACCCAGGAGCAGTACACCAACTACGCCTCCGCGATT
GAGGGCGCTTACCAGGACTTCACTAGGTCCGGCTCTGAGGACGCCTGCCGCATGCTGGTG
ACCTTCACCGACGGCGCACTGACCGCTCAAGAAGGCGCCGATGTTGCAGAAGCAGCACTG
TGCGCGCCGGGTGGCGTCACCGATCGACTGCGCAGTGCTGGCATCACCCACATCGGCATC
GGTTTATCGGCACCTACCAACCCATCTGATTTCAGCCTGCTGCGCGGAACCACCGCAGGT
GGCGGAACATGTGGTGTCGAACCAGCTAACGGTGCATTCTTCCCAGCAGATAACGTGGGC
GGACTTTTCGCAGCATTCCGTGAAGCCCTTGCGATTGGTGGTGAAACAATTGGTGAAACC
CGAGCTGGTGATCCTTTCAGCTTCACCCTGGACAACTCGGTGAACTCTGTGCGTTTCACC
GCGATCGCCAAGGATGATCTCGGCCCGAACGCCCACTTGGTGCTCACCGCACCCAACGGC
GAAACGGTTGAGCTCAAAGATTCTGGAAGCAGCGTCGCCAACAGCACTGACGTGAGTTGG
GAAGCCGAAAGCAGCCCAGTAAAAATGGCTGATGGTTCCCTCAACCTGCAGCAAGGTGGG
GATTGGAAGGGTGTCTGGCAGATTCAGTTCCAAGGAATTGATCCTGCAGCGGTTGATGGA
CGCGTATTCAACTCAGTGGAGATCCAGCCTGACCTCCAGCTTGTGTTCAGTGGCGGTGAT
TCGACGTCAGGTGCACTTAACCTTCGCGATGATCAGCAGCTGAATATGCAGCTGGTGGGC
CGTGATGGTCAGCCACGCATCCTTGAGGGGTCCGCGCTGGTCGATCTTGGTTTCACCCGC
GCAGATACCGGCGAGTTCGCCCCTTTGGCTCAAGGAATTGATATTTCTGGCGGCGAATTA
AGCTTCCCGCTGGATACGATTTCGCAGCTCCCAGCCATCGGCACGGTGGAAGCGCGTACC
ACGATCACCACCGCAGGCGTCGATGATCTCCCCGGCACCACGTTGAGCCCAATTCTCAAC
ACCACGCGCATCACCATCACTCAGCGCGATATGCCTCAGCTGCCAGCGTCGGTTCGCTTC
ACAGCGGATGAGGACGTTGTTACCGTAGACATCCCCATCACCGGCCCCGGCAAGGTATGG
ATTGCACCGGGAACCCAGCTCAGCGGAGTGCTTCCAGACGGCGTGGACGGCATTGCAGCA
TCAAGTACTTTCGACAGCCCAGATAATGCTTTGGTGCTCGGACTGGATGAGCAGGGCACG
ATTCCTGTTGAACTAACCGTGAGCGATCTTCGTGACGGACTGGTCAACGGCTCGATTCCA
CTCCAGATCTCCAACGCTGAGGGCGCCAATGAAACCAGCGTGGATCTGCCGACAGAAGGC
ACGTTGAGCGTTCCCATTAACGCCTCCACTTTCGCATTGGCATTCATTTTGGCCCTTGTG
CTTTCCCTCCTGATTCCGCTGCTCATTTTGTATATTGTGCGTTTCCTCTCCGCAAAGGTT
CCGTCCTCTGCGATGAGTGGCGTGCGCATTCCAGTGGAATTCTCCGGTGAAGCTCTGCGC
TATGCGGGCAGCACTATGCCTGATCTCGCATCGCAAACCACCGCCACCAAGCAGGTCGTT
GTTCATGGAGACACCTTCAATGTGGAAGGCCACAAACTTAAAGTCCAGCGCTTCCAGCTG
AACCCGATTGCGTCTCCTGCAGTGATCGTGCAGACCGACCCGTCGATCAGCTTCGACGGC
AAACAAAAGGGCACACAAGCTAAACTCCCGCTGGCGGTCCAAGGCAGTTGGTTCCTCACT
GCAAGCGGCGCTGACCCTTCCAAGATGGAACTCATCGCCCTGACAAACCTGCCGCTCGAG
CAGGGCCAAATCGACCGCATGATCGCAGGTATCACCAGCAAAGCCCCTGATAGGGCACGC
GAACTACAAAAATTGCTTGACGACGCCGCGACCTCCCAGCCCGCAAAGGTTCCACCGCGC
GCCCCAGCCGCGCAGGGCCACGTCGAAAAGCAAGCTCCTAGTTTTGGCACTGGTTCCGGT
GGTGGTTTCGGCTCCAGCAATGGTGGAGGCTTTGGCTCCGGTAGCGGATCCAACGACACA
AATGGTGGATTTGGTTCCAGCGGCGGCTTCGGCGCGCGA

>RXN00917-downstream
TAACCTGTAACTTGCGATTAAAA

>RXN00921
CCTGCGGCAATCCTCTTGGACCATATCGTTCCGAACTTCAGCAGAGATCGGTCTTTGCCA
GACATCGAAGACTGGACGAGAAGCGATGAAGCTCAGCAGATCTTTGCAGGAATCATTGCG
GGTGCGTCTGTTCAAACTGGTAGAAGCCACTTCATGTGGGATCTTTTGCGGGCGTATTTT
GGAGTCGCTTTGATCGGCGACGAAGATACCTACAGGGCTTTTACTACTCTCACGGTCGAT
TCTGTTCTTAGTTTCGTGCAGTTAACTCTTCAAGAGGGCAGAACGGAAGACATTAGACGA
TTCGAGAAATATGGTGAGCAGATTGCCCGAGAGGATTTGCCGTCGATTCTCACCAATGCT
CGAGCAGTACAGCAATATCTCGGCTATATCGACCAAGATATCATCAATAAGAAAGTGTCC
CGGTCTAGGGATGTTAACCAGATTTTTACTGAGATGGCGCGCGCTATCATCAGAGCAATT
AGCCGGAATAATATTGGAAAGGACATGCGGTCA

>RXN00921-downstream
TGAACGTGATTCGACTGGATTCC

>RXN00943-upstream
TAGGTACGATCGGACGAGGAGAAAAAATCTGAAAACAATCCAGTGGCCCACCTCGGCTTA
TAAAACTGGACAACAGTATTTTGATTGGAGCATCACCATA

>RXN00943

ATGATCCGCAAACTTGCTCGACCAATGCTTGCATCGGTCTACGTCGCAGATGGCGCAGAA
ACAGTATTGAACACCAGCGCACACGTCGAAGGCACTCAGGTAGTTCTGGATCGTATCCGT
TATGTGCTGCCCCGTAAGTACGCAAAGCGCATTTCCAGAGATCCAGAATTGGTCACCCGC
GTCATTGGCGGCACCAAAGTCGGTGCGGGTTCTTTGCTAGCTATTGGTCGTGCACCACGC
ACCTCTGCAGCTACCCTCGCAATCCTGACTATCCCTAACATCCTGGCTCGCAATGCGTTC
TGGGAAACCCAGGATGCGGATGAAAAGCGTAACCGCCGCAACGGTTTCCTCACCAACATT
GCCCTGCTTGGTGGCCTGTTTATCACTTCTGTTGATACTGAGGGCAAGCCTGGCGTGAAG
TGGCGTGCAACCAATGCTACAAAGCGTGGCAAGAAGCAGCTGCAGCAGGCACTTCCAACC
AAATCTGAGACTGAAAAGTTCGGTGAGAAGGCCTCTGATTGGTTCAACGATACTTCTGAC
AAGGTCACCGAGTACGCGTACACCGCTCAGGATTTTGTCGGTGAGAACAAGGATGACTGG
ATCAAGTCCGCAACCGAGACTGCTCACAAGGTCGCTGATACTGTGAGCGATTACGCTCAC
AAGGCTACCTCTTACCTTGAGGAGAACAGCGGTGACTGGCTTGAGGCTGCGCAGGCTAAC
GCCAAGACTGCTCGTAAGTCTGCAGTGAAGGCTGCCGGCAAGGCTCAGGAAAAGGCTAAC
TTTGCTCTTCAGGTCGCAGAGGAAACCTCTGGTCGCGCCAACAAGAAGGCAACTAAGAGC
TACGACAAGCTTCAGAAGCAGGCTGATAAGGCCATCGATCGTGCACAGAAGAAGCTGAAG
GGCATCGAACTT

>RXN00943-downstream
TAAGTAACTTCTTCCTGATTGAG

>RXN00945-upstream
TCACAGTACCACCCACAAGCCACAAGGAGGGTATGGAGGTGGGCGTCTAAAGCCAAATTT
TTCCCGGTGTTTGAGGCGATTGCACCGTACACTAATGTGC

>RXN00945
ATGCTTGAACGCCTCAAACGCCTAGATCCGCTCATTGTCCTCATTGTGCTGGCTGTCATT
GTGGCGATCATCATTCCAGTTCGCGGGGTTGCTGCGGATTGGTTTGATGTCGCCGTCAAG
ATTGCCATTGCGCTGCTGTTTTTTCTTTATGGTGCCCGCCTATCCACCCAAGAGGCGCTG
AATGGTCTGAAGCACTGGAGGCTTCACCTGACTATTTTGGCGATCACTTTCGGAATATTC
CCACTTATCGGCATTGGGCTCGAGCCGATGACTGCATTTGTGTCGGAAGATATTTATCGG
GGAATTTTGTTCCTCACGCTCGTTCCGTCCACCGTGCAGTCATCGGTGGCGTTTACCTCG
ATCGCTAAAGGCAACGTAGCTGGTGCGATTGTGTCGGCATCGCTCTCCAACCTTGCGGGT
GTTTTCCTCACTCCGCTGCTGGTCATGCTCATCATGTCTGCGGGCGGGGGAGTTCACGTG
GATTCCCAGGTCTTCCTCGACATTGCGATTCAGCTTCTGCTGCCGTTCATCCTCGGCCAG
GTATGTAGGCGTTGGGTGAAGAATTTTGCGGCCAACAAAGCAACAAAAATCGTGGACCGC
GGCTCGATCGCGATGGTCGTGTACTCCGCGTTTTCTGCCGGCATGGTGGCTGGCATTTGG
TCCACTGTGAGCGTTCTAGAGATTATCTACCTCATTGTTTTCGCTATTCTGCTGGTGATG
GCCATGCTGTGGTTCACGCTGTTCATGGCTACACGCCTTGGATTTAACCGGGCAGATTCC
ATCGCTATTCAGTTCTGCGGAACCAAGAAATCCCTGGCCACAGGCCTCCCAATGGCGGCA
GTCATCTTCGGTGGCGCCAATATCGGCCTGCTCATCTTGCCGTTGATGATCTTCCACCAA
GTCCAGCTGATGATTTGTGCATGGCTTGCAGCTCGTTATGGTCGTGATGCGCAGGAACAG
AAAGCCAACGCC

>RXN00945-downstream
TAAAAGTCCTCAGTAGCTAGCCA

>RXN00946-upstream
GGGCCGGTGTGAATAAAACACCTTCCCCAAATAGACAGCATGGTCTAGATTAGCTTGAAA
CGAAAGCGTACATTCGCAGCAACTAACGGAAAGCACACTC

>RXN00946
ATGACTCACACTCTGCAGGCAACTAATCCCCTTGATCAAACCGCTTGGCACGCTTGGCAT
TTCTCCCGAAACAAAGAGGCCATCAGCCGCACCGGCGCCACCAGCCTGAGTGCCACAGAG
TGGATTAGCGCCACCACACTCAAGGACGCGCACACTTTTCCTTCACTTCCCGGGCGATGG
TATAAACGAGGCGGCGGGGTAGTGGGAGCACATTTACCACCAGCTTTCGCAACAACTGGA
ACGGTGCAACTGCGCCCCGGTGAGCTCTTGATAGCGGAAGATTTCACCCTCACCGTCATT
GAACGGCTTGGACAGTTTGCACTTCAGGTTTTTGATGCACGCAATCCGAAGCGTTTTGAA
TTCCACTCCATCGCAGCTTTCCCACCGTCCGAGGAATGGCGGATTGAGGCTCGCTTCTTC
CCGGAACCTGACACTGTTAACACCGCTGCAGCTGATGGAGTTATCGTTGCCACGCCTACT

GCGGGTTGGGTGCACTTTTTGAAGGGCCGTCTGGATTACCGTCTTCGTGTAACCGTTCAG
AAAAATAATCTACGGGCACTATTTAGCGACAATTCCTCGACGTTGGGCGTTTATCAGCAT
CGTTTTGTCGACATCCCACGCCCTGATGCCGAGGGAAACACCATCATTGATTTCAACCGC
GCTTATCTTCCCCCAAAGGCATTGAACCGAAAGTTCCTGTGCCCATCGCCCAGCCTGAAC
AACCACCTCAATCTCACCGTGGAGGCAGGGGAGAAGTGGGTGGTTGCTGGAGGA

>RXN00946-downstream
TAATACTTGCTAACCGTCCTAAA

>RXN00953-upstream
CTTGCATTCCCCA

>RXN00953
ATGGCGCCACCAACGGTAGGCAACTACATCATGCAGTCCTTCACTCAAGGTCTGCAGTTC
GGCGTTGCAGTTGCCGTGATTCTCTTTGGTGTCCGCACCATTCTTGGTGAACTGGTCCCC
GCATTCCAAGGTATTGCTGCGAAGGTTGTTCCCGGAGCTATCCCCGCATTGGATGCACCG
ATCGTGTTCCCCTACGCGCAGAACGCCGTTCTCATTGGTTTCTTGTCTTCCTTCGTCGGT
GGCTTGGTTGGCCTGACTGTTCTTGCATCGTGGCTGAACCCAGCTTTTGGTGTCGCGTTG
ATTCTGCCTGGTTTGGTCCCCCACTTCTTCACTGGTGGCGCGGCGGGCGTTTACGGTAAT
GCCACGGGTGGTCGTCGAGGAGCAGTATTTGGCGCCTTTGCCAACGGTCTTCTGATTACC
TTCCTCCCTGCTTTCCTGCTTGGTGTGCTTGGTTCCTTCGGGTCAGAGAACACCACTTTC
GGTGATGCGGACTTTGGTTGGTTCGGAATCGTTGTTGGTTCTGCAGCCAAGGTGGAAGGT
GCTGGCGGGCTCATCTTGTTGCTCATCATCGCAGCGGTTCTTCTGGGTGGCGCGATGGTC
TTCCAGAAGCGCGTCGTGAATGGGCACTGGGATCCAGCTCCCAACCGTGAGCGCGTGGAG
AAGGCGGAAGCTGATGCCACTCCAACGGCTGGGGCTCGGACCTACCCTAAGATTGCTCCT
CCGGCGGGCGCTCCTACCCCACCGGCTCGAAGC

>RXN00953-downstream
TAAGATCTCCAAAACCCTGAGAT

>RXN00959-upstream
TTTGGAGGCGGAGCATCATACCTTTTAATGTCAGGATCGTGCAGTGAAGAATTCAGGATG
AATTACTCGCTGGAATATTGGTGGGGATAGAGTTGTTGTT

>RXN00959
ATGACGGTGATCGGAATTATTCTTGGCAGCCTTTTTGGCGTTCTTGCAGTCCTTCTCATC
GTGGTTGGTGCTTTGGGGTGGGCGGCTAAGCTCCCTGGCAACCCGGTTGTGGGCATTCGT
GTCCCTGAGGTGCGTAAATCCCAAGAATTGTGGGATATGGCGCACCGTGTCGCTGGCCCG
TTGTGGGTGCTGTCGGGAGTTTCCTTTGTTATTGCATCGCTAGTTGCGTTTGTTGCTTCT
GGTTGGATGTGGCTTGTTGTGGCGTTGGGTGTTGAGGCTGCCATCGCGTTCATTGGTATG
GGTGCGGGTATGGCTGCACATACTGTTGCGATGGTTGACGCGAAGCGCATTCGCGAAACC
CCGCAGGCGCCTGTTTCCGCTGAAATTGAAGAGGCCGGTGGTGTGACTATTACCTCTGCC
GATTATCAACAAGACTCCGCTGAATGCCCCCAAGAT

>RXN00959-downstream
TGACTTGGATGCAGTGCGTAGAG

>RXN00963-upstream
CTGGCTCTGACGGCGTCGACTTGTTCTGCTTCTCTGATACACCAATTTTCGAGGCCCTTA
ACCTCGCACGTACTTTTACTCCGGAAGGAATCTAGAACTT

>RXN00963
ATGCGTCTTGCAACAATCCGCACCAACGGCACCACCATTGCTGCTCGTGTTGAATCTGAA
AACACCGCTACCACCATCGAGGGCTTTGCCAACGTCGGTGAATTACTCCAGGAATCCAAC
TGGCGCGAGCTGGCAGAAAACGCTGCTGGTGAGGCTGTGACCTTTGAAAACAAGGAGCTA
GATGCAGTAGTTCCAGCACCTAAGAAGATTGTGTGCGTCGGCCTTAACTACGCCAACCAC
ATTAAAGAAATGGGCCGCGACCTCCCTGATACCCCAACCCTTTTTGTTAAGTTCCCTGAC
GCGCTCATCGGACCTTTCGATGATGTTGTCGTTCCAGAGTGGGCTAACAAGGCTCTCGAC
TGGGAAGGCGAGATGGCAGTTATCATTGGCAAGCGCGCACGCCGTGTCAAGCAGGCCGAT

GCTGCTGAGTACATCGCTGGCTACGCAGTGATGAACGATTACACCACCCGCGATTTCCAG
TACGCAGCACCTGCAAAGACTCCACAGTGGCACCAGGGCAAGTCTTTGGAAAAGTCCGCT
GGCTTCGGGCCTTGGATGACTACCCCAGATTCTTTTGAGTTCGGCGGCGAGCTGGCAACC
TACCTCGAGGGCGAGAAGGTACAGTCCACCCCTACCAATGACCTGGTCTTTAGCCCAGAA
AAGCTCATCGAATACATCACCCACATCTACCCATTGGATGCTGGCGACGTCATTGTCACC
GGTACCCCAGGCGGCGTTGGCCACGCACGTAACCCACAGCGCTACATCGGTGACGGCGAA
ACCGTAAAGGTTGAGATTGCGGGCCTCGGCTTCATTGAAAACAAGACGGTGTTTGAA

>RXN00963-downstream
TAAATGACAACTTTCCACGATCT

>RXN00971
AAAGCACTTTCCATCGGAACCCAGTGGGCACAAGTCATGGGCATTAACCACGCCGAAGCC
GAAGAACTCGACGAAGCCCTCTCCCCGCTCATTAACCGCCTCCGCGAAATGGGCTTTGAC
CCCACCGAAACCGAAGAAGCAAACTCCCTCGCTCTACACAGCTGCCCATTTGTGGTCAAC
GACAAACGCCCATCAGCCTTCGTCTGCGCCATCCACGCCGGATTCATCCAAGAAAGCCTC
GGTGAAAACAACCGCATCCAGCTGGAACTCAAACCACTCAACGCGCCGGGCACCTGTAAG
GTTCACGTGTTCAGCGAA

>RXN00971-downstream
TAATTGCTGCACTAATAAGGCCC

>RXN00991-upstream
ACTTCAAGGAAAGACGGTCCCAAGAGCTAAAACTCCCCCACGGCACGCGAAGCTGAACAG
GCTTTCACCGCTTCTAAGGGCAACAGCTTAAACCACGCTA

>RXN00991
ATGGACATACTCATAAGCATCCTCTCACTGCTAGGCTTCGTGCTTCTTACCGCGAGCACC
GGACTATTCGTGGCCATTGAGTTCGCACTCACCGGCTTAGAAAAATCCACTGTAGAAACA
CATGTGAAGCAAAAAGGCGACAGCAGCGCCCGCGCAGTGCAGAGGGATCATCAAAATCTG
TCGTTCGTGCTCTCTGGTGCCCAGCTGGGCATCACGATCACGACACTTGCCACAGGCTTC
CTCGCAGAGCCGGTTTTGGCCAAATTCTTCACCCCAGCACTTGAGCTGGTGGGATTAAAT
GAATCAGCAAGCTCCGCAGTAGCCCTCATCATCGCACTGTTGGTGGCAACTACCCTCTCC
ATGGTTTTTGGTGAGTTGGTTCCCAAAAACTGGGCGATCACCAACCCGTTGGGCGTGGCA
CGTTTTGTTGTCCACCCTGTCAATTGGTTCAACATGGTTCTCAAGCCGTTTATTAACGGC
ATGAACAAGTCTGCAAACTTTATTGTCCGCAAACTTGGTATTGAACCAGCCGAAGAGCTT
GCCTCTGCCCGTTCCTCCCAAGAGCTCACCGCCTTGGTACGCAGCTCCGCGGAAAGCGGC
GGACTGGATCAAAACACCGCAGCGGTGATCAACCGATCCCTGCAGTTCGGTGACGCCACC
GCTGATGAATTCATGACACCTCGCTCCACCATTGAATCATTGCGTGCCACAGACACCGTC
AATGATTTGATCGAGCTTGCCCTGGAAACGGGTCACTCCCGCTTCCCAGTCACCGAAGGC
GACTTGGATGAAACCATCGGCATGGTCCACATCAAGGACGCATTCTCTGTAGTGCAGGCA
GAACGCGCCACCACCATGGTGCGCGATCTAGCCCGCAAAATTCCTGTGGTACCAGCCAGC
CTTGACGGCGACTCTGTCCTCAACGCTGTCCGCTCCGCCGGCTCCCAAGTTATTTTGGTT
GCCGATGAATACGGCGGAACCGCAGGCATGGTCACCATCGAAGACGTCGTGGAGGAAATC
CTCGGCGAAATCCACGATGAGCACGACGACTCCGACGCCGAACGCGATTTCCAACAATTC
GGCGCCAGCTGGGAAGTCTCCGGCCTGGTCCGCATCGATGAACTCGAAAAACGCGTCGGG
TACGTCTCCCCTGACGGCCCCTACGAAACCCTCGGCGGCTTGATCATGTACACAGTCGGC
GCCATTCCTCGCGTCGGCGATGTCGCCCTACTCCCACTGACCGATACCCCAACCATGGAT
GAATTCGAATCCGGCTTCTCCGGACGCTGGATCGCACGAGTAACGGTCATGGAAGATCGA
CGCATCGACAAAGCCGTTCTCACCCCCATCACCCATGAAGAAGCAAAGGAGTACGAAAAG

>RXN00991-downstream
TGAGTATTTGGGCAACTGTCCTT

>RXN01004-upstream
CCGGACGCTGGATCGCACGAGTAACGGTCATGGAAGATCGACGCATCGACAAAGCCGTTC
TCACCCCCATCACCCATGAAGAAGCAAAGGAGTACGAAAA

>RXN01004

GTGAGTATTTGGGCAACTGTCCTTCTAATTATCGTCCTTCTTTCCGCCAACGCCTTCTTC
GTGGCCGCGGAGTTCGCACTGATTTCCTCGCGCCGGGACCGCCTGGATTCCCTGGTATCC
CAGGGTAAAAAGGGAGCTGAAAAGGTTCTCTACGCAACCGAGCACCTCTCCATCATGTTG
GCGGGCGCTCAGTTCGGTATTACGGTCTGTTCTCTGATTCTGGGTAAAGTCGCAGAACCT
GCGATCGCCCACTTCATTGAGGTGCCTTTCACCTCCTGGGGGTGTTCCAAATGATTTGATC
CACCCAATTTCCTTCGTCATCGCACTGGCGATCATCACCTGGTTGCACATTCTCTTTGGT
GAAATGGTGCCAAAGAACATCGCTATTGCTGGCCCTGAAACCTTAGGCATGTGGCTTGCT
CCAGTGCTCATTGCGTTTGTGAAGATTACCCGCCCGTTGATCGAGTTCATGAACTGGATC
GCCCGTCTGACCCTTCGCGCCTTTGGTGTGGAGCAAAAAAACGAGCTGGATTCCACCGTG
GACCCAGAGCAGCTGGCATCAATGATTTCCGAGTCCCGTTCCGAAGGCCTCCTTGATGCT
GAAGAGCACGCCCGCCTGTCCAAGGCGCTGCGCTCTGAGCAGCGTTCCATCAAGGAACTG
GTGATTAAGGATGAGGACGTGCGCACGCTGGCGTTCGGTAAATCTGGCCCGACCTTGCAC
CAGTTGGAGGAAGCAGTCCGCGAGACCGGTTTCTCCCGCTTCCCTGTCACCGGCCGCGAT
GGATCCTACTTGGGTTATATCCACATCAAGGATATTTTGCCTCGTCTGGCTGATCCTGAG
ATGGATCCCTCCGAGACCATTCCGCGTTCTGCACTGCGCCCTTTGAGCAATGTGGATGCC
GACGGCCTCATGGATGACGTCTTGGATTTTATGCACTACCGCTCCGCGCACATGGCTCAG
GTTCGCCTCAAAGGTGAGCTTCTCGGCGTGATTACGCTGGAGGATCTCATCGAAGAATAC
GTGGGCACCGTCAACGATTGGACTCACGAAAGCTCCGACGAC

>RXN01004-downstream
TAGAAATAGTAACTGTGTTGGAC

>RXN01016-upstream
TGCCCGTCGAGGTGAACGCCCAAGAATAGTTCTCTTTCGTCGACTTCTCACGTTGATACC
GCTCGGCATCATCCACCAAATTCTCCAGCCGGGTGAAGCA

>RXN01016
TTGTTGCCGTATGCAATAGTCGGCCTGGTCATTTTGCTGCCATCCTCCTGGTTGCCTCGT
TGGGCTGTCGCAGTCCTTGGCGAAGTGTCGCTTGTGCCAGCGGTGGTTTTCGGTGGCGGG
TTCCTGCTTATCCCCTCAATGTTCCTGATCGGTTCAGCGCTCGTTAGGTATGGAGTAGTC
GATCGGGCAGAGAACGCACCGCGGGCTATGGGAGTCTTTTTCGCCGTAAGCGCAGCAATC
GCTATACCTACGCTGATCATCCAGGCACGTGACATCACTTCTTCAGGCTTCTCGATCGTT
TCCACAGTGGCGGGACTCGCGCTTGGCGGCGTCTACATTTCTTTAGTGTTGCTGGCCTTG
CATACACCGATTCGCGGTGCACTCGCTGCAGTTTTCGCACCTTTAGGGCGTATGGCGCTA
ACCAACTACATTGGTGCAACGATCCTCATGCTCATTGGCGGGCTAATCGTGGATCTTCCA
CACAGCACATCATGGACAGCTACGGTGCTCCTAGCTGCGGGTATTCTCATTATTCAAGAG
CTACTTTCTGCTTTATGGTTGCGCCACTACACACAGGGGCCACTTGGGTATCTATGGCGT
TGGGTGACTTGGGGAAGCCGTTCCCCCTTCCTTACCCGTTCCGCATCA

>RXN01016-downstream
TGACAGGTACGGAAGTGTCCTAC

>RXN01023-upstream
AAGCGAATCCGGGAATGAAAGTGAGTGCGCCAAAGTCAACTCCTTGGTTCAAGTGTCAGT
ATTTTTCTAGTCTATCGCCCCACAGGTAGGCTCAGGACAC

>RXN01023
ATGAGTGCCGTGAACAGTGCTGGTCGCCCAGCCAACGGGGGAATTAACAAAACCCCCATG
ATTATTGCCCTAGTGTTATCTATTGTGTTGGTTTTGGCGGTGCTGTTCGGCGCCCGAGTC
CTCCTTGGCCCCGCCGGCCAGCAACAGATAGCCATGAGTGGGCTTCCCGCCCCAGACGCA
GAATCTGCTGAGTGCGCCGCATTACTCGAGGATCTCCCCGGCGAGGCCTTCGGGCACACC
CGTGCAGAAATCATGGATCCTGTTCCACCGGGCGCTGCCGCCTGGTCCACCTCAGACCTC
GAGCGTGTGACGCTGCGTTGTGGCGTCGATATGCCATTCCAGTACACCGCGCTCGCCAAC
ACCGTCGACGTCGACGGCACCACCTGGCTACCTGTCTCCGACATGACCCCCGGCTCCTCC
CTGGAGACCTGGTACTCCGTCAACCGCTTCCCCGTCGTCGCCATCACCGCCGATGACATC
AGCACCGACAGCGCCGACAACCCCGTCGCCCCCTTCAGCAGCGCCGTCGACAAGCTAGAA
AAGCGCGACGGCCAGCCCTTCGACGCCCCACTTACCGGCTTGAGCTCAGCCGGCACCACA
TGCACTTCGCTTTTCGACGCCCTCCCCCGCCAACTCGAAGTCGGCGGCGACGACGGCACA
ACGTACGAACGCATCGAGGAGGACCGCATGCAGGCCGCCGGATACTCCGACGACGCAGTC
GCGTGGGACACGCCGGGATTAGAACCCATTGTGATCCGTTGCGGCGTGGAGCCTTCTGAG

AACTACGCAGCCGGTGCCATGTTGCAGCAGATCGATGACATCCCGTGGTTCGAGGACACC
ATTTTGGCCTCCGGTACCACCTCGTCTACCTGGTATGCCCTTGGACGCGAGATCGACATC
GCCGTGTCTCTGCCTCAGGCTGCTTCCTCTTCCCTGATTACTATCTCCGGTTTCATTGAA
GACACGGTTCCTGCGGAA

>RXN01023-downstream
TAAGACATAAAAAATCGCCCCAC

>RXN01028-upstream
CGCAAGCAGCTGCACTATATTCAGGCATTTTACCGTGCCTGGGACCCATCAACGCCGCTT
CAATGACGCTGACCCAGCGGTGACCCATCCGCATCTCACA

>RXN01028
GTGATCTACCCACCGCTCACCCCTGCATCCGAAGAGAAATTCAACAAGATCACCTCAGTC
GCTGCTGTGAGCAAGCGCCCAACCACCCTGCCGTATTTCCGTGCAGATGGTTCACCTACT
CGTGGCTTTGCTAACTTCTCCACAGGAGGTATTCACGGTGCGGAATACAACGAAGATCGT
TTTGACCATGATCAAGATCTACACACAGTGGCAACCCGTGAATTCTTCGCCATTCTTGAT
GCGACATTAGCGGCTCTCTACGCAGCCCACCAAGCCGAACCTGAATCGGCGGACTACCAG
ATTGCACAAGACGCACTCGCCTGGGCAAAGAATGTACTTAGCGATCAAAAACTCATCGCT
AAGTCGCCTCAGTTATACAACCCCGAAACCGGGGTCACCTATGAGTGGGAGTTTGTCGCT
CAAGCAGCATGGTGGATTCGCAACAAACCGGTTGAGGTTATTTTACCAACAGGTGAATCA
ATGACCGTAAAACACAAATCTGTATTGGCATCTGCGTCCTACCCACTCCGAGACAACGTG
GCGTACTGGCGTAGCGAACCCAAAACACCACAGCTGTTTCCCGTAGCAAAATCTGGTGGT
TCCTCGCTTGAGAAGAAGTACAACTACACCTCTGTGGGTACTGCTATTCACGAGGACTTT
AGCAGTTACTATCCGCTCTTGCTCACCAATATGGCTGCATTTACCAATGCTGACTTAGGT
ATTGATGAGAAAACCGGGCGCCCTCGTGACCGCTACCGTGAAATCTACGAACAAAAAGAG
ATCTATGGCGCACAGCGCAAAGACCCCTCCATTGATGAAGAAACAAAGCAACGTCTAGGG
ATTTTGCGCGAAGGTACCAAGTTGATTCTTAACTCGGCCACCGGTGCTGCTGATGCTGGT
CACGACACCCCGATCCTCATGAACAATCGCGTTATTGCCATGAGGATTATTGGGCAGCTA
TTTTCTTGGAGAATTGGGCAAGCTCAATCACTGGCTGGTGCAACGATTATTTCCACTAAC
ACTGATGGCCTGTATTCCGTACTCGATATGGGGACTAACCAGCGCGTTCTTGATGAACAC
GCTACAGCCATCGGTGTGCAAATTGAGCCTGAAGAACTGGATATTGTCTCCAAGGATTCC
AACTCACGTGCCGAATTTCTCGGCAATGGCTACATCAATGCGGCCGGTGACTTGGCGTGT
TGGGATGGACCCAACTCTCGGAACTCACTAGATCACCCGGCCTTTGTTGACCATGTGCTG
GTGAAGTATTTCCAGCTCGTCGTCAACAACACTGTGCCAGAGATTCCAGAAACACCTGAG
CTTGAGGGTGTACCGCTGGCTCTTGATCAACCCATGAACCGCCACGAAGTCTCGAAGATT
GTCGCCACTATGCACAAGGAATTCGAGCCGAAAAAGCTGCTGTCGTTTTACCAAAACATT
TTGGCCTCTTCACGCGGTTCTAATACCTTCCTATTCTCTGTCCCCTATATCCCTGCAACA
GAAGGAGAAGAAACCCACCCTGCAACAGATACCAGCACTATTGCGACACCAACCTTGAGC
TTTGATGCTTATGGTAATAAGGCCGAGGTCATGCCGACTCAATCCACTGTGGATAAGCGC
GTGCCCTCTTTGCTGCAGTATTACACGCGTACATTCCATGTGCGACAAGATACGCAGCAG
GCTGTCTTTGATGTTATTGGCGCCAACCCCGTGCTCATCGCCGCAGCAAAAGCTGCATCC
ATATCACCGGCTTCTGCTGATTCACGTAGAAAGAAGGGCCTGGCCTCCACCAACGCTGAC
CCAGTAGCCAAGCATGTACTAGAAATTGCAGGAGCTGATGTGGAATCGCTGCGCCATGAA
AAGGATCTCAAGGTCACCAAGCACACTGGCCAAGACCCAGCACTGCCTGTCGTGGTCTTT
AACCAAACCATTTGGCATAACCCCAACGACGATGTGATTAATGCATTACTGGGCGCTATT
GACCAGGATGCCTACATTGACATGGCGATCTCGTCCTACAACAAGTCCTGGCACAACATT
ATCCCGGCT

>RXN01028-downstream
TAACTACCGCTGGGTAGACCCCT

>RXN01069-upstream
TCCTAAGCTCTCTTGAGTACCTGAGACCTTCTCAGCAAAACACAAAGTGCCTTCACCCAA
CCTGGGGTGGAGGCACTTTCTCATTGCTAAGGTGTGCATC

>RXN01069
GTGAACGATTTACCGAACCTACCAAAGCTGCCCTTCAACTGGACATGGGTGCTGGCAACT
GTTGCCACGACAGTGGTGTTGGCGGGTATTGGTTTGTATGTGTATTACCCGTCGTTGCCA

GATCCTATGCCGGTGCATTGGAATGGATCCGGGGAGGCGGATAATTGGACGCCTAAATCG
GTGGGTTCGTTTCTTTCACTGATTTTGATAGGGCCAGGCATTATTTTGCTGACCCTGTCG
GGTATGCAGGCGTTGCTGACCATGCAGTCTGGAGTGATCACGCAACGCGGTGGGGCGAAA
TCGGCGAATGAAGCGCACCGGCAGTGGGAAACCTACAAGGCAACAAGCATGCACATGGGT
TGGTACATGTTTGTGCTCAACGCTTTGATTTTGGTGATGATCCTCAATGAGTTCCGCCCA
AACCCTCTGCCTGGTGGATTTATCATCGGGCTTATTGGAATTATTGCTGCCACGATTGTC
CTGTTGGTTCTGATTGGAAAAACAACCACGAGTTTGGCAAAGAAATACCCCATGCCTGAC
CAAGATGGAAAGACGTGGGGGATTTTCTACAACGATCCGGACGATAATCGGATCTTAGTG
GACACCGGGATGGGGATGAATTACACGTTTAACATTGCCCATACGTGGGGCAAGATCTTC
GCGGTTTTGATCTTCGCGGTGCCAGTACTCATCGTTTTATTAACCGTTCTCCTT

>RXN01069-downstream
TAACCTCGATCCACCGATGTGCC

>RXN01071-upstream
CACCTGAATTGGCTGAGGGAGAGGCACCGACTGGCACCGAAGAGGTGCTTGCCTCGAAGG
CGGGCGCTGAGGCGAATGGCCTGGAGTAGGGGACCAGATC

>RXN01071
TTGGTCGTGGACTCCAGTGGCCGCTACAACGTCACCATCACAGGCCTGACCACCACTGAG
ACGGATTCGGCCACCGCGCTGAACCTGCAGATGTCGGAAGCTGGCTACCTGGAGCGTTAC
ACCGACGGGGCTACCGTCCCCAGCGTCATGCTGTCGGCTGCAGATGGCACCACGCCTCAA
GAGCTTGTCGACGCCCTCGCTGCCGAACTTGGATCGAACTTTGATGTAGAAACCGGCGAA
GCGCTAGTCGAGCAGGCTACAGGAATGATCACGCAGGCCTTGAGCTTCGTGCAGTACTTC
CTCGTTGCCTTCGGTCTCATTGCACTGCTGGTTGGTACCTTCATCATCGCGAATACCTTC
TCCATGATTGTGGCTCAGCGCATGCGTGAGTTCGCTCTCCTGCGAGCCCTGGGTGCGGCG
CCAGGACAGATCACTCGCTCTGTGGTGCTGGAAGCAACCATCGTTGGCCTCTTCGGCTCT
GCTCTTGGTGTGCTGGGTGGTATGGGCCTCGTAGCGATCATTTCAGCTGTCCTCAATAAC
CTGGGCATGCCGATGGGATCCAGCGTTGGCTTGACTCCTTCTGCAGTGGTTACCGCGCTC
GTATTGGGCACCGTTGTCACCATTGTGAGCGCGTGGGCTCCGGCTCGTCGTGCAGGTGAG
GTTAAGCCTGTTGAAGCGATGCGCAACATGGAAACCACCACTATGCGTTCCATGATGGGG
CGCACGATCACCGGTGGCATCGTTCTAGCACTCGGCATCATCTTTGCGATTGCCGGTGCG
ATGATGACTGATTCTTCCACCGCTACTCGTTCCATCCTGGTGGGCATTGGTGCACTGTTT
GTCATCGTGGGTACGTTCCTCTTCTCACCAGCGCTCTCCATGCCTGTGGTGGGTGGCCTG
GGCAAGGTTATCGGTGCACCGTTTGGCAGCGTTGGAAGCCTTGCTGCGACCAACTCCAAG
CGAAACCCTCGCCGTACCGCAACTACAGCGTTCGCACTGACGTTGGGCATTGCCTTAGTG
ACTGCAATTGGCATGCTTTCTGCAACCATGAAGGACGCAGTCTCCGACATGATGGCGGAG
CAGTACACCGCAGATTACATCCTGCAGGGACCAACCAACGGTTCCATCACCATGCCGAAG
GAATCTGTCAATGATGTTCGCGATGCTGAGGGCGTTGCCGATGTCGTGCTCGTTTCCATG
AACTCTGCCTCGGTGAACGGTCAGGCTTCATACAGCCAGCTGGGCCAGTCTGTAACCTTT
GTCGCTGACGGCGACCTGAGCAAGGTCATCAGCACAGAAAGCATTGATGGCTCCCTCGAC
TTGAGCAACCCAGGTGTTGTGACTAACCAGACGTTTGCTGATGAAAACGGCTGGGCAGTA
GGCGATACTCTGCAGCTTGAATCAATGGGGCAGACCATCGGCGATATCGAGTTGATCGGT
ACCTTCACCGGAAACGACGCCATCGGAAATATGATCATCTCCGAAAGTTCCTTGGCTGAT
ACACCAGCGGCAGACACTGCTGTTCCTCAGATGATGCTGGTGGTAGGCGAAGAAGGCTTT
GATAAGGAACAACTGCGCACCAACTTGGAAGACGCAGTCGCTGATTACATTGTCATCTCT
GTGAAATCAGCAACCGAGTTCGCTGGTGAAACGGTTGCGATGATCGACACCATGATGAAC
ATTCTGTACGCGCTGCTTGCTCTGTCTGTCATTGTTGCCATCATCGGCATCATCAACACC
CTGGCACTGAATGTGATCGAGCGTCGCCAGGAGATCGGTATGCTCCGCGCAGTTGGCGTG
AAGCGCGGACAGGTCCGCACCATGATCACCTTAGAATCTGTTCAGATCGCCATCTACGGT
GCTGTGATTGGTATCGCGATTGGTCTTGGTCTGGGCTGGGCCTTTGTGACAGTGATGTCA
GGCGAAGGACTAGACGCTGCGGTTAGTATCCCGTGGGGTCAGGTCGGACTGATGCTTGTT
GGTTCCGCTGTAGTCGGTGTTATCGCCGCGCTGTGGCCGGCAGTCAAGGCATCTAGGACA
CCACCTTTGGATGCGATTACCGAC

>RXN01071-downstream
TAGTTTTAGCGGCAGTTGAATCA

>RXN01075-upstream
GCGGTGCGTGTTCATTAGCAGGTCAAGCGCGTAATTGAGGGCTAGACTGGTTAGTACCGG
ATATTCTTTTTTTCTTTAGTTTGTGGGAGTGGAGATAACT

>RXN01075
ATGGACAATCCAGTCAACATCCTCAATGAGCAGGAAGCTTTGGAGCGCCTGCAGTCGGTG
TCTCTTGGTCGCGTGGTGGTTCGTCGCAGCGATGAGATGGACATTTTCCCGGTGAACTTC
ATTGTGGATAAGGGCGCAATTTACATTCGTACAGCTGAGGGCAACAAGTTGTTCAGCATG
AATCTCAACCACGATGTGCTCTTTGAAGCCGATGAGGTCAAGGACGGAAAGGCCTGGTCC
GTGGTGGTTCGTGCGACCGCAGAGATTGTGCGCAAGCTGGATGAGATCGCTACTGCCGAC
ACTTTGGAGTTGAAGCCTTGGATTCCAACCCTGAAGTCCAACTTTGCCCGTATTGTTCCG
AATGAAATCACTGGGCGGGAGTTCACCCTCGGCGAGGAGCCTGAGCGCTAC

>RXN01075-downstream
TAGCTTTGCCACATTTCACTAAA

>RXN01085
CGAAAGCGTGGTGAAGGACTTGATCCCAACTCACCAGAAGCTATTGAGCAGGCGAAGAAG
AAAGGGGAACGGAAGGCTCGTAATGAGCGTTGCCGCAAAAACTTCAAAGGTGGTGGCACC
AAAGATCTTAAGCAGACTGATCGGACCTTTGATCAGCTGCGAAAACAGCGGGTGACGGAT
AAAGCCCGCAACCGTGACGTACACAATGAGCAGCAACTGGCACGCGGTGAAATCGGAGAA
ATGCGCTCACCGATGTGGGTTGAGGTGGGTGCTGCGATTCTGGGCGTGTTTGTCCTGGTT
GTGATGTGGCTGGCCTGGGGCGGTATCGGGCTGCTGATCCAGACCATGATGAATACTGGC
TCACCTAATGACAAAGAGCTTTTTGATGAGCTTGGTGTGAGACCCTATTATGTTGCTGTC
GAACAGCAAATCGGCACCAGTAGTGCTCACACCACGTGCTACCAACCGCTTGATGAATTT
GGCAATAATTTTGGCGACTGTACGCGTAGCGTGCCTAAAGAGCCAGTGTGGTACGCCGAT
TATGTAGCTAGTGTGTTCGCAGAACATGGCTTTGATGCACCAGAACCTATTGATAATTCG
GTGGGTAGCTGGCTGTTATTTGGTCATGTGGGCATTATTCGGGTGACGTTTGTGATTGCG
GTTGCAGCGGGTGTGTATGCGATGTCACGCGCAGCAATGATGCGTCAGCTAGAAACACAA
AACGTCGCTGTGGACACCACCGATATTAACCAGCACACCAATGACGCACGTTTGGCGATT
CCGCAGGAGATTGTGCGCGATTTGAGTCTGTTCCCCGATGTCGGTGCACACTTCACCAGT
CCAGCCCTCAAGCATGATTTCCCATGTGATGCTGTCGAA

>RXN01085-downstream
TAAGGGCTTTGAAAAAGGTGGAT

>RXN01121-upstream
AAAGATTTACTGCGTACAACTCTAACCAACAATATTGGCAATGGGTTGTTCCATCTTAGC
GCTTTACCTGTGAACTCTGCAGAGCGGTACGCTTAAGCTA

>RXN01121
ATGAATCCCGAATTTATTCACGGCGCAACCGAAATTGAAACCACAAACAGGGGCCTTCGC
CCGCATCGACTCAGCAAAGAAATAGTAGAACGCTACTGTGATCCCCAGTTTAGCGCGATG
GAACGCCAACCATCGGGCGTGCGCGTTGTGTGTCGCACCACCGCCACCTCCGTCACGCTG
ACCACGTATTCCACGCGGGTGGTGTACCTCGATTCCGGCCGGCCGGGCGGCAAGATTGAT
GTGCTTATCGACGGCGCCCCCACATCTTCCACGCCAACTTCCGGGGGCGAGACCACGGAA
GTCAATTTCATCACCGGCGCCACGGAACGGCGCCTGAAAGATCCGCAGGTGCTCACAGTG
GATGGACTTTCAGAGCAGGAAAAGGTGGTGGAGTTCTGGCTGCCTCACAATGAAGAAATT
GAAGTGATCTCCCTTAAAGCCAACGCAGCTTTAAACACTGTCGAAGACACCCGTCCCGTG
TGGATCAATTACGGCAGCTCCATTAGCCACGGTTCGGTTGCCACTGCCCCAACCAAAATT
TGGCCAGCCATTGTTGCCCAGTCCAAAAACTACAACCTGCGTAACTTCGGTTTTGGTGGC
AGCGCCATGTTGGATCCTTTTATGGCGAGGCTAATCAGGGATACTCCAGCTGATCTGATC
ACCTTGGAAATTGGCATCAATATTGTCAATGGTGATGTGATGCGTCGCCGCGGACTAGAG
GCTGCTGTGGATGGGTTCATCAATACCATCCGCGATGGCCACCCCACCACGCCGATCAAG
ATTGTGTCGCCGTTCTACTGCCCCATTCATGAGAAAACTCCAGGACCCGGCGCGTTTGAT
ACCTCATCGTTTGGCAGTGGTCAGATTAGGTTCATCGCCACTGGTGAACCTGATGAGCAT
GGTCGACTGACGCTGGAGATGGTGCGTGAGGTGTTGGAGGGGTTCGTCGAAAAGCAAAAA
GACCCGCACCTGACCTACGTCGATGGTGCGAGCCTTTATCAGGCCAGCGATGCGCCGTTG
CTGGATAATTTGCACCCAGACGAGGCGTCGCACGCCTTAATTGCGCAGCGTTTGCTTAAG
CAACTT

>RXN01121-downstream
TGAAATCGGCTTCGGTGATTTCG

>RXN01128-upstream
ATTCGAGTACAAATAAATTTGAGAACAAAAAGATGGGGGGAAATATGTTAAAGTGCGTTA
TATTGCTTTAGCGAAAGTAACTTCCATGCATCAACGTTCG

>RXN01128
ATGAGCTTCACTTTCATTCGTACTTTTTTCGTACTTTTTGGCATCACGTTGTTAGTGTCA
TGCGTTCCAGAGCCTCCTGACTCCTACACTAAAGAATCCACTGTGCTGCGGTATCAGGTC
TCTGATTTCAATCTAAACTTCGTGGAATTAGCAGTTGCGCTTGGGTATTTGAACAACATT
GAGCTCCAAGTAGTCGGATCTGTACAAGGCGGCGTTGAGTCCATTGAATCGCTCAAAAAG
GATGACATTGACTTCGCGGCAGTCCCCTTCATTGGCCTTGTTGCAGGAGAGATAGCCACC
GGTGCGCCCATCAAAGCAGTGGCCGCAAGTTACGGAATTTCCCACGATTCTTCTTCTGCA
CTTCTAGTCCTTAAAGACAGTGAGATACACGAAGTGCACGATCTCATTGGCAAAACAGTT
GGCATAAACACCCTCGGTGCTCTGGGATCTGCGATGGTTGAGCGTCATCTATTCGACGCC
GGTCTCACCGAACCTGAGATCGTGAGCGTCACTCAACGTGCATTACCCGGTGAGTACTTA
GAACAACGCCTCTACCAGGGGCAAGTTGATGCAATTTGGGTCACCGATAGCGCTAAACAC
CAAGCGCTTGAAACTGGAGATTTTCGGATCTTGGCAGAGGATTCAGACCTTGTGCAGGAA
CTCAACACTGGCTGCATGGTGGTGTCGCAAAAACTCATCGACGAGCACCCCGCAGTGGTT
GGAGAATTAGTGGATGGAGTAGCTCAGGCAATCGAGTTTGAACGATCCCACTCCCCTGAA
GAAGTGCGCGAAGTTTATTTCAACTACCTCGAAGCCCATGGTCAGAGTGATAGAATATCC
AGCTTTAGATATTGGGAGCATTCGGGCATCGCAACCCGAGGTGGAGTGCTCAGTGATAGG
GAGTTCAGCATGTGGTCCCACTGGATTGACCGCCAATACGACGTCCCCGATATCAATCCA
GCAAGTATTTACACCAACCAATTCAACCCATACCGAAAAGTAAACCCCTCGCCA

>RXN01128-downstream
TAAAAGGCAAGGGGGTCGGCGTT

>RXN01134-upstream
GATATCTTGAACTTGACGCTGGCTGAATACATTCCTGCTGCCGATGAAATGATCAAGGGC
TTCGACGAGGCGGCTGAATTCCTGCGTCAGCGATGCATTT

>RXN01134
TTGAGTCTCGACCAGGTTCCATACACCGCGCAGATTGTTCCACTGGCCGTGATCCTCACC
CTGCTTGATGCAGAAGAAATGGCCACCGCACGTTCATGGGATCGTTTGAATCAGTGGTTC
TGGAGCGGTGTCTTGGGTGAGCTTTATGGCTCGCCTGCTGTGATCGCACGTTCCGGTCGC
GATACCGATCAAGTTGCTGCGTGGATTCGTGAAGGTGCCGGCGAAACTGCGGTTGTGCCA
AAGACTATTCGCGATACCGTTTTCCACGAATCACGTCTTCTCAGTGCAACCCAAGACACC
GGAGTGTGGAAGGGTATCTTCGCACTGCTCATGGGCAGGGGAGCACGCGACTGGCGCACC
GGACAGCAGTTTGATCGCTGGACTTTTGATGAGCTGGGTTGCAATTTCCACCAGATTTTC
CCCACCAAATGGTGCAAGGAACGCGGCATCGATCCTGTCCTTACGGAATCAGTACTGAAC
CGCACCCCGATGGGTCGCCGTACCGAAGTAGTCATCGGCGATACCCCTCCATCCCGCTAC
CTGTCTCGTGTTCAATCCAAGTCGCTCATGGGTGATGAGGAATTCGATCAGATGCTGGAT
ACCCACCTGCTCAGCGCGGAAGACCTGCACAGTTCCAACACCACGCACTTCTTTGCTTCT
CGACGCACCAACTTCATCGACATGGTCGAGGATGCCATCGGTAAAGCGGTGATCAGGGAC
GTCAACGAGTCAGATCTCACCGGTGGACACGATGGTCCCTCGGTACACGGG

>RXN01140-upstream
TATCCAACTTCCCGATTTTCAACGGGATTACGCTTGGGATGTTGATCGCATCCGAAGCCT
TATAACCACTGTTCTTCGTGGTTTTCCAGTAGGTGTGCTG

>RXN01140
ATGGCACTAGACACCCGCGGCGAGGAAATGCGTTTCCGGCCACGCGCGCTGTCCGGCGCC
CCAGATACGGGCAAGGATCCAGGTCTTTTGCTTCTCGACGGACAACAGCGCCTCACCACC
CTTTATCATTGCTTCAGTGGCGATGGCTATGTAAATACGGTGGACTTCCGATCAAAGAAA
GTGACCCGGAAGTTTTATATTGATGTTGCTAAGGCTGTTGAATCTCCGGTCATGTCCGAT
GAGGCTATTTTTTCAGTCGACGAAACCGGCAAAATCATCTCCCACTTCGGTCCAGTGATC
GACGGCGGCATCACCGATTTAGAAACAGCACTTGCTCATGGTTGCCTTCCAGTTTCTGTG
CTGCTGGATGATAACGGCACTGATTTCCTCTTTGACCTCGCCGATATGGCAGGAGAAGGC
GCTCGCGAACACGCGAAGCGCTTCCAATCACAAATCGTTAAGACCTTAGTTAGTTACGAC
ATCCCAATGATCCGACTGGATCGTGAAACCGCCAAGGGTGGAATTGGTTCCATCTTTGCT

CAGGCCAATAGCTCTGGCTTGCAGATGGATGTCTTTGATTTGCTCACCGCGGTGTTCGCA
GCCGATGAATCGGTGGAGACCGAATTCTCACTGCGTGATGACTGGGTGCGGGTTGAACGA
AACCTTCGCCAACACTCCGCACTTGATGGCATCGGCAGCACGGAGTTCCTCACCGCAGTA
GCCCTGTTGGTCAGTGCCCGCAAGGGACATGCGTCTGGTTACCGTGAAGATATCTTGAAC
TTGACGCTGGCTGAATACATTCCTGCTGCCGATGAAATGATCAAGGGCTTCGACGAGGCG
GCTGAATTCCTGCGTCAGCGATGCATTTTTGAGTCTCGACCAGGTTCCATACACCGCGCA
GATTGTTCCACTGGCCGTGATCCTCACCCTGCT

>RXN01140-downstream
TGATGCAGAAGAAATGGCCACCG

>RXN01148-upstream
ATAGAACAAGGGTAGCCAAATTCTTGGAAACAGCGCGGGCCCCCGAATCCACAATGCGAA
TCCACAATGTCACCTGAAGCCGTTAAAGTAGGTGATCATT

>RXN01148
ATGACCAGCCCAGTTGAAAACGTTAAGAAAAAGCCACGCCCATTGGCGCTGTCACCGTCG
CGCGCCGGGGATTACCAGCAGTGTCCCCTGTTGTATCGCTTCCGCGCGATTGATCGCCTG
CCAGAGCCTAAGACCGTCGCCCAGGTCAAAGGCACGTTGGTGCACGCTGTGTTGGAATAT
ATGCACAAGTTGCCGCGTGAAGAACGCGAATATCCAGCCATGGTGAAGCAACTCAAGCCC
ACCTGGGCGCAGATGTGTGAAGAAGACGCAGAGCTCAAAGAGCTTGTTCCAGAAGATGAG
CTTTATGATTTCCTCGTGGATTCCCGCACCCTGCTGCGTGGCTACTTTGAAATGGAAAAT
CCTCAAGGTTTCGACGCCACCGAATGCGAAATGTACGTGGACACTGTGCTGCCCAACGGC
GTTCCTGTTCGTGGTTTTATCGACCGTGTGGATACCGCCCCACCGGCCAAGTCCGAGTTA
TCGACTACAAGACTGGCAAGAAACCAAAGCCGCAGTGGAGCCAGCAAGCGCAGTTCCAGA
TGCTGTTCTATGCACTGGTCTACTGGCGCATGTTCAATGAAATCCCAGCTCAGCTTCGTT

>RXN01148-downstream
TAATGTACCTCAAAGTCAACGAT

>RXN01153
CCGTTTTTAAGCCCGATCGTTACTTCCACGCACGCGGTGGTGGCGTATTCCACCGCGCGT
GGATTTGGTGAGCACCGGGTGCGTTGGGACTATGCGCAAGAGTCCCCACTGCGCGATACT
CGTGGCTTTGATCTGCGCCGATACCACCAGGCCCCTGTGGTGGATCCGCACGCCATTGGT
GTGGCCAACGTGTTTGTGCCCAATGGTGCCAGGTTTTATGTCGATCACGCGCACCCGGAA
TACTCCTCCCCAGAGGTCACCAATGCGTGGGATGCCATGGTTTACGACGCCGCTGGTGAC
CACATCCTTATGCAGGCCGTCTCTGATGTTGCGAGTTTCACCAGCCAGAATAGGTCTGTG
TTGGACGGCCATGATCCGTGTCCAGCTTTGAAAATCTACAAAAACAATGTCGACGGTAAG
GGTGCTAGCTACGGGTTCCACGAGAATTACCTCTACTCACGTGAGACGGATTTTGATGTG
CTGGCTCAGGCATTGATCCCATTTTTTGTGTGCCGGCAGGTCATCATCGGTGCCGGACGT
GTG

>RXN01154-upstream
CCGGGGAATTCCAGGTCAGTCAGCGAGCCTGACTACCA

>RXN01154
TTGAGCAAGAAAATTTCACTGGAAACCACACTCAACCGCGGCATTATCAACACCCGCGAT
GAACCACACACCGACGCTGATCACTGGGGTCGCCTGCACGTGATCATCGGCGATGCCAAC
ATGTCGCAGACTGCGAATTTCCTCAAATTCGGCATGACCTCCCTAGTGCTGGATGCCATT
GAGGCTGGGGTGGATTTCTCTGAACTCAAGCTGAAGAACGCAGTGAGTGAAGTAGCAAAG
GTCTCCCATGATCTTTCCCTTACCCACCAGCTGCGATTGGCGGATGGTTCAGAGCTCACC
GCTATTGATATTCTGCGCCGCTATTTGGACAAGGTGCAGCCGTTTGCAGAAACCCCAGTG
GAACAGCGTGTCACTGCGCTGTGGGGTGAAGTGCTGGGGCTCCTGGAGAATGATCTGCTC
TCCACCAGCCATCTCCTTGATTGGACTGCAAAACTTGCCCTGATCAAGTCTTTTGAGGCG
CGTGGGCTGTCCATTAACGATCCCAAGATGTACCTCATTGACCTGCAGTACAGCGATATT
GATCCACAGAAGAGTCTGTATCACGCACTGGTATCCAAGGGGCGGATGAAAACACTGTGC
AGTGCGCAGGACATTGCAGATGCAGCGGCCACTTCACCG

>RXN01155-upstream

ACAGCTTGCTGGATGAAATCGACGGACTGTTGGAAAACAACGCCGAGGAATTCGTTCGTT
CCTATGTACAAAAGGGTGGCGAATAGTCACTGTGAGTACC

>RXN01155
GTGGAATCCGCATTGACCCGCAGGATCATGGGCATTGAAACGGAGTATGGCCTCACCTTT
GTTGATGGTGATTCCAAAAAGCTTCGCCCAGATGAGATAGCTCGAAGGATGTTTCGTCCC
ATCGTGGAGAAATATTCCAGCTCTAATATCTTCATACCCAATGGTTCCCGGTTGTATCTT
GATGTGGGTTCCCACCCGGAGTACGCCACCGCCGAGTGTGATAATTTGACCCAGCTGATC
AATTTTGAAAAAGCTGGCGATGTTATTGCAGATCGCATGGCTGTAGATGCCGAAGAGTCG
CTGGCGAAAGAAGACATTGCTGGGCAGGTGTACCTGTTTAAAAACAATGTCGATTCCGTG
GGCAATTCTTATGGCTGCCACGAAAACTACCTTGTGGGTCGCTCCATGCCGTTGAAGGCG
TTGGGTAAAAGGCTGATGCCGTTTCTGATTACCCGCCAGCTCATCTGCGGCGCCGGCAGG
ATCCATCACCCCAATCCTTTGGATAAAGGCGAATCCTTCCCCTTGGGCTACTGCATATCC
CAGCGCTCTGACCACGTGTGGGAGGGCGTATCAAGTGCCACCACTAGATCACGCCCCATT
ATCAACACCCGTGATGAGCCACATGCGGATTCCCATTCTTACCGCAGGCTGCACGTGATT
GTGGGTGATGCCAACATGGCAGAGCCCAGCATCGCGTTGAAGGTCGGCTCCACGTTGCTG
GTTCTGGAAATGATTGAGGCAGATTTCGGTTTGCCCAGCTTAGAGCTTGCCAATGATATT
GCCTCAATTAGGGAAATCTCCCGCGATGCAACAGGATCCACACTGTTGTCCCTGAAAGAT
GGCACCACCATGACTGCCTTGCAGATCCAGCAGGTGGTCTTTGAGCATGCCTCGAAGTGG
TTGGAGCAGCGCCCCGAACCAGAATTTTCTGGCACCTCCAACACAGAGATGGCCCGCGTG
CTGGATCTGTGGGGTCGCATGTTGAAAGCGATTGAGTCCGGTGATTTCAGCGAAGTGGAT
ACAGAAATTGACTGGGTGATCAAAAAGAAGCTCATTGATCGTTTCATTCAGCGCGGCAAC
CTTGGGTTGGATGATCCAAAACTTGCCCAAGTGGACTTGACTTATCACGATATTAGGCCA
GGTAGAGGCCTATTTAGCGTGCTGCAAAGCCGCGGCATGATCAAACGGTGGACTACTGAT
GAGGCGATTTTAGCTGCGGTGGATACCGCTCCTGATACAACACGTGCTCATTTGCGCGGG
CGAATCCTTAAAGCGGCGGATACTCTGGGAGTACCTGTGACTGTCGATTGGATGCGTCAC
AAGGTCAACCGACCGGAGCCACAATCGGTGGAATTGGGGGATCCTTTTTCCCTTTTAAAT
CCTCAACAACCAGCCCAAGAAACTGCTTTGAGCATTCTTCTCCTAGGCGGAACCTCTTAC
ATTGCCGGTGAGATTGCCACGTTGACGTTT

>RXN01167-upstream
GTGTCGTTTTATTTGCACACTAGCAGGTAAACTGTGTGAGACGAATTCTTTTGCGGCAAC
TTGGAGGCCGCATTCTAGTAGGCAAAGGACTGATACCTAG

>RXN01167
ATGGCAGATCGCGTTCTTCGTGGCAGCCGCATGGGCGCCGTGAGCTATGAGACGGATAGG
GACCACGATCTGGCTCCTCGCCAGCTCGTGAAGTACAAGACCGCAGACGGGGAAATCTAT
GAGGTTCCCTTCGCTGATGATGCGGAAATCCCCGAGGAGTGGATGTGCAAGAACGGTAAG
CTAGGCATCCTCATGGAAGGTGAGGGAGTCGAGTCCAAGCCGGTCAAGCCTCCACGTACT
CACTGGGATATGTTGCGTGAGCGTCGCTCAATTGAAGAGCTGGATGTGCTGCTGGAAGAG
CGCATCGAGGCACTTCGTAAGCGTCGTCGCAATGCAGCGAAACTGCTGAAGGCTCAGCAA
GAGGCTGAAGAAGCAGAAAAGGCAGCTGAAGAGGTT

>RXN01167-downstream
TAATCTTCCTGCCTAAGTTAGAA

>RXN01169-upstream
TCTTGATCGGAATCGGCGCAAACATCGTCTACGAACACCTCAGCGCGTAACCCTCGGCGC
ATTATCCTCAGACAGCTTTTAGCGCAAACAAGGAGCATCA

>RXN01169
TTGAAACGGGTCGTTGAAGCGTGGGATAGATTTCAAATCCCACTGTATATCACGGCTCTT
ATCGCCGGAGCACTGGTGGGTTTGCAGTGGCCAGGCTCTACAGGGGGTTTCGAAAGCGCC
ATTAACCCAGCGTTAATGGCGCTGCTTTATGCCACTTTTCTCGGTATTCCGATCACTCGG
ATTGGTGCAGCGCTGAAAGATCTGAGATTTCTCATAGTGCTCATGTCCGTCAATTTTGTT
GCAGTGCCTCTGGTGGCTTTTGCGTTGAGCAGATTCATTGCGGGTGATGAGGCGCTTCTA
ATCGGATTTTTACTGGTGATTCTCGCGCCGTGCATTGATTACGTCATTGTCTTTGCTGGT
TTGGCCAGGGCCGCCCAAGACAAGCTCCTTGCCGCCACGCCAATATTAATGCTTGTCCAA
ATCCTGCTGATCCCCGTCTTCCTGGCTGTTTTTGTGGGTTCAGATGCCCTTGGCTCAATC
TCTTTCGGCCCATTTGTAGAAGCATTTTTCCTCCTGATTCTCATTCCACTTGTTGCTGCT

GCGGGAACTCAGCAAGTGGCAAGAAAGTGGCAGGTAGGACGTACAATTATGGCTGCTGCA
GAAGCAATCATGGTGCCTTTAATGATGCTGACGTTGTTCGCTGTCATCGCATCGCAAGTG
GAAGCTGTGAGTGGTCAATTCACCGATATCGCCACAGTAGTGCCACTATATGTCGCCTTT
TTGATGGTGATGATTCCAATTGGTGGCGGGATATCCAAACTCGGTGGCTTAGGTTTCAAA
GAGCAACGAGCCATCGTTTTTAGCGGAGCAACCCGTAACTCTTTGGTCGTTTTACCTTTA
GCGTTAGCACTTCCCGCAGGCCTGGAAATAGCGGCCGTCGTAGTTGTCACTCAAACCCTC
GTGGAACTGATTGGCATGGTTGTCTACGTGCGCATCATCCCTTTAATTTTCCATGAAAAG
CAGACATACAGGAAACTTTCAGGCATAGGGGAGTCA

>RXN01169-downstream
TGAAACAGAACGGCAAGCTAAGG

>RXN01173-upstream
AGATCTGTTTCTATGTATTAAAGATCACACCGAGTGGTGGAATTTCCTCAAGTGATTTAC
CCACAATGGACTTTGTTGATACCCAATTCGAGAAAGGCCA

>RXN01173
ATGCACGTGAGCACTCTTCCAAACAAGAAACTGCGTACTCGCATTTTCGCAGGCACCGCT
GCCGTCGCACTGTCACTTGGTGTTGCGTCTTGCTCAAACGCAGAAGATGCTGTGGATAGC
GCAACAGATGCTGCCAACTCTGCAACCTCCGCCGCGGGATCTGCAATTAACGATGCCACC
GGCACTTCCAGCGCATCCACCACAGAGCCTTCCGGAACCTCTGGATCCGACTCCGGGTCT
GACTCTGCTGGAGGAGACACCACTGAAGTAGAAAGCGCCGATGGGTCCACCATCAGCATC
CCAACTGCCGTCGTCACCGCTGCAAATGCTGCAGGATTCAGTACCCCGGAATCCGTGGAA
GAAGGCCCGAATGGTGAGTCATTGGTGACGTTCCCTGAAGGCTACATTGTTAACTCTGCA
GAAGGTGGTGCACAAGCACTGGTCGGCATGATCGGTGAAACCTGGATCGGCGAAGGCGGA
CTATCCGCGGCAGTGGGTCTCCCAACTGGGCCTGAAGAAGCAACAACAAATGGTTGGACT
CAACAGTTCACATCTGGAGTAATTAGCTGGCTTGATGATGGATCAGGACAGTTCGCAGCT
TCTGTTGAACCTGCT

>RXN01173-downstream
TAAGGGAATCTCACCTGGCCTCC

>RXN01174-upstream
ATATCGCAACCGCTGTTAATGAAGAGGAAGAGGCTCGCGATATCGCGAAGCTGTGCCAGG
AGATGGTGGAATTAGCTCGGAATATTGAGAAGTTGAGGTA

>RXN01174
ATGAGCAACATGCAGGGAAACGATTCCAAGAAATCTAGCGGCGCGAGTCGTGCGGAGAGC
CCACTGATCAAGTTCCGGACATTGATTATCGTCATCTTTGTCATCTTGATCGTTGGTTTG
GCATCTATTGCAGTGGGACCTGTCGTGTACCAGCTCATCATGGGACCTGGTGTGAAAACC
GAAGGAATCCAGGCTGATGGCGCAGCACCTGCGTCCACCGACATGAACGGCACCTGGGAT
GTTGCCCCAGGGAGTATTCCAAACACCACCTCAGCTGGATTCACCTTCGCTGAGATCCTG
CCAGGCGAAGAAAAGATCACCTCCGGCTCAACCACTGGTGTCACTGGCGAAGTGGTCATC
GAGGATAACTCCCTGATCTCTGGTCTGATTACCGTCAACATGACTCACATCACCACCGAT
CAGGAAAAGCGCGACATCAACGTGCGCACTAAGCTCTTCCACACCGATCAGTACCCAGAA
GCAACCTTTGAGGTTACCGATTCCGTTGATCTTTCTGCGCTCCCAGACACCGGATCCATT
GCTCAGGTTGTCATCCCAGGCGAGTTGACCATCCACGGTGAAACCAAGGCTGTGGAGCCT
ACCTTTGATGTACTTCGTACTGGTGACCAAGTTATCGTGGCTTCCGATATCGAAATCAAC
CGCCTCGACTTCGGTGTAGAAACCCCAGAGTTCATCGCCGCAAAGATCAATGAGACCGGC
GAGATCAACGTCCGAATCGTATTGGAGAAA

>RXN01174-downstream
TAAACCATGATGGCATCACGGAT

>RXN01206-upstream
CCGTGCCAGTGATGAAAAGCCGGCGAGCCGCCAAACTTGATTAAGTGATTGTCACTTTGG
ATTGTCATATTGGGCGAATAAACCGGTAGGATTCCCCTTC

>RXN01206

GTGAGCGCCGAAAATACCGAGAACACAGATTCCCCATTTGAAATCTCCGAGTTTGATGAT
CACCGACGCCCCCTCCAGCGGGCCCTCAAATTCGGTTCCATCGCCCTAATTGTCTTCACC
CTGATCTCCCTAGCGATCTGGGGTGCAACTCGTGGCGTACCCGGCGTATCAGCAGTTGTT
ATCGGCGCAGCAGTTGGCGCAGGCTTTGTCCTCTTAACGGCTCTCAGCGTCCTGTTTACA
ACTAATTCCAACGTCACCACCACCGGTGCGGTGGTGCTCGGTGGCTGGCTGCTGAAGATC

>RXN01210-upstream
TTCGCTGCAAAACCCGCCACCTTGGAATCCGTATTCATGGACATCGCCTCACTCGAGAAC
ACCTCGCTGCAAACCGCCTAGAATCTTTAAGGAGACCACA

>RXN01210
ATGACCACGTCACACACCGCCCGCGGGCTGCAACATGCAACCCCGGAGCGCCGCAAGACT
TCATTTTTCAAAACCTCTCTGTTTAAGGCCGAATGGCTCCAGTTCCGCAGAAATAAAACC
CTGTTGTTCATGGCCACCGTATTCCCAGTCGGAATCCCTTTGTTGCTCTTTCTCATCGGA
AATGGTGGGGCAGCAGAGTCCGCGAACTCCTTCGACTACTTCGTCATGTACACCCTGCTA
TTTGTGCAGTTCTACACGGTGCTGTCCATGGCAACCACCCGCCGTGATGAACGTGTGCTG
AAAAGGCTGCGCACGGGAGAAGCCCGCGACATCGATATCATCGGTGCCATCTGTTTCCCC
GGCGCGCTCCTCACACTGATCTTCACCGTGGTGATCATTCCATTGCTCATGGTTTTGGGA
GCTCCCGCGCCCATCAACCTTGTGCCCATTGTGTTTGCCGTACTGATCGGACTACTTCTT
TGTAGTGCTCTTGCCTTGATGACCAGCGGTTTCACCCGAAACGCCGAAGCCGCACAGATG
ACCTCCATGCCCGTGTTCATGCTTGCGATGGGTGGACTTGGATCAATCCGCTTCGTATTC
GGCGACAGCATTGTGGCTGATATCTTGGCCTACACCCCATTCGCCGCGATCAGTGACCTT
GTCCAAATCGGCTGGGCTGGCGCCACCTTCGCCGACAGCGTTGGTGGAGTAGAGGCAGCA
AACTTCGCTGGAATTTTCCAAGACATGCTCATACCACTTGGAATTCTGGCAGCGTGGACA
GCTGCAGCGGTGTGGGCGGCGAACCGCTACATGCGCTGGGACTCGTACCGC

>RXN01210-downstream
TAAGCCTGCAGCCGACGGGATTA

>RXN01229-upstream
TAGCCCCGAAAGACGGCGAGGGTTGGCTCTGCTTCGTTGTGGGAAAACTAGGCCCTTAAT
AAGCTGTGCTTATAGGGTCTCCTGCACCGATAAAGGACTG

>RXN01229
ATGATCATCTCCACTAACACCGCTCACCCCCTGCACGAACCGCACGTACCCAGCCACCAC
AATCGTATGAATACTCTGCGTGCCGGTGTGCTGGGTGCTAATGACGGTATCGTCTCCATT
GCTGCGCTACTGCTCGGTGTGATCGCCACCGGCGCCAGTGACACCGTCGTGTTCGGCGCT
GGTTTGGCCTCAACGATCGCGGGGGCGGTATCTATGGCTCTCGGTGAGTACGTCTCTGTC
TCCTCACAGCGTGATACCGAACGGGTGCTCATCGCAAAAGAAGCGAAGGAGCTGGCCGAA
GACCCGACGGCCGAGCACGTCGAGCTGTCGGAGATCCTACACTCCTACGGCATCTMCMMT
GWGAMTSMRRASSMSGCSRMMAYCGRGAWMGGGMASGGCGACGCCTTGGGCGCCCACCTT
CAGCTCGAGCTCGGTATTGATAATGAGCAACTGACCAGCCCCTTGGCCGCCGCCTTCTCC
TCGGCCGTGGCTTTCCTGCTCGGAGCACTGCTGCCGATGGTGTYGGTATTCMTYGCCCCY
KCAGGCTGGGACGCCGGCGTKGKCTTCGTAGTCACGSTGCTGGTCCTGGCGGKKACCGGG
TTCATCTCARCCCMGRTCYCGGGTACCTYCCCMATGCGCGSGTGCSGGSGCTTKGKGRTC
GGKGGTKCCCTCSGSCYGGCCCTGACCMTACCGTCTTGGAAWCWATTSKKSGSSGCMGYW
KTMKGWGSYKCSKSRRRAMARARRRGGRRKRMKGSKKKTKTKGTGGYKGSKSGKYKTTKT
CGWCGMCKSSWSRAMGWRRTSRKCGSCGMCSWCCTYSYWGMMSAYCMKSSGSSKSCWKGR
WSSRCYGCYSCMSSMGGSKSKCSMSWKWTRKKSYSSSKSWSWMTWCKYKTTTYYCYYCSG
SMRGKWAMCMMMMYKGKKSYWWKRRRWTKTTTYYKRRRARRMSRMYWMCSRRKWRGGCCA
CCACTGTCAGGCGAGATTCTGCTTGCTGGCCTCGGCGGTGAGATAGGCATGGGGGAACCG
AGGATCCCAGTGACTACTGGTGACCTGGAAACCCGCGGTCTCCAGTGCCTGGGCAAGCTC
GGGCAGTGGCCACCGGTAGGCGGTGGCCACGGGATGATACATCGGTTCCAGAGAAGGCCC
GGAGAAAAAGGACATCAGCAGGCCACCACCATCCTCCACCGCCATCCGCAGTGCGACCAG
GGCGTCGGGCAGCTCGCCCGGGCCCATGTGGATCAGGGAGTACCAGGCCAACAGGCCTGC
CCAGCGCTTCGGCGAGTC

>RXN01229-downstream
TGAGAGGTCGGTAATAGTGCCGT

>RXN01231-upstream
TCCTGGGACGTCTTCCCCGAGGCGTGGGAGACATTGAAGGTTTACCTGGGCTTTCGTGCC
CCAGGCATCGAGCACTTCACCCCCCTATGACGCCTTGCAA

>RXN01231
ATGCTGGGCTACACCTTCGTCATCTTTATCCTGGCGCCGTTTCTCATCCTCACCGGAATA
GCGATGGCCCCGGCCATCCGGTCCCGCTTCCCGTGGTACGTCAAACTCTTCGGCGGCCAC
CAGGGTGCACGTTCCCTGCACTTCATCGCCATGGTGTTGATGACGGGCTTTGTCATCATG
CACGTCGGCCTGGTTTTTTGGTCCATGGCGACTACAACATGGTCCACATGGTCTTCGGCG
ATA

>RXN01231-downstream
TGAACACTGACCGTGCGGCGCAG

>RXN01246-upstream
GGGAAGGAGGAGAAGGCTGCTGTGAGCTCTGCAGCCCCCGTCCGCTGACTTTCAATGCTT
CATGGACTCCCCGATACACAACCTCCGAAAGGGAACCCCC

>RXN01246
ATGAAGCGCACTATCACCATCGCCGCTCTCGCCTTGACCTCCACCCTGGTTTTGTCCGCC
TGCGCAGATAACACTGAGGGAGAAAACACCGACACCACGACCATCGCCACTACGTCCGCC
CCCGACACCACCGAAACGACCGGGGCCACCACGGATCCTGAGACAGAGACGGGGGCGGCC
GGAGAGGTCTCCGCCGAGCACAATGATGCGGACATCATGTTCGCGCAGATGATGATCCCG
CATCACCAACAGGCCGTGGAGATGAGTGAAATCCTCCTGGCCAAGGACGATATCCCGGCC
GAGGTCATCGAGTTCACCCAGGGTGTTATCGATGCCCAGGGCCCGGAGATCGACCGGATG
AATACCATGCTCGAGACCTGGGAAGAAGATCCGGTCACCGGTGATATGGGTGAGATGGAC
CATGGCGGGATGAGTGGAATGATGAGCGAGGAGGACATGACAGCCCTCGAGGACGCCCAG
GGCACCCGAGGCTGCCCGGCTCTACCT

>RXN01246-downstream
TGAGCAGATGACCGCCCACCATG

>RXN01249
TCTCAGATTGTGGCGGTGTCTTCTCACGGTCTTACCACGATCCAGGAGATTGACGTGAAA
CGAGCAGCGATCGCAGCCGCCGCCCTTACCCTCGCCCTCACGGGGTGTTCGGCCGCCGAC
CCGGAACCCACCGCCGACGGGACGGTGTCCCAGGATACATTCCTGACTACCCATGGCCTG
GCCGCCATGGACGCGGTGGAGATCATTGATCACCTCGACCGGCAGAAGGTCACTGAGCGT
CCCACGGATCTGATCGCCTCAGTGCGTGCCGATGAACTGCTGCTCTCGAGCGATGACCAG
GAAGTCGTGGTCGATCTTCCCGACAATCAGACGTATGTCTCGATCGCACCCTACCTCAAC
TCCACCCACGACTGCTTCTACCACAGCCTCACGACCTGCCTGGGGGATCTCGACAATGAG
GATATCCATGTCATGATCACCGATGAAGCGACCGGCGAGGTCCTGTTCGAT

>RXN01251-upstream
TGTAAGCCGAGAGCGAACCTGCCAAAAGTAAGGGGCGGGTTCGCGGTGACGTCGGTAGGA
TCGAGCGAAGAAACCAACAAACTTCTTAGGAGCCATTCTC

>RXN01251
ATGACCCAGCCAGATATGTCCCAGATCCTCGCCCAAGCTCAGCAGATGCAGGCTCAACTA
CAGGCCGCTCAGCAGGAAATCCTGGCAACCACCGTTGTCGGAAATGCAGGAAACGGGCTG
GTTACCGTCACTATGGCCGGCAACGGCGAGGTCTCCGCAGTGACCGTTGACCCAAAGGTC
GTTGACCCTGAAGATGTCGAAACCCTACAGGACCTTCTGCTCGGTGCATTCAAGGATGCC
CATAACAAGGTCGCAAACGTTGCTGAAGAGAAGATGGGCCCACTATCCCAGGGCATGGGT
GGCCTCTTC

>RXN01251-downstream
TAATTAGTTGCTAAACGCAGGGC

>RXN01263-upstream
AGTGGCCTTTGGAGTTATTTTGATGACGGTATCGGCGACTGCTGGGATCCTCCTCTTTTT
ATCTCCAAATAGAAGCCAAGCTGCGCCACCCCAATTTAGT

>RXN01263
TTGACCCCGTATGATCCAACCGCTGTAAATAAGGAGTCGGAAAAAGAAGCAGCAAAGAAT
CTGTTTGGCGCTGAGGCGTTGACAGTGGATCCGGATGCCGGTGAGGTTGTTGATCGAGTA
GATAATTTTTATCCGACGACTGCTAAGGCAAAACGAGATTACCCAAGTAACTATGCAGCG
GGTTGTCACCAAGAAGTCAATGAGACTAGTCCTGAGTCATGTGTTTATGGTGATAAAAAT
TCTGATTTTTCTGTAGCACTTGTCGGTGACTCCCACGCTGGTCATTGGCTTCCTGCCTTG
GAACCAATTGCTGAAGCACAGGGGTGGAGATTGGAAGTTTATACAAAGTCACAGTGTCCA
CTCATAAGCACTGCGATCAAACTTGGTGAAACTTTTTATGCAGAATGCTATGAGTGGAAT
GAAAAATTACTTGCTAAGCTAACTGGACCTTCTGCACCAAATCATGTGATTGTAAGTAGC
CAACGTTACGCTTCTGCAAATCCGTTAATCGATAGTGTCGCGACGGGAACCGTTTCCGAA
GGATATGAAATGGCATGGAATTCATTAAAAGATGCAGGTGTTTCTATTTCTGTACTTCTT
GATACTCCTCGGCCGCAAATTGATATCCCAGAATGTGTAGCATCAAACCGCGATAATCTC
TCAGAATGTTCAGTTCACCGGAGCGTTGCGCTTGGGACTGAAGCTCATCCTCAGCAAAAA
ACTGCAGCTCAAAATATAGACGTGCCTGTATTGGATTTGAGTAATTGGATTTGTCCGGAA
GAATATTGCTCCGCTGTTATCGGAAATGTTTTGGTATACAGGGATTCACATCATTTGACC
GCTACGTATGCTCGTAGTCTCTCTAGCGCATTATGGAATGAGTTGGTTGCCTCAAATGGT
GAGCCTTTTAAG

>RXN01263-downstream
TAAGAGGTAGTTGTTCAAGTAGC

>RXN01266-upstream
GATTGTGAAGTTTTATATCTGTCATATTCTGGTGATTTTCGCCCTGCTCATGAAGTGGCG
GACGAGCAATGGCCCGATATAGATTTAGTAAGGAACTAAA

>RXN01266
ATGCCAAAAGTAAGTGTGGTTACTGGTTTTTATAACCGCTGTGAGCATTTAGAACGAACC
ATTGAGTCTATTCTTAACCAAACTTATAGCGATTTTGAATTAATTGTTTTTGATGATGCA
TCGACAGATGGAACAGCTTCACGATTGTTAGAGTTAAAAGAAAAATATGATGATCCGCGT
TTCCGATTTATCATTCATGAAGAGAATAAAGGTTTCGTAAAAGGGTTATCAGAAGCAATT
TCTGGAGCTAAAGGGCAGTATATTGCAGTCCAGGGATCAGGCGATGTATCTCTTCCTCGC
CGTTTAGAGCTTCAGGTAGAGTTTCTAGACGCGAATCCTTCGGTAGGTGCTGTGGGTGGT
GCTATCTATAATATTCAAGAAGATACGGGAACACGCAACCCACAGAGATTTGAAAAGCCA
ATTGCTACATTCGATGATTTATTGACATCTAATCCGTTCACTCACGGAGAAGTGATGTAT
CGCTTAGACCTTTATAAGAGTATAGGTGGGTATCGAAGTGGCTTTACTTTTGCTCAAGAT
CGTGATTTATGGTTGAGGATGGCGAAAAAAGCAGATCTGGGTATCATTCCAGATTTTCTT
TATCACCGTTACACACTTTTAGATGGTGTCTCTTTCGTCCCGGATAAAACTATACGTCAG
CGATGCTTTTCAGAAGCTGCGGTGCGACTGGCATTAATGCCAGAAGAGGAAGGAGCTTTA
GCCTACTCTAGGCTGGAAGCTGAAGGGCCTACTGCCGTAGTTCCTATCGCTGATAGAGCT
GTTCAGAAATTTGTCCCTAAAGCGGCTATTCGCTTATGTCTATATGGTGCTCCGGAAACT
GGTTTACACATGGCTCGAGACTATATCCAGAACCCTCTGCGCCGTACCATAGTTGTAGTT
TTGATCAGCATCTATTCGTCTAGATTAATTAAGCCTCTTCAAGATATTCTATATAAGTCT
ATTTTTAAGGGGGTCTCGATTTCTAAACCTATTAAGAGTTCACTCGTGAAGTTTACAAGA
AGAATTCAAGGGAAG

>RXN01266-downstream
TAGCGAAAAACCGCATCTACCAA

>RXN01275-upstream
CGCCATACTAGGCTCGGCCTTTTCGACGGGAACTCGGATAGGCTTCTGTAAAACCATCCC
CGTTGAAGAGAGACTCGTGGCTGAAATAACCACCCCATTA

>RXN01275
ATGGAAAAAATTCGCTCACCCGCAGTCCAATCAGATGCACTGCAGGTTTTTAAATCAGCA

CTTGCTGCGACAGTCACGTGGTGGATTTCGGTTAACCTCCTTAACTCCCAACTACCCTTT
TTAGCTCCCTGGGTAGCGTTAATGACGATGCAATTCACCGTCTACCACACCTTTATCAGT
GGAATTCAGACTGCAATTGCTTCTGTCATCGGAGTTGGACTTTCCTTTGTCATAGGCACT
TACTTAGACGTAAGTGTGTGGACTTTTGGCCTTGCAATGGTCATAGGATTAATAGGTGCA
CGAGTACCAAAGCTCCGCGCGGAAGGAATAGGTATTGCTACTACATCCATTTTTCTTCTT
GCCTCCGGGTTTGATGATCAACAACCCCTTCTATACGACCGTATTTTAGAGATCCTGCTC
GGCGTGGCTGTTGCCATAGCCATCAACCTCATCATCTTTCCTCCCTTACGCGACCAGGAG
GCAAACATGGTGGTAGGAAACTTAGATCGGAGGATGGGTGAGGTTTTACAAAAAATGGCC
GATGAGCTTGCAGAAAAGTGGAATATCGACAATGCAGATGAGTGGCTGGAAGAAATTAAT
TCTATTAACAATGACCTAGAAAAAGCGTGGCACTCCGTGCGGTTCGTTCGCGAAAGCCGT
CGAGTTAATCCTCGTAAAATCCGCATCCAAGAGGGCCGCCCCCAGCCTACGGAAACAAGT
TATGAATCAAACCTCACCAGCATTGATGAAGGGATCGCTCATTTACGCCACCTTGCCCGT
ACTCTTCGTGATACCCCGATTATAGATTCCGACTGGGGATCCAGTATTCCAGCAACAGTG
GGTATCCCTTATGCACGATGCCGGAGCTTTGCTCGCAGATCCGAATCAGGAAATAGATCC
TATCCGCGACCGGCTCTC

>RXN01275-downstream
TAAACTTTCAAGTGAGATGAGTG

>RXN01276-upstream
TGCGTAAAACCCTCATCACCATGCTCGCGACCACCGCGATCGCCTTTTCCGCCATCTCAC
CAGTGCAGGCGCAAACCGTGGACACAGACACTGACGCCTC

>RXN01276
GTGTCATCTGAGCTGAGCAGCGGCACAAGCTCAGGAAGTTCAGAGGATTCCGAAGATTCT
GACATCTCCAACCGGGACATCATCTTCGGCATCGCAGCTATCGCTGCAGTCGGCGGACTT
ATCGCAAGTGGTGTGCACTGGGCAGTACAACAGCGCATGATCCCAAATCCCCTCCCAGGA
ATCATTCCAAATCCCCCTGCACTGGCACCTCAGGCGCCTGCCCCAGCACCTGCTCCCGCT
CCTGCCCCTCAGGCAGTCGCGCCCCAGGTTGTCGCTCCCCAGGTTGTCGCGCCTGCTCCA
GCCCCAGTACAGACCAACCGCACCTACAAAAACTGCACCGAAGTATGGAACGTCCTGGGA
AGGTCCATCCGCCAAAGCGATCCAGGCTACGGCACACACCTCGACCGCGACCGCGACGGC
ATCGGCTGCGAATCACGCCCTAGG

>RXN01276-downstream
TAGTTTGGGTTTTGGGGATCTTC

>RXN01281-upstream
GGACAACCTCATCAAATGCAAACATGCGCCACCGCGTCCCGGAAAACCAGGGGCGATACC
GCGCTTGAGTGCGAGGTGCCGTCAATTCCCAACTACAAGA

>RXN01281
GTGGGACTCAGCCGTTCACATTATCAGCTAGCCGCAGAAAACACCAAATCCCTTGTTAGA
ATGGTTCCCATGACTGTTCCTCAAGGAAACGAACCAGCAAAGAAGCTCGCCACTGACCTT
AACCGAAACCAAGTCGTGGATGAACTTTCTGCAGCTGTTTCCCGAGGTCAACTCACTTTG
GAGGAATTTGAAGATCGCTCCTCCAAAGCATGGAATGCCCGCCACTTAGACACTCTTGTA
GAGCTGATCTCTGATGTGAACGACAATCCCTACACTCTGCTTGGTCAGCAATTTCCCGGC
GCCTCCTATGCGCCGGCGGCCTACGAGACCACTCCCCCAGCGATGCCCAATGTGTCAGAT
CCTGTAAATATTGTCCGCAACAGGATTACCGGCAACCCGAATGGCTCCAAAATGTCGGTC
TCGTTTATGGGTGGCACCGTGCGCAAAGGTGGATGGCATGTGCCTAATGTTCACACATCC
TTCGCCATGATGGGCGGCAATCAGATCGATTTGCGCGACGCCTTCCTGGAAAGCGACCGC
ATTCAGATCAACGCCTACACATTCATGGGTGGCATCGAGATTATTGTTCCCGAGGGTGTT
TTTGTCATTTGTGATGGCATGGGCATTTTCGGCGGCTTCGAACAGTCTGTGGACAAGGCC
GGTGCACTCAATCCCGCGCGCCTGCCAAGCAACGCGCCCACGGTCCACATCAAAGGCCTG
GCGTTCATGGGCGGAGTCAGCGTAGTCACCAAGAAAAACATT

>RXN01281-downstream
TAAAAAGCTTGTCGACGCGCCCC

RXN01296-upstream
TAAAACTCCTGTTCGAAATTGCCCAGACAGGTGTCCACCAACACTGCTACATTGCATTGG
AGATCCAGAATCGATCACTCTACGACCAGGAAAAACTTTC

>RXN01296
ATGTCCATCGAGCAAGCAATCACTTCACTCTCCGCAAGAGTGCGGGAACTAAAGCCCATC
ATCGAGACTGAAGAAGCCACCAAAACCGCACTGATCATCCCCTTTATCAGCAACGTTCTC
GGCTACGACGTCACTGATCCTCGTGAAGTCATTCCGGAATACACTGCTGATGTTGGCGTC
AAAAAGGGTGAGAAGGTCGACTTCGCTATCAAAACCGGCGATGATTTCCACTTCCTCATC
GAATGCAAAAAGGTCGGCTCCCCACTCAGCCTCGATCACGCTAACCAGCTCGTCCGCTAT
TTCAATGTCACAGACACCGAATTTGCCATTCTCACCAACGGCGAAATCTACCAATTCTAT
GGACAACTCGATGCAGCCAACCGCATGGATGCAAAACCATTCATGACCTTGGATTTGAAC
AATATTGATGCCCGTCAGTTCCCTCATTTGGAAATGTGTACCCGCAAGCATTTCAACCCA
CAAGCGCTAGCCGCCAACGCTGAAGAACTGAAGTACATTGCTGAATTGAAGAAAGTCATC
GCGAATCAATTCCAAGAACCTGACGTAGAAATCGTCAAGATGCTTGCGGCGACAGTCACC
ACAAAGCGTATGACTGCACAAAATCTGGAATTCTTCACCCGCTTGGTTAATACTGCGTCT
TCCCAGTTCCTCAAAGACGAGGTCAATCGTAGATTGCGCTCCGCCCAAGTCTTTGAGGAT
CCTGTCCAAACACAAGGTGCTGATGCAGAAACACCAGCAGAGGACGAAGCAGTAATCGAA
GAAGTGGTTTCAGAAATCGTGACGACAGAAGAGGAAATCCACGGTCATTCAATTGTCCGT
GCAATTTGCTGCTCAGAGGTATCGGCACAAGAAATCACCATGCGTGACGCAAAATCCTAC
TGCGCTATTCTCTTCCAAGACAACAACCGAAAGCCAATCGCCCGTTTCTACTTTGATCGC
AAGATTCCACGCATCGGCATCTTCAATGCTGAAGGCGAGCAGGAACACTTTGATTTGGAA
TCCATCGAAGATATCTACAACCACGCTGATCTTCTGCATTCCCGCGTCGTAGCATTGAAC
GCT

>RXN01296-downstream
TAAGTTCTGCCTTTAGTTCTGCA

RXN01301-upstream
AGGCAAGAACGCAAAGTTCTAGTACGCTGCTAAAGTATGCAGCTTGGCCCGCACGGTTTC
CGCGTGCGGGACGTGTTCATTTCTGTATAGGAAAACTACC

>RXN01301
TTGATCGTTGATACCCAGTTTGAGAAGATCCCTGCTCACGACGTCGTGGGCATCCGGGTA
ATCCTTTCCTCTGAGGATCTCCCTGAGCTCTTTAAACGCGGCTACGCGGAAGTAAAGAAA
TTCCTCCGCCTAGAAGGCATCGAACCTAAAGGTCCTGCCCGCGCCTACTACTTTGGCGAT
GTCTCTGACACCGTAGACATCCTGATTGGTTTCCCCGTCAGCCCCGCGCAAGCAGAATCC
CTGCGCCGCGGCGCATTGAGCCAATCCGGTGGCGACATCGATGACGTTGTCCTCCACCAC
TTCCGCGACATGAAAACCATGCACAGCCGCCACTCCGGCCCCTTCGATGGAGTCGAGCGC
GTCTGGGACGAAATCCTCGATGAAGTCGAAGACCTCGGATGCACTCTGCCATCCAGCAGC
ATCGGTTGGGAAGAATACATCGAGGGCCCAGCCACCGCTGATACCTGCGACCAACTGGCC
TCTGAAGTTTATGTTCAGGTGTGCCAAGCACCGGTGAAGTCTGCA

>RXN01301-downstream
TAAAGATTCACCCGGAATTTCCC

>RXN01306-upstream
TGTTTTAGAGGTAGAGCGAAACGTGCCTGTAAAACTGGCGCTCGCTGTGCTCGAAGACCA
CCCAGACAATCACCCCGCTCCGAAGGAGAATCGCTAAGCC

>RXN01306
ATGACTGAATGGTATGTCGTTTTACCCGCCACTATTCTACTCATCGCGCTGTCTGCGTTT
TTCGTCATCATTGAGTTCGCTTTGCTTGCAGCTAGGCGGAACCGGTTAGAGGAGACTGTG
GAAACCTCGCGGTCTTCCCGCGCTGCGTTGCGAAGCCTCAATGAACTTACTCTCATGCTC
GCGGGCGCGCAGTTGGGAATCACCATGGTGACTTTCGCGTTGGGTGCTATCACGAAGCCG
TGGGTTCATTATGCTTTGATGCCGCTCTTCGAATGGGCGCGTATACCGCTGGTTATGGCA
GATGTCATTGCGTTTATTTTGTCGCTGTTTATCGTAACGTTTCTGCACTTGGTCATCGGC
GAAATGGCTCCGAAATCCTGGGCAATCGCGCATCCGGAGACGGCACTTCGAACTATCGCG
ATTCCCGCACGGGGCTTCATTAACCTGTTTCGTCCATTGCTGCAGTGGATCAACAAAATG

GCGAACGATTTGGTCCGCAAAGTTGGTGAAACTCCCGTTGATCGAGCTGCAGCTGGTGGC
TATGACACCGATACCCTCCATGCCCTCATTGAGCATTCCCGAGAAACTGGCGCTCTGGAT
CAGCAATCCGCCGCCCAAATCAGCGGAATTATCAAGCTGGATAAAATCACGGTCGGTCAA
ACCCTGACCGCATCTCCATTTACGCACAGCGCCAGCGCCACGGTTGCTGAGGTGCAAGCC
GCAGCTCAGCGCAGTGGCAGCTTGCGTGTGCTTATCGACGCCCCCTCCCACCTTTTCCCA
CACGTCATTCATGTGCGAGACACCCTTGGTGCCTCGCCAGACGAGAAGGCTTCGAAGTGG
TCTCGCCCAATCCTCACCGTTGCTGAGACCGACACGTTACACCAAGCGCTGGAATACATG
CGGGAGCATAACGAGCAGATCAGTGCGGTGCTTTCCGCTGATGGGAAAACGGTGCTTGGT
GTAATAACTTGGGATCACATCTTGAAATACCTGTGGCCTGCATCGGTG

>RXN01306-downstream
TAGCTAATTTGAGGTGCGCTGAA

>RXN01324-upstream
TCCTCAACCCAATGCTTGCCGGCATTGCGATGGCCTTCAGTTCAGTTTTCGTCGTCTCCA
ATTCCTTGCGTCTGCGAGGATTCAAAGCAAGGAGCAACTA

>RXN01324
ATGTCCAACAGCGAATGCCACACCCACGGTTACATCGAAGAAAAGCAGCGTTACCTCGCA
CGCCTCAAAAGAATCGAAGGCCAAACCCGAGGCATTCACCGCATGATCGACGAGGAACAA
TACTGCATCGACATCCTCACGCAGATCTCCGCAGTGAACTCCGCACTCAAAAACGTGGCG
TTCGGCCTCCTCGACGATCACCTCGCTCACTGTGTCAAAGAAGCAGCTGACCTCGGCGGC
GACGAACTCGACGCAAAACTCAAAGAAGTTTCCGACGCCATCGCCCGCTTCAGTAAGGCC

>RXN01324-downstream
TAAACGGATCCGGTGGCATTGGA

>RXN01326-upstream
GTCCTTGAGGCTGCTTACACTCTACTTATTGTAGAAATGGGAGGGTCGTGGCGTCGAAAA
GCAAACATCTTTTAACGCTTTTGGCCCGTATTATGGTGGC

>RXN01326
ATGGCTTTCCCCGTGACAGAAGACAAAATCCTGGCAGCTGAGGAAACCCTTGGCAGGCGC
CTCCCCGAAACTTTGCGCGAACGACTACTTCAAAACAATGGTGGCGAAGTCATCGACAAT
GAAAACAACGACTGGATTCTCCATCCAGTTCGTGATGACAGCGACCGAAAAAGGCTTGTC
CGAACTGCCAACGACATCATCCGCGAGACCGAATCTGCACGTGAATGGGACAATTTCCCC
GAAAATGCGATCGCAATTGCAAATGACGGAACGGGCGACTTAATAATTCTGCTTCCCGAC
GATGATGCTTTCTACATCTGGTCGCACGAAGATGAACCCCTGATCGAAACTGAACTTGAG
GATGCC

>RXN01326-downstream
TAAAACAGCTGGACAGAATTCGA

>RXN01331-upstream
CTAAACTCGTCTCTCGTATCTTTCAGTCATTTATGTCTGATAAGCAGGCGCGTGCGCCAC
ACAATTGGCACAATCACAAGAAAGTGAAGTGGGAACCTAG

>RXN01331
ATGCTGACGACACTATGGATTGCGGTGTTGGTATTTACCGTTCCAGGATTGGTCGTCTCG
TGGGTTTCTGGCCTTAAAGTGCCCTGGGCTATCGCAGCCTCCATCCCAGCCACCTTCGGT
ATTTACGGCCTGTCCGCCTGGTTGCTGGGCTTGTGGGAGATGCGTTTTGATCTCCATTCT
GTAGTTATTTCCACATTGGTTTTCGCTGCGGTTGCTTTGGTATGGCGCTTGTTTTTTGTC
GGTGGTTGGCTTGTACGTCGGCGTAAAGCACGTATCCGCAGGCAGACGCTCGCGGATGAA
GAGCGGGCAGAAAATGCTGAGGTATCTGCAGGGGAGCCTGCCGAATCGAGCACAAACGAA
GCAGCCGAATCTGAATCTGAAACCTCGGAGCGTCGCGGAATCTGGCGCGTGATCTTTGAT
TACATGCGCGACGGTGGCATCTTGGATCACCGTTGGCTGCTGCCTGCCGCAGGTGCTATC
ACTGGTGCGTGGCTGATCATTGATCGTGCCGTTGATCTGCTCTTGAGCACCGAGCATGGT
TTGGGCGATATCGTCCAAGGCTGGGATGTCCATTGGCATGCTTCGACTGTCCGTTTTATA
GATGAGACCGGCATTGCGTCATCCACGATGATGGGGCAGCTGCGCAATATTGAAACGCAG
CAAGATCTGTTCTACCCAAGCGCATGGCATGCTGGTGCATGGGTGCTGTCGGATGTCGGA

AATCTGACGATTGTTGAAGCCACCAACCTCACTGGCATTGTGCTGTCCGGATTGTTGCTG
CCGTTAGCTGTTGCACTGATTGCATGGCGGATGATCAACAATCGTGGACTGACCGCGCAG
ATTGGTGCGGGCTTTGCTGGACTGATCACCATTGCCTCTCCGGTACTGTTCTGGGTTGGT
AACTACGTGGGTGCGTGGCCTTATGTTGCTGCGATCGGTGCTTCAGGTGTGGTGCTTGCG
CTGTTTATGTCCACTCCGTCTGTGCCGGTAAGAATCTTTGCCGCAGCATTGGCGTTCATG
GGTATGTTCCAGCTGCATCCAGCCCCATCCACCATCGTGATCATGGTGTTGCTGCTGTGG
TGGCTGCTCAAACTCGTGGTGGTTCCAAGCCAGAAAGTGAAGGGCTGGAAGGCGGGCATC
GGTATCCGTTTGAAGGATGTCGGCATCCTGGCCATCACGGGCATCATCGGTGTGCTCTTC
ATGCTGCCTCAGGTGATTTCAGGTTCCGAACAAACCGAAGATGTGCTGTCATATTCTGCT
GAGGAACAAGTCACCCGCAGCGAGTCCTGGTTGGTGTCTATTTTCATGGAGACCCGCCAT
GTTGATTTCTTCGGAAATATTGACATCGTCCCAGTGCTGGTATTCGCAGCAATCGGTGGC
GTGGTTGCTTTGGTGTGGCGCGGAAACTTGTGGGCGCCGGTGTTTTACTTCGCCAGCGTT
GCGTTGACCGCTAACTCGCTGAAGCCTTTTGAAGAGCCGTGGGGTGATTGGCTCAACATC
GTGGGCGGTCTGCATTACTCCACAGGACACCGTTTGATCATGCCTGTCGCCATGTTCACT
TTTGCTGCCGCAGGTATCGGCGCTGCCGCAGTGATCCGTTTGATCTGCTTGGGACCAATA
AAGAAGTTCACCACTGTTTCCGGTGTTGTTTCTGTGGTGATGGCTCTTGTTGTGGCTGTG
CCATTGCAGACTTGGGCGAAGGATTTTGTAGAGGAAGGATCCGAAACCACAATCCTTGCG
CCACACAATGATGAACGTATGGTGAGCAACAACGACTTGGCTGCCTGGGACTGGTTAATC
CAACAGCCAGGTGGAGCTGACATGAACATCATGGGTGACCCCGCAGATGGTAACGGCTGG
ATGTATGCCTACAACGGCTTGCACTCCGTGGCCCGCCACTATGCATGGCCAGCAGCAGGC
GAAGGCTCTGCCACCGCGATGCTGTTCTGGTGGCCTCAACTTCTAGGTGTGGGCACCGAT
GAAAACCCAGATCAAGTCAACGATGTGGATCAGGCTGCTCGTGATCTCAACGTCGGCTAC
TTCATGATCAGTCCGTGGACGTTCTGGGATTTCCAGATCCCCAACTTCCGCCAGATCGAT
CTGCTGTGGCAAACCCCAGGCGTGACACCGGTGTGCAAGAAGGGCGACTCGGTGATCTTC
GCAGTCAACGATATGTTCACTGACGCCGAACTGGATCAGATGCGTGCACCTGGTAATTCT
CCAGAACCACTGCCAGAGCTTCCTACCTTGGGCGAGCTTGGGTTGGCTGAAACTGAAGAC
GAGGTAGATCAGACTTATTACCATCGTCCAACGGTTCCTGCTGGTGTGAACTCAGAGATG
CCTTCAGCCGAAACTCTGTATGCACCGGATCCAACGAAGCCGCATACGGTCCCTAAC

>RXN01331-downstream
TAATCACAAAGAGTATTCAGTAA

>RXN01337-upstream
GCTGGCTATCCTCAATTCCGCTCGGGTCGCACTGCCACGCGGAGCGATTAGTGATTTTGA
TACGCAAGAAAAAGTTTCTTAGCAGGGTAACCTAAATGTC

>RXN01337
GTGACATTTCGAGGCGGAAACACTGGCGCAAAGCACGCGGTCGTTGTTGGTTCTGGCCCC
AATGGGTTGACCACGGCGGCGGTGCTGGCCAAAGCAGGTTGGCAAGTAGATGTGTATGAG
GCGGCGCCAACCCCTGGAGGGGCGGCGCGCTCAGAAAGCGTTCTGGGGGAGGGGACTATC
AGCGATTTGGGTGCCGCAGGGCATCCTTTCGGGGTGGCAAGCCCAGCTTTTCACTATTTG
GGTCTGGAAGATCACGGCCTGGAATGGGCGTATTCTCCCTTTGCGATGGCCCACCCGTTA
GATTATGGCAGGGCCGGACTGCTGGAAACGTCACTCCCAGAGACCGCCAAAAAGCTTGGA
CCTGATGCACGTCGTTGGAAGAATTTGCACCAGGGCTTAACCAAAAACATTGATAAACAC
TTGGCCAATCTATTAGGGCCGGTGCTGAAATGGCCAGCACATCCGATTCGGATGGCAAAG
TTTGGCCCATTTGCGTTGCTGCCCGCGAAACGTCTAGCCAGTGCCGCTTTTGAAACAGAA
GAAGCCCGATCCCTGTTTATCGGTTCGGCGATGCACTCGGTGACTCCACCACACAAGCCG
ATGACCGCATCACTTGGATTGCTTTTTGGCGCTCTGGGGATGTCGCGAGGATGGCCGGTT
GCAGTTGGGGGAAGCGGACGGATCGTCGATGCTCTGGTCAATGTCATAAACCATCACGGT
GGCACCATTCACTGCGATTCACAGATTGATTCCCTCTCACAATTCCGCGACACCGATGCC
ATTATTCTGAACCAAACCCCCTCACAGGTGCTGAAACTCAAAGGAACTGACCTTAATGCA
GGGCTTCCGCAACGCATGAGCACCTGGAAACACGGACCAAGTTCCTACAAAGTGGACTAC
CTCCTTGACGAACCAATTCCCTGGAGCAATCCCCAGGTAGGCCAGGCCACAACCGTCCAT
GTGGGCGGAAGCTCTGAGGAAATCGCTTTCGCAGAAGCAGAAGTCGCAGCGGGGCGGATG
CCCGAACGCCCGTTTATCATTTTGTGCCAACAACAAGTGGCGGATCCTTCACGCGCCCGG
GAGGGGCGCCACGTCGTGTGGGCCTACGCGCATGTGCCGCGGGGTTTCGTCGATAAGCGA
GCTGCTTTATTAATCACTGCGCAGATTGAACGCTTCGCCCCCGGTTTCCGTGATCGCATC
GTGCATTCAGTGGATACCAACGCGGAGGATTTAGAGGCGTGGAACCCCAATCTTGTTGGC
GGAGACATCACCGCAGGGTCCGCGCTGCTTCGGCGAATGCCGACCAAAATCGGCGAGAAA
ACGTACATGGCATCCGCCTCCAACGCGCCGGGCGGGGGAGTCCACGGAATGCCCGGCTGG

TGGGCAGCGCAAGCCGTTTTAGCAGATCACAGG

>RXN01337-downstream
TAGAATTGCGACATGGAGCCCAC

>RXN01351-upstream
CTGGAGATTTCCGATTTCCAGCGCGCCCGCATCGACGCGAATGCTCAGGAATTGCAGGCC
GAGCGCGAGGCAGTGCGCGACTTGCTCTAATCTTTAACGC

>RXN01351
ATGACTTCGCTTTTCGACGCCCCAACCCTCCAACGCGTCACCGTTTTCACGGGCTCGGCG
CTCGGCAGTTCCTCGCTGTACACGCAAGCGGCTCAAACCTTGGCGAAAACCGCGGTAGAC
CGCGGCATCGACTTGGTTTACGGTGGCGGAAAAGTGGGGCTCATGGGTATCGTCGCGGAT
GCGTTCCTGGAATCAGGTGGCGAAGCCTTTGGCGTCATCACGGAATCACTTATGAAGGGT
GAGCTTGGGCATGAAAAGCTCACCGAACTTGAAATCGTTCCTGATATGCACATCCGCAAG
CGTCGCATGGCAGAACTTGGCGATGGTTTTATCGCCATGCCCGGTGGCGCCGGCACCTTG
GAAGAACTTTTCGAGGTCTGGACCTGGCAACAGCTGGGCATTCATCAAAAGCCCGTCGCA
CTTTATGATGTCGATGGTTTTTGGCAGCCCCTGCTGGAAATGCTTGAGCAGATGACCCAG
CGTGGATTTATCAAGCGAGACTTCTTTGAGTGCCTCATCGTGGAATCCGACCCGCATGCC
CTGCTAAAGGCAATGCAGACCTGGACTCCACCAGCACCAAAATGG

>RXN01351-downstream
TAACTAAATTGTGTGCTCGACGG

>RXN01362
AAATGGCTTGGCACGCCTGCGCAGAGCTTATTCTTAATCCCCCCAGTTACCCAGCATGCT
CGCACGGGCACCCACCTTTATGATTCCCTGCAGCTGCTGTTCACTCTGGTGGATAAAGGC
CACCACCCAACAGATGCTAAGGCTGTAGCTTTTGATGCCGAGGCTGGAGAAGAAGGCCTG
CACTTCCGCAACCTTTCAGCGGATCTCTTCCTCCCTGCAGCCACAGAACTTATTGATCGA
GTTGGTCTTTCCAATGAAGCCCTAAACAAGGTCTTGGAAAACCTCCTGCTCTCCCGGGTG
CAATCCGGTAAAGACCGCGGCTTTATCTCCTATGCCACCTTGGGTGTTACCGAGCTTGGC
CAAGTTTATGAGGGTCTGATGTCCTATACCGGCTTTATCGCCCAGGAAGATCTTTTTGAG
GTTGCACCACATGGCAAAGCCGATAAAGGTTCCTGGATGCTCCCGGTCTCAAAGGCTGAT
GAAGTCCCTGCCGATAGCTTTATCGAAGTTGATCAAGAAGCCCCTGGTGGCGGCGTAATC
AAGGTGCGTAAACGCCACCCGCGCGGATCATTTGTGTTCCGTCAGTCCTCTCGTGACCGC
GAACGCTCAGCGTCCTTCTACACCCCACAAGTACTCACCAGCTTTACTGTCACCCAGGCT
ATTGAAGAACTCCAGGCATCAAAGCGCATCACCACAGCCAATGATGTTCTCAGCCTCACC
ATCTGTGAACCTGCCATGGGTTCCGGCGCCTTCGCTGTGGAAGCAGTACGCCAATTAGCA
GAGCTTTATTTGGAATTGCGCCAAGAAGAACTAGAGCAGCAGATTCCAGCGGAAGACCGT
GCCAAGGAACTCCAAAAGGTCAAAGCGCACATTGCGCTGCACCAGGTTTATGGTGTGGAC
CTTAACAGCACTGCTGTGGAGTTGGCGGAAATCTCGCTGTGGCTAGACACCATGAATGCA
GAAATGGACGCACCTTGGTATGGCCTGCACCTGCGTAATGGTAACTCCCTCGTTGGTGCC
ACCCGTTCGCTGTATGCACCTAGTCTGCTTAATAAAAAAGCCTGGTTAACTGCTACTCCA
ACCCGCTATCGGCTTGATGATATCGCGCAGGCTATTGATGAAAACAAAGCAGAACCCCTC
TTCAACCACGGCATCCACCACTTCCTCTTGCCCTCTACTGGCTGGGGAGCCACTGCAGAT
GCCAAAGATCTTAAAGATCTTATGGCTACTGAAATCAAGGAGCTTAAATCTTGGCGTACT
TCCATCCGTGCGTCTTTGAGTAAAACTCAGATTAAGCAGCTCAATAACCTTGCCCTACGC
GTGGAAACACTATGGCGATTTGTGCTGATGCGTATTCGCATTGCAGAATCCCAGATCTCA
CGTAGCACTACTCTCTGGGGTCAAGAGCCAGCTGAGGTTTCGGAGGTTGTCACACGTGAG
CAAATTGAACAAGACCTCTTTGGCAATATTGATGGTGCATATAACCGTCTACGCTTGGTG
ATGGATGCTTGGTGTGCGCTGTGGTTCTGGCCTTTGGATGCTGTTGCTACCGCTGAGCAT
CCGGAGCGTCCAGCCCTTCCAGATCTTGATGAGTGGCTAGCCACCCTGACGGAGATTCTG
GGTATTGATCTCCCTCTGAAGTCCAAAAACGAAAATCAGATTGTCTTAGGTCCAGATACC
AATTGGCTAGCCATTAATGATGCCGAGGCTACTGATCTTGGTTTTTCTGGGGCATTGAGC
TTTGAGCGTGTTAGCGCGAATCACCCGTGGATCAATGTTGCCCGCCAAGTGGCTAAACAA
CAGAGCTTCTTCCACTGGGATCTAGACTTCGCCCACGTTTTTGCCAAGGGTGGATTTGAT
CTGCAGGTTGGTAATCCACCATGGGTGCGACCAGATGTGAACTTTGAGGATCTGCTTGCT
GAACATGATCCGTGGTGGGCTGTAATGAGTAAACCAACCCAGGCATCCAAAAAAGAACGC
CAGAAGAATTTTCACAACAATCCTAAGAGCCTCGAACATGTGGTCAGTGGTGCAGGTGAA
CCCGTGGCTACTTCTGCGATCCTCGGTTCGGTTACTCTCTATCCGCATCTTAAAGATCAA
CGCCCGGACCTCTACCGGGGCTTTATGGAAAAGACTTGGTCTAATGCCTCCCCGGCAGGT

GCGATCTCACTGATCCACCCCGAATCCCACTTCACTGAGAAAAAAGCTGCCCCGCTACGT
CGGGGAGCATATGAGCGTCTGCGCCGCCACTGGCAGTTCATTAATGAGTTGATTCTTTTT
GACGTCCACGACTTGGTTAAATATGGCGTACATGTCTATGGCGCTCCGCAGGAATCTATT
AACTTTTTAAGTGCTGCGTCGCTTTATCACCCACAAACAGTGCTTGATTCATTTGATCAT
GACGGTTCAGGTAATCTCCCTGGTCTTAAAGACGACAATGGCAACTGGGACCGTCGCCCA
CACAAGGACCGTATCCAACTGGTCAATGCCGATACTTTGACGGTGTGGAAGTCCATCCTG
GAGGATGAACAAACGCCATACTTGGATACCCGCATGGTTTATACCGTCAACACGGAAGCA
GCAGCAGCGTTGGAAAAGTTGGCTTCTGCACCTCGTATCAAAGAACTCGGGCTGCAGTTC
TCCAGTGGCTGGAATGAAACCACCGATAAGAAAAAGGGATACTTTGACGTTGGTTGGGGC
TACCCAGCTTCCTGGTCTGATGCCATTTTGCAGGGGCCGCACCTGGGTGTTGCTACACCA
ATGATCAAGCAGCCCAATCCGACAATGAAGCATAATCAAGATTGGTCTGAAATTGATTTC
GAGGCCATTCCTGCAAACTTCATACCTGCAACGGCGTACCAGCCCGATCGCCAAACAAAG
CCCACTTATGATGCTGACTACGGCACCTGGACTTTCGGGGACAAGCAGGTACCAGTTGCA
GACACTTTCCGAATTGCATGGAGGGAGATGGCTGCCACCACGGGATTTAGGACTGTCTAC
CCATCAGTAATTCCACCGGGAGCCAACCATGTGCACACAGTTAATAGCGCTGCATCACGT
TCAAACTTAAAAACCATTCTCGTTGGAGCACAGCTTGGTGCAATTCTAAGTGACTATTTT
GCTCGGTCCTCGGGTTCAAGCCACATATTTAACGACATTGTTCGCAAGATTCCACTTCCA
AATTTCACATCCTTGGAAAAGCAGTTCGCCCGCACATACCTCCGCCTCAACTGCCTGACC
TCAGCTTATGCCCCATTGTGGGAAGAGATCACCGGTGAGCCGTGGGATGTTCAGGTGCCT
TTGCGCAATGCCGAGCAACGTCGAGCAGCGCAAAACGATATTGATGCCATGGTGGCATTG
TCTTTGGGTATTAGTGCTGATGAGCTGTGCATGATTTATCGCACTCAATTCCCAGTGATG
CGTAGATATGATCAAGAAGATCATTTTGATGCCAATGGCCGTAAAGTTCCTAAAGAGATC
ATCAAGCTGCAGCAGAAACTTAAAGATGGCCAAGAGCTCAGCGTGGAAAAGCGCACCTGG
GTGCATCCCCAATCAGAAGTGTCCTATACCTTTGAATATCCTTTCCGGGTGTTGGATCGT
GAAGCTGATCTGCGTGCTGCATATGCAAAATTTGAAAACCAGCTTAAGGAGCCA

>RXN01362-downstream
TAGAGCGCTTATGTCCTCACTCA

>RXN01379-upstream
CAGAAATTGAGTAATGCTCTCGAGCCAGACCGTGAACTTATTAGGCCTTTGGCCGTCATT
CTTCCGCAGCCCGCAACTTTGAACACCGAGGTTTAACACA

>RXN01379
ATGAGTGCATTTGATTCGATCCTAAATGTTGAAGAGTGGATCAGTGACCACTACCTCACC
AATGACGATGCCAAAGGTGCCTCATTTTCCAAGCGGGTGCGCGAGCGCATTAAAGAATGG
AAAACCACCGAGGACGCAACCCAGCAGAGTGGCCCTTTAACTCGTTTTTCCAGCAACCGC
CTGCAGTTGCAGCATGCTCTTTCTGAGCTTGACGACGCCACCACCGCCGCCAGTTTAGTG
GCCTCTGCACTGGGGTATGGTGTCCCCAGCGCGCGCCACGCGCAGCGCGGCTCCGACACA
ATATCCTATTCCTCTTGGGTGGGAAATGCCGGCAGTGTGGAATTTCTTGCAGCGACTCCC
GCTGAAAGCTTTGAAGAGAACTTCCGATCCCTTCCCCTTGAGCCAGTAGCGGTCAATGAC
AAGCCCCAGGATATCACCGCAGCCAAATTGGTGGGCCAGATTTTCCTTAGTGATACTCCC
CCTGCTTTTGTTGTTATCACCGCTGGTAAATGGGTGGTTTTAGCCGAGCGTGAAACCTGG
CCTCTAGGCCGCCACCTAGCTATTGATATTTCCCTGGTGGTGGAACGTAATGACACCAAA
GCCCAGGGTGAGATGCAGCAGACGGTCGTAGCACTAGCCCGCGAAAATACCGAGCGTGCC
GCCGATGGCACCACCTGGTGGGAAGAAACCATTGAGCAATCCCGCGAACATGCTGTCAAG
GTTTCTGGCGAGCTACGCAGTGCGGTGCGTGAATCCATTGAAATCCTGGGCAATGACGTG
CTCACACGCTATGAAGCTAAAGAGCTCTCCACCGCTGAGATCGACGGTGGCGAGCTAGCT
AAGCAATCTTTGCGCTATCTCTACCGCATTTTGTTCCTGCTTTTTGCCGAGGCTTCACCA
GAGCTTGAAATCCTGCCAACCGGCACCCCGGAATATGACGAG

>RXN01390-upstream
CGTCCAGATAATCAATCTGCGAAGCCAGTGGCTTCCGAAGCTCCAACAACTATTACGCCG
GCAAGCTCTGGTGCATTAGCATCCGATGCTCCGACGTCTT

>RXN01390
ATGTTCAGGCGCAGCCTTCCCAGCAACAAGACATCCTCAGCAAGTTCCGCCAGCTCCGCC
GACACAAGTTACTCAGTCAGATTAGGCCGTCCTGAAGAGCCTGGTTACCAGCCAGAACCG
TCTTATTCGGAGCCTTACACTGACTCTGATTTCGCGCCAGCAGGTGCGGCCGCTGCGGCA
GCTGCAGTAGCTCCACCAATGATTGCGGAACAGCCACAAATTGTTGAAGATGCCCGCCGA

GGTACCCTCGATTTCGGCCTGTTGATTATCCGCGCAGTCATTGGTGTCTATTTGATCGTC
CGTGGAGTCTTTACATTCTTCACCCTTGGAGGATCTGCCGGTCTTGCTGGCCTCGAGGCA
GAGTTCGCTGGTTACCAGTGGCCTGAAATCCTCGCGATCCTGCTTCCATCTATTGAACTT
GCGGCTGGTGTCTTCCTGCTCCTTGGTCTGATGACCCCAGTGGCAGCAGCGGTAGCCACG
GTGGCGACATCCTTTACCACCCTTCACCAAGTCAACACTCATGAAGGTGGTTGGGGTGAA
CTTAGTGAGCCATTGATGCTGGCACTGATCCTCACTATCGTGGTTGTCGGACTTCAGTTC
ACCGGCCCCGGCAAGATTTCCCTTGACTCTGGCCGAGGTTGGCAAAGCGTCCACTGG

>RXN01390-downstream
TGAGCTCGTGGATCTTCGTGGTC

>RXN01391-upstream
ATGGTGTGAAACCATCATGGCTCGATCACAAAAAAGAACACCTGCTATCAGGTCAACCAA
AAAAGTTAAAAGTGTAATATCCAGCATCATCACGATTGCC

>RXN01391
GTGGCTGCAGTCGCTTTTGCAGCTTACGTTATAGATGGTGGGGTAGAAGAGGCGTCTGGA
ACACCGACGTCTTCGGAAAGCTCGGTAGCGGCAACTGCTCCAGCGGCATCTAGCGAGACT
GCGGCTGAATACCGTGCGATGCTCGCTTCCCTTGACGTTAAAGGTCGTGCGCCAGGAACA
GGATATGACCGCGAATTATTCGGACCAGCATGGACCGACACTGTTTCCGTGGAATATGGA
CACAATGGCTGCGATACCCGCAACGACATCCTGCAACGCGACCTGGATGACATCCAACTT
CGCGAAGGCACCAAGGATTGTATCGTCACGAGCGGCCTGCTCAGCGATCCATTTTCTGGC
GAACTTATTGATTTCGTTCGCGGTGAACGTTCCGGCGACGTGCAGATCGATCACCTGGTC
CCATTACATGACGCATGGGTCAAGGGAGCACAGCAGTGGGATGAGCAAACTCGAAAGAAC
TTTGCCAACGATCCCGACAACCTTCTCGCCGTTAAAGGTACGCTTAACCAGCAAAAAGGT
GCAGGCGATGCAGCAACCTGGCTTCCACCAAACACAGCTTTTAGGTGCGATTACGCAAAG
AAAATCATCACCGTTAAAGATCGCTACAACGTGTGGGTGACTGAGGCTGAAGCAAGCGCC
CTGGAACGCCAATTAGATACGTGTGCTGCA

>RXN01391-downstream
TAACAGTCACATAAGCATTTGGG

>RXN01400-upstream
GAGCAGCTATCACCCTTATGCATCGGCTCCGGGTGAGGCGGTGCCGGTGTCCTTTGATCA
GCAACGACATGTGGGTGCCGGCGAGCGACCGGGTAGTTGG

>RXN01400
ATGGCGATTAGTGTTTCTATGCCTAAGGCGATCAGCCGTGAGGAATTGGAGCGCGCGTGG
CTTGAAGTGATTGAACGGCACGGCACCTTGCGCACAGTATTTAGCACGGGAATGGGTGGG
GAAGTGCAGCAACACCGCATTGATGTGGGCCCGGGAAAATGGATTGACCACGCCGTTGCG
CCTGGTGAGAGCATTAATGAGGCGTTGCGGGCGGTGTTGAATCGGCAGTGTTCGCCGTAC
TCGAGGCCATCGCATAGTTTGTGCATTATTGATGCGCATCCGCGTCCCACGGTGATTATT
GGTAGTGATCATTCGCATGTGGATATGTGGTCCATGCTGGTGATTGTGCGCGATTTGTTG
GCTGCGCTCGATATGGAACTTCCCGTTGAGCCGCCGTTGGCGTTTGAATCGCACACCGCG
GAACTCCTCGCGGCTCCACCTGCACCGGAGCGGATTCACCAGCGGTGGCGTGAAATTTTG
GAAGCTGGTGGTGGAAAAATGCCTCAGTTCCCGCTTCCGCTTGGCGATGCCATCTCCATG
CCTGAACGCGTTGAAGTCCGCGACATTTTCGGGGTCAATGGCTTGGCGATTTACTCGGCA
CGCGCCCGCGCACAACAGGTAAGCTCCCTGGCCTTGACTATTTCAGTGATGGCTGATGTT
ACGGCGGCGCTGGCGGACCTTCCGTTGCGTGCTGTATTCCCAGTCCATAGCCGTTTCGAT
CAGCGCTGGCACGATAGTGTCGGGTGGTTTATCTCCAATTCGGTCATTGAGGTGCCAGAT
TCCGATCCTCACACTGCAGCCCAAGCTGTTCGCGAGGCTGTTTCTTTGGGAAGCTACCCG
CTGGCTGAGCTGCTTGAACCGTGGGGTGGCATGCCGGAAACGCCAGGAATGTTTGCTATT
TCTTGGCTTGACCTGCGCCGACTCCCAGTGAGCATTGACGATATTGGCCTCCAAGCCCAG
TATGTCAGCGCTTCACTGCGCACCGATGGTGTGATGCTGTGGTTTATTTTGGATCGCTCC
GGCGCGCACCTTCGCTGTCGTTATCCTGACTCTTTGGTGGCGCGGGAAAATGTAGGCCGC
TGGATTGATGCGATTGTTGCTCAGATGCGCGCCGAAGCTGGGACGGTGAATCTGCAGGCC
GGCGGGGAACAGCTGACACTTCGGCATGGAACTCGCGCCGATATTTCCGAGATCGCCCCG
CTACTTGCCCGAAACGCAGCTGACCCTTGTGAGCTGGTGGATCTTGAACATGCCCTTGAC
CTGCTGACACACGAGTCTTCGCATTTCCTGGCGGTGGTTCGAAACGCTCGTGGCAAGATA
ATCGCAGCGATGCAGTTGACTATTGTTCCGGAGTTTTCCCGCGGTGGTGCGCTTCATCTT

CACATCGAGGGGCCGTTCATTATTCCGGAATATCGCACCACCGATTTGGATAAAAAGCTG
CGCGCCTGGGCTGTGGAGCATGGGCGTGCGCGAGGGGTGAAGGTTGAGGAGGTGGTGGGA

>RXN01400-downstream
TAGTTGGTTTATTGGCGCCTCGT

>RXN01403-upstream
GTGCGTCGCATACGGTGAATTATCTTTCGGCGGATCGTTTCCGCACGGTGTCGAGTTTCG
TAGAGTTTGCGGCCGATCGCGGTATTCAGGAATTCAGCCA

>RXN01403
TTGGTGCGCGGTCGGGGCTATTTCAATGCGGTGGATATTTATGAGACCTCCACGCAACCT
GACCAGGAATTTCCTTTCGATTTTGACACTTTTTCAGCCGACCCCACGCCGTTTCAACTC
TCTGCGGTGCGTGCCGATACCGGCGAGACCGTTTTTTTGGGGCAGGGAAGACACCCCGGAT
TTGAGCGCTCTGATGAAGCGGGTTCGCGCGTCGTCGACCATGCCTGGTTTCATGCCGATC
ACCTACATCGACGGCCATCCATATGTCGATGGCGCGGTCGGGGAGACCGGCGGTTTGATG
CTACAGCCGGCCATCGATGCGGGCTTCACCCGCTTTTTCGTTATCGCCTCCCGTCCGCGC
GATTATTGGCGCAAGGAGATCGGGCGCCCGGGTTTCATCAAAGCTGCTTTACGACGTTTC
CCCACAATCGCCGACCTCACCATCGCGCGTCCTGCACTGTATAACTCGGTAAAGCAACAG
ATCCTCGACCTAGAGAAACAAGGCAGCGCCTATGTGTTCTTTGCGGACAACATGAACATC
CAGAACACGGAAATCAATCTGAAGAAACTCCGTGCATCTTTCGATGCAGGCATGCAGCAG
ACCCGCAAAGATTGGCCGGAGATCATGAGCTTCCTGAACCAAACCAGA

>RXN01403-downstream
TAATGAAGGTTTTTAGTCCAACT

>RXN01409
TGGGTGGATTTCCCCGACGTCACCGCACGTTTGGGGTATGAATACATGCAGCTGACCCCT
CATGTAGATTTCGGTCCTTTCTTCCGCCACCCCAAGGCAGACGATGATCTCGTGGCAGCC
CTGAAAAAGCGTGCCAAGGATGCCGGAGTCACCATTCCTGCACTGTTGCCAGTGCAGCGT
ATTTCCTGGCCGGAGGAAACCCAGCGTGTTGCAGCAGTACGCAACATCAAGCGCATCATC
CAGTTGGCCGTTGATCTGGAAGTAGACACCCTCAACACGGAGTTTTCTGGACGCCCAGAA
CGCTCCGAGGATTCCGAAGATGCCTTCTACCGCTCCATGGAAGAACTCCTGCCAATCCTG
GAAAAAGAGGGCATCAAGTTCAACATCGACCCACACCCTGATGATTTCGTGGAAAACGGT
ATTGAAGCATGGCGAGTCATCCGCGGTCTGAACTCCAAGCAGGTGGGCTTTGTTTACGTG
GCACCTCACTCATTCCACATGGGTGATCAGGCTGAGGCAATCCTGCCAGCAGTAGGCGAT
CGCCTTGGGGCTGTGTACCTGTCAGATACCTTCGACCACCACAAATCCCACGGCCTGCGC
TACATCACTAACCCTCCAGGCAACGCAGTGCGCGTGCACCAGCACCTAAAAATCGGTGAT
GGCGATGTGAACTTTGAAGAGATCTTCTCACTGCTGCGCTCTACCGGTTACCTTGACCGT
GAAGATGCACTGTTGGTCTCCAACGTGTTTGCAGAAGATGAAGCAGCAGATGAAGTATCC
CGCTACCAGCTGGAGAAAATCCGCTCACTCATCGAAAACGCA

>RXN01409-downstream
TAGAGTTATCTCGAAACTACCAA

>RXN01422-upstream
AATGCATTGAAATCGTGATCGCCTGTTATTGTTTTGTACGTCGAATAACAGTCCCACAAC
AGTTCCCCAAAAGGTGCGAGCGGGAAAAGGAGAAGCAAAC

>RXN01422
ATGGCTCAGCGAAAACTGGCCTCTGTGATCGGTGCAGCATTGGCAGCATCTGCTGTACTG
GTTGGATTAATGACACCCGCAACAGCACAAAGTAGTGGCAGCTCATCAACAGACATCACT
CGAGCACTCACCTCAAGTGGTGGTGTGGCTGATAGCCGTGCTCCTGAAGGTGGCGCAAAG
GTCGTTGTTTTCGGTGACTCCCACACCTCTGGCACCAATGCTCCATTCCGTACCGATGAG
CGTGGCTGCCTCAAGGGTGCAAACAACTGGGCAGATCAGCTGCAGTCTCAGCTGGGACTT
GGCGCGGGAGACCTCATTGATGTCTCCTGCTCCGGTGCATCGATCAACTCTGATGGATTC
CACTTCTCTGATGAAGTCCGCCATGCTGAAGCTCGTGGCGCAATCGGCCCAAACACCACC
GATATTTTTGTTCAGTTGGGCAAGAATGATCAGTGGGGCCTTTCCAATGTGAACCTTCTG

CAGTCTGTTCAGACCTGCTTGACTGATGTGTTCGCTGGTTGTGGCGATGCTGCGGTTGCT
GCTGGCAAGATGCAGGATCCAAATGCAGTTACTGCTGAAAACTATGCAGAGCGCATGAAG
CCAGTCATTGACTACTTGAAGTACTACGCACCAAACGCAGAGATCACCTTGGTTGGTTAC
CAGGAATACACCGCTCGCAGCGGAAGTCAGGTATGTGTTCGCCTTGGTGGAACCCCACTG
GTGAAAAATGATGCACCTGCGCTGGTTTCGTTCATGAACAAGTTGGACATGGCGATTGAT
GGTGCTGCTGGAATCCTCGGCGTCAGCCACGTTGATCTGCGTAGCGCGACTGAAGGGCAC
GACAGCTGCTCCAACGATCCTTGGGTCAACGGTGTCTTTGATGCACGTGCAGAAATCGTC
GGCGGTCCGTGGCACCCATCTGTTAAGGGAGACTCGGTTACTGCAGGGATCCTGCGAGAT
CGAGTAAACGCC

>RXN01422-downstream
TAAAGATGACGTCGAAAAGCATT

>RXN01434-upstream
GGTTTCCTGCGCACCGTGATGATTGGTGCGGCGCTGTCGCCGGCCATCGCTTCGGCGTTC
AACACTGCCAACACGCTGCCCAACCTGATCACTGGAAATC

>RXN01434
GTGTTGGGTGCGGTGCTGACATCGCTGGTTATTCCGGTCCTTACCCGCGCGGAAAAAGAA
GACGCCGACGGCGGTTCCGGGTTCTTCAGGCGGCTGCTCACCCTGTCGGTGACGCTGCTG
GGTGGTGTCACCATCCTGTCGATTATCGGCGCGCCGCTGCTGACACGGATGATGCTGTCC
TCTGAGGGACAAGTCAACGTGGTCATGTCCACGGCCTTTGCGTATTGGCTGCTGCCACAG
ATTTTCTTCTACGGCCTGTTTGCCCTGTTCATGGCTGTGTTGAACACCCGTGAAGTGTTC
AAACCCGGCGCGTGGGCACCTGTTGTCAACAATGTGATCACCTTGACCGTGCTGGGCGTG
TACATGGTGCTGCCTGCGCGTTTGCACCCGCATGAGCAGGTGGGCATTTTTGATCCGCAG
ATCATTTTCCTCGGCGTGGGCACCACCCTTGGTGTGGTTGCACAGTGTCTAATCATGATT
CCGTACCTGCGTCGCGCGGGCATTGATATGCGCCCTCTGTGGGGTATCGATGCGCGTTTG
AAGCAATTCGGTGGCATGGCGATGGCGATCATCGTGTACGTGGCAATCTCCCAGTTCGGT
TACATCATCACCACTCGCATTGCGTCGATTGCAGACGATGCTGCGCCGTTTATTTATCAG
CAGCACTGGATGTTGCTGCAAGTTCCTTATGGCATCATCGGCGTCACCTTGCTCACCGCG
ATTATGCCGCGACTGTCCCGCAACGCGGCAGACGGCGATGATAGGGCAGTAGTCTCTGAC
CTTCAGTTGGGTTCCAAGCTAACCTTCATCGCACTGATCCCCATCGTGGTGTTCTTCACC
GCCTTCGGTGTCCCTATTGCCAATGGCCTTTTTGCCTACGGCCAATTCGATGCCAACGCC
GCCAACATCCTTGGTTGGACTCTGAGCTTCTCTGCTTTCACGCTGATTCCTTACGCTTTG
GTGCTGCTACATCTGCGTGTGTTTTATGCGCGTGAAGAGGTCTGGACCCCAACCTTCATC
ATCGCCGGCATCACCGCCACCAAGGTCGTGCTTTCCCTGTTGGCACCGCTGCTGTCGAGC
TCCCCGGAGCGTGTGGTGGTGCTTCTTGGTGCGGCCAACGGTTTCAGTTTCATCACCGGC
GCGGTCATCGGCGCGTATCTGTTGCGCAACAAACTCGGCCTGTTGGGTATGCGCTCTTTG
GCTAAAACCTCCCTGTGGGCGTTGGGCTCTGCGGCGGTTGGTGCAGCAGCAGCATGGGCG
TTGGGGTGGCTGATTCAAGCCGTCGTGGGCGATTTCTTGCTGGGCACTCTAAGCTCCGTA
GGCTACTTGTTGAACCTGGCTGTGTTGGGTGTCTTCTTCATCTTCGTCACCGGCATCGTG
TTGTCACGTTCTGGTTTGCCGGAGGTCCAAAACTTGGGCCAGGCACTGACCCGCATCCCA
GGTTTGAGCCGGTTTATTCGCCCGAATACCAAGATCTCTTTGGATGTCGGCGAAGTCTCC
GAGCAGGATTTCTCCACCCAGCTGGTCGCGCCAAGCGAGTTCGCAGCAACCCCTGTGCCG
CCACCGATGTCCGCCGGTATTGTCCGCGGACCTCGCCTGGTTCCCGGCGCCCCAGTCGGC
GACGGTCGTTTCCGTCTGCTCGCCGATCACGGCGGCGTCCAAGGCGCGCGTTTCTGGCAG
GCCCGCGAGATCGCCACCGGCAAGGAAGTCGCGCTGATCTTTGTGGATACTTCCGGCAAC
GCCCCATTTGCGCCACTGTCTTCGGCAGCCGCAGCGGGCATCGCCTACGAGGTGCAGCGC
CGCACCAAGAAGCTGGCCAGCTTGGGCAGCTTGGCGGTAGCCCCCAACATCCACTCCGAG
GCGTACCGCAACGGTTGCCTCATTGTGGCCGATTGGGTGCCTGGCTCCAGCTTGAGCGCC
GTCGCGGAATCCGGTGCCGATCCCCGCGCCGCCGCGTTCGCGCTCGCGGAACTAACTGAA
ACCATCGGCGAGGCCCACGAGATGGGTATCCCGGCCGGCTTGGACAACAAGTGCCGAATT
CGTATCAACACCGACGGCCATGCCGTCCTCGCCTTGCCGGCGATTTTGCCCGATGCCTCA
GAGCTCCGCGACGCCAAGTCCCTGGCCTCGGCCGCCGAGATGCTTATCGACGCGACCCTC
GCTCCCAGCGACGTCAAGGCAATGGTCACTGAAGCCCAGGGGCTAGCTACAGAAGACAAT
CCCGATTACGCATCACTTGCCATGGCGATGCGCACCTGCGGACTGTTCACCGAGGAACCA
ACCCACCTTGTGGTGAAGAAGGAAAAGACACCAAAGCCTGCGACACGTGATGGTTTCGGT
GCCTCCGACTACACCGTCAAGGGCATGGCAGCCATCGCCGCTGTGGTGATCATCTTGGTT
TCCCTGGTGGCCGCCGGTACCGCGTTCCTCACCAGCTTCTTCGGCAGCAGCACCAACGAA
CAATCCCCGTTGGCCTCTGTTGAAGCCACCACCTCTGCAACACCAGAACCTGTGGGGCCA
CCGGTCTACCTGGATCTGGATCAAGCCCGCACGTGGGATGACGGTGCAGGAACAGATGTC

ACCGACGTCACCGACGGCAACACCTCCACCGCATGGACCTCCACCGGCGGCGACGGCCTC
CTAGTTGACCTGTCCACGCCTGCCCGCCTCGACCGCGTCATCTTGACCACCGGCACCGGC
TCCGACAGCAACGTGACCTCGACCGTGAAGATCTACGCATTCAACGACGCCTCACCACAC
TCCCTGTCGGAAGGCATCGAGATCGGCACCGTGGATTATTCCGGCCGCAGTCTCAGCCAC
AGCATCCGCGATTCCTCCAAGCTTCCGGGTCAGGTGGAATCCGTGGTGATTCTGGTCGAT
GAGGTTCGTTCCTCACAAACCTCAGACACCAATCCACAGATGCAGATCGCTGAAGTACAA
CTTGTTGGTTGG

>RXN01434-downstream
TAAATTACGCGTTTGTGATTGAC

RXN01448-upstream
GTAATCTCAGCAGTTAAAAAGGGCAGTTCCGCATCAGGGGGACTGCCCTTTTTCGTGTCT
TCTCATGCTCTTGTGAATATGCATAGCTAATCTTGAGGCC

>RXN01448
ATGGCAAAGAAGAAACTGGGGACTGTCGCCAGACTGTCTGAACTGGATAAGTCCCTGCGC
AATAGATTGCTGCGGGTTCGTTCCCGACTGCTGTTTATTGTTCATTCCGCAATTGGTGCG
GGTGTGGCGTATTGGATCGCCGTGGAAGTGATCAAACACGGACAACCGTTTTTCGCACCG
ATGTCCGCGGTGATTATTTTGGGTCTCTCCGGAGGAGACCGCATCAAAAGAGCCACGGAA
CTCACCCTGGGCTGTGCTTTAGGCGTTGGTTTGGGTGATTTACTGATCATGCAAATCGGC
ACGGGCTATTGGCAGATATTTGTGGTAGTTGGATTAGCGCTGCTGGTGGCCTCGTTTGTT
TCACCGGCACCGTTGGTGAGTAATCAGATGGCCATTGGTGGCATTTTGATTGCCACGATG
TTCCCGCCAGGTGATGGTGGAAGCATTGACCGTATGATCGACGCCTTCATTGGTGGTGGC
GTGGGAATTTTGGTCATCGCACTTCTTCCCTCATCTCCTCTTGACGCAGGCCGGCATCAA
GTGGCCAACGTTTTGGGGATCGCAGCTAGTGTGCTGGAAGACGTGGCAGCTTCCCTAAAA
GCCAAGGATGCAGCCAAACTCAACAATGCTTTGGAAGCATTGAGAAGGTCGCAGGCGTCG
GTGAACAAGCTGGAAACTGCGGCATCTTCAGGCAAGGAAGCAACCACCGTATCGCCATTT
TTATGGGGAGATAGGGCCCGCGTGAGATCGCTGTATCGCATTCTGGCGCCAGTGGACAAC
GTCATCCGAAATGCTCGAGTCCTTGCGCGACGGGCAGTGGTGCTGACCGAAGACAATGAC
ACCGTCAGTGATGAACAAATCCACGTGATTGAGGAAATCGCAGACATTGCACTGCGACTG
TCAGACCTTTATGAGCACCACAAAGAAATCAGTGAAGCACTGGAAATTCCTGAGTTGGTT
AACCGACTGCGTCAACTGGGCAGTGAAGTGGGCGAGGACATCGCCGAAGATCGAGTGCTA
TCCGCACAAGTAATTTTGGCGCAATCGCGATCCATCATTGTGGACCTGTTGCAGATCTGC
GGCATGTCCAGGGAATCTGCGGTGGCAGTGTTGGTTCCGACCTCAGAGAGTCCGGCTTAC
CCTCCGGAGCTGTGGGATGACGAAGAC

>RXN01448-downstream
TAGCCTTTTATCGCGGTTCGGTT

RXN01459-upstream
GATTCGGCGATTCACGAATATCCACCCTACAACCTGTGTTCGCTTACAGCGTTGTTCGGA
TCGTAGCAATAGGAAATAGTTGCCTTGTAGATTGGTAAAT

>RXN01459
ATGAACTCTAATGGCTTTGGTTTCTCTTTTGGCAACAACGATGACGACGATGACAAAAAC
CGCAACAACGACCCATTCGGCCTTTTCGGTGGCAACTTCGGATTCGGAGGACAAGGTGGC
GCTGGTGGCCCCGGCGGATTAGGCGATATTTTAAACCAGTTCGGCCAGATGCTGTCCGGA
ATGGGAGATTCGATGAACTCCCCCGAAGCAGCAGGCCCGGTTAATTATGATTTAGCAGCA
CGCATCGCCCGCCAGCAGATTGGTCGCGTAGCGCCGGTGAAGGATTCTGAGAAGGAAGCA
GTCGAAGAGTCCCTTCGCCTTGCTGAACTCTGGCTCGATAACGCCACCCAGCTCCCCACT
TCCGGGCACCGCGTCGAAGCGTGGAATCCAGAAAACTGGTTAGAAAACACCCTGCCTGTG
TGGAAGCGTCTTGTCTCCCCTGTTGCGGAGCAAATGAACAAAGCCCAATTAGAAAACCTC
CCTGAAGAAGCCCGCGAGATGATGGGCCCGATGTCTTCTTTGATGAACTCCATGTCTTCG
ATGAACTTCGGAGTTCAATTAGGAAATGCGCTGGGCGACCTCGCAAAGCAGACCCTCACC
GGCTCTGACTTCGGTTTGCCTATCTCCCCAGTCGGCGTATCTGCCGTCCTGCCCGGCAAC
ATCGCCGAAGCATCCAAAGGCCTCAACGTGGCACCGCAAGAAATGCTCGTTTACATCTGT
GCCCGCGAAGCCGCCGCCAACGCCTCTTCAAGCACGTGCCGTGGCTTGTCGAGCGCCTCG
TTTCCTCCGTTGAGGAATACGCCGTCGGCC

>RXN01459-downstream

TAGAAATCGACACCTCACACATT

>RXN01460-upstream
GCAACATCGCCGAAGCATCCAAAGGCCTCAACGTGGCACCGCAAGAAATGCTCGTTTACA
TCTGTGCCCGCGAAGCCGCCGCCAACGCCTCTTCAAGCAC

>RXN01460
GTGCCGTGGCTTGTCGAGCGCCTCGTTTCCTCCGTTGAGGAATACGCCGTCGGCCTAGAA
ATCGACACCTCACACATTCAAGAGGCCATGGGCAACTTCCAAATGGACAACCCAGATCCT
GAACGCCTCCAGGAAATGATGAACGAACTCCAAGGTATGGACCTGTCCCCACGCATCGGA
TCCCGCAACGCCAACGCAGTATCCCGCCTGGAAACTCTCCTCGCACTCGTCGAAGGCTGG
GTCGACATCGTAGTTACCCAAGCCCTGAGCGAACGCATTCCATCACCGACGCCA

>RXN01460-downstream
TGAACGAAGCCTGGAAGCGCCGC

>RXN01471-upstream
CCTCCAACCAGAGCTATAAAAAAGGTTGTAGAAGAAATTTCTTAACATACATCGTTGTGT
TGCCAGGGGTTTAACAGATTAGTTGCTAAGGTCTGTCTCC

>RXN01471
ATGCAGAGTTTTAAGACGCTTGAATCTTGGCCTGTCGACAATGTTTCGGCCAGTGTCATC
TCCGACGGCGCCGTGCACTTTTACGGCGACGTCGATCGTGTTTTTGAACTCATGAGTGTG
ACAAAACTCCTGGCCACCTACGGTTTCCTTGTTGCCATCGAAGAAGGTGTTTTTGAGCTC
GATTCACCGATGGGTCCTGAAGGATCCACAGTGAGGCATCTGCTCTCACATGCTTCCGGC
GTGGCATTCGATAAGCCGGTAGCGGAAAAGGGAGTGGGGGAGCGCCGCATTTACTCCTCT
GCTGGCATGGACATCTTGGCGGATGCTGTTGCCGCTGAAGCTGAAATGCCGTTTGCAGAG
TATCTCCGCGAGGCTGTGTTCGAGCCTTTGGGAATGGAGAACTCTGAACTATGGGGTTCT
GCGGGCCACGAGGCGCGCAGCACAGTGGCTGATCTGACCAAGTTCGGCCAAGAGCTCACC
GCACCAACTCTGATCTCACCAGAAACCCTTGCAGAGGCTTTCCAGGTGCAATTCCCGGAA
CTGATTGGCACCGTCCCCGGTTATGGCATGCAGAAGCCGTGTCCGTGGGGATTGGGCTTT
GAAATTAAGGGACAGAAGTCGCCGCACTGGACAGGTGACTTGATGCCGGAGAACACTGCT
GGACACTTTGGACAGTCGGGAACATTCTTTTGGACTGTTCCAGGCTCAGGTCAAGTCGGG
GTTGTTTTGACTGACCGAAATTTCGGTCCTTGGGCTAAACCGTTGTGGACTGCCTTCAAT
GACGAAGTCTGGGCCGAGTTAAATTCA

>RXN01471-downstream
TAAACTTTTGCCGTAATTACGGT

>RXN01479-upstream
AGCGCTGCCCGTGCCATAAATTTCGAAGAAGCGCGAAACAGGTAGAGTCTAAGGTGTCAT
TCTTGGTACAAGTTTTATATTTAGGGAGAGTTATCCACAC

>RXN01479
ATGATCCAGTTAGTGATAGGCGCTGCAGCAGGCTACGTGCTTGGCACAAAGGCCGGCCGC
AAGCGTTACCACCAGATCAAAAAGGGATATGAGGCAGCGATTAACTCCCCTGCCACCAAA
TCTGCAGTAAACGCCGCCCGCAAAGCCATTGCCAACAAGCTGGATCCGCAGCCCCGCATG
AAGGAAGTAAAAAACCTGCGGACTGCGGACGGGCATGAAGTCCTCGAGCAAGACCAGGAC

>RXN01479-downstream
TAAATTACCCTCTAAACGCCCGG

>RXN01484-upstream
GAGTTTACTCTTAACCGCAGTAGTGCAGCCAGCCCTGAGGGTGGTGGCGTATTCGATGCT
CAGAACGCCTAATAATCGGCACAAAATTGATTCAATTTTG

>RXN01484
GTGTTGGGCACAGCTCAATATGATGGAGTTCCATCGAGGCAGTTTGCTGCTCGTTTGAGG
CATGCCGCGAAGCTGTGGCGTCTTCATGAAATCCAGCATGTATATACTGTCGGCGGAAAA
CTTCCTGGCGATCGTTTCACCGAAGCAGAAGTCGCGCGGGAGTATTTGATCAAAGAGGGC

GTGGATCCGGATCTGATTTTTGTCTCTGCAGTTGGCAATGACACTGTCTCCTCCTATGAG
GCGCTTGATCCGGAAAAGCTTGGTCGGGTGCTGATTGTTACTGATCCGAACCATTCGTAT
CGGGCGGTGCGCATCGCGCGACGCATGGGCTTTGACGCGAAACCTTCCCCGACAACCTAT
AGTCCCGCGAAGTTTCCGTCGATAGTTTATTTTCTGACCTTGTCCCATGAGTGGGGCGGG
GTAGTAGTACAGGACGTGTCGCGGCTCTTGGGTGAACGGGTGCCCGATAAGGTGAAGCAT
CTTTGCGCGCAATCCAAGGTCTGCTGCGCCCTTCGCGGCGTGCACGCCATGAGCAACTTC
GGAGGC

>RXN01484-downstream
TGAAAAAGTAGATGTACCCCTAT

>RXN01485-upstream
CTCAGGGCTGGCTGCACTACTGCGGTTAAGAGTAAACTCTTGGCTAAAAATCTTCTCACG
TTAACTAGTGTGCCAGCTGGACTCGTCTAAGGTGGGGACC

>RXN01485
ATGAACTTTAGTTTGGTGCATCTTCGGGAAAACGTCCGCCGTGTATCGGTCACTGTGGCA
ATTGGAGCTGGCGCGCTCCTTATCAGTGGACCATTTTTTACTGCTCACACTGCAGAAGCC
ACAGAAACATATGTCTTGGCTGAATCACCAGAATTTTACCAAGACAATGTCACTGACTAC
ACCGGCCAGATTTCCTCGTCCGATATCACCAACATTCAGGCTGCCATCGATGATGTAAAG
GCATCTGAACAAAAGGTTATTTTCGTTGTTTTCCTAAGCTCTTTCGACGGAGTTGACCCT
GAAACGTGGACGCAGCAAGCACTCCAAGCCAACGGCGGCGGAAACGTCTTGATTTATGCA
CTCGCTCCCGAGGAACGGCAGTACGGCATCCAAGGTGGTACTCAATGGACCGACGCTGAA
CTCGACGCCGCCAACAACGCTGCTTTCCAGGCACTTTCCCAAGAAGATTGGGCAGGCTCT
GCACTAGCGCTGGCAGAATCAGTTGGTTCTAGTTCTTCCAGCTCTTCGGGCTCGTCCAGC
TCTTCCGATTTTTCCGGCGCTTGGTTGGCTGCTGCGGGCGTTGGCACAGTGGCCGCTGGT
GGCGGAATTTGGGCCTATTCCCGCAGCCGCAAGAAGAAAACAAGTGCTGCAACCTTGGAA
GATGCACGCGAAATCGACCCGCGCGATACCAACCGCCTCATGCAGCTTCCCATGGAAACT
CTCGAACACCTTGCCCAAGAAGAGCTCACCTCCACTGATGACTCCATCCGTCGCGGAAAA
GAAGAGCTCGCTATCGCTACCTCCGAGTTCGGACCAGAGCGCACCCGCAGCTTCAACCGC
GCCATGAACCACTCCACCGGCACCCTGCAAAAAGCCTTTGAGATTCAGCAGCGCCTCAAC
GATTCTATCCCAGAATCCGAAGCCGAACGTCAATCCATGCTGGTAGAAATCATTTCATCC
TGTGGCCAAGCCGACGATGCCCTCGACGCCGAAGCCCAAAACTTTGCCGATATGCGCAAC
CTGCTGATCAACGCGGGCAGCAAATTGGATGCTCTCACCCAAAAATCCGTCGACCTGCGC
ACCCGCCTCCCCAAGGCCCAAGAAACACTCGCTGGCCTGCGCACTCGCTACTCAGCAGAG
GTCCTTGAAAGCATCGACGACAACGTCGACCTCGCCAGCGCTTCGCTCGACGAAGCAGAA
GAAGTCCTGCCACAGGCGTACGAGATAGAGTCCATGCCCGCAGGCGAGCAGGGCGGGCTT
ATCGACGCGATCCGTCACATCGAGCACGCCATCACTACCGCAGACAAACTCCTCGCGGGC
GTCGAGCATGCCGATGAAAACATCTCCACAGCCAAAGCAAACGTTGCCGATCTGATCCAA
GAAATCTCAGACGAAATCAACGAAGCCGGCCAACTCAAACAAAGCGCAGGAGCCGACGGT
GCCCGTGCCGACTGGGCCTCCCTCGACGATGCTGTCCGCGCAGCCAGCGCAGCACTAATC
ACCGCATCAGCAGACGCCGAAAAGGATCCGCTCGGAACCTACACAGAACTTGTCGATGTC
GACTCCGCCCTCGACACTCAACTTGACACACTTCGCGCCACCGCAGCTGATCAAGCCCGC
CAGCTACGCGTATTCGACCAACAGCTGCAATCTGCAAGAAGCCAAATCCAAAAGGCCGAA
GACCTCATCTCCACCCGCGGTCGCATCGTAAAATCCGAAGCCCGCACCCACCTGGCCAAC
GCACAAAAGCTGTACGCCATGGCACAACAAAACCGCACCCGCGACACCCGTGCAGGAATT
GATTACGGACGTCAAGCAGCAGTCGCAGCCCAACGCGCCAGCAAGTCAGCACAAAACGAC
ATCACCACCTACAACAATCGCCACAATTCCGGTGGCGGAACCACCGGTGCGATTGTCACC
GGCATGGTGATCAACTCGATTCTCAACAGCGGCCGCGGTGGCGGTTTCTGTGGAGGCGGA
GGCTTTGGTGGAGGCGGTGGCGGCTTCAGCGGTGGTGGCGGTGGCGGAGGAGGGTTCCGC
GGAGGCCGCTTC

>RXN01485-downstream
TAGCCTGAAACGAGCAAAACCAA

>RXN01492-upstream
TGAAGTGGGCGCGTTAGCTTCGGCGCGTGGCAAACCACATTTGCTGGACTGCAGGCATAA
TGGACAAAGACTTTTAGCAACAACTATGTGGAGGTGACAG

>RXN01492
GTGACCACAACTCTGTGGGCGGTTTCTGACCTCCATGCAGCGGTGAAAGCTAACGCTGAT
CCAATTGAGAATATTCAGCCTAAGGATCCGTCTGACTGGTTGATTGTTGCAGGTGACGTG
GCGGAACGTACCGAATTGGTGCTGGAAATTTTGGCACGTTTGCGCAGGCGCTTTGCCAAG
GTGATCTGGGTTCCGGGTAACCATGAGTTGTTTTCTCGCTCCGCGGACCGCTATCAGGGG
CGCGATAAGTACTCTGAACTCGTTGAAGGCTGCCGCAAGATTGATGTGTTGACTCCGGAG
GACCCTTACTTAACCTTTGGTGGGGTTACTATCGTTCCGTTGTTTACACTCTATGACTAC
TCGTTCCGTCGACCTGGTTTCACCGTGGAGCAGGCTGTGCAAGCGGCGCGGGATCGTCAA
GTGATGATGACTGATGAGTTTTCTATTGCGCCTTTTGTTGATATCCGAGCGTGGTGCTGG
GATCGCTTAGCCTATTCCATTAAGCGTTTGAGCAAGATCAACGGGCCAACAATTTTGATT
AACCACTGGCCGCTGGTGGTGGAACCGACTTATCAGATGCGCTGGCAGGAACTTGCATTG
TGGTGCGGTACTCGCCACACCAGGGGATGGGCCGAACGCTACAACGCGGAAGCCGTTATT
TACGGTCATCTGCATATGCCCGGAATAACCAACGTCAACGGTGTGAAACACATTGAAGTG
TCGTTGGGTTATCCGCGCGAATGGGAGCATTGGTCTGGGCAGCATGTGTGGCCATATCCA
GTGATGGAGGTGGACAATGCTGGA

>RXN01492-downstream
TGAGTCTTTGTTTCCAAATTCGG

>RXN01518-upstream
AGCAGAACCTGATGCCGTCCTGCACGGCACGACCATTGCAGAACATGTGGATAATCTTGA
TCCCACAGACATTGAAGGTGTCACCAAGATTTAAGGAGTC

>RXN01518
GTGGCTTTCATGCAGAAAACGTCAGCGGGTTGGTTGATCGCAACGGGAGGTTTCCTCGCC
GCTGTGTCCGCCATTTTGACGTGGCGTTTTTATGGATCCATGACCTCTATTTCCATCACG
GTATCCATCACTTTTTGGTTGTTGGCCGTGGTGTGTGGTTTCGCAGGTGTGAAGGTCCAA
GGTCGCCTCGATGAGGGGCTGATCGGCCAGGACAAATCCCAAATGAACCCCGTGACCATT
GCCTATCTGGCCATGCTGGGTCGAGCGTGTGCGTGGGGTGGCGCAATTTTCGGCGGCGTT
TATGTGGGAATTGGCAGTTATGTAATCCCACGCGCCGGTGAGTTGTCCGCAGCATCGAAT
GATCTTCCGGGAGTTATTGCCTGTGCGCTGGGCGGAATCGCACTCTCAGCTGCCGGACTT
TATTTAGAGCGAAGCTGTGAGGCTCCGCCTCCCCAATCTGGCGAAGCGATCAGC

>RXN01518-downstream
TAGATTGGAATTCATGAATCAAG

>RXN01539-upstream
GAACAGCACGGTTGGGTGCCGCAGAATTGTTGCGTCGTTTTGAACGCACAGGTGCAGCAG
CTCAGAATAATCAGTTTGACGATATGGACTTTTAAGGAGT

>RXN01539
GTGGTGACAGTGGCTGGGAATGAGAAGAATAAGATACGAGAAGAGCGGGTGGCTCGGCGT
GCCCAGGCAGTCGTAGAGGCGGAGATTAGTCTTGCTGCACAAGCAAGTGAGCAGGTGCGT
GAACAAGCAGAGGCGCCTGATGTAAATGAACAGGTAGAAGAGGTTAGTGTCGAGGTATCT
TCTGTCCAGTCATTAACCCAGCCTAAGACGTTGGGGCAGCTGCATGACCCAAGGAAAAAT
GTCATGAGTAGCAGCGACTTGGCTTCTATTATTGGTGTAGAGCAACAGCCTGTTGCTTAT
GGTGAGTCTGAGGAACCAGAAACACTGCGTGATGTGTTGCCTCGGCGAAAGCTTCACCCA
TCTGAGATAACACCGAGTTATGAGGTTGCTGATGGTGAACAGCGCAGCATTTTTGGTGAA
TCAGCTCCGTCTGATTTTGATGACCTCAGTGATGTCGAAGAATTTGATACCAGTCATTGG
GTGCGTGCTGGACAAGATGATCGTAGTGATGATGATCGACTCGCTGATGAGGCTGGTGTA
CCGCGTAGTGGCGCACAAGATGTAGCTGATAATGAGGCTAATCTTTCTGGTGTGGATGAG
CAGCTGCACATGCGTGAAGTCCATGCACAGAGTTTTGACCCTATTGACGTTGCCAAAAAG
GAACGCAAAGCAGCGGAAAAGAAGTATGCCAAGCCACCAAAAAGTGATAATCCGTACCTA
GCACGGGATGCCAAAGATGCAGCTGCTCGTAAGCGGAAGATCAATGCAGCTCATGATAAT
TTTGCCCAAGAGATGGCACAGGCTGCGATGGGACCACTGCGCAAAGGGGTCAACACTCAA
ACGGTGATGGCCGCGTGTACGACTGCTGCGGTGATGTGGTGCATGAGCCCACGTATGACC
GGTGTGAACGTGGATATGAAGCGCAAGTTTAACAAGGATCTGGAACAGGCTAAAGACACT
AAGTTGTCGAAGTATGTGTCCAAAGATTTTTGGAAGTCAAAGCTGACGCGCGATAAGACG
GAGAAGGAAGCGAAGTCGCTCTCTGATGCGTTCATGCAGCAGAAAACAGCGATCATCAGC

AACCGTGAACGAATCCCCATGAGTGTTGCTTCTGCCGCGCAGACCGTGGTTCGGTTGTCT
GATCAAGCGTATGAGGCGATGCGTGAAGTAGATACGGATGGTCAAGCGATAGTGGATGCG
AAGGATGTCTCTGCACAGGTGGCAGAAGATATTGACATGGTGGTCAAGCAGGGTGAAGAG
CATGGCCTGAAGTCGAAGGATATTTATGGCGCTGCCCGCGATATTGTGGGTCGTCGCATG
GAGCGCGATCCAGGCTATGCTGCCCGGTTTAATGAGACGGCTTTTGGCACCGTGCGCCTG
GGTGAACAACGACGTGGCATGGTGATTTCAAAGACCCCGACATGGCAATTCCCTGATGGT
GCAGGTTTGAGTAAAAACGCCGGCTGGTTTAGTGTTCGTGAGCCGATGGGTAATGCGCAG
AACTTCGCTGACAACCTGGCTGCGACTTTGGCGACAGAAATGCGGGTAGCTGGTGAGCAG
TACGGTTCCGATGGCGTTCGTGATGTAGTTGCCGGCTTCATGACAGCGACTGATGTCTCA
GAAAGTGGCCTCGCCTCTGCGAAGAAACTGTTACCTGACTTTGATACACGTGGTCGCAGT
GCTTCTCGGGTGCGCCAGATTGCTATGGCACAGCGCACACAGGCAGCGATCAAGGTGTTG
CAGGATGATGGTAATCAGACCGCGATGACGACTGAGCAGGTCAAGGAGGTTCAGGTATGG
GCGATGGATCAGGCTGAGAAGGTGATGCAGCGTGATCATCCAGCGATTCTGGATAAGTTT
GTGCGCAAACATGGGCAGACATTTGGGCAGGATGCGGACGCTTTTGTTAAATCCATAACT
ATGGAAAAAGACACGAGCAGCGAGTACACTGATGCTATGGTTCGACCTCAAGAAAATCGT
GGATCAGGTCGAGAACTGGCAGCTCGTCGTCGTGTACAAGCAGCGCAAATCAATCAGGCA
GCACAGCTGGATATGAATGTTCATGATTTCCGTGAATCGAATCTGCCAGAGGAACGACCC
GCGAATCCTTATGAAGCGTATGTTCGTGAGACTGAAGCGAAAACCAATGATCCGCAGTAC
GGTTAT

>RXN01539-downstream
TAATAGAAAATGATAGAAAGAAG

>RXN01549-upstream
TGAATTCCGTTTCTAGATTTTTTTTATTGATTGTGAGAGTGCATT

>RXN01549
GTGGCTAATGATTTTATAGAACCAAATGATGCCCCCGATGCACCTGATAATGGTGACTCG
GGAAGCTCGGGGTTTGTTGATGAAGCAAAAGATAAGACCCGCTCAGCTGCACAAGGCTTA
GGTTATGGCGCACTACGTGTAGGTTTTGGTACTGCAGCACTTGCAGCCAATGGTGCTCGC
TCTATGGGTAATTTGGCTAAAAACCTGTGGACACGAATGATGGGGCTTGCCCTGTCTGCC
GGTACTGGTATCTCTGCTGCCACAGGTGGCATGATCACTGCACGTGTAGGCGCAATGCTG
GCAGGTACAGGCTCGGTGTTGTCGTCGGTGACGACTATTGCGTTGATTGTGTCGATGATT
GTGGTGCCGGCAGGTCGAAAAGACGGCATTATCGAGTTGTGTGAGCCGCCAGTAACGGCC
AACCCGTTTACCATTGACGCAGGTGATATGACTGAGAACGCGAAGTTGGTGTACGGTGCG
CTGTCGTATCTTGGGATGAATGATCAAAATATCGCCGGTGTCTTGGGCAACTTTGAGACA
GAATCAGGTATCGACCCGACTGCGGTGGAGGGTATTTTTGATGAACCAAATACCATCGGT
CCTCGGAAGAGAGCTGCGTGGGATAAGAACTTTGAACCTCAGCCGATGGGTATTGGGCTT
GGGCAGTGGACAGCAGGGCGCACACAGATGTTGCTAGATTTTGCCGCCGATAGAAACCGA
GACTGGCATTACATCGACGTGCAGCTTGCATTTGCTATTAGTGGCGATAATGAAAGCGAT
CGCAAGGTTTTTCTGGAAATGGTTGATAATAAAAACTCCAGTAGCAATAGCCCCACCGCA
GCGTCCGAGTACTTCCTGCGTGAGTGGGAGCGCCCGGCAGATGTCGCAGGTAATGCACCC
ATTCGTGCAGAGCAAGCATCTAAGTGGTACGCGCAGATGGGTGGTTGGCAAAAGAACTCA
ACCTTGGGTGAGTCTGTGATCGCTATGGCTGATGGTGCAGCAGCAAAATCCACGGCGCGT
GATGAGCAGGATGCTCTTAATGATTGTCCTGAAGAGGACCGCACCTCAGGTGGAAATACG
TCCGCTGCAGAAGCAATGGTGACTATTTCACATCCTTATCTGGCTGATTCTCGTGGCAAT
GACGGTACTGATATTTACCGCTATATCCATGATGAAGTGCTCACCGGTGATCCGTATTAC
GCATCCTGTGACCGTGGCGTTGCTACCGCTATTCGCTGGTCGGGCACGGATGATACGTTC
CCAGCAGGTCCAACAGCAGCACAGTATGAATACGTTGTGGGCACAGGATCGGGCCGTTGG
GAGGAAATCGGCAATCTTGCCACCATGTCAGAGAACGATTTGTTACCTGGCGATGTGCTT
CTTGGTGCACCGAATCACGTTGCGATGTATGTCAGCAATGAGGTTGTTGTGGACATGTTG
GGCCCTGGTAATGCAGAGCCTAATGCAGCTATTGGTCATGCATCGTTGAATGACCGCTCA
CCTGGTCTGGATACCTTGAGTCTGGATGGATGGGGCGTGAACTTCAAGGTGTTCCGCAAC
ACCCAGGCTGAGACAAACTCAGTGTTCTCTGGTGTACAGATTCCGGCTGGTAAAGAAATT
GGCGAAATGACTAACCCAACTCGAACTACTCCTGCAGGA

>RXN01549-downstream
TAAGTTTTTTTCATCGCTGGGTT

RXN01557-upstream

TAAAGGTGTGAAAATAGTTCCTCACGTGGGGAACTATACTGATCCTTGATGCGTTAACTT
GATTGACGACGAAAAATCAATTGAAAGGATCGGGGACTCC

>RXN01557
GTGCGAAGCAGCAATCCCGTTTTTAGTTCCCTTAAGGAAACTCAACGTCCACAAGGCCAG
AACCCATACGGTGGTTACGACAACTTCGGTGGTGTCTACCAGCAAAACGTAGCTCCACAG
AAGGCGGAGCGCCCAATGACTGTGGATGATGTGATCACCAAGACTGGTATCACTCTCGCG
GTTATTATCGTTTTTGCATTGGTCACCTTTGGCGTGTGGTTGGTTAGCCCCGGCCTCGGA
ATGATCTTGACCCTTGTTGGTGCCATCGGTGGTTTCATCACCGTTCTGGTCAGCACCTTC
GGCAAGAAGTACGGATCTGCGGCAGTCACTTTGATTTACGCAGTATTCGAAGGCCTCTTC
GTCGGCGGAATTTCCCTTCTGCTGTCCGGCTTCACAGTTGGTAACGCCAACGCAGGTGGC
CTCATTGGCCAGGCAGTCCTTGGCACCATCGGTGTATTCATTGGCATGCTGTTTGTATAC
AAGACTGGCGCTATCAAGGTCACTCCTAAGTTCAACCGCATCCTCACCGGCATGATGGTT
GGCGTCCTGGTTCTTGTCCTGGGCAACGTTGTATGGGCACTGTTCACTGGTGGCGCAAGC
CCACTGCGTGACGGTGGAATCATCGCGATTATCTTCTCCCTCTTCTGCATCGGCCTGGCA
GCATTCAGCTTCCTCTCCGACTTCGATGCAGCTGACCGCCTCGTCCGCGAAGGTGCACCT
TCCAAGATGGCATGGGGCGTTGCGCTTGGTCTTGCAGTGACCTTGGTCTGGCTCTACACC
GAAATCCTACGTCTGCTTAGCTACTTCCAAAACCGC

>RXN01557-downstream
TAGTTTACGCAGCACAAGACCCC

>RXN01574-upstream
AAAAATCCGCACACCCCACATTGCTCAAAGGAATTGACAAGGCGCTTCGCAAGGCCGAGT
AAGGTGGGCAACGAGTCGGTGAGAGTATGAGGAATATTTG

>RXN01574
ATGAGCAACAAACGCATCGGTGTAGTGATCGTTTCCTACGGACACGAACAAGATGTTGCC
AACCTGGTAGACACATTTGCAGATCAGCTGAAAACTGGTGACCGCGTAGTTGTCGTGGAC
AACCGCAAACCTTGGGTGTTAAAAGACGCCGTGGGGGAGCGCCTGGAAAAACACGGCGCA
GAGATCATCAACCACGACAACGGTGGTTTCGCCGCTGGCTGCAACGTGGGCGCAGCGCAC
ATCGTGGATGACGTTGACCTGCTGTTCTTCCTCAACCCCGACACAGTGATCGACGATCCC
ACCCTGTTCAATTCGCTGAGACGCGTCGATGAACAGTGGGCAGCATTCATGCCGTACCTG
CTGCTTCCTGACAGCACCATTAACTCCGCAGGCAACGCCCTGCATATTTCCGGACTGTCG
TGGGTGACTGGTCTGGATGAAAAACCAGTTGAAGGCTCATCTGAAGTTACCGATATTTCC
ATTGCCTCTGGCGCCTGCCTTGCCGTGCGCGTGGACTGGTGGAAACGCCTCGGTGGCATG
GAAGAACTGTATTTCATGTACCACGAAGACACTGACTTCTCCGCCCGCTTGCTGCTGGCC
GGCGGTCGAATTGGTCTCCTGCATTCCGCGTATGTCACCCACCATTACGACTACGCCAAG
GGTGACTACAAGTGGATTTACATCGAACGAAACCGACACGTTTTGCTGCTCAGCGTGCTG
CCGCTTCCATTGCTGTTCGTGCTGATCCCGCAGATCCTCGGTGTGAACCTGGGACTGTGG
GCGATTGCCGCAAAGGAAAAGAGGGTCGGACTCAAGGTGAAGTCCCTTCGCCTCCTGATC
CGCGATCTACCAGCGATTTTCAAACTGCGTAGGAGCACGCAGGAGCTTGCCGAACTCACA
CCATCGCAATATCTGGCAAAAATGGAATGGCGCCTAGACAATCCCAACCTAGGCAACATT
GGATCCAACAAGATTGTTGCGACTGGATATAAGACCTATTACAAGTTGTGTATGAGTATC
CTGAAATTGCTCGCT

>RXN01574-downstream
TAACACCCCATAAAGAGGGTGAA

RXN01589-upstream
AGGGATGTAGATGCGCCCTCATATTGGTACAAAAATATAAATTATCAGCATGATTTGGAC
GCTTTAATTCAAAAATTGTAAGCTGTTAGGAGGTCCACAA

>RXN01589
ATGGTAGAACAAATAAAAGATAAACTAGGACGTCCCATCCGTGACTTACGGTTATCTGTG
ACAGATCGGTGTAACTTTAGGTGTGATTATTGCATGCCTAAAGAGGTATTTGGAGATGAT
TTCGTATTTTTACCTAAAAATGAACTGTTAACGTTTGATGAAATGGCTAGAATCGCTAAG
GTATATGCAGAATTAGGTGTAAAAAAAATACGCATTACAGGTGGAGAACCATTGATGCGA
CGCGATTTAGATGTACTTATAGCTAAATTAAATCAAATCGATGGTATTGAAGATATTGGT

TTGACTACAAATGGTTTGTTATTAAAAAAGCATGGACAAAAGTTATATGATGCTGGGCTA
CGCAGAATTAATGTCAGTTTGGATGCTATTGATGATACGCTATTTCAATCAATCAATAAT
CGTAATATTAAAGCGACTACGATTTTAGAACAAATTGATTACGCGACGTCTATTGGTTTG
AATGTAAAAGTAAATGTTGTTATACAAAAAGGTATTAACGATGATCAAATCATACCAATG
CTTGAATATTTTAAAGATAAACATATAGAGATTCGATTTATAGAATTTATGGATGTTGGT
AATGATAATGGATGGGATTTCAGTAAAGTTGTAACTAAAGATGAAATGCTTACAATGATA
GAGCAGCACTTTGAAATCGATCCTGTAGAACCAAAATATTTTGGGGAAGTAGCAAAATAT
TATCGCCATAAGGATAATGGTGTTCAATTTGGTTTGATTACAAGTGTTTCACAATCATTT
TGTTCTACATGTACACGCGCAAGGCTGTCATCAGATGGGAAGTTTTACGGATGTTTATTT
GCAACTGTCGATGGATTTAACGTTAAAGCGTTTATTCGTTCTGGCGTGACCGACGAAGAA
TTAAAAGAACAATTTAAAGCTTTATGGCAAATAAGAGATGATCGATATTCAGATGAGAGA
ACTGCTCAAACAGTTGCCAATCGTCAACGTAAAAAGATAAACATGAATTATATTGGTGGT

>RXN01589-downstream
TAATGTGTAGGGACCACTACATA

>RXN01590
TGGGGTCAAAAAGATCACTGGGGCAAAGCTCCACTGGGTGATCACGATGCTGTGCGTATC
TATAGGCAAGCAGAAGCCTTGATGAAACAGCGCGCAGCAAACAATAAGGGCTTAGACCTC
AATGATGAAGCGACCTATGGCGCCATCATGTTTGCGTCTTTCGATGATGCCTTCGCCGCT
GATGCCGAAGCTCATGGCTGTGTACACCGACCACAGTTCGCGAAGGTAACTAGGCGAAAT
ATTCTTAATTCACCGCAATACACGGCGATTAAGTCATCTTATGACGCGCTGGTGCAGCAG
GATCTCGTGGCCCAACAGCAGCAGGCACAAGCGCTACAGCAAGCTGCTTATGAGCAAGAG
CAGGCAGCTATTTTCCAGGCACGTGATCAAGCAACATTCCAGGCTGAACAAACGCTCGCG
CAAGAGTCCGTTCGCCAATCAGAGGGTGTGGGTTTACCTGTCATTGATCCGATGGAGAGC
TATTTCCGGGAGTACGCCTTCTATGAAGGTGTCGAGATGTTTGGTACCTGGGGTACGCAC
GTTGATGCTGGTGTGTCGCAGTTTAGCACCTCTGATGGCCGTGCGATCCGAGCGCTTGTT
GATGAGCATCTCGCAACCTATGAACCAGTAGAGCAGCGGGGGAGTACTCAGGCATTCTTC
GCCTCTGTCAATGCTGCCTTTGCTGAGGTGGCACCTCACGCAGCACCCATGTTTAGTGCG
ATTGCTCGCGAGGGTGAGGGTTCAAAGGGGTACCAGGCGCTGCGTCACCGTTTCGACAAG
ATGGTCGGCACTGCAATTGGACCTAATGGTTTGCCTGAGGGACCTGATCTGGGTGGTCGT
CGTTTACCTATTTCGCCTTATGATCCACGCTGGTCAGACCGCGAAGTAGTCCGTGTGCAC
GGTACCAAGCTGCTATCACTGTCCGAAGAGAGTGTTGGCATGATCAGGGACCTTGATCTA
GCAACGATCCACCTACAAGATAATGATGTTTACGAGGGCACTCATCGAGAAGACGACACT
AAAGGCGGTGTGCGACCGTTGACTCAATGGGTCAATGGTGAAGCTATTGCCTGGCGCACT
ATCACCGAGAATGACCAGATGCGACTGCCCAATATTGGTCAGTTTATGACGGCTAAAGAA
TACCGTGCCGCAGCGTCATGGCTGCGTGCTGGACTCATTGATACCGCAGATGTTGCGAGT
CAGAAAATTGACCCCAACAAGGTCATGTCTGATGAGGGTATCGCGCGCTCGGAAGCTATT
TTGACGTATCTGTCGGATGAGGGTGTGGATTTTAGGATCGAGCCAGATCGTGAGCCGGGA
CAGCTTAAAGTGCGTATTGAGGGCACCCGTATTGATATTCGTCTCACTGATACTCGCGCC
AATGAACAGTGGGTGGGTCGTGTCTATGATTCTGGCACTGTGATTAAGTATTCCGCCGAA
CAAACAGCGGAAGAACGTCTACGAGCTCGTGAGCGCATGGAGAACGGTGATGGAACGTGG
ACACCGGCTACTGATTATGAACCAAGCCCAACTGAAGTTGTCGATCTCGTGAAATTTGCT
CTCGGTCGAGAGGTTGAGCGACAGGATGGCAAAGGTCTTGTTGGTGTGCCTAATGCTCGA
CACCCACGTGCTTTAGAGCAGGCACAGGATGCATATTTCACTAAGAATCGTTCCGCATTC
ATGGTGCGTGAAGGGCTCTCGATCGTTCAGGATGCACGTGATCGAAGTGCTGGTCCTGGA
AAGTGGTTTGATAATGAAGCGAAAGCATCGGAGTGGCTTGGTAACAATATCGCCCTTACT
CGTGCGCGTGTGGCCGAAGAGCTCGGCGTTGAAGAACTGATTGCGCTTTCTGCACAGTAC
GCCGATGATCCTGACTTCATGCCGGCTTTTGCTGGTGAGGATGAGCTCATGGCGATAAAG
CAGGACTATTGGGCGATGCTGCGAGGTGAGGAAACCGATCTGCTTAACCCTGGGGTTAAC
CGCGATGATTATATGGCTGCTATCCGCGATGGTGATCATGAGCAGATTGCTGCGATGACC
TCAGCAATGAATGCTGTGACCGTGGAGGATCGTGTGCGTCAGCACGCGGCCCTTGTTCTT
GATGATTATGTCGGCACGGTGGAGCCTGATCCTGTTACCGGCTTGCGTTTTAATCCGGTG
ACAGTTGCTCAGCACATGCCGAGTGCTAAATCCCTGTGGTCAAACCATGACGATATTATT
GCCGCGTTGCGAGCGACTTCGATTACTGGCGATGAACTGCGCGGTGACGAATTCTATAAC
GATGTTATTAATCAACAGTTGCTCAAATTTAATCCTGAGACCGCGCAGAAAATGGTTAAT
AACCCTGATCTTGACCCGCAGTTGGCTCGATTTGGCACTGTCATTGCCGAGACTATTTCC
CGCAATGGTGCTGATGTGGTCGATATTGCTGTTGACGATAACGGTGTGGTGCGGTGGACC
GCACAGCGACGTGTTGGTGCGAAGGATAGTCGTGCAGTAGATAGTAAGGGGCAGGTTCGC
GGTGAACGCACCCGTCATGTGCAGGGTGAGATAGGTCAGATTTTTACTCGCGGTGAGCAT
GGTGAAATTGTCACCAAATTTAATGGTGGCGAGAACTATATGTTTGCCCCTGGCTACACC

GCGTCTGTGGTACCACAAAAGCCTGGTGAGACAAAGAGTTTAGAAGAGCGTACCAAGCTC
AAAGGCTATGAGCAGGTGATGTCAGAGGCGTTGGTGTACCGTGTGCGAGAAGATTTGATG
TTCACTGAGCGATCCCGAGTGGGTGCTACAACCAGCATCAACAGTGCATATAAGCGACTG
TATGACAATCGCTTCCCTGTGGACTTCTTCGAGCGCAGCGCCGAAGAAGGTTTGAGCGAT
GAGTGGCGTGCTGCGTTGCTTGAGACTGCGAGTTTGCGTGTGCGCTACGACAACTCTATT
CGTGATGGTGCGAATGTGATGGAGGATATTCGAGCACAGCAGCGTGGTTTTGATGCGCGT
AATGATAACTCCCGTGATGCGCTGGTGCTTACCGGTGGGCGTAACATTTCTGTACTTGAT
GTTGATGCGGGTAAAGGTTTCTTTGATCCCATGATGACTGGTATGGCGGCGAACCAGGGT
TCTGTTCGCTATTTGTTGCCTTCTGCGAAGGTGGGCGCTGATGGCATGATTACCCCTGGT
GATCCGGCTGATCGAGTACCTGTTGCAGCGCATCCAGAATCATGGGCGATGGGCTTTGAC
CCACATGACCGTCAGAACATGACTTTCTCGAACATCATGCAGGCTAGCGCTGTGACTGGT
GGTGCACGCACTGCGATGATACAGCTGGGCGGTTGGAACTTTGAAGATGGCATTATTGTC
TCTGCCGATTTTGCGAATACCCATGTTATTCGCGATACGGAAGATGAGATGCGCCCCTTG
GTTGCCGGCGATAAGCTGTCTGATTTTCACGGTAATAAGGGTGTGACCGCTCTTGTTGTT
GATCCAGCGATGAGTGATGCTGATGCACGTGCAGCAGGGCTGGAATCAGAGGTGGCGTTT
TTCCGAGACAACCCTGATCTAGAGGTTGTCATGAGTCCGTTTTCTGCCATTTCTCGTTTT
AATGGTGGCACGGCACGTGAGCTCATGACCAACCCGCAGGATGTGGTGTTCAGGAATAAT
GATGGTTCTACTCGTGTTCAACCAGGTGCCTCTGGTGATCTCAACTTCATCGTCACGCAT
ATGGCTGTTGATGCGAAAACCAATGTCTATGATGAAGAAGCTGTTCGTGAGGGCCAAGGA
CGTAAAGCGTCTTCTCAGCTGGCGTGGGTGCTCCAAGCCCAGGAATGTCATGAGATTATG
GAGCACTTTTATGGCAACAACGTCTCTGCATTGGCTAACTTCCAGGAATATCTTCGCGTC
ACGGGGCTTGATGTCACCCCGTATGGTGAGTTGCGCGAGGGGTTCAGCGAGTCCAATGAG
CAGCGCAATATCATCGAGATGCCAAGCATTTACGATGAGAACGGTGAGCTGAATAATCGT
GTTAATCGTGCACAGGTGCGCGAAGCTTTTGTTGAGCAGATCAGTCGCGCTGGTGGTGTT
ATGGAGATTCCTTTCCAGTTACAGTTGCGCAATGGTGCACAGCTAGAAGAGTCACCTAAT
AATCCAGACATGTATCAGTTGCCACTACTGAGCCCGCATTTGCGCAGTGATGAGGATTTA
GCGGACGGTAGTACCTCTCGACATGAGTACACCACGCGGTATATGGCTATTTTTGATACG
TGCTACAAGCTGGCAGAAGAGCAAGCCAAGATTGACGCATTGCGCCAGGAGGAAGCGCAG
CACGGCACGTTGCCTCGTGCTGCGGAAAAGCGACTGAGCGAGTCACAGAAGTTTGTTGAT
CAAGCACAGAAAAAGGTGCAGGCAAGCTTTGATGGAATTGCTAATGATATTGTCGCCAGC
CGGATCGAGACCAAGAACAATGTGTTCAAGGACGGCTTTATGTCGGCGCGACAGTCACAC
TCCGCTACTGCTGTGTGGACAGGTGATCCACGCCTGTCAGTTGATGAAGTAGCCATGAAC
TCTTCGATGGCACGTGAACTCGGCGTTCTCGATAACGGTTATGCAATGGTGTGGCGTGAT
CCGGTGATCCGCGATGGTGGTGTGCGCTATTTGCGTGTGGTTATTAATGATGATCTGCAC
GGTGTGGCAGTCAACCCTGTGTCGGTGAAGAGCTTTGACGGTGACTTCGATGGTGACTCT
GTAGGTCTGGTCGGCAATCTGCCGAAAAAGGCGCATGAGGAGGCATTGTCCAGGCTCACA
GTTGAGGCAAACATGCTTGATCTTGGTGATGGTAAGCGTATGGAGGACGGCACTATGTTT
TATGGGCTAACTCTGCATGACAGCCTCGATGTACAGGTAGCGCAGCACCATGATCCGGCA
ATGGCCGAGAACATGAAGGTTATTGTCTCTGAGCTTAACCGCTACCAGCGTGAATACGAG
GCCGGCGAGATTAGCCGCGAAGAATTGCTAGAGGTCAACCGTGCACACATGGATGATCTC
AATGAGCACTATGCACAGGCTTTTGCCAACCGCGATGGTTTGGTGACCTTGCGTTTTGAC
GGTATGGAAAACCATATGGCTTCTGTTGCGCAGTGCTTCGAGACGGGTGCGAAAGGTTCG
CCTGGCAAGCTGAAGGAATATGCCACCTATATCGGCGCTGATCCGGCGCAGGGTTTTAAA
GACGTAGGTCAACCAACGCCAGAAGCGCTGCGTAGCCACTATGAGGGTTCGCAGAAGGCG
ACTGCAATTAAGGTGCTCTTTACCGGTGTGGCTGGTAAAAAAGAGCAGGAAATGGTGGCA
TTGTGCCGCAATCTTGGTCTGACCAAGGAAGCTATGGCTGCATCAGCACCGGCACAGCAG
TCGATTCTGCAGGCGAAGCACGACCCGATTGACGCGCTCTATCGTGCAGAAACTCTTATG
GGACCAGTAGGTGATCTCTACCAAGGTCGCAAGATGCGTCGTGGTGAGAATGAGCAAGGT
CGCTATGAGTGGGAAGTCGTTAGGGACGAGAACCACCAGCCTATCCAGGCCACCAAGGAT
GAATGGGTACAGCAGTACATGGAGATGTACGCCGATGACAAGGGTATGGGTGTCTCGGTT
GGCGTTGACCAGGTGGAGAAGATCGCGGAAGAATTCTCTGATGAGCAGGGTTATATGCGT
GTGCTTAGCCATGATGAGCTACCCACTGAGATTAAGCCACTAGCACTTGATCAGCTTGCC
TATGGCGATAAGAAGAACCGCTTTGATTTGTTGTGCGAGATGGCAAAGCAGCAGGTCAAC
ATCTACGACGGTGATGCTTATGACTTTGCCCCTCGTGTGGTGCGCGCCAATATGAAGGCA
ATGGAGGATGCAGCGCGTTTTGGTATCCCTGATGTGGAGATTCAGTCGATTTCTGCACAG
CAGTCATTGGCGAGCTTTGAGCGAGTCCCACAACGTTCTGGTTTCCGTATTGAGCGTCGT
GTGCCGGCAGAAGTAGGTACAGGGATTGCTGCACCAGCACCGTTACCTGATGCAGGTGTA
CAGGGGAATTATGTTCAGCAGCAGGTGCCTGCGACCCCGCCAGTTATGCCTGTCACACCT
CCGGCACAGCAACCTGTTTCGCCTGCTCAGACGGACTTCCGGGGCGTTGGTCAGCCACTC
GACCAGGGCGGAAAAATCGGGAATTATGGACATCAGGGACCTGCAATGGGGGCGCAACAG
CCAGTTGTGCCTCAGCAGCAGAATATTCCGCCTGTGCATAATCCGGTACCACAGAATTCT

GTTCCGCCTACTCCGGTTGTGCCGAAGCCAGGTACAGGAAACCCGTTTACTCATGGTGGT
GCGAACAATCAGTTTATGGGTCGATTTGATACAAGCCGTTACAACCAACAGGAACCACCA
CAACGACAGGATGGCGGGTTTGAGCTC

>RXN01590-downstream
TAAATAATGGCAGTAGATTTCAG

>RXN01592-upstream
GATTCAATGGTAGAGGTATTTCATTTCCTCCCATTGGATCACACTCTTTTTGTCGTTCTA
TAATAAAGTCTTTACCCGGTTCTCAACATCAAGGAACAAC

>RXN01592
ATGGCTGATAACTTCGACCGCTCTCGTGACAACGATCGCTCAAGCGACCGCACTCCTCGT
GGAGACCGCGGCGATCGCGGTGGCTACCGAAACTCCCGCGGCAACGATGACCGCGGAAAC
TACCGTCAAAACCGAGATGGTGAATCACGAGATCGCGGCGGATACCTCGGTGACCGTCGC
GACAACCGCTCAGGTGAATATCGTCAACGTGACGATAGGCGTGACGATCGTAGGGACAAC
CGAAGCGATGACCGCCGCGGTGGTTACCGCTCCGATCGCAACTTTGACGATCGCAACAGC
AACATGCGTGATGATCGTCGCGGCGGCGACCGTTCATACAGCCGTAATGATCGCTCCGAT
CGTGGCTATCGTAGCAATGACCGCTACGACCGTAATGATCGTCGCGATGACAACAGGGAC
ACCAGGGGTGGCGATCGCGGAGACCGTCGCTACGACAGGCGCGATGACCGACGTGATGAT
CGTCGCGATGATCGTCGTGGCGGACAGGGCCAGGGGCGTCCAGGTGGAGATCGTCGACAT
GCGAACCGTGCAGGTGCAGGTCGCGATCAGCAGCGTGATTCGCTGCATCCACAGCGCGCT
GGTTTCCGTGAAGAGCGCTTGAACACTCGTCTCAATGAGCCTGATTTGCCGGGCGATATT
GATATCAAGGACTTGGATCCTTTGGTCCTGCAGGATTTGAAGGTTTTGTCTAAGGACAAC
GCAGATGCCGTCGCAAAGCATATGATCATGGCTGCGACCTGGCTGGCCGACGATCCTCAA
TTGGCACTGCGCCACGCCCGTGCTGCGAAGGATCGCGCGGGACGCGTGTCCGTCGTGCGT
GAGACGAACGGCATTGCTGCTTACCATGCTGGTGAGTGGAAGGAAGCTCTTTCGGAGCTT
CGTGCTGCGCGCCGCATGTCGGGTGGTCCTGGTTTGATTGCTGTGATGGCTGACTGTGAG
CGTGGCTTGGGTCGTCCTGAGAAGGCGATTGAGCTGGCTCGAGAAGAGGATTTGAGCTCT
TTGGATCAGGATAACCTGATCGAGTTAGCGATTGTTGTTGCTGGAGCACGCCATGATTTG
GGTCAGCATGACTCTGCGATTGTGGAATTGCAGAAGGTTAATCCAAGCTTGAAGAGCACC
GGTTTCACCCATTCTCGTTTGTCTTACGCTTACGCCGATGCGCTTGTTTTGGCTGGTCGT
GGCGATGAAGCACGTGAGTGGTTCCAGCACGCTGCCACCTTGGATGAGGACGGCTACCTC
GATGCAGAGGAGCGTATCGAGCAGCTCGATAATGGGAACAAC

>RXN01592-downstream
TAGACTATTGGTCTAGAGTGTAA

>RXN01597-upstream
GAGTAGAACCACTTCTCGCCGCCAGTGCATAAGAGTTTTCTTGGAATTTTTTAGGCGCGC
CTCCACCAAAGGTTGAGACTTTGGTTCCACAATGGGCTGC

>RXN01597
ATGAGTCTGTTCAACCGCAAAGCCGACCTGCCCGGCCTGCAAGGTGCCACCCGAATCTGC
ACCCCGCAGGGCAAAGGGCTAAAGCGCCTGTCCGAAGGCGATCTCGCAATCATTGATGCA
CCAGATCTATCCAGGACCTTCGCCCAACGATTGCTAGCAGCAAAACCCGCCGCAGTCCTC
AACGTTTCCCGGTTCACCACCGGATCGGTGCCCAACTTTGGACCGCAAATGCTTATCGAC
GGCGGCATCCAGCTCGTGGAAGGCTTTGGCCAGGAGCTGCTCGACGGCACCAAAGACGGT
AAGAAAGGTCGCCTGACAGAAGATGGACAGCTCTTCTACGGCGAACGACTGATCTCTAAC
GGCAGTGTTCTCAGTGGACCTGCGGCTGAAAATGCATTTGCAGACGCCCAGCAATCACTG
CTGGACCGCATGGAAGCCTATTTCGGCAACACCATTCAGTTCATTCACTCAGAAGCACCG
CTCCTGATCGATGGCCTCGGCATTCCCGATACCGGAAATGCCATTGAAGGCCGCAAAGTT
CTCATTGCCTCACCAGGGGATAACCACCGCAGCAGGCTCAAAGAACTCCGCAGCTTCATC
CGCGAATACGATCCAGTACTCATCGGTGTCGATGGGGCAGCAGACACCTTGGTGGAATTG
GGGTACAAGCCCGCGCTGATCGTCGGCAATCCCACTGGTATCGGCGCAGATGCGCTGCGC
AGTGGCGCCAACGTAATTTTGCCAGCTGATCCAGACGGCCACGCTGTTGGTCTGGAGCGC
ATCCAGGATCTTGGCATCGGTGCGATGACCTTCCCATCCTCAGTAAATTCCTCCACGGAT
CTGGCGCTCCTGCTTGCGGATTTCCACAACCCGCAGATGATCGTCAACGTCGGCGGTCCT
GTCACCCTTGATGGTGTTTTTGAAAACCGAGAAGATTCCGATCCCGCGGCGCTTTTGACG

CGCGCCAAGCTAGGCACCAAGCTTGTCGACGGATCCGTCATCGCAAGTCTTTACACAGTG
CGCAGCTCCAGCAACCTTGGATGGATGTGGGCACTGTTAGCCATTTTGGTGGTTCTTGCA
GTCGTGATTGTTATCGCTGGCACCGCAGGATCAGGCTCTTTTACCGACAACCTCATTGAC
ACCTGGAACAGCTTCGCGCTGACAGTGCAGGGTTGGTTCAAA

>RXN01597-downstream
TAGGAAGGCAACATGGCTAAACG

>RXN01598-upstream
CGCTGGCACCGCAGGATCAGGCTCTTTTACCGACAACCTCATTGACACCTGGAACAGCTT
CGCGCTGACAGTGCAGGGTTGGTTCAAATAGGAAGGCAAC

>RXN01598
ATGGCTAAACGACGTGGAAGAGGCGCCGCAACCTTCGCCGCACTGGGATTTGGTGCAGCA
GCCGGCATTGCCTTTGGAACTTATGTGCTTGCACCCAACCTTCCTGAAAACATTGACCCA
AATGCACCAACATCAGCTGAATTAGTCGAGGCAGAGACCTTGGCTGAGGTTAATGCGGTG
CAGGCCGATCAAGCAGACAGCATCATTGACCACATCGTGGAAGACGTGGTGGCTGGCACA
CTGACCGATCGCCCCGTACTGGTGATGCGCACCGCTGACGCTGAAGAATCAGACGTTGCC
GATGTGTCATGGCTGTTGCAGCAAGCAGGAGCTATTAATGCTGGATCCATTACACTTGAG
GAGAATTTCTTCTCCCAAGACGGCGCGGACCAGCTGAAATCAATCGTGGCAAATACGTTG
CCTGCAGGCGCTCAGCTTTCTGAAACCCAACTGGATCCAGGAACTCACGCTGGCGAGGCA
CTTGGTGCCGCTTTGCTGCTCAACCCTGAAACTGGTGAACCACTAGCCAGCACTGCAGAG
CGCGGACTATTGCTCAACGTGCTGCGCGACAACGGTTACATCTCGTACGAAGACGGCACC
ATTTTGCCAGGCCAGGTCATCGTGATGATTACTGGCGATAGCGACGGCTCAGGTGATGGT
GCCTTCGCTGCAGAAACACAATCGCTGTTTGCTCGCGCACTTGACGCCCAAGGATCAGGC
GTGGTGGTTGCAGGACGTATTCACACTGCTGCTGATACTGGAGTTATTGGACGGCTTCGT
GCCAACCCTGATGCTGCAGAAAACGTCTCTACAATTGATTCCGTGAATCGTACTTGGGGC
AAGATGGCTACCGTGCTATCAGTTCGTGAGGAACTAGCCGGTAGGTCTGGAGCGTTTGGT
TCCGCTGCCTCCGCAGACGCGGCAAGTCCGTCTCTCGATGGAACTGCAGCAGCGCCAGCG
CAG

>RXN01598-downstream
TAGGTTTTCCAAGCCTTTAAAAC

>RXN01618-upstream
GGCCGTGCGCGCCTCCAGCGAGCCTGGCCGTGCCGGAAAAGTGCTCATTCGTTTCTAAAC
GTTTAAGGCCCATTAGACCCCTGATTTAAAAGGATCTCAC

>RXN01618
ATGATCATTATCGGAGCAGTTTTCGCCATCCTCGCAGTTCTACTGCATGTTTTCATCTTC
TACATGGAATCATTCGCATGGACTAGTGAGAAAGCACGTGGAGTTTTCGGCACCACCGAA
ATCGACGCCGAAAACACCAAGGAGATGGCCTACAACCAAGGCTTCTACAACTTCTTCCTG
GCAGTCATCGCCGGCGTGGGTGTTGCGTTCCTCTTCGCTGGTTCAACTGGCATCGGCGCA
GCCCTCGCACTCGCTGGCACCGGTTCCATGCTGGCAGCCGCTGCAGTGTTGGCTTTGAGC
TCACCCGACAAGCGTGGTGCAGCCTTCAAGCAAGGCACGTTCCCGCTGCTCGCAGTGGTG
TTCCTTGTGATTGGATTGCTGGTT

>RXN01618-downstream
TAAGCAGTTTTTTAAAGGAACTT

>RXN01634-upstream
ATTGGATCTAGGAAAAATTATGAACATCTCAAAGCTCGGACTGAGGATCGCGGTCACAGC
AACGGCGACCACAACGGCGCTTGCCCTCGGTGGCACGCAC

>RXN01634
ATGGCAGTTGGTCAAGAAACTGATCTGCTCAACGCTATGGAAACACTCGCTGGGGTTCCC
TCAGACTTGGTGGTCACTGAAATCCTCCCCGATACCACCAGCTATGACAATTTTGAATTC
TTTGAAGTTCACAACACCGGCAGTGCACCCGTGACCATTGGGGAAGGGGAGTACACCTTC

GCCTATTCCTTTGACGATTCCGCCGATACGTCCCGCGACAAGGCACTGGATCTTGGCGGG
GAAGTCACGGTAGATGCAGGCGAAACCATTGTGGTGTGGATTGAGTACTCCAGTTCAACT
GTTGATACCGCTGCGTTTAGTGAGCAAGACTTCCGTGATTTCTACGGCATGGATTCCTCA
GCCCGCATCTTCCGAGCAACTGGCCAGGCGGGTCTCGCTAACGGTGGTGATCGTGGCATC
CGAGTTCTGTACAATGGTGAAGTTTCTGGTTGGTCCCACTACCCATCAGATAGCGCAGCG
GTTCAAAAGGGAATTGACTTCGCGCTGCCAAAAGTAGGGGAGCAGGCCAGCATTGCAAGT
GCGCACCAAAAC

>RXN01634-downstream
TGATCCAACTCCAGGATCAATTA

>RXN01635-upstream
AGGGAATTGACTTCGCGCTGCCAAAAGTAGGGGAGCAGGCCAGCATTGCAAGTGCGCACC
AAAACTGATCCAACTCCAGGATCAATTACTTCTGATCAAG

>RXN01635
TTGATTCCTGGCGGATTGGACACTCCAGAAGAGCCTGAAGCCCCTGAAGACTCTCTTTTT
GAAGGGCGCACTCCCCCTAGGGATGCAAGCACCCGCTTGATCCTCACTGAACTAATGGTC
AACTCCACCAACATGGGCAGTTCTGATGGTTTTGAGTATGTGGAAATCACCAACACTACT
GCCGAACCCATCGATTTTTCCGATTACACCTTGAACTACCTGTACCCGCAGGATGAGTTC
ACCAACACCAACGAAGCCGTCTGGGCTGCGGAACCTGGTGATGTCATTATTCAGCCTGGA
AAATCTCTCGTGTTTTGGATCAAAAATGGCCCCAATGATGAGGCAACCGCAGCAGATTTC
AATGCAGAATATGGCACCAACCTGGAGGCTGGAAAAGACCTTGTTGAAATCTCCTCAGGT
GGGATGGCCAATGGTACTGCCAGAGGAATGCAGATTCAGACCAACACTGGCCACATAGTC
AACCGTGGTTTCTACAACATGGCTGGCGCTTCTGATGTGAAAGCCAACGAGGGTCTTCAT
TTCGCAGTGGATGAGTCTGATCTTCTGAAGCAAACGCTTGTCGGCAGCGGTGCGCCAACC
CCGGGCACTGTGTACACTTCGCAGATTCCTAATCCACTGTCTGCCGTTATCGCTGATTCT
TCTGTACCACTCATCACAGATAATACCGCAACCAGTATCAACCCTGCGGAGCCGTTTACC
TTCGCCTTCAAATATCACCGA

>RXN01635-downstream
TGATGTCCAGGTGCGCACGGCAA

RXN01638-upstream
AGGCATCAAACCCACAGCACAACCACCAGGACGTGCCACGATGTCCATCCGTGGTGAAAA
CATCGGTGTTGCACAGATGGCACCGCATAGGTGATGACTC

>RXN01638
ATGAGCACCCAAACAATCACCATCACAGTCCTAGAAACCGCCACCATCTTTGACGGCCCT
GAAACCATCTACCGCTATGACCTGGCTGCCGAAGGCATCCTTGATGGATGGGCTCACTCT
GCTGTGCTGGATCAAGTGAAACAAATAGCAGGTGAAAACTGGCCGACTGTTGAGATCGTG
GTGGATGGCACCGACAACGTAGTCAATGCACTCACCTCCATGTTTGCTTCCAAAGGCGTG
ACCTGCGGTGGGGTTGGAGTAGAAGCACCTCCCGTTGCGGAGGAACCACCGAAAATTAAA
CGGCCCACGAGTGGAAAACAAGTCCGCCAGTTCTACGGCATCAAGCCACTACACCTGTTG
TTGGTCAGCATATTGGTTGGTTCTATTGCTGGTATTTGGGTGATTTCGGGTTTCACTGGG
CCAGTGGACTCACGGCCGGTAGATAAGGTGGCGGAGATTTCAACGCAGGGGGAGACGTCG
ATAAGCAATCAACCCCAACCCCAGCCCACCGTGCTCGTGACCGAGGACCTGCTTATTGAG
GCGCCATTTGGTTTTGAAATGCGAAGCGACGAACAGTCGCGCTACCTGGAAGGCCCCGAC
CCGAATCTGCGCATCCACGTGGGCGTCGATCCGCTGCACGGCGCGGACGCCGCGCTGGTT
GCCGAAGAGCTGCGCCGCCTGATCACCGAGGATCCTTCGCTGGAGGAAATTCCCGCAGGG
GAGTGGGGCGAGAAAACCACCATCGACTACCGCGAAACACCCGGCGATGGCTCTCATGTG
CTGTGGGTGACCTGGTTTGACACCGACCGACAACTCAACGTTGGGTGCCATAGCAAAGCC
GCCGAAACCCTTGTTCACAAGGCACAATGCCGAAATGTGATTGAGCATCTGACGCTGAAA

>RXN01638-downstream
TGATGCCGGTTTCTATCCGGAAT

>RXN01647-upstream
GCTGGGGGAATACATGGCTGAAGGCATGTTGATGCCCACGACATCGGCGCAGGTGTCGGG

GCATAAATTTCTGGTGCGGCGCATCGAACATGGGTTGGTG

>RXN01647
ATGGGCGATGTGCGCATGATTCATGATCCACTTGGTAGGCGCCGGCGGGCGTTGGTGTTT
GGGGTGGTGGCGTGCGTGATGTTGGCGGTGGGATCATTGGCGTTGGCTATTTTTCGACCC
GCGAAGGATCCGGCCGATGCGCCGTTGATCCGCTCTGAATCCGGCGCGCTCTTTGTGCAG
CTGGATGGGTCGGTGCATCCGGTGGCTAATGTGGCCTCGGCTCGGTTGATTGTGGGGGAG
CCGGTGGATCCGGTGAACGCCAGCGATGCGATCATCGCGGGCATGCCGCGCGGAGTGCCG
GTGGGGGTTCCTGATGCGCCGGGGCTTTTCAGCAGCACCGAAGAACCCGAGCAAGATTGG
TTTGTGTGCCAGGATGTCGGCACTGGGGATCTACACATTACGGTTCCTAGGGGCGGACTA
GGGCCCACCCTGATTGCGGAAGGAAATGGGTGGCTGGGGGCGTCGAAAAGCGAAACCGGC
GAGGTCACCTGGAACCTGATTACCGCGGACGGGCGCCGCGAACTGCCGGCGTGGGGCAGC
GAACATGGGCGCATTATGCGCCGCCACCTGGGGATTTCCGAGGACACCCCGCGCGTATAC
CTGACCACTGAGCTGCTCAACGCGATCCCCGAGCACGACGCGGTCCGCTTCCCAGCCCCG
CTGCCCGAGCTTGTCGACGCCTCCACCCGCAACTGGTTACGGCTCGACGGGGCGCTCGCC
GAAATCACGCCGCTACAGCGCGGGTTGCTTATCGACGCCGGTTCCGGTGTTTTCCCCGAC
CCCACCGCGCTTCTTGGTGTGCATGAAGAAACAGCCAACACCTTGACGCTGCCCGAGCAA
ACAGTTTCTTGGCAAGATCTGGACGGTGGTTTTGCCTGCGCGGATGGTGAAGGCCAGATC
GGTTTCCTGGAAACTCTGGAATCGGGGGTGGCGCTATCTGGTGATTCCAGGGCGAAAAGT
TTCAGCACAAACGCTGGTGGGGCAGTGGGCGTGGACAGTGGCTTTGGCTACTATGTGGTC
TCTGATTTTGGGCTGATGCACCCTGTTTCTACTGGTGAATCGATGGTTGCCCTAGGAATC
ACTGACGTGCAGGTCGTGCCGTGGAGCGTGCTGCGATTGTTGCCGCAGGGAAGTGAATTA
GCAAAAGAGACAGCGCTCGCGCCCACCTAT

>RXN01647-downstream
TAAGGAGTATGGTGGCCTTACAT

>RXN01658
GATCCACAGATCCTGTCACCAACCTTCACCCAGCAACAGCAGCTGCGAAACTTCTACGGT
TTCCCAGACCAGCTGGCGATGGACCGCTTTGAAGTAGATGGCAAACTCCGCGACTTTGTT
GTGGCAGCACGTGAGCTCGATCCAAACGCCCTGCAGCAAAACCAGCAGGACTGGATTAAC
CGTCACACTGTTTATACCCACGGCAACGGCTTCATTGCAGCTCAAGCAAACCAGGTGGAT
GAGGTCGCCCGCGACGTCGGATCCACTCGTGGTGGTTACCCTGTCTACACCGTCTCTGAT
TTGCAGTCGAATGCTCGTGCTGCAGAAAGCGAAGATGCTGAGGAGCTTGGCATCAAGGTT
GATGAGCCTCGTGTGTACTACGGACCACTGATTGCTTCTGCGACTGATGGTGCTGACTAC
GCAATTGTCGGTGACACCGGCGATGGCCCAGTCGAGTACGACACTGACACCTCCAGCTAC
ACCTACGAAGGTGCTGGCGGCGTGGACATTGGAAACATGGTCAACCGTGCGATGTTTGCA
TTGCGCTACCAGGAAATGAACATGCTCCTGTCTGATCGTGTTGGTTCCGAATCCAAGATC
CTATTTGAGCGCGATCCTCGTTCCCGTGTGGAAAAGGTTGCACCTTGGTTGACCACTGAC
TCCAAGACCTACCCAACTGTGATTGATGGTCGCATCAAGTGGATCGTCGATGGCTACACC
ACCTTGGATAGTCTTCCGTACTCCACGCGCACCTCACTGACGGAAGCGACTCAGGATGCT
GTCATGCCTGACGGCACCCCACAGCCACTGATCACAGATAGGGTCGGTTACATCCGCAAC
TCCGTGAAGGCTGTTGTTGATGCGTACGACGGAACTGTTGAACTCTACGAATTCGACACC
GAAGATCCTGTTCTGAAGGCATGGCGTGGCGTGTTCCCAGACACCGTGAAGGACGGGTCG
GAGATTTCCGATGAGCTTCGCGCACACCTGCGTTACCCAGAAGATTTGTTCAAGGTCCAG
CGTGACATGCTGGCCAAGTACAACGTTGATGATTCTGGAACATTCTTCACCAACGATGCG
TTCTGGTCTGTCCCAGGTGACCCAACTGCAGCGGAGGGCCGCCAGGAACTTAAGCAGCCT
CCTTACTACGTGGTGGCAGCAGACCCAGAGACCGGTGAGTCCAGCTTCCAGCTGATCACC
CCGTTCCGTGGACTTCAGCGCGAGTACCTCTCTGCACACATGTCTGCGTCGTCTGATCCA
GTTACCTACGGTGAAATCACTGTTCGTGTGCTGCCTACCGATTCTGTGACCCAGGGTCCA
AAGCAGGCCCAGGATGCGATGATGTCATCTGACCAGGTTGCTCAGGACCAAACACTGTGG
CGTGGATCGAACGATCTGCACAACGGAAACCTGTTGACCTTGCCAGTTGGTGGCGGAGAG
ATCCTCTACGTTGAGCCGATTTACTCGCAGCGCAAGGATCAGGCATCGGCCTTCCCGAAG
CTTCTGCGCGTGCTGGTCTTCTACAAGGGTCAGGTTGGTTACGCACCAACGATCGCTGAA
GCCCTATCGCAGGTCGGCATTGATCCGAAGGAAGCGCAGGACATCGAAGAGGTAGATGGC
ACCGCTACGACGCCATCGACTGATGAGACTGACACTGACACTGATCAGCCTGCAACCGAA
ACCCCAACTGCACCAGTGAGTGAGGCGGAAGGAATCGCGGCCATCAACGATGCGTTGAGC
AACCTTGAAGCTGCTCGCGATAGCTCTTTCGAAGAGTATGGTCGTGCACTCGATGCGCTT
GATCGTGCCGTCGATAGCTACCAGTCCGCACAG

>RXN01658-downstream
TAGCGTTTGAGTAAACAGCCCGA

>RXN01659-upstream
TTGATGCGCGCCGCGGTGAGCAGCCTGCCGATCCAGAGCGTGAAGAATCTGATGATTTAG
TCGAGATTGATACCGTCTCTGGATTCCGCCTGCTCAGTAC

>RXN01659
GTGGCGGGGGTTGCGCAGCGTTTTGTCGACGAGCGCATTCACGTCGGTTTGGATTCCATG
CCAGAAGCTGTGACTGCTGTGTGGATGGAATCTGATTGGGTGTTGGCGGAAACCATCAAG
GGTTCCACGCCTTCCGATTGGGAAGAGATTTTGCGGCCGTTGGCGCTGCTCACGGACGCG
TCTTTCACGTTGCCACCTCGTTCCACGCGTGCGCAAACCTTGGATTTGAAGCATTTGGAA
CCAAGCCGTCTGAAGCCGGAGCAGCCAGAAAAGCCAGCGTTTACTCCCAATGCTTCGGAA
GAAGATTTGTCTCAGCCGTTGGTGATCCGCCCCGAGGAGCCGTTGCAGATGCCGGTTCGC
GGTGTGCAGGAAAGCCGCGGAGTGGTCGAGCCACGGTCATTGGGTGCGGATGATGTGGAG
TCGATTGCGGAGGGCGATCCAGAGCGTCCGAGCGATCTTTATGGCACGCGTGTGCTGCGT
GATCTCAATGGTCAGTCCAGTATTTTCCAAGATTCCACCGACGCGGATGAGCCACCAAAA
AAGTGG

>RXN01659-downstream
TAGAAAACTGGTGTTTTTCGGCC

RXN01663-upstream
TATTTTGCTGGTTGGTCACAGTGGAGCGCTAACCCCGAGAATCCTATCGAGGCCTAAAAT
CGTGGCTTGAGTACGCACTGCCAGTAAGGTGTGTGATGTG

>RXN01663
ATGGAAATAAGTGTCTTGATCATCGCCGCACTGATCTTGGTGGCAGGCATCGTACTGTGG
CGCGCGGACTCGTCTAAACAGGCAGCTAAAAAGGCTGAATCACCTGTGGGCTCAGTCGCA
CCTGCGCCCGTGCTGGTTGAAGAAGAGCCGGACCCTGAGTTTGAGCCAGAACTGGACCCT
GAACCAGAAGCGCAACCAGAACCAGAGCTGGAAGTTGCGCCTAGATTTGCGCCAGAACCA
GTTCAAGATCTTGAGCCGGATCAGGCTGAGGACATTTATTTTGATGATTCCCCTGAACTC
GATGCTGATGTTGAAAATGCCTTGGCTGAGCTTACTGAGGTAGAAGACTACCCGGAAGAG
CCAGTGCAGTCTGAGCAACCTCAAGCCCCTGCCACGGCGGAGGTAGCTGCGGACGAGGAG
CAACGGGGCGTCGATAAGCATTCGTTTTTGAGCTCTTTGCCTGGTTCGCAGCGCCGGGAG
CGCCGAAACTGGGCGGCGAAGCACCACTTCGATTTCATCAAGGAAGATGCCTTTTTGACC
GATGAATGGTCAAGGGGTGCGGCATCGACTGGTGCCGTTGCACGTGATGTGGTCAGTGGC
ATGGCTGAAGGATATGAAACGCATCTGGTGGATTTGGCGGGCGTGCCCGTGATGGCGATG
CGCCGTGGAATTACCTCTGACGTGGTCATTGATGCGCGCCGCGGTGAGCAGCCTGCCGAT
CCAGAGCGTGAAGAATCTGATGATTTAGTCGAGATTGATACCGTCTCTGGATTCCGCCTG
CTCAGTACGTGGCGGGGGTTGCGCAGCGTTTTGTCGACGAGCGCATTCACGTCGGTTTGG
ATTCCATGCCAGAAGCTG

>RXN01663-downstream
TGACTGCTGTGTGGATGGAATCT

RXN01669-upstream
CACCCACAGTCACCAAGAACATAGCCACTCCACACACAACCACTCCACACACAACCACGA
GGGTCACGACCACCATCACCCCACCGGATTCAAAGGATTT

>RXN01669
TTGTACGAGATTTTCGTTCCACACTCCCATGACACCGCCGACTCGATTGATGATGCTATG
GAGGCGAACTCAGAGGGTATTCGAGCGCTGAAGTTTAGCCTTGTATTGATGCTGCTCACG
ACGGTTTTGCAGGCTATCATTGTGTCTTTTTCTGGATCTGTTGCACTGTTGGCGGATACG
GTTCACAACCTTTCCGACGCATTGACTGCGATTCCTCTTTGGATTGCTTTCATACTTTCC
CGGCGCGCAGCGACTCAAAAATATACGTATGGATTCAATCGTGCAGAGGATTTAGCGGGG
TTGTTTATTGTCGCGATGATTGCTCTTTCGGCGATTGTTGCTGCATGGCAGGCGATCGAC
CGGATGATTAATCCTCGCCCGATGGAGAATATTGAATGGGTGATTGCGGCAGGTGTTATT
GGTTTCTTAGGAAATGAGGCTGTGGCAATGTATCGCATTCGGGTTGGTAAGAGGATTGGC

TCGGCTGCTTTGGTTGCAGATGGCGTTCATGCTCGCACGGATGGTTTTACTTCACTTGCA
GTTGTCGCAGGTGGTGTTGGAGTTTTTCTGGGATTCCCCCTGGCTGACCCAATTATCGGA
TTGATCATTTCTGCGATGATTGCCACCCTTCTTGTTGGTACGATCCGTTCGGTTGGCAGA
CGCCTCATGGATGGAATTGAGCCGGAGTTGGTAGAGAAGGCTACGCACGCGATCTGGCAT
GTGAAGGAAATTGAGTCGATTGATCGACTGAGGTTGAGGTGGGTTGGACACCGTCTTCAC
GGCGATGCCACGGTCAGCACTTCTACATCATCGCTATCGGAAGCCACCGCAATCGCCCTT
GAGGCTGAGCTTTCCGTCAAACAACATCTTCCCAATGTGGATGAAATGACTGTGACCATC
ACCCCTTCCAAACCT

>RXN01669-downstream
TGAGTCCCGTGATACAATTGTTG

RXN01672-upstream
AGTAGCAAAGGGTGCAGTCGAAGGACCAGCATCCAAGACTGCTGCCGAAGAAACCGACTC
CGTTGACAACGGATCCGACGAAAACGGCGAGGAATAATTT

>RXN01672
ATGGCATCCCGAGAAGTATCCATCACCCGAATCTCACCACTAGCAACCTTCCGAGTTGCA
CTGGCAATGTCCATCATCGGACTCGTGGCGTGGATCATCTGCGTAACCGTCCTCTATTTC
GGACTTAACGTGGCTGGCGTCTGGCAGAACTTCAACGATGTCATCGGCGGTGTTGGTGCA
GAACAAACCATCACCTTCGGGCTCGTCCTGAGCATTTCCGCACTTCTGGGAGCTATCGGA
GCGATTACCGTCGCTGTGCTTGCACCATTGTGTGCAATCATCTACAACTCGATTGTTGAC
CTCTTCGGTGGACTGCAGATTCAACTGCAAGAAGAAGTAGAC

>RXN01672-downstream
TAACCTCTGAAACACAAACCCCT

>RXN01694-upstream
CGACACCAATAATTTATTGGGTATCCACCAATTACCGCTGTGAGCACTGCAAATTACGTA
TTCGAAAAGCCATGTCCACCACGTGTTCTATCCTGGCGGC

>RXN01694
ATGCAAAAAATCACCCCAAACATCTGGTGCCAAGGCACCGCAGACGAAGCAGCCGAATTC
TACGTCAATGCGTTTTCTGAGTTTCCGGGTGGCGCAGAAGTACTCACCACAGTTAAGTAT
CCCGAAGCTGGCTTGCTGGACTTCCAGGAGCCTTTCGCAGGAAAAACCTTGACGGTGGAA
CTCGCTATCTCAGGCTTTAAGATCATCTTGATCAATGCTGGTGAAGAGTTCACTCCCAAC
CCATCGATCAGCTTCATGGTGAATTTTGATGCGGTGCGTGATGAAAATGCCAAAGAGCAC
CTTGATGCGGTGTGGGAAAAACTCCATGAAGGCGGCAGCACACTGATGCCAGTCGATACT
TACCCATTTTCGGAATACTACGGGTGGGTACAAGACAAATATGGTGTGAGCTGGCAATTG
ATGCTCAGCCGCCCAGAAGAAAAGCCAGGTCCCGCAGTAATCCCAACGCTCTTATTTGGT
GGGGCAGCTCAAAATCAGGCAGGCCCAGCTCAAGAAAACTACGTTGAGGTGTTCCCGAAC
TCCCAACTTGGTGATCGTGCACCTTATGGACAGCAAACAGGTCCTGCCACTCCTGAGGCC
CTCATGTTTTCCCAGTTCCAACTCGACGGTCAGTGGATTTTCGCGATGGATTCCGGAGTT
GAGCAAGATTTCACCTTCAGTGAGGGTGTCTCATTGATGTATGAAGCTCATGGTCAAGAA
GAACTCGATGCCATCTGGAATGCACTCTCGGCAGTTCCAGAAGCTGAGGCTTGTGGTTGG
TTGAAGGACAAGTTCGGCGTGAGCTGGCAGATTGTTCCCGACAACATGGAGGAGCTCATG
GCTAAACCCGGCGCGTATGAAAAGCTTCTTGCGATGAAGAAGATCAATATCGCGGAGTTC

>RXN01694-downstream
TAGCAGTTCTAAGCGCTCCACGC

>RXN01696-upstream
AGGTGACGGTGATACAATTTTGCCATAACTGACTTAACCCAGAACGTTGTCCGGAAGCAC
ACAGACCTTTGTGCGGCTTCCTTTTCTAGGAGCATGTAAC

>RXN01696
TTGTCTACCCCAATCGGCCTTGGCCTTCCTCCGACCCCACCTCCAGTGTTGGCGCCACGT
CGTAAAACACGCCAACTCATGGTCGGCAAAGTGGGCGTTGGTTCGGATCACCCGATTTCC

GTCCAGTCGATGACCACCACCAAAACCCACGACATCAACGGCACCCTGCAACAGATCGCA
CAGTTGACAGCCACCGGTTGTGACATCGTCCGCGTTGCCTGCCCAAAGACTGTTGATGCG
GAAGCACTGCCGATCATCGCAAAGAAGTCTCCGATCCCAGTGATCGCAGATATCCACTTC
CAGCCCAAGTACATCTTCGCGGCAATCGATGCAGGTTGCGCCGCCGTTCGTGTGAACCCA
GGCAACATCAAGGAATTCGATGGTCGCGTTAAAGAAGTAGCAAAAGCTGCAGGCGATGCC
GGAATTCCAATTCGTATTGGTGTCAACGGCGGATCCCTGGATAAGCGCATCCTGGACAAA
TACCACGGCAAAGCCACCCCAGAAGCTCTCGTGGAATCCGCAATGTGGGAAGCCGGCCTG
TTTGAAGAGCACGGCTTCGGCGACATCGCAATCTCTGTGAAGCACTCCGACCCAGTACTC
ATGGTGGAGGCCTACCGCCAGCTCGCTGAACAAAGCGACTACCCACTGCACCTCGGTGTT
ACTGAAGCTGGTCCCAAGTTCATGGGAACAATCAAGTCTTCCGTAGCATTCGGCGCTCTG
CTGTCCCAGGGCATCGGCGACACTATCCGTGTGTCTCTTTCTGCTGACCCAGTGGAAGAA
ATCAAGGTTGGCGACCAGATTCTGCAGTCCCTCAACCTGCGCCCACGCAAGCTGGAAATC
GTGTCCTGCCCATCATGTGGCCGCGCACAGGTCGATGTGTACTCACTTGCTGAAGAAGTC
ACCGAAGCACTCGACGGCATGGAAGTTCCACTGCGCGTCGCTGTCATGGGTTGCGTTGTT
AACGGCCCAGGTGAGGCTCGCGACGCTGACCTCGGTGTTGCATCCGGTAACGGCAAGGGC
CAGATCTTTGTCAAGGGCGAAGTCATCAAGACTGTCCCAGAATCCCAGATCGTGGAAACC
CTCATCGAAGAAGCAATGCGTATCGCAGAGGAAATGGACCCAGAAGTCCTCGCTGCAGCA
AGTGCTTCCGGTATGAAGGCTGAAGTGAAGGTAACCAAG

>RXN01696-downstream
TAAGTTTTGGTTAATTAAGGCAC

>RXN01697-upstream
TAGATCAACTAAGTATGAACGCGAATCCGACTTTGGTCGTACTGCAAGAATCGACCAGAG
CCCGATTAAAAAATGCCCCCGCGCAACGAAACTAGTAATC

>RXN01697
ATGTTTCAAGGACTAAAAGAACTCACCGCAGCAAAAGGCCGCACGCTGCTGATCACCGTC
ACCGTCGGGCTGATCGCCGTGCTGGTTACTTTCCTCTCTGCCCTCACCGCCGGGCTTGGC
CACCAATCAGTATCCGCACTGAAATACCTAGCGGGTGATAATGAACTTATCCTCGCCGAT
TCCGGATCCACCACGCTTTCCGCGTCCACGCTTTCTGATCAAGCAGTTGCCCAACTCGAA
GACGAAGGCGCACAGATGCTGTGGCAGGTCCGCGACCGAGTAGCAGACACCCCCACCATG
CTCCTCAACTCCCCTGACCTTGCGCCTGGTGAAGTATCCCTTCCTGCCGAACTCGCTGAT
TCGGAACTCGCTACTGCGCATGATGTAGTGGATTCTTCCAACGATCTGTACCTCGATCAC
CTGCCCGTGGTATTGATGAACACCTCCGATTTAGCCTCACTCGCGCAAGTCCGAGGCGTG
ACAGGACCAGCAGGCGCATTCGCCTCTGACGTTGCGCTCCCCTCCGACACCGTTGCGCTC
TCTGGATCCGAACGGTGGAACGCATCCGCCTCCTACCAGGGCGAACAGATGTCACTCAAC
CTCATGATCGTCATGCTGTATGTTATCTCCGCACTCGTGCTCGGCGCATTCTTCACCGTC
TGGACCATCCAACGCCTCCGCGGCATCGCCATCTCTAGTGCTTTGGGAGCAGCCCGCCGA
GTACTTATCGCCGACGCTCTCGGCCAAGCCATCATCGTCTTAGGAATCGGCATCACCGCA
GGCACATTGATCACAGTCATCTCCGCATTCGGCATGGGAGACGCAATGCCCGTGGTCATC
TCCTCCTCCACCACGCTCTTCCCCGCACTTATCCTCGCCGCAGCAGGACTCATCGGTGCC
GCCATTTCACTCGGCCCCATCCTTCGCGTCGAACCACGCTCCGCACTCATGAACGCA

>RXN01697-downstream
TAAGAAAAGGAACCTCACATGAC

>RXN01701-upstream
GCCGATCAAATTCATTGATTGTTAATCGGAAGTTTTTTGAACAGGTAAAGCTAGGGGACC
TGTTCAGTGCCTGTTGGCGGATGTATTAAGGAGAATGCCC

>RXN01701
ATGCTGAGCCACGAAGAAATTGTTGCGATCGCAGAAGATTTGCTGTCTAAACGCTACGGC
GGTGTACAAACTCTTTCTGACGTGGAGCAGCTCAACGGTTCCGGCACCTCCGCGGTGCTG
CGTGCCAGGGTGGCTAACTCCCCATTCCTCCAACAGCGCTCCGTGGTGCTGAAGTACGTG
CCCAGCACCGGAGACGTCTTTGATGATTCTGCGCTGGTGCGTGAAATCGTCTCCTACCAG
TTCACCACCTCCTTGTCGGAAGATGTCCGCCCAGGGCCAGTCATTTTGGCCTATGACATT
GACAAGCGCATCCTGGTCATTTCAGATTCCGGCAACGGCGACACCTTTGCGGATCTGATC
GATCAGCGTCCG

>RXN01703-upstream
GTTAGACAAATGGGTAAACAGAGCTGACCTAGCGGAATCCGCCATCAACGAAAGGCATTC
CGCGAGGGTTTGGGGTCTGCCTCGAACAAATCTTGGGTTT

>RXN01703
GTGGCATGGCCATCCAACGCCAAAGAAAAACTGTTTATCCACTGGCACTACTGGTGGCAA
GCGCATTATCTAGACTGCCTGGTGGATGCTGCTCGTCGACGCACCACAAAGGCCCGTCGC
GACCGCATCAGGGACACCATCCGCGGCATTTCGGTGCGCAATGTGGGCAAGCTGACCTCG
AATCGTTATTACGACGACAAAGCTTGGCTGGCCCTTGCTCTTGGGCGTGCCGGAAAAGTG
CGAAAGGTGCGCACACCAAAATCATTGCCCTCGTTGGAACAAAACATCGTCGATGGCATT
GATTCCCTTACTGGTGTGCTGCCGTGGCGTTCCGGCGAAACCTTCTACAACGTTCCCTCC
AACGGTCCTGCTGCGATCATGATGGCCCGCACCGACCGTTTGGACGAGGCTATGAAAATC
ACCGATTGGATTTTTGACAACCTGATCGATGGCGACGGCCTTGTGATGGACGGATTGCGC
ATGCGCATGCACGGACCTGAGCTTGTCCGTTCCATCCACCCGTATTGCCAAGGTGTCGCC
ATTGGTGCGTGTTTGGAAATTGCTCTCAAACTGCGTGAGCGCGCAGGCTTGACCACTACT
GTGGTGGATCACTGGTCGGATGCCGATAAGGCAGAAGACTCCCTCAAATACTTTGCACAC
ATCCACGCTGTGGTTCAGGCTGTGTCGCGGAAGATGACCAACTTCCACGGCGTTATTGAT
TGGGACACCGGTGACGGCGACGGCGGTTTGTTCAAGGGCATTTTGGTCCGCTATTTAGCT
GATGTGGCCATCCGCCTGCCTGACGATTCACCAACCAACCGGGAAACCAAAAAGATTGCA
GCACGCCTGGTACTGGAATCGGCGGAAAGCGTATGGAACCACCGATTGGAAGTTGATGGC
CTTCCGGTATTCGCCACAGACTGGACAACGGATGCACGCCTGCCACAAAACTTTGGTTTG
AGTTCCTCTAGTTTGAGCGATCTGGTGAGTGTTGTGCGCGTGGATGAACGTGATCTGTCC
GTGCAATTGTCCGGTTGGATGCTCATGGAAGCAGCAGCGAAAGTGGCCGAAGAACTGGAA
AACAACGGCAATAGTTACACCGGTCGCTCCCGA

>RXN01703-downstream
TAGCCCCGATAGTGTATGTGCTG

>RXN01709-upstream
GCAAGTGGAACCACGATGGGAACGGTAACTGCTGCCGCTGCGGTATTACTCGTAGTTTCA
GAAATTAGGTGTCGATGCAGCAATACGGAACTTTGCCAAT

>RXN01709
GTGTTTGAACAAGCTCTCGGGCTCACCACCCTTGCACAAACAGCTGGAGCGGGCGCAGCG
GGGGGCTTGGGTTTCATGGCAATGGCGTTGTTGTCTGCAGGGATGCGCTCCGGCGTGGAC
ATGATTCTTAATGAAACCGGGGGGTGAAAAGATGCTTGCACAGGCAGATTTAGTCATCACT
GGAGAAGGACGCATTGATGCACAGACCCTCAGCGGGAAAGCTCCTACTGGAATCGCCAAA
CGGGCACGTGCGAAAGGAATTCCAGTACTGGCGGTTTGTGGGCAGAGCCTATTGGGTCCA
GCAATCTCAAATGAGCTATTTGAAGACATCTACAGCTTTACCGATTTCGAATCTGACATC
AATGAATGCATTCGAAACCCGCTCCCAATTTTGGAAGGTATCGGTTTTAACATCGCCAAA
CATCATCTGAGT

>RXN01709-downstream
TAGCGATATTTCAGCAAACCGAT

>RXN01711-upstream
TCTCGTGAGTTTCTCCCCGGTAGCACCTTCTATATCAGCCCCCACGCCGCGTCGGAGCAG
GTGGGATAGCATCGGCAACGCGGTTGCATGGCCGTTGGCC

>RXN01711
ATGTTGTTGATGGCGCATCGCTTCTTCGTGCTTGCGATTAACGGCGCAGTCACCGACGAT
TTCACGACGGTTTATAGTGCTTTACGACGTTTCGTTGAAGGTATTCCGGTCTACAACGAG
GTCTACCACTTCGTCGATCCGCACTACCTCTATAACCCGGGCGCCACCCTCCTATTGGCA
CCATTGGGATATATCACCCATTTCACGTTGGCTCGGTGGATGTTCATCGCGGTGAACCTC
CTTGCCATTGTTTTAGCGTTCGGGCTGCTGACCAGACTCTCCGGTTGGGCGCTGCGCAGC
ATGGTGTGGCCGATTGCGATCGCCTTGGCGATGCTGACAGAAACCGTGCAAAACACCCTC
ATTTTCTCCAACATCAACGGCATCCTGCTGCTCATGTTGGCGATTTTCCTGTGGTGCGTG
GTGCACAAAAAATCCTGGTTGGGCGGACTAGTCATTGGTTTGGCCATTTTGATCAAACCC

ATGTTCCTGCCACTTCTCTTCCTACCTTTGGTGAAAAAGCAATGGGGATCGCTCATCCTC
GGCATTTTAACCCCAGTGATTTTCAATGCAGTGGCCTGGTTCTTAGTTCCGGGAGCATCT
GAATACGTCACCCGCACGATGCCCTACCTTGGTGAAACTCGAGATTTTGCCAACAGCTCA
CTCCCAGGCTTGGCCATCTATTTCGGAATGCCCACCTGGATGGAAATCACCTGGTTCCTC
ATCTTCGGCGCAATGGTCGGCCTCGCAGTGCTGGCACTCCTGAGATTCCGTAACACCGAG
CCATACTTCTGGGCAGCAACCACCACCGGTGTACTCCTGACTGGCGTATTCTTCCTGTCC
TCACTGGGACAGATGTACTACTCCATGATGATCTTCCCTATGATCTTCACCCTGCTCGGA
AGCCGATCCGTATTCCACAACTGGGTTGCCTGGGTCGCCGCCTACTTCTTACTATCCCCT
GACACTTTCACCTCCCAGCGACTACCCGATGTAGCCCGCTGGATGGAATTTTTCAGCGCG
ACCGTTGGTTGGGGACTATTGATAGTGGTTACATTTGTCTCGGCGCTAATCTGGTTTATT
GGTGATATCCGAGCCAAGGGAACTCCGAGCTCACCCATTACCACTGATCCAACGCACGAC
CATCTTGAGAGGACAGCA

>RXN01711-downstream
TGACAGACTTCAAACTCATCAGC

>RXN01721-upstream
TTCGCCAACGCCGCCCCGAAATGATCGGGAGGGGGCGTCGAAAAGCACTTCTGCGAGCAT
CAAACATGATGCGTACCTGCCACCCGCAGACGGCAATCGC

>RXN01721
GTGCTTGTGGACAGATTCGGACGCATCGCGCGTGACCTGCGGGTGTCACTGACCGACCGA
TGCAACCTCCGCTGCACCTATTGCATGCCCGCGGAGGGTTTAGAGTGGCTGCCCACCGAG
CAGACGCTTAACGACGCCGAGGTGCTGCGACTCATCCGCATTGCGGTGGTTAAGCTGGGC
ATTCGTCAAATTCGATTCACCGGCGGCGAGCCTTTACTGCGGAAAAATTTGGAAGACATC
ATCGCCGGCACCGCAGCCCTGCGCACCGACGAAGGCGAAAAAGTTCACATCGCTCTCACC
ACCAACGGCCTTGGCCTAGACAAACGCATCGCAGGACTGAAAGAAGCTGGTCTTGACCGG
GTCAATATTTCACTCGACACCATCGACGCCGAACGCTACGTCTCGCTAACCAAGCGTGAT
CGATTGTCCGGTGTGTTGGCGTCCATCGATGCCGCTGTTGCCGCTGGCCTTCACCCAGTG
AAGATCAACGCCGTGGTCATGCCTGGGGTCAATGAAGTAGATATCGTCCCCCTTGCGGAA
TACTGCATTTCCAAAGGCTCCCAACTGCGATTCATCGAACAAATGCCACTTGGCCCGCGC
GAGCAGTGGAAACGCGGCGATATGGTCACAGCCGAAGAAATCCTGGCGCGCCTGGAAGAA
AAATTCACCTTATCCCCCGCCAAGGAACCCCGAGGAGCTGCACCTGCTGCGCTGTGGAAT
GTGGTAGATAAATCCAACCCTGATATCACTGGACAAATCGGCATCATCGCCTCGGTGACG
CACCCATTTTGCGGAGATTGCGATCGCTCCCGCCTCACCACCGACGGCACCATCCGAAAC
TGCCTTTTCTCCCGCACTGAAACTCCCCTACGTGACGCGCTTCGCGACGGCGCCTCCGAC
GATGAGCTCGCGCAACTGTGGGCAGGCGCCATGTGGGAGAAGAAACCCGGCCATGGCATC
GACGATGAAGGCTTCCTCCAACCAGATCGCCCCATGTCTGCCATCGGGGCTAGCCCATAC
CAG

>RXN01734-upstream
ACGATCTGCCGGAGAATCTCAAGAAAGTGCTCACTGCGCAGCACACCGTCACCGTCCAAG
ACACCGGCACCGGGCGGATTTCACTCCTGGATGTGCAACC

>RXN01734
ATGACAGATCCAATTGAGCAGGCATTTGAACGCATCCGCGCCGAAGCCATGCGCAGAAAT
GGATCCGTTCCCGACCTCAATAAAAACGATGCTTTTCGACGCCCACCTGCGCCGAAAGGG
GGCGTCGAAAAGCGCAAAAAAGGCCGTGCAAGCGGCCTAGACGGCCGCCAGAAACGATAT
GTGCGCGGCGCGGAGTCGCTGGGATCGGTGCTGAACAAGGAAATTCAGCGTCGTGGCTGG
GGCAAAGACATTGCCGGCGGTTGGGTGACGTCCAACTGGGAAGAGCTTGTTGGCGCGAAG
ATTGCGCAGCATACGCGCGTGGAAATGATCAAAGATAAGAAGCTTTTTATCACTTGTGAT
TCCACAGCGTGGGCCACCAATCTGCGCATGATGCAGCGGCAAATCCTGCAGGTAATCGCT
GAAAAAGTGGGTCCAAATATTATTACAGAGCTGCGTATTTTTGGGCCTCAGGCCCCAAGC
TGGCGCAAGGGGCCGTTGCACGTAAAAGGACGCGGTCCGAGAGACACATACGGA

>RXN01734-downstream
TAGTTTGGTGATAAAAACCGTCG

>RXN01742-upstream

TGGCTAAAGCGATGTGTGTCATCTGAAAAATTTCCCCCAAAACTTAATCGACACAGTTAC
TTCATCTGGCCTTATTTCATCACAGTTACAATCATCTGTC

>RXN01742
ATGCAGGAAAAGCCAGAGATGCCAGCGATTGAGGTCATCCGTTCAGCGAAACGCACCAAA
ACTGTTCAAGCTCGAATTGTGGACGGGCAAATCCAGGTGCGCATCCCTGCGAGGATGTCT
AAAGCGGAGGAAGAAAAAGCGGTGGGGGAGATCGTCGCAAAGCTAAAGCGACGCACCCAA
TCGGCCGTCTCAAGCGACGCTGACCTGATTGAGCGCGCCCATAAGTTGAACAAGACTGTG
TTGGAGGGGCGGGCGCGGGTGGAAAGTATTCGGTGGGTGAGTAATCAGAAGGGGCGGTGG
GGGTCGTGCACGGTGGCGACTGCGGAGATTCGGATTTCGGATCGTTTAAAGCACGTGCCG
GATTATGTGTTGGATGCGGTGTTGGTGCATGAGCTGACGCATACGTTTATTGCGGGGCAT
TCGGCGGAGTTTTGGGAGTGGGCAGACAAAACGCCCCTGGCAGAGAGGGCCAAGGGCTAT
TTGGAGGCGTATCAGCGGTGGGGC

>RXN01742-downstream
TGAAGGTTTAGTTCTTGTCGGAG

>RXN01754-upstream
TGTGGCTGAAGACAAGAATGAATAGCATTCATCTCGTCGAATTTCATGTAGAAATTTGTC
CCCCTTTTTTTTGATGTGAAAGTTGAATCGGTAAGCTCCT

>RXN01754
GTGAAAATTAAATCCGTATTTTTGAGCACCGCTTTAAGCGCTTCCTTACTGCTCGGAATC
ACCCCACCCGTGCTGGGAGCAACGATCAACCCCAGTTTGCCTCTTTCTGCGTTGAGCTCC
TCGGACGATATCGCCGTACCCAACTTCGCCAAAGAATTACCGTTAGCTTTTGATGTACCA
GCAGGCACTGTTCCCCAAAGCTTGAGTGGAACGCTGCAGATTCCTGCCGAGTTTTCTGGC
GGCGTCGTGGAGTTTTATGACGGTGACCGGCTCTTTCACACCCTGCGCCTAGAAGTTAAT
GATTCCCGAGCACACATTGAGGTTCCGCTGCAAAGCGTTCCTGTCGAAGACGGCCGCGCC
ACCTTTTGGTTGCGCGCCATGTTGGATCCTGTAAACAACCAGTGGTGCTACGAGGAGCAG
GAAGTCCGCTTCTTAGACGGAAACGTCACCTTTGAAGGGGCGACGATTAACCCAGCTGTG
GTGGCTGATTACTTCCCGTCAGTGCTGCGCGCGTTGACAATTTACGTCCCGGAAAACCCC
TCTGAGGCAGTACAAGAAGCCACGTTAGAGGTTGCGACCTCCCTGGATTCGGTGTACCGA
AGATCAGGTCTGGATGTCAACGTAGAAACGCTTCCAACCGGCACCGATGCTCCTCCTACA
CGTCCTCAAGATTTTGAACGCCAGATTGTGCTGGTTGACGAGGCAACAGAAAGTAACACG
CAAAAAACCGAATTGGTCAATCCCGGCCAAGACAATGCATTCTTGCGCCTGAACGGCAAC
GCCGACGAGCTTTACGATCAAGCGCGCTTGCTTACCGACGCAACCCTGCCACTTGCCGTA
GACACCGAAGTAACGGCCTCAGGTTTTGGTGATGTGCCCAACCTTTCTACAGATGTGGCC
ACCCTCCAAGAACTGGGTATCACGCAGCTCACCTCTGAATCAGTTGCGCGCACAAGCGTC
ACCTTGGGCATTGAACGCTCCCGCCTGCGGACCTACTCGCAGTCCATGGACCTGCACATA
ACGGGAACCTACACCCCATTGCCACCCCAAAATGCAGGACAGATCACGTTCTCCATTGGT
GACACCGTGTTGGACTCCTTGACCACCGATGACACTGGCATCATTGACCGTGAGTTCAAC
GTTCCTGGAGACTTGGTCAACCGCTACACGGCGATCGTCGTGGAATTCACCAGCACCGGC
GACGTTAATTGTGGGGTCACCCAGCCCGTAGGCCTCAACATTGATTCCGACAGCCTTGTC
ACCTCCCAACATTCAGATGTTCCTGTACTCAACGGCTTCCGGTCCCTACCGCAGTCCTTC
CAACCTCGTGTGGACGTGGCGTTTGCTGATCCCAGCGTGCAGGAACTCTCCCGCGCTGTC
AGCGTAGTGTTGGGAATTCAATCTATGAGCTCCCAGCGCATCCGCCCACACCTGGTTAAC
TGGGATGAAGCCGTAGCCAGCGAGCGCCCAACAATTTTCATTGATGCTGCGGGCGCAAAG
ACTGATCAAGTGCCAAGCTACCTCGCCCAACAAGGCCAAACCCTAGAGATCACCAGCAAG
AACGACCAAAATGCGGACGGCGAACAACTCACCCGATCCCTGCAAACCAACGCTGCGCTT
GTTGTCGGTTCCATTCAGGCCGTGTGGGATGCCGATAAGAAGCGCACGGTGATTGTGGCA
AGTTCCCAGGACAACCCCCCCGATTTGGATGCCTTGATTTCGTGGATGGGAGAAGACCGC
GAACGCTGGAGTGATCTCAACGGCGACCTGATTGTCAAAGTCCGAGACCGCGAACCTGTG
CAATTGACCACCGTGGAAGCCCCAGATCAGCCTGGTCGATCGGCCACAGCCTTTATTGCG
ATCGGCGTCAGCCTTGTGGTCATTGCCCTGATTGTCGCAGCCGTGGTGTCAGTGTCCAGG
CGTTCGCAAAAAGGATACAAA

>RXN01754-downstream
TGATTTCTTCTTTACCCAGTAGA

>RXN01761-upstream
TTAAAGTTTCTATATTCCATTCTAAAATAACTTTGAATTGGGGATTAATGAAACTTTTTA

AGCAATTGTTTAAAACGAATATTGAGGGGGTGGCGGGCAA

>RXN01761
GTGACTGCGACAGTTTTAGAACCGCAACCTGTACAGCTTAGTGAGCAGGACGTAGATGCT
GAGATTGCGCGCATGGAGCTTAAACACAACCGACACAAGACGTGGCGACGCCGAACGATG
GCTGTTGTCATGACGCTCTTGATCTCAGTGGGTTTGAGCTTTGGTGCGTTTGGTAACAAG
GAACGTGAAGCTAATGCTTTCGCCAGCGCTATTATTGCCCAGGTTGTCGGTGCTATGGGC
GAGGTTGCCTTTGAAGCGATTTGTCCCAGTGATGGTGACACCGAGATGCTTCTTAAGTGC
ATCACCGAGAACTTAGGTGAAATGCACATTATCGAGAAGTGTCTCGAAGCAGAAGATGTC
TTGAAGTGCTTCTACGATGCGAAAAACGAAGAGCAACGTAAAGAACAGAACCTTGATAAA
GCCCCTGATTACTCCATGTACCGTATGGCCTCTGCGATGGCATCGTTCTATGGCAATGGT
CGGGCAGCTACTGCCGGTGTAGAGGAAGGCGGACCGAACGAGTTCCTCGATTCTGAGGAC
GCCGGTCTTAAGGTGTGGGAGGGCATTCTCAGTAAGGCCGCCAACGGAGGCAATGTCCTT
GGTTATGCTGACGCGAAACACAACGAGGACTCTGGTTGGTTCTTTGGTAATGGTGTTGCC
AACAACGAGAAAACGTACTCCTATGATTCTCTAGCTGATCATGCCTTTCAAGGGCCTTAT
CACTTTGCATTATTTGGCGCGACACTGAGTGGCTTAGGCTTTGATAGCTCAAAGGCGGAG
GATTCGCAGACTGATTTTGCTCAGCGTAAGGGCATGGGGTACGCGATGATGATCGCGTAC
ATCATCTCCGGAGGCATTGATCTGGTTTTTAACACTGTGCTGAATATCTTGAGCACCATA
AACCCATTTAGACTGCTCGTTGGACCAGTATCTCAGAATACTAACAAGACATTCACTGAG
AATATGGCTGGTGGGCAGACCACAGAAGGAACACCGTTTGAAGGAATGACTGATTTCTTC
GGGTTGATCTATAACTGGTCAGTGACTGTGGGCTGGCTCATCGGTATTCCTGTCTCCATT
GGTCTGTTTATGATGGGTGCGTTGATGTTTCGACGCATGGACAAGGGATCAGCGTTTAAA
AAGGTTGTTATCCGCGTCGTGTACGGTGTCGTTGGCCTGCCACTGCTTGGTGTCTCTTAT
ACCGGTGCGCTGGATTCCTTCCTCGACAGCGGTAGTTCCACAAGTGCTGGATCAAATGCG
ACAAAGATTGTGTTGTCCACCTACGTGGATTTCCAATCATGGGCAGAAAACACCCGTATG
CGTGTTCCTGACAAAGTAACACTGGCGTGGAGTCTGGAGGATCAGGCGCCAACAGGGCAG
TCCATGCGGATGGTACGCAATTCGGCGTTGGAAATTAATGCTCAATCAAATGAGAGTTTT
ACTACTTTTAAGAATCCAGGTTCCATGGATCTAGGCTATAGCATGGACTGGATGGAAAAG
ATGGCGGATCCAGCCAATTCTGGCACCGATGGGACCTCATCAAGTTCGGCGACGACTATT
TTCCAGGGAACCATCGCGCTACTGAGTCGTTATATCGACAACGACAGTATCTCCTCTGGC
AGTTTCGAAACCTCTATTCGAAGTGCGATGGAATCTTTGACCTCGAAAGAGGGAAGTGGC
GAAGCTGTTGCCGGTGGTGATGTAATGGCCTGGGTTACTGGTTACAACACAGCCTCTGGT
CTTAATGAGATCACTGCTGCTGAATTAGCTGATGCGAACAATCCATTGCTTGAGGTCAGC
GACTCAGCTGGTCTGCAGGGACGACCTATTGACCGCAATGCGGTGTCATTTAAATCTGGT
GATGCGACAGCGTCATGCAACAACTCAGTCGTGACAGGTTCTCGTGCTGTGGTCGGGGAC
TACCGAAGTGACTGCAATATGTCGCCCTTGACGATGTACAACTTCCTCAACACCTCATTC
CATCCAGCTGATGCAAGTGTCTTTTCTACGTCCACTTCTGCGTCAAGCTACACCCGTGCA
TCGCATAGCGCAGTGAGTCTTATCGGTTCTGGTGCCATGAACTTTGTGTACTGGTTCTCT
GCAATGTCCCTGATGGGTAGCTTCATCGTGATCGGTATCGGTTACGCCGGTGCCATGCTG
TTTAATACGATTCGACGCACGCTGTCGCTCATTGGTGCCGTTCCTTTTGCTGCGATGGGC
TTTATTGCTGGTGTTGCCAAGGTCATTGTGTACACCATCGCTATGCTCGTAGAGGTTATC
GGAACGATCATTTTGTACCAGCTCATTACCCGGTTCTTGATGGCTGTACCAGCACTCTTT
GAACAACCTTTGGCTGATTCCTTAAGTAGTAACGAGAGTGCTGAGCTGGTTGCCGGTGCT
GGTATGGGGCTAGTCGGTATGGCACTAGCTACCTCAGGCAACTGGGCGATTGCCGGCATG
GTGATCACAGTGGCCTCATCCATGGGGGTCATCATCTTCACGATTATTGCGATGAAGGTG
CGCGGATCTTTGGTATCAGGTGTCGATGAAACCGTGACCAGTGTTATTAACCGCTTCTTG
GATACACAGGTCTCTTCTGCAGGTGCTACCTCTGGTGACGGCATGATGCGTCGTGCAGCC
GCAACGGGTCTTGGTATTGGTGCGACACATATGGTACTCAACCGTGATGGTGACGGTGGT
GGATCTGATTCAGGCTCTGGTGGATCAGGTGGCGGTAGCGATTCAGGCTTGGGTGAGAAG
GCTGCTGGTCTGGCGAAGGTTGTCACAACTGTGGCTGGTGCCGGATTAGTCGGTAAGTAT
GCTACGGATGCGCTCGATAATTATGCAGATGGCGTTATCAACGGCGACGGTGATGGTGCG
TTCGCAGCAGGTGGTGACGCTACCGTTGATGGCGACTATGTAGCAGATGGAGATGCAATT
GCTTCTGCTGATGCTAACGCTGATTTTGTAGACGGTGTTGTTGATGGTGCTGGTCGCGCG
TCATTTAGCAATGCTGCGTATAGCTCCGATGGAACCACTCTCGACGGTGAGGGTGCGAGC
GTTGATGCACAGGGTAACCCGCTTCATGCTGATGGCACACCAATGAGTGCTGCTGAAGCT
GAAATGAAGATGGCTGGTCTGAGCTCGTCAGGAACCATGATGGAGAAATCTGGTGTGAAA
TCGAGTGGCATTACCACTGCAGCGGATGTCATGGACGATCAGTCTCTGGCAAGCAGTGTC
ACTGAGTCTGGTCTGTCCAAGATTCCAGACACCTATGGTGCAGATGTCTCGGGTGCTGCG
GGCACAGTCGGAACTACCGGTGCTGATTACAGTGCGACCGATTCAAGCGCAGGTCTGAAC
ATGAGCGAGGCTGCATTGCAGAGTGGCACCCCAATGGGCGCTCTCGCTGGTGGATCTGTG
TCGAGTTCCGATCAGGCCATGAATGACGCAGCTCTTCAGATTGCAGCGTCTCAGGGTCTT

GCACCAGCAGGTTCCATAGCTGGTATGGAGCAACTTAGTGCTCAAGCCACTGAAGCACCT
GCTGGAAAGGCCGGCAAGCAGCTTGGCGATCTTTCTGGCTCAGCGCTCAATACTCAGCTG
GCGTCCATGGGACAGCAGGTAGGTGACAGTGTGAACAGCGCTTATGCTGCAGGCGGTATG
GGTGGTGTTGATGTGGCTGGCAAGGTCACCGAGGCAGCACAGCACTTGTCTCAGGTTCCA
GGTCAGATTCAGAATGCTGTGACCAATGCGGATGCTGGTTCCTCTGGCGCAAGCTTTGGT
CAGATGGCACAGGGGGCAGCTGGTATTGCCGGTGTCGCAGGTGTGATCGGTGCAGCGGGC
GCAGCAAGCTCTGCAGCACAAGGCGCAGGTACTGTCCAGGGTGCGATGGGTAATGCTGCA
GCTGGTGCGGGAATGATCAACAACGCTGTTTCCGGTGGAGCTACTGGCTCAACAGGTGCC
GCACATGTGGTCAATGCATCACATGGACCAGTGGCGCCTGGTCAGGCTCACTACCAAGAG
TCTGGTCATGCACAAGCATTTGTGCAGAACAACCAGGCCAACACCGCGCACACAGCAAAC
ACGCGTGCACCGTCATCAGCTCAAATTATGGGCGCGAACGTTGCTGGCTCACTGGCATCA
CAGGCTGTACGAGGAATCGGTCAGCCTGGTCAGATGGGTGCTAATGTTCGCGACGCGATG
GGTGGCAGCGGACGCTCTGGTGGCCGTGGTGGAGCAACTCAAGGCGGTCGAGGCGCACAG
CGCAGCGGTGTCAGTGCTAAGAACGGTATCCGTGCACAGCGAGGTCAGAAGCCTTCTGTG
ACCGGCCAGGCGATGAATGCAGCAATGCGTTCAGCAGCGGTAAGCGGTCGCATGGCAAAC
ATGGACGGCAACAGTGTAGGTGGCACTGAAGCAGATCCACAGCAGGGGAGTGGCGTAACC
GAGAAGGGTGATAAAGGCGTTAAA

>RXN01761-downstream
TAGCGTGTAAAACACAATGACCG

>RXN01765-upstream
GCAGTCCGTCGGTGTCGTTTTCCCTGAACTGCCGGCAGAGCTTCAGCCACAAATCCCAGT
CAAGGCATAACACCGCACACCAAGAATTTTAGGAGGGGTC

>RXN01765
ATGAGCAACAACGTAGTGAAATATGAGTGCGCGGTCGACGCCGACAACATTGTCGCAGTC
GATATGCATGTGCACTTGGAAGTCGACAGCTGCGGACACAAATCGATGCCGGCAGACATC
ATGGCGGCATCCTCGAAGTACTTTAAGACCGCGGAACGAACTCCCTCAGCAGATGCCATT
GCTGATATTTATAGGGAACACAAGATGGCGGCGGTGGTTTTCACCATCGATGCGCGGACC
CAAATGGGGCATCTGCCGAACTCGATTGATGATTTGGTGGCAAGCTGTGCCCGCAACAAT
GACGTGCTGATCCCTTTTGGCAGTGTGGATCCTCGTACCGGCGAGGACGCGCTGGTGGAA
GCTCGCCGACAGGTGGAAGAACTCGGGGTGCGAGGCTTCAAATTCCATCCATCGGTTCAA
GGATTCGACCCATCCGCGCCAGAGTTCTACCCACTGTGGGAATTGCTCGAAAGTTTTGGA
TTGCCATGCGTGTTCCATACCGGACAAAACGGCATGGGTGCAGGTCTTCCAGGTGGTCGA
GGCATTAAGCTGCGCTTCTCCAACCCAATGTTGCTTGATGATGTTGCGGCGGACTTCCCG
AACCTGACCATCATCATGGCGCACCCTTCTGTTCCTTGGCAGGATGAGGCTAACTCGATT
GCCACCCACAAGGCCAATGTGTTCATTGATCTTTCCGGCTGGTCGCCGAAGTATTTCCCA
GAGTCTTTGGTCAGACAGTCCAATAACGTGCTATCCAAGAAGGTGCTGTTTGGCACGGAC
TTCCCGCTGATTACCCCAGAGAAATGGCTTGCGGCTTTCGCGAATCTGCCACTGAAGGAT
GAGGTTCGTCCGGGAATCCTCAAAGACAATGCGGTGAAGGTACTTGGCCTAGCCGCTAGC
ACTGAGCGCGGATCTCAAGCAGAAAAGGTCGTGCAACATGCG

>RXN01765-downstream
TGATCCCATTCAAGGTGCTGTTA

>RXN01767-upstream
ACACCAGCCCTCCACAAGAGCGTCGAAGCAATCTACGCTTCGACGCTCTTTTTTTCACTA
CCTACTCATCCCCCACATAAGAAAAAAAGACGACACCACC

>RXN01767
ATGATTGACCATAAACTGTGGTTTAACACAGTAACCAACAACGCCTCTGTCCGAGAAGCT
GCAGGAAAATGCGACATACCCATCAGAACGCTCAACGAGCAGCTTAACCGTCGAATACTC
CCTGAAAAGACCGTCATCGCTCTAGCACGCGCTTATGATCTCTCACCTGTTGATGCGCTC
GTTCGCACCGGACACCTCACCGAAGAAGAGGCTGGTAGTCGTGAAGAAGATGCCAGCCCA
GATTCAGCTGACGACTACCCTACCTGGGCACTGAACTCGCACCTTGACTATGGCATTCTC
GGAGCTTTTGGCGACATCGCTGAAGAAGTAAACAGCGAAAGAGTTAACCGCGACAACGCC
ATAGAGCAAATTCGCGCATGGCTCGACGAGCTTCCAGGCAGCCTATTCAACAACCTCCGC
AGCACTAAAACAGGCTACATCGAACTATTCGAGACCTATCTCGAT

>RXN01767-downstream
TAAACCCAACCAGCACAACAATA

>RXN01769-upstream
ATTTTCAACAACCAGGACTAAAACACCTGCTGCTGTTGAGCGCTTCTCACACATCATCCT
CACAACCCCGTTGCAGCACCAGCATAAATCTATATTCGCT

>RXN01769
GTGACGGGGTTGTTGGGGCGCGCCCCACATTCACTCTTTTTCCCGATTGGTTTCTACTAC
ACACCCATGACCTCTATTACTACTACCGATACCCCGCTATATACAGCACTGCCCCATACC
CGTATCTCTGATGCGGAATTGTTGACACCAACAACAACTGTGCACGAGATTCTCGTTTAC
GGACCGGCTGAGTGCCCAGGGTGTACAGCAACGCTTGACTTCTTTGCACGCAAAAACATG
CCGGCCACCAAAGTCACTGTAGCTGCCGGTGATGTAGCACATACCTACATCACCCAAGAC
TTAGGTTATCTCCAAGCACCGATTGTCACTGTCCGTATCAGTTCCTCTGCTTCTAACCAC
GACAACGAACACAACACCCAGATCCTGCACTGGTCCGGCGTTAATCGCTACCTCATGCAG
GCACTCTCCCGTACTCATTTC

>RXN01769-downstream
TAGAAAGGTTTTTCCCGTCATGT

>RXN01771-upstream
TGCCCCGCTGTTGGTGGTTCCGGAGCGGCGATAATCGCTAAACGTTTGAGGTGATTGTAT
GGGTATTTTCAGGTCGCGGTCGCAGGATTTTGGGTGGAGC

>RXN01771
ATGCACCAGGCTGGCCAGCTCATCAATGATCCCAGTCAGGGTCTGTGGCGCACTTCTGCC
CTGCGCTCGCCGGTTGCTCGGGTTGGACATGCCGTGTTGCGCCAGCGTGCCGGTGAGATC
TCGCGCATGCAAGGTCGTGAGTTTTCTCGCCCTGGGGATCAGTTCCGACAGGTAGATTTG
CGCAGGCGACTGATTCAGGTCCATCCCCAATCAATTCCTACAGCGGATGCGATGGCCGTA
ACCATCACCATGGCGCTCACCGCTGCCACGATTGATCCGGTGAAGTTCGTCGCGGATTCA
CAGAACCCGGATGAAGAGATTTATTTGGCAGCTCAGATCGCATTGCGGGAAATGGTTATC
GCTATGCCTTTGGAGGATTTCATCGGGGTGCGCATTGATCTAGAGCCTGTTTTGGTGGCT
GCTCAAGCTGCTGCGAAGAATGTGGGCGTGGAAGTCTCGTCAATCTTGCTGAAGGATCTG
AATCTTCCCCAGGAGTACTCGGGAGCGTTGCAGGAATCGATCGTTGCGAAAATTCAAGCC
GAAACTGATCTGGAACGTGCACGAAATGAAGTGAAAACTACCCGTGCTCGACTTGCCAGC
GCGAAAGTGTTGGAGCAAAATCCGATTCTTGCCAAAATTCGGATGATTGAAGCGCTCCCA
CCGGGATCCACAATTGAGGTTCGGGAGGGTGACTCAAAGGCA

>RXN01771-downstream
TAAAGTTGCCCATTTCGGTGCCC

>RXN01774-upstream
CTGCGCAAGAAGAGAAAAAACAACGACAGCGAAGCTGCGTTCGGGCGAATCGGCGATAAT
CACACACCACTCTTCCTGAGAGAATCCTGAGGTCATCACC

>RXN01774
ATGTCACCGAACTTCCAAGCTCGCGGTACTACTGCGCCCACTGTTGCTTTGTCCATGCGC
CAGATCGCGCACATCCGTGAAGAAATTAAGAAATCACCACTCGCTGCTTCCGTTTTCATC
ACACCCACCACCAAACAAATGGTTGTCCGAGATCTAGAATCACTGTTCCAGCAGCTCTAC
CACACAGATCTACCTGAACCATCCATCAAAGACAGTGGTCTTATCAGTGCTATCGGCTCT
AGCGCCGGCAATACCAATAATCCAGCACTCGCCCTAGAAACTCAGATGGCTTACCACCTG
GTGCTTGCTATGCACCACACCGATGTTGCTACCTGGCACAAGGTGGTGACCAAAAACATC
ACCGAATCTGCTGCTGCACAAGATGCTGCGGTCGAGCACAGTGCTAAATACGATGCTGTG
TACGATGCCGCACAACTTATGGGCATCACTGTTGAGGAAGGTAATGTCGGTAGCATCGCT
ATTGCCTTTAGCACAGCACGTGCAGACGGTAAATCTGATTGGTGTGTTTCCGGCATCAGC
CGCTACATCGAGGTCACCGAAGCCTTGGATGCTGCGCGAGCTGTCACTAAAAATACTGAT
GCGCTCAATAAAACTGCTCTACCAGACGTGCAGCCGGCGCCGGTTGTGCATTCAGCACAG
TTCATGAACAAGTCCGCACACGATCATGGGGTTAATACTGCGGAAAAAGATCAACCAACC

CTGTTT

>RXN01774-downstream
TAAAAGACTGTCCATTTAACAAC

>RXN01787-upstream
CAGAAGCACGTATTTTCTTCTTAACTCGCACCTCATCTGGTGTGGGTTTTTTTGCATTTT
TTACACACCCCACTCCACACACACTCGCAAAGGATTCATC

>RXN01787
ATGAGCAACAATGCTCTTTTAGTAGCAAACGAAGCCGACATCGGTCTCTACCTCCACTGG
AATGGTGGTCGCGACTCGATTGAGGCGTTTCTCGCCTACGCCGCATACGCGCAGTTACCA
CCCATCAACGAAAATAACGATTGGTTGCCACCGTTTATTACTGTGCTGAAGAACTTCTTC
GGCAATGATGGTTCTGGCGTCTACCTCGAACCTGTCAATCAGGATTATCTCGACGGCATC
GACTATGACAACGGTGTTTACATGCTTGACGATTATGAGATCACTGAGCGTATTAATCCA
CCCGCTGTTGAGCAAGACTCCCACGATCTCCACGACATGTTGATCAAAATTGATAAAGCT
CAACCACCTGTCGATCAACTCGGGAGTTTTCTCCATGGCCTAGAGACCTCTGTCGCAGAT
TTGGGGGTTGGTGATCGCGTATTTTTGCCACGTTTTAGCACCTTTGATAAGAAACTCGGT
CGCTACCGCATCCACACTGTTCTCGGATTCGCTGAGAACGATCCGTTTAACCCTATGACC
AGCAGCGAGCGATTTAAAGGTAAGCCCTATGTCGATATGTTCGACAATCAAGACAACGCC
TTTAACCCAAATTCCTATATCACTACAGATACCGTGCGCATCGTTGTCGATCCTGTACCG
GAAACTAATCCCGACGATGAGAAAGCAGGACGC

>RXN01787-downstream
TAGCCATGTCTCGCAGCTACCCC

>RXN01796-upstream
ATGTAACTCGATCAGGTGGAAATGCCCGCAAAAGTGGCGGCGGTGGCCGAGGGATGGCCG
TTGGTGCGGCATCGGTGGCCTGCTACTAGTCGGGCTCTTC

>RXN01796
TTGCTCCTTGGCGGTAACCCTGCCGAGATCGACCAGGTTTTAGGTGGCGATCAAACCCAG
ATCGAGTCTGGAGAGTCCACCGGAGCCGGCGACTTTGATCACTGCCAAACCGGCGCAGAT
GCCAACGCCAGTGATGATTGTCGCCTTTACTACACCTCATTCTCCGTCAATGAAATGTGG
CAGACTTTGCTTCCAGCTCAGGCTGGTATCGAATACACCGAGCCGACATTGACTCTTTTC
AAAAACTCCACCCAAACCGGCTGCGGTTTCGCTTCTGCGTCCACTGGGCCGTTTTACTGT
CCGTCAGACCAAGATGCTTATTTTGACTTGACTTTCTTCGATCAGATGCGTCAGTTCGGT
GCAGAAAACGCCCCGCTTGCCCAGATGTACATCGTGGCGCACGAGTACGGCCACCACGTC
CAAAACCTCGAGGGCACACTCGGACTGTCCAATTACAACGATCCGGGCGCTGATTCCAAC
GCCGTCAAGATCGAGTTGCAGGCCGATTGCTACGCAGGCATTTGGGCTAATCACTCCAGC
GAAGGCCCGGATCCGCTACTCCAACCCATCACCGAATCTGAGCTAGATTCCGCTCTCCTT
GCTGCAAGCGCCGTGGGCGACGACAATATCCAGCAACGATCCGGTGGCGATGTCAATCCT
GAAAGCTGGACTCACGGCTCATCGCAGCAGCGCAAAGACGCGTTCCTCGCCGGCTACAAC
ACCGGCCAGATGAGCGCCTGCGACTTCCTCGGCCGGGGCGTCTACAACGACGCT

>RXN01796-downstream
TAAAGCATTGCTTTTCGACGTCT

>RXN01803-upstream
CTAGCGGAAAGGCTTTAGCGACAAGGCTTTTTGCATGTTTTAATGCAGGGAATATTAACT
TTTTGTTAATCTCTGACCATTGACCTTGTACGCTTAAAAC

>RXN01803
ATGCGAAAGAAAAAAGACGGTCAAAATCTCCCAGACTTCCGGAAAAATCCGCCAAAGCTG
GATAAAAAGGCTTATGAAAAAGAACTAAAAAGACTTCAAGCCGAACTCGTCGATTTGCAA
CAATGGGTTGTGGAAACCGGTGCGCGCGTGGTCATCGTCATGGAAGGCCGCGACGCCGCT
GGTAAAGGTTCTGCGATCAAGCGCATTACGCAGTACCTCAACCCCCGGTCCGCAAGGATC
GAAGCGCTGCCCACCCCAAACTCTCGGGAAAAAGGGCAGTGGTATTTCCAGCGCTACATC
GAAAAATTGCCGACTGCTGGTGAGATCGTTATCTTTGACCGCTCCTGGTACAACCGTGCA

GGAGTCGAGCGCGTCATGGGATTTTGCACCTCCCAGGAGTACCGCCGATTCCTTCACCAG
GCACCAATCTTTGAACGCCTGTTGGTGGAAGATGGCATTCACCTGCGTAAATACTGGTTC
TCTGTATCTGATGAAGAGCAGATTGAGCGTTTCGAAGACCGCCTGAGCGATCCGCTGCGC
CGGTGGAAGTTGTCGCCAATGGATTTACAATCGATCACCCGCTGGGAAGATTACTCACGC
GCAAAAGATGAGATGTTCATCCACACGGACATCCCGTCAGCACCGTGGTACACGGTGGAA
TCTGAGGACAAGAAGCGTTCCCGCATCAACGTCATTTCGCATCTGCTCTCGACGATTCCT
TATGAGAAGATCGATCGTCCATTGCCGGAAATCCCTCATCGCCCAGATTCTGAATCTGAT
TATGTACGTCCCCCTCGCGATGAGTTCCGTTATGTTCCAGATGTGGCAGCACACTTGGAA
GAAGAGCGCATCAAGAAAGAAGAAAAAGCCAAGAAGGCAAAGAAGCCAGCTAAGGCTGCA
GGAAAGAACTCGGATAAGCAGAAGTCTTCCGGAGGAAAAGGCAAGAAGAAGTCCAAGAAA

>RXN01803-downstream
TAGAACGCCTTTTAAGGGGTTGA

>RXN01809-upstream
ACAACACGACAGTTGTAACTAGTGGTTTCAACACCATTATCGGTATGACTCGTGGCGACT
CGTATCTCTCTGATGATCTCGATGACCTGGGTTAAACCCG

>RXN01809
ATGAACGAGCAGGAACGAGAAGCCTTAGAGGATGCTGCCCTTGAGGAAGCTGCCTTAGCC
GATGAATTAGCTGCATTAGAGGCTGAAGCTGGCGTACAAGGGTCAGTCGAGCCTTATGAC
TATGCAGCAGACCTTGATGATGAGGACGAGTTTGATGAGGACCCTTTTGCTCAGGATGAA
CCCCGTGACGCTGGTCCGCTAGGTGAGTTGAGCAGTGATAACCATGTCTCTGAGGCTGTT
GCTGAAGACACTGGGACAAGTACAGAAGAGTCTGCACAAGAGGGCAGTCACGAAGAGTCG
GTAGACAATCCCCGTGATTTCACCGGCACTGCGACAGCGGTGCGATCTTTTCGACCCAGA
CTTCCCGTACCCAATGCACTGCGACCAGGACCACCCATCCGAACACAACCGGCAGTGAAC
ACCGACATAGATGATGGCGGGCAAGAGAATACAGCTGGCGCGACTGCCGCAGATGTGGGG
GCGGGAGTGTTTTTTGGTACGCATTTTGAGCTGGCTTTTGGGCAGGTTGATGTTCACCGC
CACATAAGGCATGAGCAGGCTATGCGAGATGGACACCAGGATCTCAGCGTCTTTGTCGGT
GCTGATGGGGCGATCATGCTGGAAGAACTTAAAAATCGTTACCAGCGCCCACCGGAGAAC
GAGCCCCATGATGATGATGTCACCGAAATGATAAAGACCACCGAGGAAACAGAGAAGGAG
AACGTAGAGATGGATCAGGATATAGCTGTAGTAGACAACGTTGATGAACAGGTTGTGGTG
ACACCTGCTCATGACGCTGACAGCGTAGCGGTTGTTGCTGAACAGGTCGTTGCGTCAGAA
CCAACGCCAGAGCCGGTACCCAAGGTTGAGCACGTAGAGATGAGTGTCGATCTAGCGGGT
GAGACTATTACACCGATTGATCAGGCAATTCGGTCTTTTATGCAGCTCAACGGTATTGAG
CACAGCGTGGTGTTGCGACGCTTGGGGCTGATGACTCAGGTGGCACATAATAAGGAACTT
GATGAGGTCTACGCTAAGGCACTTGCCGAGGGTGAATCCCATGCTCAGCAGCAGCATGAA
TTAGAAGCAGAAAATGAACGGCTTAAAAAAGAAGTTGATGCGCTCGCTGCAGAGCTTAGT
GCTGCGTTGATGGGCGAGGGTGGTGGTGATCATGAC

>RXN01809-downstream
TAAGGCCGTGACACCAATTGTGG

>RXN01811-upstream
GAAGGAGAAGAGACATTGTCTCAAGAAGAGCTGACATTAGTCGCATTGAATTCTTATGAA
AAAGGAGAGTTGCCAAAGAAGAATATCATTATTTGAAAAC

>RXN01811
GTGTTTGAATTTGATGATACCTTGGCAAAAGATATACAAGTAGACCGTACGTCCATGCAA
GTATTCGAAGCTTCAGAAACCGTCAAAGAAGCGATAAAAGCTTCGATTGAACAAGGACAT
ACTCGCTATCCGGTTATCTTAGAATCAAAAGACAATGTTTTAGGTTATGTCACCTTGCCA
GATTTGATCAAGCAATCTTATAAAGATGACCAGCTGACAGTAGAACAGTTGATTGAAGAG
CCGATCGTAACAACTGAAACGATCCCTATAAAAAAATTATTGACGATCATGCGAAAAAAG
GGAAAGCATATTGCTATCTTAAAAGATGAATACGGAGGGACAAGCGGCTTAGTGACGATT
GAAGATATTTTAGAAGAAATCGTCGGGGAAATCCGAGATGAGACAGATTTGGACGAAGCA
TTGATAGCGGAACAGTCAGATGGCTCTTATATCATCTCCGGCAAACTAACATTAGATGAT
TTCCAGCGTTATTTTCATGTAGAGATTCCAGAGTTTGAAGAAACGAATTTTACTACACTT
GCGGGCTTTGCTTCTAGCCGATATAAAGAAATAAAAGCAGGAACAATCATTGAGATTGCA
TCATTCCGTTTCACGGTATTAGAATACCAGCATGCACATATCGATTATTTCAAAGTAGAG

TCCACGGAAAGAAAAACAGAA

>RXN01811-downstream
TAAAAGAAAAAAGGCTGTGACAT

>RXN01813-upstream
GCGAGAATTCAAGAAAACAAAACAGATCAAAGTAAGGCAACAAGTGAGCAACAAAGTTCA
GAATCCGAACCAAGGTGGAAGCAAGAACTTCCTCTGGGCA

>RXN01813
ATGGTGGCGATCGTCGTCGTTGCAATCGTCGTCGTCGGCTTCATCGTCATCCAAGGCCAG
GGCTCAAAAGCAGCCAAGCTTGGTGACCGCGACTACGAAGACACCTCTTTGGCAATGGAA
GTAGGCTCCGACTCCATCACGCTGACCTCCGCAAACACCTCCGCCGACGCAAAGTCCGTG
CAGCTTTTTGAAGACTTCTCCTGCTCTCACTGCTCCGAGCTCTCCCTCGCCACCGACGCT
GACATGAAGACTCAGATCGAAGACGGCAACCTGGTCGTCGAAATCAAGCCACTGAACTTC
CTTGACCGCGAAAACATCGACGGCCACTCCACCCACGCATTGGCAGCAGCCCTTGCAGTG
GCAGACTCCAACGACGCAACCCTCTACTGGAACTTCCGCGCATTCCTCATGGAAGATCAG
TCCGAGATCTACAACCAGTGGTCCGATGATGACTTCGCAGACGGCGTTGAAGCCCTTGGC
GCAGACTCCTCCGTAGTAGACGCAATCCGAAACGGCGACAACATCCAGCGCGCATACGAC
CTGGCAACCGCAAACGGTGAAGAACTCACTGAAGAAACCGGCAGCCTGTCCTCACCACGC
GTCCTCCAGGACGGCAAGGATGTTGAAGGCAACATCTCCGACTGGATCACCACTGTTCTA
GCTTCT

>RXN01813-downstream
TAAAGAACTGATCTAGAAGGAAA

>RXN01815-upstream
GAATGAAAAGAAGTGGTGGCCGATGCTTGGCTATCTCAGCCTGACTTTTACACTTGGATA
TTCTGCTGTTTTTCTCGGGATGCGGCTCTAGAATTGTAGA

>RXN01815
ATGAATCGTTCAACAATTTCCCCAGTTGAAGCCCGCCAGCAATTCCGCGCAGGCCTTATC
CAACCCACCTCCGGCTGGTCCGCGGGTTTTGCCCAAGCCAACCTCATTTCCATGCCCCAG
GATCTGGCTTATGATTTCCTGCTTTTTGCTCAACGCAACCCCAAGCCCTGCCCCATCTTG
GAAGTATTAAATGCTGGCGAAACCTTCGGCGGAATTTTCGGCTCAAACGCCACCGAAGCA
GACATCCGCACCGACGCGCCCCAATACCGCATTTACGCACACGGCGAACTTATCGATTCC
CCCGCCAGCGCCGTCGATTATTGGCGCGACGACCTCGTCAGTTTCATCATCGGCTGCTCC
TTTACTTTTGAACATCCCATGGTCCAAGCAGGCGTTCCCGTCCGCCACCTCGAGGCCGGC
CGCAACGTCCCCATGTATGAAACCTCACTTGCCTGCCGACCAGCCGGTTCCCTATCAGGA
AACCTCGTGGTGTCACTGCGCATGATCCCCGCATCCCAAGTCGCGGATGCCGTCCGCATT
ACCTCCCGCTACCCCGCGGTTCACGGAGCACCAGTCCACATCGGCGATCCTTCACTGATC
GGAATCGATGACATCAACAACCCTGATTTCGGCGATGCCCCGCTGTCCGAACCAAGCGAC
GTCCCCGTGTTTTGGGCCTGCGGAGTTACCCCTCAAGCAATGGTCATGTCCTCCAAGCCA
CCGCTGGCGATCACTCACGCACCCGGACACATGCTGATCACCGACGCCCCAGATCTGGGA
TTCCAGGTTCCT

>RXN01815-downstream
TAAACCTGGATCCACCGATGTGA

>RXN01825-upstream
GTCAAGGTAGCTGGCCCGGCAACTGATACGTTAAGCTCAAACAAGATAAGTACCAGTTGC
TGGGGTTTTTCCAAGACAATAAATTATGAAGGTGTGAACA

>RXN01825
ATGCCAAAGGCAAGAGTAACTAAAAACGAGACCGCACCGGTTTCAAGCAACCCAAGCGCA
AACCGCACCCCGGTTAAGATCAATTCCGCCGGAACCCCAATGTGGTACAAGGTCATCATG
TTTGCCTTCATGATCGTCGGCCTAGCCTGGTTGATCATTAACTACCTCGTGGGCCCACAG
ATCCCATTCATGGCTGATCTTGGTGCATGGAACTATGGCATCGGCTTCGGTCTGATGATC

ATCGGCCTACTCATGACCATGGGTTGGCGT

>RXN01825-downstream
TAATCCTTCAAAAAAGTGACTGC

>RXN01831-upstream
CCTGTGGATAATTGGTTGTTGGCTGATGGTGATGTCATTACGGTGGGTCATTCCAATATC
GAAGTTCGTATTGTTAGTCCCTAGAGGGAGAGGTTGATCA

>RXN01831
ATGGATTCTCTGGTCCTTCTTGGGCTTCGCATCGCTTTGCTTGTGGTGTTGTGGTTTTTC
GTCTTGATGGCGCTGCGCGCTATGAGGGCAGATTTGAAAGTGACGGGTCAAGCGTCGACA
AGCAGCTCCTCCGTCGCGGCACCGCAGGGCCTTGCCCGGGCTTTTAATCGCTCCAGCCCG
CCTCGTCTTTTGACGGTGGTCGAGGGCCCGTTGGCGGGCTCCTCGATTGAGGTGTCGGAG
GATATGACGATGGGCCGTAGCCCTGAGTGCACGTTTGTGGTGGGCGATGATTACGCCTCC
GGCATGCATGCGCGGGTGTTTAAGCGTGGTTCGGAGTGGTTTGTGGAGGATCTGGATTCG
CGCAACGGCACTTTTGTCGGTGGTACGCGCATTGATCAGCCTGAGCAGATTGCGGTGGGC
ACGGATATCCGTATTGGTCGTACAGCAGTGAGGCTTGTTCCC

>RXN01831-downstream
TGATGTTGAAACTTAAATATGCG

RXN01834-upstream
ACTAAGAACGTGAGCTTGGTTTCATAATACCCCCCAGGGTATTGTTAGCCAGGTGATTCT
AGCCCTTCTTGGCGGCCTAATAATAGGCCTACTTCTTGGC

>RXN01834
ATGCTCGGTGGTGGCGGTGCCATCCTTGCCATTCCGCTGCTTATTTATGGATTTTCTTTT
AGCGCCACGCAAGCTACTGCAGCTTCATTAATCATCATCGGACTTGGCGCCCTCATTGGA
CTGATCAGCCAATACGCTGCCGGGCACGTCCGCCTTAAAGAGGGTCTAAGCTTTGGCCTT
TTAGGGTTGGTCGGCTCATTTGTGGGCAGTCACCTTGCTAGCAATATCCCCGATTCCCTA
CTCCTGAGCGGCTTTGCCATCCTCACGCTCGTGGTGGCGTTGACCATGATTTCTAAATTA
AGAAGCACCCGAGAATACATAACCAGAAGGCCAAGCATCCTTGCCATTGCTCTTAGTGCC
ACCGGCGTGGGATTTTTGACGGGATTTTTTGGTGTGGGTGGCGGTTTTGCCATTGTGCCA
GCCTTGATTTTTGCGCTCGGTTTTTCCATGCGGCAGGCTAGCGCCACTTCCCTAGTGGTG
ATCGCCGTTAACAGCGCTATTGCCATGGGATTTAGATATTCCGATTTGGCAAGTATTGAC
TGGTCAGTGATCTCGCCAATTATCATCACCACCGTATTGGGCGCTTTTAGTGGCGTAAAA
CTAGCCAAAAAGGTCAAAGCATCATCACTGCAACTAGGTTTTGCTGGCTTCTTGATCTTC
ATTTCGATCTATATGGGATTTCAGAATTTCCCGGACCTTTTT

>RXN01834-downstream
TAAAACTTCAAAATATACCCCCC

>RXN01846-upstream
GTATTTAGGAATTGAAACCCACTAAAAAACAGACTAAGTTACTAGGTGATAACAAAAGTT
GTTTATTACTTATGGGAATAGTGTGGAAAGTAGGGTGAAT

>RXN01846
ATGTCAATTCCTGGAAATGTTAGTTATGTTGCACAGGGTGGCACCGGTTGGGATGGTGCT
GATCAGTACACCACGGGTGAGAGTTGGGATCTACAGTCGTTCCTTGAAAACTCGACTGAC
TACCTCATGATTATTGGTGGTTCGCTGCTGGCACTTGTTGGTGGTGCTGCTGTGATTTGG
GGCTTTGTCAACGTGATGCGCAAGCTCTTCGGTGGTCAGAGTGGTCAGCAGATTCAGTGG
TTCACCACTATTTTGCTCATCATTGTCGGTGGTGCGTTGCCT

>RXN01847-upstream
GACGTGTGATCATAGGTGACAAATATACCCTCTCAACTTGGCTTCGACTGCCCTGCCCCC
TCGATTTAAGAGGCAAGGCTTTTACAGTATCCTCTCATGC

>RXN01847
ATGCTTATTGTGTTGCCTCCCTCAGAAACTAAGACCCACGGCGGTTCAGGAAAACCTCTG
GATTTTCACCATTTGAGTTTCCCGTCGCTCACCAAGGCACGCCAAACAATACTCGCTGAC
CTGCAAGCTTTGGAGGTAGATGAGGCGCTGAAAGTTTTGGGCATTTCTGAAAAGCTCCGC
CCTGAGGCCGAATCCAATCGCGCGCTGGAGACCAGCCCTACGATGCCTGCGATTTTTCGG
TATTCCGGAGTGCTTTATGATGCGCTCGACGCTGCAACGCTGCCGGAGAAAGCACTGGAA
CGCCTCGCCATCGGCTCGGCACTTTTCGGCGTCATCCACGCCACCGATCCGATCCCGCAT
TACCGCCTGTCCGGCGGCACAAAACTGCCCACCAAAAGCGGCGAGCTGCCCACCATGAAG
GCGCGTTGGGGCACAAGCATCAGCGAAGCGCTTATCGACGTCAACCAGCTGGTGATTGAT
CTTCGCAGCGGGACCTACCAACAGTTGGGTCGCGTAAAAGACGCCGTCACGGTACGCGTG
GAATCAGTCATGGAGGATGGCTCCCGCAAAGTAGTCAGCCACTTTAACAAACACTACAAA
GGTGAACTCGCCCGCGTGCTCGCGCTCTCTGAAAAAGAAGCACACACCGCAGAGGACGTA
ATGAGCATTGCGCAGGCTGCGGGCCTTGTGGTGGAGGAAAACCCCAACCACAAGGAAACC
CTCACTCTGGTTGTC

>RXN01847-downstream
TAGGCGTTAATCACCATTTTGAT

>RXN01874-upstream
AGTGTCGGCGCGACGATTGTGGGCGGTGCTTTGGCGTGGCACGCAGCAGTTTGGCATCAC
AGTTCCGGAGCGCAAAACGCGGTCAGCCTTTCGCGTCGCA

>RXN01874
GTGATCGCGTATGTTGCCAGCGCGTGCTGCCTGCCGTTTGGCGCATTTGCCGGAGCGTTG
TTGTCCAAGGAGCTGTCGGGACATCTCCAGGAACGAGTCCTTCTCACCCACACGGTGATT
AATTTTCTAGGTTTCGTGGGATTTGCTGCGCTCGGTTCGCTGTCGGTGCTGTTCGCCGCG
ATTTGGCGCACCAAAATTCGCCACAATTTCACCCCGTGGTCTGTGGGGATCATGGCGGTG
AGCCTGCCGATCATCGTCACGGGCATCCTGCTCAACAACGGCTATGTCGCCGCCACAGGC
CTGGCCGCGTACGTGGCAGCATGGTTGCTGGCCATGGTGGGGTGGGGG

RXN01875-upstream
AATCCTATCCCTAAAAAGTTTCTAACAAAAGTATTGCACTTACTTTTTGATAGTGCTATC
TTCAGTTGTGTACTTGAAACACACACGAATGGAGCAAGAA

>RXN01875
ATGCGTATTGCAGTAACTGGAGCAACGGGATCTTTGGGTGGACATGTTGTGGATAGTCTT
CTAAACAAGGGCGTCGCAGCATCAGACATCGTTGCCATTGTTCGAAATGAAGAAAAGGCA
GCAGACCTCAAAGCCCGTGGAATCGCTCTTGGTGTGGCTACTTTTGAAGACGAAGCGGCA
CTGACTGCAGCTCTTGAAGGTGTGGATCGCCTTGTGTTTATCTCTGGCAGCGAAGTGGGG
CAGCGCGTTGCGCAGCACACCAATGTCATCAATGCCGCTAAAGCAGCTGGCGTGACATTC
ATTGCATACACCAGCTTGCTCAACCTTGGTACCTCAAAGCTTGCACTTGCTCCAGAGCAC
ATTGCAACGGAAAAGCTCCTGGCAGAAAGCGGCATTGACCACGCGCTGCTGCGCAATGGT
TGGTACTGGGAGAACTACGAATCTTCAATTGGCGCAGCGAAGGCCACCGGGAAGGTATTC
GGCGCAGCTGAAGGCGCACGCGTTTCCGCAGCCGCACGTAAGGACTACGCAGAGGCAGCT
GCTGTTGTCATCACCAGCGACAACCAGGCAGGCAAGGTCTATGAGCTCGCAGGCGCACCA
GCTTTGACCTACCCAGAGATCGCAGCTGGCATTGGTGAGGTCATTGGTTCTGAGGCAGAA
TACGTCAACCTCTCCGTGGAGGAGTACCAAAATGCGCTGGAGCAGGCTGGCGTTCCAGCT
GAATTTGCAGCACTTCTCGCAGGCATGGATCCCATCATTGCAGAGGGCGCGCTGTACTCC
GACAGCACCGACCTACAGGATCTCATCGGACGCCCGAGCACCTCAATCGTTGAGGCCCTG
AGCTCA

>RXN01875-downstream
TAACCTGCTACTCACCTAAAATG

RXN01877-upstream
GTACCCGTATTGTACTAATTGTAATTCCCCGGAGAGGGAAGAAGTTTACATGGCGCCCCA
TCAGAAGTCAGGGATCAACCGGATCAACAGCACCCGCTCG

>RXN01877
GTGCCGTTGCGTTTGGCTACCGGTGGCGTGCTCGCCACCTTGCTTATCGGCGGAGTCACC
GCTGCAGCTACCAAAAAGGACATCATTGTTGATGTCAACGGCGAGCAGATGTCCCTAGTG
ACTATGTCCGGCACTGTTGAAGGTGTGCTGGCGCAAGCTGGTGTGGAACTTGGTGACCAG
GACATTGTTTCCCCTTCACTGGATTCATCCATCAGTGATGAAGACACTGTGACTGTTCGT
ACTGCCAAGCAGGTGGCGCTCGTGGTGGAAGGTCAAATCCAAAACGTGACCACCACTGCG
GTTTCCGTGGAGGACCTCCTGCAGGAAGTCGGTGGCATTACCGGTGCTGATGCGGTGGAC
GCTGATCTTTCAGAGACCATCCCAGAATCTGGTTTGAAGGTGAGTGTTACCAAGCCGAAG
ATTATTTCCATCAATGATGGTGGCAAGGTCACTTACGTTTCTTTGGCAGCTCAGAACGTA
CAGGAAGCCCTAGAGCTGCGGGATATTGAGCTGGGTGCTCAGGACCGCATTAATGTGCCT
CTGGATCAGCAGCTGAAGAACAACGCTGCGATCCAGATCGACCGCGTTGACAACACCGAA
ATCACTGAAACTGTGTCTTTCGATGCTGAGCCAACCTACGTGGATGATCCAGAAGCTCCA
GCTGGCGATGAAACTGTGGTCGAAGAAGGCGCTCCTGGAACCAAGGAAGTTACTCGCACC
GTAACAACCGTTAATGGTCAGGAAGAATCTTCCACGGTGATCAATGAAGTTGAAATCACC
GCAGCAAAGCCAGCAACCATTAGCCGTGGCACCAAAACTGTCGCTGCAAACTCCGTGTGG
GATCAGCTGGCACAGTGTGAATCCGGCGGAAACTGGGCAATCAACACAGGTAATGGCTTC
TCCGGCGGCCTACAGTTCCACCCACAGACCTGGCTCGCATACGGTGGTGGAGCTTTCTCC
GGTGACGCTTCCGGTGCAAGCCGTGAACAGCAAATCTCCATCGCAGAAAAGGTTCAGGCT
GCACAAGGTTGGGGAGCATGGCCTGCTTGCACCGCAAGCTTGGGCATCCGA

>RXN01877-downstream
TAGTAGAAATCTGGCATCCAATA

>RXN01879-upstream
CTTTGCGGGCCGCTGATATTGATCCAACGCTTCGTGGCGAAAAGCTTGATGTCACTGACT
ATGTGCGCCTAGCTGGGGTGTTGCAGCAAAAGGATGAGAA

>RXN01879
GTGAAAATTACCGCTAAGGCGTGGGCGAAAACCAACCTGCATTTAGGTGTGGGACCGGCT
CACGACGATGGATTTCACGAGCTCATGACGGTGTTTCAAACCATTGATCTGTTTGACACC
GTCACCTTAACCACCCTCGATGAGGAGTTGGTGGAGGAGGGGAGCGTCGTCAAGCAATTA
TCTGTGACCGGTGCCCGTGGCGTGCCTGAGGACGCCAGCAATCTTGCGTGGCGCGCTGTG
GATGCGTTGGTTAAGCGGCGCGCGGAAAAGACGCCGCTGTCTGCAGTTTCGCTGCATATT
TCCAAGGGGATTCCGGTGGCTGGCGGCATGGCTGGCGGCTCTGCGGATGCGGCTGCGACA
CTGCGCGCAGTGGATGCCTGGATTGGGCCTTTCGGCGAGGACACATTGCTGGAGGTTGCC
GCGGAGCTCGGCTCAGATGTGCCGTTTTGCCTGCTTGGTGGCACCATGCGCGGTACCGGT
CGCGGCGAGCAGCTGGTAGATATGTTGACGCGCGGCAAGCTACATTGGGTGGTGGCCGCG
ATGGCGCATGGCCTGTCCACGCCTGAGGTATTCAAAAAGCATGATGAGCTGAATCCGGAA
TCGCATATGGATATCAGCGACCTCAGCGCCGCACTTCTCACCGGCAACACCGCCGAGGTG
GGGCAGTGGCTGCACAATGATCTGACCAGCGCCGCACTCAGTTTGCGCCCTGAACTGCGC
AGCGTCCTCCAAGAAGGCATCCGCTCCGGCGCGCATGCAGGAATTGTCTCCGGCTCCGGC
CCGACCACGGTATTCTTGTGCGAATCGGAGCACAAAGCGCAAGACGTTAAAGAGGCGCTA
ATCGACGCCGGCCAGGTGTACGCTGCTTACACCGCCACCGGCCCTGCGGCCTCAACCGCC
GACCAGCGCGGCGCACACATTTTGACTGTTTCA

>RXN01879-downstream
TAATAAAGACAAACTTAAGTATC

>RXN01896-upstream
TTATTGGGCAGCTCTTTTGGACCGCGAAGTCACCCCCGAGCTGCGCCACAGCATTGCTTA
TTGGATCCGCGCGAACCACATCAAACGCTAGAGTGATTCC

>RXN01896
ATGACGCATGCGATCCTCTTTGACCTCGACGGCACCCTCGTTGATCACGCTTCCGCCGCC
CGCGCCGCCCTGCACGCCTGGTCGCCGACCGTGGGCGTCGACACGGATGTTGAGCGCTGG
ATTGAGCTGGATAAGTGGGGTTTTGCCCGTTTTGAGCGCGGCGAAACCACGCATTTAGGT
CAGCGGCGCGACCGCATCAGGGCGTACCTCAACAGAGAGCTTGACGACGCCACCTGCGAT
GATATTTACTCCGGCTACCTTAAAGCATATGAGCAAAACTGGACTGCCTACCCCGATGCC

AAGGGCGTTCTCGATCGCGCGGTAGCCACCGGTGCCCCTGTGGGAATCCTGACCAATGGC
GCAGCCCCCATGCAGCAAGACAAGCTTGATCGCACCGGCCTTGGCCTGCCAGAACTCGTC
ATGTTGGCGGCGTCCACTCTGGATTCTGCGAAGCCTCGCCCCGAAATGTATGCCCGAGCG
CTCACCCATTTGGGTGCCCGAACCGCAACAATTATCGGCGATGATTGGACCAACGATGTC
GCAGCTCCCCGCGAACTTGGCTGGAATGCTCTCTATTTAGATCGTTCCGGAACCGATCCA
CGCGCCGATATCCACTCCCTGGATGAACTCTTTCAC

>RXN01896-downstream
TAGGCTGGCCTTTATTGTTTCCG

>RXN01899-upstream
CCTCGCAGCACTTCGCGCAGGCGAATCCACAGTGGCCGCAACCTTGATCAAAGAACACAT
CGAAGGCTACTACGAAGAAACCGCTGCCGCCGAGGCCTAA

>RXN01899
ATGTCCCGCACTCTGTGGGCGGTTTCAGATCTACACGTCACCTTCGCCCAAAACCAAAAC
ACCGTTGATGCCCTCATGCCGCAGGACCCCGGCGACTGGCTGATCGTCGCTGGCGATGTA
GCAGAGAAAATCCCCGATGTGGTACGTACCTTATCCGCGCTGGTCAAACGCTTTGACACC
GTGATTTGGGTGCCGGGCAACCACGAACTCTTCAACCGGAAAACAGACCGCGTCAACGGC
AAAGCCCGCTACCGAGCATTAGTCGGACAACTCCGAGCCATCGGCGTGATCACCCCCGAA
GATCCCTATCCGATCTTTGGTGGCGTCACCATCTGCCCACTTTTCACACTTTACGATTAC
TCTTTCCGTCCCCTCGGCCTCACCGCGAAACAAGCCCTCGCCCAAGCAAAAATAAAGCTA
GACGACGAACTAGCCATCGCCCCCTACGTAGACATCCCCGCCTGGTGCGCCGAACGAGTC
ACCTACACAGAAGACCGCCTAAAAGCCACCAAAGGCCCAAAAGTCCTGGTCAATCACTGG
CCGCTGGTCATTGAGCCCACCCACCGGCTCTTCCAAAAAGACATCGCGCTGTGGTGTGGA
ACCACCGCCACCAGGGATTGGGCCGTACGATTCAACGCTCTCATGGCCATTCACGGTCAC
CTACATATTCCTGCCGAAACCCGCGTTGATGGGGTAAGCCACGTGGAGGTTTCTTTGGGT
TACCCCTTTGAAAAACACCCACCTCACATGAAGCGTCCGTGGCCGTTTCCGGTCATGCAG
ATTAAC

>RXN01899-downstream
TAACTCTGTTGCTTAAATGGGGG

>RXN01902-upstream
GGCTGGTCCGAAGTGCAAACCTTCAACACCGGCACCTACGGTGACAACTGGAACTTCCTC
TTCTTCGGCGACACCCAGCTGTACAACACCCACTCCAACC

>RXN01902
GTGCAGAAGAAGTCCAGAACTGGGCAAACAACCTGGAACGGCGGCCCACCAATCGAAAAC
CCAGGAACCTCCTTCATCCTCTCCGCGGGTGATCAGGCAAACCACTCCAGCTGGGACGAG
CACTCCGCATACATCTCCCCAGAAACCCTGCGCAACTACCGTCTGGCCGTGAACAATGGA
AACCACGACCAGTACAACTACGACGCCTACAACGCGATGTACCCACGCCCTAACCAGGTC
GATGAGAACTACTTCTTCGAGTACAACAATGCACTCTTCCTGTCCCTGGACTCCAACGAC
TACTTGGACATCGACGACGACATCGCATTCCTTCGCGACACCGTCGCAGCACACGGTGAC
GACAAGGACTGGATCGTCCTGACCTACCACCATTCCACTTTCTCCCAGGCCTACCACATG
GATGACGCTCGCATTAAGTACCAGCGCGAACGCCTCACCCCAGTGATCTCTGAACTGAAC
GTTGACTTGGTTCTCGGTGGACACGACCACATCTACACCCGCTCCCACCTGATGAACGGC
TTCACCCCAGTCGATGCAGGCCGCGAAGCAGTTGTCGGTGAAACTCTGAACCCTAAGGCC
GGCGAAGTTGTTTACCTTGCAACCAACTCTTCCTCAGGCTCCAAGTTCTACGACTTCTAC
GACTTCCAGCTCGGCCAGCGTTACGACACCGGACTGGATTTCCAGGAAACCGTCGATCAG
AAGAAGATCCGCACCTACACCGCAGTCTGGAACCAGGACCAGGTTCAGGACTACACCAAC
GTTGAACTGACCCCAGAAGGCCTGACTGTGACCACTAAGGACGCAGTCTCCGGCGAGCTG
GTTGACCAGTTCACCCTGAGCAAGCAGGACCGCGACGAAGAATCTGAAGTCCCAGTTGAA
GATGACAAGGACGGAGACAACGCGACCGGCTCCTCCAACCTTGGTCTAGCTGCTATCTTG
GCTCCAGTTCTGGCCATCTTCGGTTTCGTCGGTGGACTCTTTGTTGGCGGCGGCTCCCTC
GCTGAGTTCTTTGCCAACCTCGGCGTGAAGATGCCTTTC

>RXN01902-downstream
TAATACTGTCTGAGATTCAAGCA

>RXN01908-upstream
TCCACGACATCTGACACAGAAAGAAGATTCACCATGTCTAAGAACAACGCAGCTCACCCG
CAGTCTGTCTTCCATATTTCATATCCCAGCACATACCACT

>RXN01908
ATGCACTCTGACCGCTTTGAGCACCCAGACAACGGCTATGGCTACACCATTCGTCAGGAC
ACTGATGCAGAGAACCCGATGACCCATCACGATACGAAAGATGCAGCTCTCTGGGTTCAC
AACCGACCACGACGCGGAGATACCGTCGCCGATAAGCCAGAAGGCAATGAGATTCTCGAC
ATCTTTGCCAAGTTCATCTGCGGCCAGCACGATAATGATGACAACCCGTTCGAAGTCTGG
TCCGACGGTGACTCGGATGCATCACTCATCCGCACCAAGGCGTATGTTGCCGAGCACCAC
CCCGAACTTATATTCGACATCTCTGCGAAAACCATCACGGGTTATTCCCAAGGCGATTGG
CTCGATGTGGTCTGTGTTACTACTGCCGCCACTTGCGACGAACTTATCCCTGCTGACAGT
CTTATTGACATCTACCGCCAGTGGGCTTTTGGTGATGTGTGGACAGTGATTCCTGATTCT
CAGCCAGGTCTCGCAGGTATTTATGCTGACGATCCAGCTGACGCCCTTGCGTACTATCAA
GAGAATTTCGAAGATGAACCCATCTGGGATCTCTTAAGCCGCCACGACGCTGACAAAGAC
GCCGCAGCACTGGCAGCTGCCTCTGCTGCAGAAAACCACGCACTAGCGCGAGGTACTACC
CCAGTCGTTATCCGTACCCAAGACATCATCACTAACGCGCGATACCTCATGTCTGATAGT
GCTGATGACAATCCAGAATACGATCGCGCCTTGGTCGAACTTAGTGCTTATCTCTTAAGT
ATCGACCTCGATGATCGCGTTGCTGCAGAGATGACCATTTTAGGTCGCCCTGTGCCTAAA
GAAGGA

>RXN01908-downstream
TAACCACCACACCAGAAAAGAAG

>RXN01909-upstream
TTAATAAGAATTGTTCTGGGAAGTAATATAAAAAGTCCCGAACAAATTAGTGTGAAAGGG
TTTGTATC

>RXN01909
ATGGCTAATTTTCGAAGCAAGGATAAAGATGGCAATGTCATCAATCCGAACGCGTCTACT
AAAGGTGTAGATCTTGTTGTCAACGTCTACGACAGCGCCAAGCATGTGACCGAAAAGGGT
AACACTGTCCACTTTGTGGATGTTCAGGTAGCGCAAATTCCGATTGACGCTGACGGCACT
CGTGCGAATGCGAATCTTGCACCACAGACTATGCCTCATCTGCATCTTGACACTAAGGAC
GGTCAGCGCAACACAGGTGTTGCGTATTCTGATGCGCAGATTCAAGCGATGCAGACGGTG
GCAGCACAGGGGCGCAACCATATGACCCCGCTCTTGAGCAAAGACGGTGAGACAGTTGGT
TACTCCATGTTGGTCAAGGCTGATGTCATGTTCCCGAAGACCAAGGACGGCAAGTCTCTC
CCTGCGGTCATGAACACTAAGTCTCTGCAGCCATCTGGGGTTCCTATTTCGGACGCGATG
AATATTCAGCAGCAGCAGTTTATGGCTGTGGCAATGAATCGCCAAGCAGCAGAAGCGCAG
AAGGCTGCACAAGCCCAAGCGACCCAGGCTCAAGCACCACAGGTGGCACCGCAGCCAGTT
ATGCAGAATCAGCAATTCCAGGCACCAGTGCCACAGGGCCAGCAGCCAGCATATGCAGGA
GCCCCTGTCTATGCAGACGCGGTAGCTCATGCAACCGCGCAGCAGCAGGCAGCAGCAGCT
CAGGCACCGCAGGCACCTGCTGGGAATCCGTTTAACCAGCCGCCAGCAGTAGCAGCAGCT
CTGGCACCGCAGACGCAGCCGCCAGCAGTAGCAGCAGCTCTGGCACCGCAGACGCAGCAG
CCGGCAGCACAACCTCAGATGGATAACGAGCCACCGTTT

>RXN01909-downstream
TAAAGGCGCAATACACCACACCC

>RXN01910-upstream
CACCGTTTTAAAGGCGCAATACACCACACCCCAACAAACTTTTTGATTGTTGGGGTGTTT
GTCTCAGATCATGAACAGCACAATGTAGGAGAAGATTGAT

>RXN01910
ATGGCATTTCCGCTTCTAGCGGTTGCTGGCACAGTTGCCCCCGTTGCAGCAGGATGGGCA
AAAGATAAGTTTCTCAGCAACTCTCAGAATAATCAGCAGGCCCAGAATCAGCAGATGAGT
TTTGGACAGGTCAACAACAGCGCACAGAATTCTGGATCAGAAAACAGCGGTTTCATGGGT
CAATACGGCAATCTGGGTGCAGGTTTGGCAGGTGCTGCTACAGGCGCAGGGCTTGCGTAT
AGCGATTTTGAAGATGGTCAAAGTTTGTCCTCGAAGGCCCGCAACATGGTCGGCAAAGGG

CTCGCTGGTGCCGGAGCTGGTGTGTTCACCAAGCTTGCCAATGATGCAATTCAGGCCGAG
GGTGGCTCGATGAAGGCTAGTGCTTATTCTGCCATTGCAGGCGGCTTGGGATCGTATCTC
AAAGACGGCGGTCCGGGTGTGATTAAATCCGCGATGGCCAGCGGTGCAGCCGGTTTTGGT
GCGGATAAAGTGCACGATAAATTAGCTGAGTCTGGTCATGAGGGGTTGGCTGATTCCTTG
TCGGGCGCTATTCAAGGAGGTGGTCTTGGTTACTCCACGCTTGGCGGTGTCACTGGTGCT
GGTATTGGCGGTGCGACGGGCGGTCTCGCAGGACTAGCACAAAACTACTTTGGTGGTGGC
GATGACTACAGCAACGCTGGGGCATCTGCATCGGGGTTTAGTGCCAACCAGGTTAATAGT
GAGATCAGCACCGAGATTCCGCAGTTTGCGAATCTTGGTCAACCACAGCGATCCGAGCTT
GAACAATTAGCGCTACCTCAAGAATCACGGTCTGTAGATAAGAGCTACGACCAAGGCTAC
GAAGCG

>RXN01910-downstream
TAAGCGCTTTATAACAACCCCGT

>RXN01911-upstream
AGATGCCGCAGATCACCGAGTGAGCGTTACTGAGATCACTGAGTCTCGATGGGTAATCCA
TATAATTGTGAGCGGGATTCTTAGTGCGCTCGCGGTTCTG

>RXN01911
GTGTTTATTATTGGCGCCGGCTTGCCACTGTTGTACGTGCCGATTTTTGTGACTGTCATC
GTCATGGTGGTGTATGCGCTATTGCGCTATGAGCAGCGCATGTCAGGCACAGTCTACGAG
GAAGCAGATCCTGTCGAAATGGATTCAGTGATCTGGGAGGGCATCAAGTGCGATATTGCC
TCGGATATTGCAGCCCGAGCAGAAGCGAAAAAAGCGAAAAAGCCAGTTGCGTCAGATGCT
GTTGCTGTTGGTAACTATATCGCGTCCTTGCGTCAGCATATGTTGGTAGAAACCCAGCGA
CGTTATCACCACAAGCTTGGTCGTGAGCTGCATAATGATCCAGCGCAACTAGAGGATTAT
GGCTCTGGTCTGCGTGACTGTGAGTGTCGGGCATGTGTGGTGGCTCAGAAATTGGGTGTC
ACGGTGCACGCTCATGGTGTGGTGCAGGCGAGCGCACGTAAAAAAGATCGCGTCATTATT
GGGCGAGCCGATGGTATTGATGTGGCCGGCTGGTGGAACCACCGCCAAGAAGCTCGACGT
AAAACGAGCGCGGCTAAGCAGTTGGAGCGCGATGCACAACGCAAGCGAACCCAAGCTGAG
CGCGATAAAGAGATTGAGCGTAAGCGTAAGGCTCAAGAATTTGTAGCGGAGCAGTCAGGG
AAAGCTGCTGCAGCACAACGGCGGGCCGAGAAAAAGGCTGCGAAGCAAGCGCGTGTAGAT
GAACTGGTGGCGCAGAAACAGGCTGCTCAGGAGCAGAAAACTCACTGTAAGCGGGACAAG
CAGCGTGCGAAGAAAGCACAAGGGCGCAAAGTTGGTGCCGTTGATAATTCCGCTGTGGAC
GATGTGTTGGCGTATGCGGAGAAAACCCGCAGTATAGCTGGCTGTAGAGATGACGACAGC
GTTGTGCACGTTGATATGGCAGCGGGTGTCCGCGATGTC

>RXN01911-downstream
TAAATCGCAGGATGATCGAAAAA

>RXN01930-upstream
CGAAAGAAGCCATAATTTAGAGAGGACAATTCTCTACTATTGGTCAAGGCTCCCACCCGG
TGTCATTCGACATTATTACCGCTCACTCACAATCGATGAA

>RXN01930
GTGATTTCAACAAATGAGATTGAAAATATTCACTCAACTCGTCGGGATATTGAAATAGCG
CTTGATGAATCTTCCACTAGTGAGCCAAAGAGATTTTCGGAAATTTCACACCTTTACCTC
GCACTTGCCGAAGGTAAAATATCCTTTCCGGAAAGCCCAAGTGAACTTCGAGAACTCTAT
GACCATTTAATGCACGGCGAGCTAGGTAAAGAAAATGAATTAGATGGTGAGATTTTCCGC
CAAGGACCCGTGGAAATCCGCGATAGTCGGCAAAAAGTGATTCATTCAGGTTTTTCTCCA
GAATCACAGATCATCGAAGGAATCAACGCAATTATTAAGCTGGCGCACTCAGAAGAGGAA
TCCAACCTTGTTGGCATCATGATGTCACACTTCATGTTTGAATCAATTCACCCGTTTTAT
GATGGAAACGGAAGAACTGGGCGCTACCTTCTCGGGATACAATTAAGCAAAATTCTCTCC
CCTGCTACAGCACTGACAATGTCTTCGGCAATTAATCAATTTCGAAACAAGTACTACAAA
GCGTTTCATGCCGTAGAACACCGATTAAATCGCGGAGACGGAACACCGTTTGTTATTTCC
ATGCTTGAGCTGTTAATTGCAGCGCAAGAAGGTCTCATTGAGAATATAAAACAAAGAATC
GACTTTTTGGCAAGCCTTGAGGACGCCATTAAAACGCTTCGGGGTACCAATTCCTTTAAG
AACCATCAGATCAATCTGTTGTACATTCTCGGCCAGATTCAGCTTTTCGGTAAGGACGAA
ACACTTTCACTTGAATCGGCAGCAAAGTTTCTTAAAGTTTCTAAGGCAACTGCAACGAGG
TATTTTAGAACTCTCCGAGAAATGGAATTAGTTCACGAGGTCAGCAAACGCCCTTTGCGG
TTTGCGCTCACGGATAAAGGTCGTGAGATAGTAGGTCTTGAGGTAAAAATT

>RXN01930-downstream
TGACTCCATAACGAGAACTTAAT

>RXN01944-upstream
GCTGATTCTTCTGTACCACTCATCACAGATAATACCGCAACCAGTATCAACCCTGCGGAG
CCGTTTACCTTCGCCTTCAAATATCACCGATGATGTCCAG

>RXN01944
GTGCGCACGGCAACACTGCATGTTACTTCCAGTGCTGGCGAAGCCGCGACAACCATCAAC
CTCACCGAGGATGACGGCTCTTTCAATTGGGCTCTGCCTGCAGCGGATCTCACCGGAAAA
TCCTGGTTCGAATACACCGTAACCGCCACCGACGGATTCAACAGCGTTACCACCGAGCCG
GTACGCGTCACCGTCGACGGCGCCAACACCGACCCGCTGCGCCTCAACCTGGAAGAAAAC
CAATGGGTCAGTGGCACCACCGATGTTATCGGTGCTTCAGATGTCTTCGGCGACAAGCTT
GAATTGCTTATCGACGACGCGCCTGCAGTCACCAACTCCAGCCTGTCTGCGGCCCCGACG
TTTGCGATGGAAGTAACCCAAACTGATGTGTTCTTCCGCAACGGCATCCTTGCCGGTGGG
GAAGAACTCCGCATTTTCGATCAAGGAACTTACGCCAACACCGAAACCATCTCCACACCA
GTCCCGCTGTATCACATCAATGAGGACGGTACCCTCACAGTCAGTGTGTATGCGGGAACT
AAAGCAGCACCAGAAATTGACCTCAACGAGAACAATGACGATTTCCAGATCAGAAACCTT
CGACTAATTCTGCCTGATGGCCGGACCCTCACCCCTGCCGGAATTTCCGATTCTAATGCG
TGGCTCAACATGGGAGACAGCGCTGGAAAACTCGATTTCTTCGATGCCACCTTCGCCCTC
CCTGAGGATGCTTTCACCGGTGTGGCACACGCATGGGATACCACCCAAAGCACAGATGGA
GAACACCACATCACCATTTCCCGCGAAGACGGCGGGGAAATCAGCCGCACCATCCGGGTT
GATAATACTGCCCCAGAACTCACCGTTTCTGGAGTTGAAGAAGGACAAGAACTGCGCGGC
ACCGTAGAAATTGATGCCCAGGCAACCGATGCGGGTGCGGGCGTGAAGAGCGTCGAGACG
CTTCTCGACGGC

>RXN01944-downstream
TAACGCGTGCAACTTCCACTAAC

>RXN01945-upstream
AGAAGGACAAGAACTGCGCGGCACCGTAGAAATTGATGCCCAGGCAACCGATGCGGGTGC
GGGCGTGAAGAGCGTCGAGACGCTTCTCGACGGCTAACGC

>RXN01945
GTGCAACTTCCACTAACCACCGGTTCCATCGCTTTGGATAAAGGTGAACACACCTTGGTT
ATCCGTGCAGAAGATGAAGTAGGAAACCGCACCGAGAAAACCATCACGTTTAGCACTCCG
GATGAAAACCCCATCAGTGGTGACTACGCTCCAAGCAATGGGGCCACCGTGGGCGTCGGT
GACGTTAAGTTATCTGCACGAGCAAGTGATCCAAGTGGCGATACTGTCAAGATGACGTTC
CTGGAAGCCGATTCACCAAAATTAGATAGTGGTCGCGTCCGAATGTCATCAGGAACGGTA
GAAGATGCCGGAAGTGTCTCGCGCGCCGAGGCGAAAATGTTGGAGAGGGGAGACGTCGAG
AAGCTATCCAGCCTGGATGGGCTGGGCATGGAAGTTACCTCCGACGCCGCACTGCCGTAC
CAGCTTTTTGAAGTCGATGCGGCGGATGCACTCGCGGCCGACACTGAAGTGCGCCTGAAT
TGGGCGGGATCCGCCGATGGTCGCGCGCAGGTGATCATGTATGTTTTCGATGGCGAGGCG
TGGGTTGAGGTGGATCGTCACTTGACCGGCGATGAGCTGGAAGAGTTTACGCTGCAGGGC
GTCGTCAATGCGGAAAAATTTGCAATCGGCGGCACTGTCACCGTATTGATTCAGCACTCC
GAAGGCTTCGCCGGTGCGGATCATTCAACTAGAAATTCCGACGTGACCGCAGCGCACCCG
GATGATGTGGCTCGCTCTGAGTACGATTTCACCCTCGCGTGGGAATCTGACACCCAGTAC
TACAACGAGGAATTCCACGAGCACCAAACCAACATCCATGACTACGTGCTCGCCGAACGG
GAGAACAAGAATATTCAGTTCATGTTCCACACTGGCGATGTTGTCGACGACTGGGATCAG
CCCGCGCAGTGGGCCACAGCCAACCCCGAATACCAGCGCCTCGACGACGCCGGCCTGCCA
TATTCTGTCCTTGCCGGAAACCACGATGTTGGCCACACCAGCAATGACTACACCGAATTC
AGCCGACACTTCGGCGAACAGCGCTACGTAGACAACCCGTGGTACGGCGAATCCTACCAA
GACAACCGAGGGCACTACGATCTATTTTCTGCCGGCGGAATTGACTTCATTAACGTAGCG
ATGGGCTGGGGTCCAGACGACGAAGAAATCGCGTGGATGAACGAGGTCCTGGCCAAGCAT
CCCGAGCGTGTGGCGATCCTCAACCTCCACGAATTCATGCTCACCACCGGCGGACTTGGC
CCGATCCCGCAGCGCATTCTCGACGAGGTCGCAGCCACCAACCCAAATGTCAGCATGATC
ATGTCCGGCCACTACCACGACGCATTCCAACGCACCGACTCCTTTGACGACGATGGTGAT
GGAGTAGATGACCGCACCGTCACCTCTATGCTTTTCGATTACCAAGGCCTACCGGAGGGC

GGACAGGGGTACCTCCGACTTCTCCACTTTGATAACCAAGGCCAAAAGATGATGGTGCGC
ACCTATTCACCATCCCTGAAGGATTACAACTCTGATGAACCCTCACTGTTGGGGCCTGCA
GAAGACCCCAACATGTATCAAGAATTCGAAGTGTCCTACGAGCAGCTCGGCATCAAACCA
GAGGGCCGCACCCTGATCGGCGATTCCTTCAGCGCCGATTTCTTGACCTCCAATGAAATT
GGAATAGTTGATGAGGTTCCTTCTGGAACGATCGCTTTCACGAACTGGAAGGACGTAACC
GAAGGTCGCCACAGTTGGTATGTTCGCTCCGAGGATCCTTTCGGCGGCGTCGAGATTTCA
CCCGTGCAGTCCTTCATTGCCGGGGAAGAGGCTGGCGGGAACGCGCCCGGCACTGGAAGC
TCCAATGGCGGTTCATCCCACGGATTATGGGGTGCGCTTGCGGAATTCTTTGCCGGAGCG
GCAGCCCTGGCTGGAGCTGCGATCGCATTTGTCCCCGGAATTTGGGACTATGTGACCAAC
GCATTCAAGCGA

>RXN01945-downstream
TAATTATGGATAGGTAAACGCTC

>RXN01960-upstream
TCCAGATTGATCGTGCCAACAAAGACTAAGCCACTCTAGCTAAACCAACTTACCCCACCC
CAACACCCCATGAGGCATCTGCTTCATGGGGTGTTTTGCT

>RXN01960
ATGCCGCAACACTTTTCTCAAGAAAACTACAGAAAGGCCCCCGTCATTATGTCTGCACCG
CTCACCATTCATGATCTGCTGTCCACCAATTCGAAGCTTAACCTCAAGTGGCTGACCTGC
ACTGTCTTGAACAGCCCAAATCTCACCGAACCCTGCATCACGGTTTCTGTGAACCACACC
GAAGGCATGTCCCTGGTCTCTTTCGAAGGTGGTCACGGGCTCACCGAGATTGCCAACACC
CAGCTAGTGCCTGTGCTTGAGCTACCAAAGTTCAATCCTTTTGAGGCACTTGCTATCCAC
CTTGAAGCCGCCAACAAC

>RXN01960-downstream
TAAGAAAGCATCCTTCATGACTG

>RXN01985-upstream
GACGTGAGACATTTCCTCCAATACCTCTCCAGTGATATTCTGTCGGGCAGCCTAACCTAA
GTTATTCCGTTGTTGTTCGAGAAAGAGAGAGAAACTTTTC

>RXN01985
ATGCGTACGTCTCGCGTTCTAGCCGGCATTCTTGCCGCAACCCTCACGGTGTCCCTCGCG
GCCTGCTCCCAGGATTCTTCAGAAACGTCCTCCAATTCGTCTTCAGCAGCATCCCAAAGC
TCTGACGTTTCCAACGAGGCGTTCCCTGTCACCATTGAGCACGCTTTCGGCGAGACCACC
ATTGAGTCCAAGCCAGAACGCATCGCAACTGTTGGCTGGTCCAACCATGAAGTCCCTCTC
GCATTGGGTGTGACTCCTGTCGGCTTTGAGAAGGTCACGTGGGGCGACGATGACAACAAC
GGCATCTTGCCATGGGTGGAAGAAACCTTGAGCAAGCTCGGCTCCGATGAGCCTGTGCTT
TTCGATGCCACCGATTCCATTCCTTTTGAGGAGATCGCCAACACTGCTCCGGATGTCATT
TTGGCGTCCTACTCTGGCATCACCCAGGAAGACTACGATCAGCTGTCCCAGATCGCACCT
GTGGTTGCCTACCCAGAAATCGCATGGGGCACCTCCCTGGATGAAATGATTGAGATGAAC
TCTAAGGCGATTGGCTTGGAGCAAGAAGGCAAGGATCTCATCGCAGATCTGGATGCAGAG
GTTGCTTCCGCCATCGATGCCAACCCAGAGTTGAAGGATGCGAAGCCTGTATTCGCGTTC
TTCGATGAGAGCGATTTCTCGCAGATTGGTGTGTACACCAGCATTGATCCTCGCATGAGC
TTCTTGCTTGATGCGGGTGTCCAGGAAGCTTCAGTCCTCAAGGAGCACTCCAGCCCAGAT
AGCTTCTACGAGCAGGTTTCTGCAGAAAACCCTGAAACCTTCGACGATGTTGATGTGATC
ATCACCTACGGCACCGAAGATGATGCTGCAAACGCTGAGCTGTTGTCCAAGATGCAGGCT
GATCCACTGCTGTCTCGAATCCCAGCTATCGCCGAGGGCAAGGTTGTGTTCTTGGGTGCT
AACCCACTGGCTGCTTCAGCGAATGAATCCCCACTATCTATTCCTTGGGGTATCAACGAT
TACTTTGCAAAACTCGCCGAACCTCTGAAG

>RXN01985-downstream
TAAAACTGCTTGATGTCAACAAC

>RXN01987-upstream
GGGTTAGGAGAGGGGAAATCCCCGATGTGCTCTAGGTTCTTATTGGCGATGATTGAAGAA

GAAAGAAAAACTCAATCAGCCATAAAGGAGCTTGATCCCG

>RXN01987
ATGACTTTCCCAGCACAATCTCGACGACTCGCCCGAAGCACCACCGACAAATGGATCGGC
GGCGTCGCTGGTGGCCTCGCAGAGACCTACGGTTGGAATCCGGCCTATGTGCGTCTCGCG
TTCGTGGCGTCGGTTCTGTTTCCACTGCCAGGTTCACAGATCCTGTTCTACGCCCTAGCG
TGGCTGATCATCCCATCCCGAGAAAATCGCTTC

>RXN01987-downstream
TAACGTGCGTTGCATAACGCAGA

RXN01988-upstream
TTAAGAATTGGATTCGAGTCGGTACCGCTTGAAAGTACTTTGCGTAAGTTCCCACCGACT
GCCCCTAGTTGTTGCGAATATTTATAGATTGTTGAGAAAG

>RXN01988
ATGAACATGAAGACGCACCCGGCTTCCGCCAAGCAGACCACCGAGCTTCGACTCCTGACA
GCCACCGTGTACTTCAAAGCACTCAATGAAGTCCACAACGTCATGCAGATGATCGACCCA
CTAACTCCAGTCGTTCCCATCACCACGGGCACCTCAGTTGCCGAGCTTTATGCTGACGCC
CGCGAGCACCTCGACAATGGTGCAACCCAGGTGATGATCCCCGTCATTTCACCTTCCAAC
CTGACCTTGTCAGTAGTTGCCCTGGGCAATGAAGAGGTTGACGCACTGGGCCATTCCGAA
GGACAAGCAGTTCACTCCCTTCTGGAAATTCATACCCCGAAGCGCAGCTGGCCTCTTTCC
GAGCTTTATATTGATGACAATGAGGGTTTGGCTCAGGTGTCGCGCTGCTTCGCCCGCCTT
GTTGGC

>RXN01988-downstream
TAGTCCCACCCCACCAATTGCAT

>RXN01991-upstream
TCCGGAGGTGGATTTGAGGATTTCGACGTTTTCTCGGAAGTTCCTCGGGTAGAGGAAACA
TCGACGAGGATCAGCTATTCTTACAAAAATTCATTTGAAT

>RXN01991
ATGACGAATTTGTTGCCGCATTTCCCGAGTACCGACGTAGCTGCGTGGGAACCAACCGTT
GTGTATTCAGCGGATAAGACCACAGCAACAGCGACGTTTAAGAATATTCCTTCGGATATT
TCCTTTAGTTGGACTGGTATTGAAGCACTAGAGCCATTTAGCCCTGGTAAAACCTTCGAA
CATAAGGTGCAAGGTTCTGTTGGTGAACCAGCGGGGGCGTTCACTAGGGATAACTATTTC
ACTGAGGGTGAGCTCTACAAACATCGCCACGCAGACGATCTGCTTTCCGGTGATGGCTTG
TTTGGCCCCAACATCACCGATGGCGATGGCAACCTCCCCTCTGTTGATGACGGCAAGGAC
GGTGACGATGGGTCTGATGGCTCAGACGGCCGAGACGGTGTTGTCGCCATTGATGTTGTT
GACAATGCTGACGGCACGGTGACTGTCACCTTGTCCGATGGCACTACGTTTACTCTTGAT
GCTGGTCAAGACGGCAAAGATGGTCTTGACGGGCTTGATGGTACTGGCCTAACGCTGGAA
TCTGCTACCCCTGATGAGGACGGCAACATCACCTATGTTCTTTCTGACGGTACTGAGTTC
ACTGTGCGCAACGGTGTTGATGGGTCAGACGGTAAGGACGGCAAAGATGGAGTCAATGGC
ACAGATGGCGTAGACGGGTCAGACGGTAAAGGTCTGGTAGAGGTGTCCCGAGTTACCAAC
GACAACGGCTCAGTGACCATTACCTACGAGGACGGTTCACAGATCACCACGAAGCCAACG
CCGACAAACTGGCTGTCCAAGCTGCTTGATTTGCTTCTCCCGCTGTTTAATCTGTTCGGT
CTTGGTGGCGGCTCCGTCATTAGTTCCAGTAAG

>RXN01991-downstream
TAGTTTTTTCACTCCCTGTTTTG

>RXN01996-upstream
CTAGTATAGAACGGAACACGGCAGCGACACAAACTGCACAGATGCAAGAGTGTCGGTACC
GTTAAAAACGAAACACACTTTCACCGAAAAGGACTTCCCA

>RXN01996
ATGAGCAAGTTGACTGGCACCTGGACCCTCGACCCTGCACACACCGAAATCAAGTTCGTG
GCTCGCCACGCAATGGTTACCAAGGTTCGCGGTGAATTCACCGAGTACACCGACTCCATT

GTCGTAGATGCTGAAAACCCAGAGAACTCCTCTGCAAAGGTTGTTATCAAGACCGCTTCC
GTTACCACCGGCAACGCAGACCGCGATGCACACGTTAAGGGCGACGACTTCTTCGCAGTA
GACAAGTTCCCTGAAATGACTTTCGAAGCTACTTCCTTTGTTATCAAGAACGAAAACGAA
GGCACCGTTACCGGCGACCTCACAATTCGTGACACCACCAAGTCCGTCACCCTGGACGTT
GAGGTTGGTGGCGTTGCTGAGGATCCATTCGGCAACACCCGCCTTGGCTTCGAAGCCTCC
ACCGAAATCAACCGCAAGGACTTCGGCGTAGATTTCCAGGCTCCACTCTCCACCGGTGGC
GTTCTGGTTTCTGAGAAGATCAAGATCGAGATCGACGGCTCCGCAATCAAGGCTGCT

>RXN01996-downstream
TAAGCGCCCACAAACAAAAAGCC

RXN02007-upstream
TGGAAGCCCCAGCCGCGGTCCAAGAGACAGTTGCGCCGACGTCCACCCCTTAGGACGCTG
ATTACAGACGTGTCCCATTTCTTTACTACTATTGGAAATT

>RXN02007
ATGAGTTCAGACGCAGAAAAGGCATCCGTGGAGCTTTCCGAAAAATTTCACCCAGAACGC
ACCCATATTTTGGGCGCCGTTGTTTTTGGCCTGATCTCATTATTAGTCATCGGCGCAGCC
CCTCAGTACCTGTTTTGGCTGCTCGCGCTCCCTGTCATCTTCGGTTACTGGGTTCTAAAA
TCATCCACGATCGTTGATGAACAGGGCATCACCGCAAACTACGCCTTCAAGGGCAAAAAG
GTTGTGGCCTGGGAAGACCTCGCAGGAATCGGATTCAAGGGTGCCCGCACTTTCGCTCGC
ACCACCTCCGATGCAGAAGTCACCCTCCCGGGCGTCACCTTCAACTCCCTTCCCCGCCTT
GAAGCTGCTTCCCACGGCCGCATCCCCGATGCGATCACCGCAAGCAAGGAAGCAGCCGAC
GGCAAGGTTGTAGTCGTTCAAGAAGACGGCTACTCCGTGATGATGTCCAAGGAAGAGTAC
TTGGAGCGCCAAAAGGCACTGGGCAAGCCAGTTCAGTTGAACTTCGATGACGACACCGAT
GGGAATACAACACAAACAGAAAGCGTTGAATCCCAAGAGACCGGACAAGCCGCGTCTGAA
ACCTCACATCGTGATAACCCTGCGTCACAGCAC

>RXN02007-downstream
TAGAGTGTAATAAGCCGTCCGAA

>RXN02014-upstream
AGAGGACAACAACATGAGAGCAGACGCACTAAAACGCCGCGAACACATCATAACCACAAC
CTGCAATCTCTACCGCACACACCATCACGATTCGCTCACC

>RXN02014
ATGGAAAACATTGCAGAACAGGCAGGAGTGGGTGTTGCAACTTTATACCGAAACTTCCCC
GATCGCTTCACACTGGACATGGCATGCGCCCAATACCTTTTCAACGTGGTGATCTCCCTC
CAACTCCAAGCCATCAGCACCTTCCCCACCGACCCAGAAGGCGTGTGGACCTCCTTCAAC
CAACTACTTTTCGACCGCGGCCTAGGCTCCCTCGTCCCAGCACTTGCCCCAGAATCCTTA
GACGACCTCCCCGACGAGGTCTCCGCCCTGCGTCGCACCACAGAGAAAAACACCACAACA
CTCATCAACCTAGCCAAGCAGCACGGACTCGTACACCACGACATCGCGCCGGGCACCTAC
ATCGTCGGTTTGATCACCATTTCCCGCCCACCTATCACCGCGCTGGCGACAATTTCAGAA
AACTCCCACAAAGCACTGCTTGGCCTTTATTTGTCCGGTCTTAAACACGGCATGATGGCT
AACATCGGAGAACATGACGGAAAGTCC

>RXN02014-downstream
TGATCTAGCAGTTTCCTTTTTAG

>RXN02019
GAAATTCCTGCTGGCACCAAGGTTGAGGCCTCTGACCTTGGACTTCAGGCAATCCCTACT
TCCCTACTGCCCAGCACCTCCTACGATTCGATTGACGATGTAGTTGGGCTCGTTGCGGCC
TCCACATTAAGTTCCGGGGAAATAGCCACAAAGCCTCGATTCGTGGGCACCGAATTGATA
AACTCCATTGCGACAAACGTCACTGATAGCTCTTTGGTGGAAGAAATTAACATGGTTCCA
CTCAGTTTGGCTGAACCTTCCGTCATCCCCCTACTGCAGCATGGGGACACCATTTCGGTT
GTTTCCCAAGACCCAGACACCGGTCTCCCAGAGAACATTGCTGCAGGTGGAACAGTAATT
CTGGCGGGTGGTACAGACCCCTCAACCATCTTGATTGCGCTTCCACAATCAATCGCTGAA
AAGGTTGCAGCACAATCGCTCAATACCCCTCTGGCGGTAGTCCTGACCGGAGACAGAGCA

GATAATTACACAACCGAAGAA

>RXN02019-downstream
TAGTTCCCTATTCAAAAAAAAGG

>RXN02023-upstream
GATGTGGCAGCAATTTTGAAGCAGTACCTGAGCGAGTAACCGCATTCGGGGTTATCGTGG
GACTTCCGAAATGTAACTAGAGACTAGAGGAGGAAACACG

>RXN02023
ATGGCTCCTAAACAAACTCCCAGCCCAGAGAAGAATCGAAACCTGGTGGGACCAGTTCTG
CAACGTCGGCAGACAGAGGGTACTTTTGATCAACGCTTGCTAGAAATGCGCGCTGATCAC
AATTGGAAGCACGCCGATCCATGGCGTGTACTGCGTATTCAGTCTGAGTTTGTGGCGGGT
TTTGATGCCCTCCACGAGATGCCAAAGGCCGTAACCGTCTTTGGTTCCGCACGCATTAAA
GAGGATCACCCGTACTACAAGGCGGGTGTAGAACTTGGTGAAAAGCTCGTTGCAGCGGAC
TACGCAGTTGTCACCGGTGGCGGTCCAGGTCTGATGGAAGCCCCCAATAAGGGGGCAAGC
GAGGCCAATGGTTTATCAGTTGGTCTGGGCATTGAGTTGCCACATGAACAGCATCTGAAC
CCTTATGTGGATTTGGGTCTGAACTTCCGGTACTTCTTCGCACGCAAGACCATGTTCCTG
AAATACTCCCAGGCTTTTGTGTGTCTGCCTGGTGGTTTCGGCACGCTCGATGAGCTTTTC
GAGGTCCTCTGCATGGTACAAACCGGCAAGGTACCCAACTTTCCCATCGTGCTGATCGGC
ACTGAGTTCTGGGCAGGTTTGGTGGATTGGATCCGTCACCGCCTGGTAGAGGAAGGCATG
ATCGATGAGAAGGATGTTGACCGGATGTTGGTCACTGATGACCTGGATCAGGCCGTCAAA
TTCATCGTCGATGCACACGCTGGATTGGACGTAGCGCGTCTCCACAAT

>RXN02023-downstream
TAAGCAGTGGCTACATTAGGTGT

>RXN02032-upstream
CTTAAAAAGGGGCTTTATCGGTTCAGGCGAGCGAGACCTTCGGCGTTCACACTTCGCCGG
GGTCTATTTTTTATGCCCAGGCACGGCTCATAGGAGAACC

>RXN02032
ATGCCCTTTCTACAAATCTCTCTGCTTTCCATCGGTGTCGCCGCCGATGCGTTTGCTTGT
TCCGTTGTCCGCGGCACCGCCATTCAAGTCAACCTTTTCAAACGCGCACTTGTTCTCGCG
GGCATCTTTGGTGTCTTCCAAGCGGCAATGCCTTTAATCGGCTGGTTCATTGGCCGTTTC
TTTGCTGGAATCACCTTCATCGCTGAAATTGATCACTGGATCGCTTTTGCACTATTGGGT
ATTGTCGGCACCAAAATGATCTGGGATGCCTTCCAACCTGAAGATGATGAAACCATTGTC
GATGACGGCCGCGTTCAATTTAGACCAGCAATTATCCTGGGGCTAGCCACCAGCATTGAC
GCATTAGCCGTAGGCATGGGCCTGGCATTCGTGGAAGTTTCCATCCTCAAAGTGGCACTG
TCCATGGGCAGCATCACCTTCGCACTTTCGCTTGCTGGCGCCTGGATCGGACACCATGGT
GGAGGAAAGTTTGGCAAGTGGGCTACGATTCTTGGCGGAATAATCTTGATCGGAATCGGC
GCAAACATCGTCTACGAACACCTCAGCGCG

>RXN02032-downstream
TAACCCTCGGCGCATTATCCTCA

>RXN02039
AAGGCGTCGATAAGCAATTTAAGCTTTTGGACGTCCACCTCCACCACCGCACCCCTTTGG
CTCGTGGGCACGCTTGTGTGGCTGGCGGTGCAGGCGGTGATGCATGACGGCGAGCTTTAC
CATGTGGAAGTTCCCACGATTGCGCTGGTCATCGGCTTTGGCGCGCAGCTTCTGATCGGT
GTGATGAGTTATCTACTGCCGTCGACGATGGGTGGCGGCGCGAGCGCGGTGCGGACTGGA
ACGCACATTTTAAACACTGCGGGGCTGTTTAGGTGGACGCTGATCAACGGTGGCCTGGCG
ATTTGGCTGCTCACCGACAATTCGTGGCTGCGCGTCGTGGTGTCTCTGCTGAGTATCGGA
GCGTTGGCAGTTTTTGTCATTCTGCTGCCCAAGGCTGTGCGGGCGCAGCGCGGAGTGATC
ACCAAAAAGCGCGAACCAATTACTCCGCCGGAGGAGCCTCGACTCAATCAAATTACCGCG
GGAATCTCTGTGCTTGCCCTGATTTTGGCAGCATTCGGTGGGCTCAACCCCGGTGTTGCG
CCGGTGGCAAGCTCAAATGAAGACGTCTATGCTGTGACCATTACCGCAGGTGACATGGTG
TTTATCCCTGATGTGATTGAAGTGCCTGCTGGTAAATCACTCGAAGTCACGATGCTCAAC
GAAGACGACATGGTGCACGATCTGAAATTTGCCAACGGTGTGCAAACCGGACGTGTGGCG

CCAGGTGATGAAATTACGGTGACCGTCGGCGATATTTCCGAAGACATGGACGGCTGGTGC
ACCATCGCTGGGCACCGCGCGCAAGGAATGGATCTGGAAGTAAAGGTTGCGGCTCCGAAT

>RXN02039-downstream
TAACCAAGGGCTGCTGAAAAACT

RXN02044-upstream
TTACTTTCTTAAGTAATTTAACGAATTTGGTCTCGAAACTGACCTAAAACCCCATGTTGC
TAGTTGGTGCAAACCAATAATAGCTATAGCCCCAATACAA

>RXN02044
ATGGTCACCCCAATCATGGGGAATTCGAACTCTATCCTGGGCATTTACCGTCAGAAAATC
CAAAATCGACATTTGGTTTCTACGCTTTTTAGGGCATACTTCCCAATCGTGACCGAGCTG
ATTATTTTATTGATTGTTATCGTGACGGCGCTCGCCTTCGATTTCACAAACGGATTCCAC
GACACCGGCAATGCGATGGCCACATCCATTGCCACAGGCGCTCTAAAACCTAAAGTCGCC
GTGGCACTATCCGCCTCACTGAACCTTGTTGGCGCATTCCTCTCTGTAGAAGTTGCGACA
ACTGTTGCCAAAGGCGTTGTTGACCTCGACCAATTCGACCTAAGCAATGCCTGGGATTCC
CACCAGCTCCTGCTTGTCGTCTTCGCCGGCCTCATTGGCGCCATCGTCTGGAACCTTCTG
ACCTGGCTGCTAGGCATTCCTTCCAGCTCCTCTCACGCACTTTTCGGTGGCCTCATTGGC
GCCGCAATTGCTTCACTCGGTTTCGGCGGAGTGGTGTGGGAAGGTGTCTTGTCCAAGATG
ATCATCCCAGCATTGGCTGCACCAGTTGTTGCAGGTCTCGTGGCCGCCATCGGCACTTTC
GCCGTGTACAGCATCACAAAGGCAGTTGGAGACAACGAGAAGAACCGTTACTTCCGCTGG
GGTCAGATCGGCTCCGCTTCCTTGGTTTCCCTGGCACACGGCACCAACGATGCCCAGAAG
ACCATGGGCGTTATCTTCCTTTCCCTGGTTGCCACCGGTCACCTGGGAACTGACGCTGAC
ATCCCATTCTGGGTCAAGGCTACATGTGCATTGGCAATCGCAATCGGTACCTACTTGGGT
GGTTGGCGCGTTATCCGCACACTGGGCAAAGGCTTGGTTGAGATTGATTCCCCTCAGGGC
ATGGCAGCAGAAACTTCTTCTGCAGCAATCATTTTGACTTCTTCCCACTTCGGTATGGCA
CTGTCCACCACTCACGTTGCTACTGGCTCCATCATGGGTACCGGCATTGGACGTAAAGGG
GCGAAGGTTCGTTGGTCCGTCGCAGGACGCATGGCAATGGCCTGGGTTATCACCCTCCCT
GCCTCCGCGATCGTTGGCGTTTTCTGCTGGTGGGTAGCTCACGGAATTGGTCTTATCAGC
TCAGACCTCCTCGGAGTCCTCGTTGCATTCGCCATTCTGGTCATTCTGTCTGGCTACATT
TACGCCCGTTCCCGTCGCGTGCCTGTTGATCCAAGCAACGTCAACGCTGACTGGAATGAA
GAATCAAACAGCGTGGAACCTGCAACACCTTCCGCCCCGGCTGCTTCTGAGATTACAGAA
GCTCCTGCCGCTCCAGCCGCTCAAGCCGTTCAAGATCTCAACAACGAGAATGAGGTAACC
AAG

>RXN02044-downstream
TAATGAACTTCGCTACTATTTTC

>RXN02045-upstream
CACCTTCCGCCCCGGCTGCTTCTGAGATTACAGAAGCTCCTGCCGCTCCAGCCGCTCAAG
CCGTTCAAGATCTCAACAACGAGAATGAGGTAACCAAGTA

>RXN02045
ATGAACTTCGCTACTATTTTCGGAAGCATCTTTGAGGTCACCCTCGTGGGCATTTTGCTC
GGCGCAGGCCTTCCAGCCCTTTTTGCATTAGGAATCCGCTTTGCTCACAGCCCTTCTTCC
AACGGCACCAACGCTCTTGGAAAAATTGCTTCAACCATCTGCTTTGCCATCATTGCGGTT
GCTATCATCGCTGGCATTCTCTGGGTCACCAAAGCAACGATCTACCAGTACTCTGGTTTC
GACATTTTCGGCACTGAAGGC

>RXN02045-downstream
TAAAAGCACCAGCTGCGAATAAC

>RXN02049-upstream
TCTACGCAGTCTCCACAGACCACGCAGCTTTAGATGCAGTGTGGCAGTCCTGGCTTCGCG
ATCTGGAGTTGCCGGAGTTTCCTTCTGGTGGTTTGGACTA

>RXN02049

GTGCGCTATCTGACGCTGGCCACAATCATCGCAGGTCTCTCCGGGTTCGTCGTCATCATC
ATCGCTGCCTGGGCCCTTGGTGATTCCAGCCAACTTTCCGAAGAATTCACCGCCTACTGG
GGTCTGTTCTTTGCAGGAACCGGAGTGCTGACTGGGTTGACGCAGGAGACGACCCGCGCG
GTGACGGCCGGTTCTCGTGGTGGTTCTCGTGGTGGGCGTGCTGGTTCTGTTGTTGGATTT
AGGCCGTTTTTGTTTAGCTTCGTGGTTGCGGCGATAGTGCTCGTGGTGCTTGGCGCTTCG
GCGCCGCTGTGGATCGGCCAGCTTTTAAGTAATTTGCAAGGTGTTGGTGTTGGGCTACTT
GCTGTAGGTCTTGCTAGCTACGCGATCCAAGCGACAATCTCCGGCATTTTTGTCCGGCTG
CCAATTGTGGAAAGAGTATGCCTCGCTGATTTCTTTGGACACCGGCGTGCGCATGGTTTT
AACTGTTGCCGCCTGGTTGCTGGGTTATCAATTGCTGGCGTTCTTGATCATCACCGTTGT
GGGATCAATATCCTGGCTGGTCATCGTGCTGTGCTTCGGTTCGGTGCGTTCCGTTTTGGG
ATCGGTTGC

>RXN02049-downstream
TGATGTTTCACGGGGCGTTTTCA

>RXN02050-upstream
CTACTTGCTGTAGGTCTTGCTAGCTACGCGATCCAAGCGACAATCTCCGGCATTTTTGTC
CGGCTGCCAATTGTGGAAAGAGTATGCCTCGCTGATTTCT

>RXN02050
TTGGACACCGGCGTGCGCATGGTTTTAACTGTTGCCGCCTGGTTGCTGGGTTATCAATTG
CTGGCGTTCTTGATCATCACCGTTGTGGGATCAATATCCTGGCTGGTCATCGTGCTGTGC
TTCGGTTCGGTGCGTTCCGTTTTGGGATCGGTTGCTGATGTTTCACGGGGCGTTTTCATC
CGACAGGCTCTGCTTGCGATGGCAGCATCCGGCGCCACGGCAGTGCTGATTACTGGTTTC
CCGACCCTGCTGAAATTCACGAACCCTTCAGCGGTTGCAGGAGGGGTTTCGATGGCCGCT
GTTTCCTACGCCGTCATCCTGACCCGCGCTCCCCTGCTGGTTCCGCTGCAGCAATTCCAA
TCGGCGATCATCGTTCGTTTTGTCAAAGGTACGTCCGGTCCATTGAAAACTTTGGCGGGT
CCGTTGGCAATTGTGTGGGCAGTCGGACTTGTTGGAGCTGGTCTTGCATGGTTAGTTGGC
CCATGGATCCTGGACGTTGTACTCCAAAAGGAACTCTTCGCGGTCCCTGGCTGGCTACTC
GCGATGCTCACCTTAGGCGCCACCACCACCGCTTCATTGATGGTGTCCGGCTGCGCGGCG
ATCGCCTTTGAACGTCACGGGATCTATCTCACCGGATGGGTTGTTGCCACTGTTGTTGCC
GTCGGATTCTTGCTGGGACCTTTTGATTTGGGCGTCGCTGCTGGCCTTGCGCTCATTGTT
GGCCCACTCTGCGGTTTGCTGGTACACATGGGAGCGTTTGTTGGTGGGGATCGGAATCGG
GTTTTGACTGCGGGA

>RXN02050-downstream
TAGTTTGGTTTGATTGGGGGATT

>RXN02059-upstream
TCGGGAAATTCCACTCATGAACGCCTAGTCTACGGGAACCATTTCACCAGCGTGTACGTT
GTAAATGTGAACTGAAAAAGTGAAAAGGAAGATGATAAAG

>RXN02059
ATGACTCAACCACGGCCCGATGCCGCATCTGTGTCGCTGGAAAAGAAGCGCCCAGAAGGA
TGGCCAGTGGGAAGCTTTGAAACATACCCAGAAGCCCAAGCAGCAGTGGATTTGCTCAGT
GATAATGCATTCCCCGTCACCGAATTGACCATTGTTGGTGTGGACCTGATTGAAGTGGAA
CGCGTTACAGGTCGTCTCACGTGGGGTCGTGTGATTGCCGGAGGAATGGCATCTGGCGCA
TGGTTGGGTCTGTTCTTTGGCATTGTCATGGCCTTGATGTCTGGATTCTGGTTCTCTTCC
ATCGCAGCGGGAATAGGTATGGGTTTGGTGTTTGGCATTGTCGGTGCAGCAGTTCCTTAT
GCTGCTTCCAAAGGCAAGCGGGACTTTACCTCTTCAACTCAAATTGTGGCGGGGCGCTAT
GATGTGATTTGTTCCCCAGAACGTGCTCGGGAAGCTCGAGACATGATTGCCCTGAAAACT
CGAGATCTCCGCCAA

>RXN02059-downstream
TAAGTTAAACTAACGCCTATGAA

>RXN02066-upstream
GGAACTTATCACAGGCGACATCCGTTTTGAGTAGTAGGTATCTTGGATAAGAAGTTACCC
ACATCCTTGAAAGTCGAGACACAGGAGGTCATCGGAAGAT

>RXN02066
ATGTTCAATTCCGACACCACCGCGAATCTCCAAGCTAAAAGTCGAGATCGTGCAGGATCT
AAAGCAAAGCGCAGCAGGCCAAGTTTTGATTCAGTAGCGCGGGATGTTTTGGATGTTCGA
ACAAAAACAGCACAAGTTAAAAACAAGGCTAAAGAGTTTTCCTCTGTTGATCACCTTTCA
GCAGACGCCGCAGCCATGTTTGTAGACAATGAACTGTCCCGTGGCGCCATGCATCGCGCC
AGGCTGCACATTGTGCACTGCGCTGAATGTAGGGAAGAGATTAACCGTCAGCGGGAAACC
GTTGATTATCTCCGCTCAGAGTGCAAAAACGAAGAAGTGTCCGCCCCAATGGACCTCAAA
GCACGGCTTGCCAGCCTCGCCACTGAGTGCATGCCTGGCCCTGGCGCAGAGAATTTAGCA
ATGCAGCGCCCAGAGTCTTTTGTGGCTAAAGTTGAGTCCGTAGTGCGCGCAGTTCGTAAG
AACCAAGGCCGC

>RXN02066-downstream
TAATTTTTAATCCTTATTTACAT

RXN02067-upstream
TAAAGTTGAGTCCGTAGTGCGCGCAGTTCGTAAGAACCAAGGCCGCTAATTTTTAATCCT
TATTTACATTTTCTGAAAGACCGGTCTGATGTTTTCTAGC

>RXN02067
GTGGGTTGGGGAGAGATCTTCCTCTTAGTCGTTGTGGGCCTTGTTGTCATCGGCCCGGAA
CGGTTGCCTCGTTTGATCCAGGACGCACGCGCTGCGCTGCTCGCTGCACGTACCGCTATC
GACAATGCAAAGCAGTCGTTGGACAGTGATTTTGGTTCGGAATTTGATGAAATCCGAAAG
CCACTAACCCAGGTTGCACAGTACAGCCGGATGAGCCCCAAGACGGCCATCACTAAGGCG
TTATTTGATAATGATTCCTCGTTCCTGGATGACTTTGATCCAAAGAAGATCATGGCCGAA
GGAACAGAAGGCGAAGCTCAGCGCAACAAGCAGGCAGCTGACAACAATGCGAATGTGGTG
GAACGTCCAGCTGATGGTTCCACCGCACGCCCAACGCAAAACGATCCAAAAGACGGCCCG
AATTACTCAGGTGGCGTCTCTTGGACCGATATTATT

>RXN02067-downstream
TAGCTTTTATTTAACGCCAAGCC

>RXN02075-upstream
AGTTTTCGAATACCGTCTACGTGGAGCTTTGCGGAAAATACGCACCGAGACCTAGGCGCG
CCATACGCATGGTTCACAGGATTTCAGTACGATTAACCCC

>RXN02075
ATGTACAAGGTCTTCGAAGCACTGGATGATTTAGTTCAAGCCGTTCAACGCGCATACGGC
GTTCCCATGACCGGAAATTGCGTGGTTCCCCGTCAGGAAGTGCTTGCGCTTCTCGATGAT
TTACGTGATGCGCTTCCTGTAGAACTTGATGATGCACAAGATGTGCTGGACCACCGTGAT
GGTGTGATCCGTGAAGCTGAAGAAAAGGCCATTGCCTTGGTCGACGATGCAGAAAACGAG
GCCCGAAACCTCCTTGCACGCGCAACTGAGGAGTCAGATGCCATGGTGGAAGACGCCACC
AAGCATGCGCATTCTGTCGTTGCTAAGGCTAATGACACAGCGGATCGCATCGTGAGTGAC
GCTCGTCGAGAAGCAAACAGCGTCACCGAGCGCGCCCAGGCTGAATCTGAGCGCCTGGTC
AACTCCGGCAATGATGCGTATCGCCGCGCGGTTGCTGAAGGCCAGGCCGAGCAGGATCGC
CTGGTCAGCGAGGCAGAAGTGGTGCGTCGCTCCACGGAAGAAGCACACCGCATTGTGGAT
GCAGCGCACGCTGACTCCAACAAGCTGCGCAATGAATGCGATGACTACGTGGATACCAAG
TTGGCAGAGTTTGAAACCTCGCTGTCCACCACGTTGCGTTCTGTCACTGCTGATCGTTCC
GCACTACGCCGAGGAGCTGGAGCTACTGGCCGCGAGCTGCGCGATGAGCAACCGGCAGCG
CGTGGTGAATATGAGCGGGACTACGAGCGTGATTATGAACGAGGCTACGAACGCGACGAT
CGAGACTAC

>RXN02075-downstream
TAGTTTCCAAGAAACCATTTAGG

>RXN02076-upstream
TAGTTTCCAAGAAACCATTTAGGCTTTTTCACCTTTCCGTCTAGCGATCCTCATCTGATG
TATGTAGTCACGATGAGGTACGAGTAGGATCTTCCTGGTC

>RXN02076
ATGAAATCTCCATTTATTTTTGATGTCGCCGCACTCCTTCGTGGAAGTGCCCTTCCGGAA
CACCTCACCCAATCAGGTCCAAGCCCGACCCGCATTGGTCCGGAAATGATCGCGATCCCC
GAGGGCGGAAAAGTTATCGTAGAAGCCCAGATCATTCCACTCGGTGGAGGCCTGGCCGTC
GAAGCAGATATCGAAGCGCAGCTTCTGGGACAGTGCTCCCGCTGCCTCCGCGAACTCACC
CCAACCAAGACGCTGCACGTCTCTGAGGTTTTTGCTGCCGATCCAGACTTTGTTACTGGT
GAAGATGCAGCAGATGACGAAGATGAGCTGCCAATGGTTAACCAAGACCAGATTGATCTG
CTTCAGTCTGTCATTGATGAAGCTGGTCTGACCTTGCCGTTTAACCCTGTCTGCGAAGAA
CTTGGGTACGGCGCATGCCAGGATGATGAAACGCCAGCTCCTGACGGTGTCTCTGAAGAA
GTAGAAGACGAGGAAAAGGTCGATCCGCGCTGGGCTGGTTTGGAGAAGTTCCTG

>RXN02076-downstream
TGAGCAGGAAAAAGAATCGCCTC

>RXN02094-upstream
TTCCACCTCTACACCGGAGTTCTTCCAACCAACGACCAGATCATTGCTGCGGAGGAGTTC
TCCAAGTAAATTTCTCTCCCCTATTTTTAGGAGGCACCAC

>RXN02094
ATGGCTGAACACAACGCCATCATCACGGATGCAGTACATTCCGACCCCGCTGTTTTAGAA
GACAACGCCGGGTTCAGCGGAAAGTACCTAATCCGTGCCCTGGACAAGGCAGCTCATATG
CAAACAGGTGCCATCGAGGGATACATTTCTTGGCTTCGGAAGCACAATCCTGAGAAAACA
CCGGCGCAGCTGCAGGTACTCGTCGACAAGCATTTTATGCGCCTTGCCACCGGCTCTGGC
GCTGGTGTGGGCATGGCTGCGGCCGTGCCAGGCATTGGCTTTGTCACGGGTGCTCTTGCC
GTTGGTGCTGAATCGTTGGTGTTTTTGGATGCTGCTGCGTTTTACACCATGGCATCCGCG
CACCTGCGTGGCATCGACATCCGCCATCCTGAACGCCGACGTGGTTTGATTTTGGTGGTT
CTGCTGGGCACCGCAGGCAAAGCCATTGTTGACGCAGGCGTCGGTGATTTATCCAAGAAA
AACCACGCGCCGGGCATTGCGATTTCCCGGTTTAATATCGGTGGCTTGATGGAAGTCAAC
GGCCGACTGATGCGCTACGCAGTGAAGGAAGTAAGCAAGCGTTTCCGTTCGGCATTGATT
GGCAAAATTCTGCCGTTTGGTATCGGTGCGGTGCTGGGCACGATGGCCAACCGCAAAATT
GCCAAGAGGACTGTCGGAAACGCATACGACTCTCTTGGTCCTCTCCCCACCCATTTT

>RXN02094-downstream
TAAGTACTCAAGACCCTTCCAAC

>RXN02104-upstream
CATGGATTCCCATTTGGAGCCTTATTTACACAGGCCACCTGGCTTGTTTCCCACCGCGAT
GTGCCACAATAACGCCATAACAGAAAGGCATACTGACACA

>RXN02104
ATGTCCAACTCCCCCACCGACGTTTCAACGAGCGCACCTCGAATTATGATCGCGCCAGAT
TCCTACAAAGGAACCGCTACCGCATCAGAAGCTGCGCAATACTTAGGCGAAGGCGTGTTG
GAAATTTTGCCCAACGCCTCCATTACGTTGGCACCCATGGCCGACGGTGGCGAAGGAACA
TCCTCAGTTTTCGGCGGGCAGGTCATAACATTACCCACGACAAATGCCGCGGGACGCCTC
ACCGAAGCCAGCTACACCTTAGATTCCGAAACAAACACTGCCTACATTGACATCGCCGCA
GCCTCCGGTTTGCCCGCCGTTGCAGACGATCTAGTCCCCACCACCGGCGATACCTACGGC
ACCGGCGTTTTGATCGCAGACGCGGTCACCCGTGGCGCAACTCGCATTGCTTTAGGCCTT
GGCGGATCAGCCACAACTGACGCCGGCTCAGGAATTCTCATCGCCCTCGGCGCCGTCCCA
CGCAACAAAGAGGGCTACGCACTACGAACCGGTGGCGCCGACCTCATCAACCTCGATTAC
ATCGATACCGCCGAACTCAACATCCCCGCAGCCGCCGTCGAATGGATCCTGCTCACCGAT
GTCGACGCCCCCGCCACCGGCCCGCAGGGCGCGGCCACCGTATTCGGGCCCCAAAAAGGT
GCCACCGAAAAAGACATTTCGCTTCTCGACGCCGCCCTCCACCACGCCTGCGCCCAACTG
GAAGTTGATGGCACAAAGCCAGGTATGGGCGCAGCCGGGGGCATTGCAATCGGACTGACG
TGGCTGTCCACCCTCATGCACGGCAACGACCAACAGATCCATATCCTCCCCGGCGCGCCA
CTGATTGCCCGCTCCAACGGAATCGAGGATGCGCTGCCAGAAACTGACTTGTTGATCACC
GGTGAAGGCCGACTAGATTCCCAATCGTTCACCGGAAAGGTTGTGGGCACCCTCCACGGT
TTAGCTAAAGCCCACGATGTGGATCTCGCTGTTGCGGCCGGCATCGTGGAAGGCGGTATT
CCCGATGATTTCCTAGCGGTAGAAATGATTAAATCCTCCGACGTTGCAGCACAATTACGT
GATGCAGGCCGAAGGATCGCTCAAGAATACGTAGCTCAAAAC

>RXN02104-downstream
TAGCGAAGGATCTCCACAGTCCA

RXN02107-upstream
AAGAAGTAGAGCTCAGCGATGAAGATTTCGCGGCAGGCCACGACCTAGTAAAAACCAAAT
ACGCCACCGAGGAGTGGACTAAGCGAGTTCAATAGTTTCT

>RXN02107
ATGGATCTGCACAAGGTAGCTGCAGCGCACGCGGCGACTCTTCCCCTGAGCACCAAAGAG
TTTCCTTTCGGACCCGAGCACGAAGTGTACAAAGTGCGGGGCAAGGTATTTTTGCTGCTC
ACGATACTAAATGATGAGCCGATTATCACGCTGAAATCAGACCCCGAGATTGGCGCTTCA
CTACGCAGTGGCTTCCCCACCATCCAGGCTGGATATCACATGAACAAAGTGCACTGGCTG
AGCATTAGCGATGGTGAACGGATCACGAAAGACTTCATCGAAGGTCTCGTGGAAGAGTCC
TATGAACTGGTAATTTCCACCTTGCCGAAGTATAAAAGGCCT

>RXN02107-downstream
TAACTTGGTTGCTTGCGGGTGGC

>RXN02108-upstream
AAGACTTCATCGAAGGTCTCGTGGAAGAGTCCTATGAACTGGTAATTTCCACCTTGCCGA
AGTATAAAAGGCCTTAACTTGGTTGCTTGCGGGTGGCAAG

>RXN02108
ATGGGTGATATGAAAATTACCCGCCACATCCATGCATGCGTTGAGATCTCACAGGGAAAC
GATCGAATCATTATTGATCCCGGTACTTTTGGCGCCCCAGATTTATGTGGCGCGACCATC
CTGGTCACCCACAATCATGCCGATCACGTTGATCCCGAGTTGCTCAAGCCCGGCATGACG
ATTTACGCGCCTCGATCAGTAGCACATTCAATTCCAGTAGAATGCCACATCGTGGAACAC
GGCCGAAACTTTACCGTTGGGTCCCTATCCGTTGAGGTTCTTGGTTCTGAACATGCGATG
CTCACCCATTCCATGCCGATCGCGGAAAACGTTGGATACTTAATCAACGGCCGAGTGCTC
CACCCCGGCGATACCTTCCAACCCATTAAAGATGTCGAACTCGCCCTGGTTCCTGTCAAC
GGCCCCTGGGTGAAAATGCTGGATGTGGAAGGCTATTTGAAGAAATTTCCACCAAAGCGT
TTCATCGGCATTCACGATGGCATTGTTAATGATCGCGGTTTGGCGATCAACAAGAAGTTC
TTAACGCATCTTGGTGAAACCTATGGCTCGGAATACTCGCCGCTTGAAGAGGGAGAGTCG
TTGGAAATT

>RXN02108-downstream
TAGATTCTTGGTTTAGATTCTTG

>RXN02114
TCCATCGGCTACGCCTGGACCACCGCATTTCACGCACTCACACCAGGCCTTGGCGGCATC
GCCATTGGTATTTGGCTGCTCGGTGGTGTGCTCGGTGGGTTGGTTATCCGCAAGCCGGGT
GCCGCAATTTTCGTTGAAGTAGTGGCCGCATGTGTCTCTGCAGCGCTTGCTTCACAGTTT
GGTATCTCCACCATTTACTCCGGCTTGGCGCAGGGAATCGGCGCTGAAATCATCTTCGCG
CTGTTCCTCTACCGTCGCTACAGCCTGCCCACCACCATGCTTGCAGGTATGGGCGCAGGT
GGCGGCGCAATTTTCCTGGAAATGTTCTTCTACGGAAACCTCGCAAAGACGATGTCCTTC
AACATCATCTATTCCACCACTGTCCTTATTTCCGGTGCGATCCTTGCCGGCCTGCTCAGC
TGGTACCTGGTCCGCGCGTTGGCGAGGACTGGTGCACTTGATCGTTTCGCCGCTGGCCGC
GAGGTA

>RXN02114-downstream
TAAATGACCACCGCACTTGGAAC

>RXN02121-upstream
CCGGGAAATCTTCAGGCGTCTCCTCCCATATGCTGCTGACAAATTCCAGAACAGGATCGT
TGGGATACCTTCGAGACAAACTTCCGAAAGCTCCGCAACC

>RXN02121
ATGATCACCTCACCATTTGAGCGCGAGCTGAAGCTGCTCAACGAGGGGGAACTGGGTATT
GTCCAGCAGTTGGTGGAATCAAGCAACATCGGATTCATCGTCGATCTTGAATTAGATGGC
GATTATGGGTGGGCGGTCTACAAACCGGAATTGGGGGAGCAACCCCTGTGGGATTTCCCT
CCTGGCCTGTACAAACGTGAACGTGCAGCCTTTGTGATCAGTGAGTTTTTGGGTTGGAAC
ATCGTGCCTCCAACGGTGATCATGCACGATGCCCCGGCTGGTGTGGGCTCGGTGCAGTGG
TTTATTGAAAACAATGGCGAACACTATTTTCCACTGTTTGACACCCGCGCTGACCTGCAT
CCGCAGTTTGTCCGCATGGCTGTGTTTGATCTGTTGTGCAACAACACTGACCGGAAAGCG
GGCCATGTGTTGTTAGACGGCGATCATATTTGGGGCATCGATCACGGGTTGTGTTTTTCC
GTCGAACCGAAGCTGCGCACGGTGATTTGGGATTTCGCAGGCTGCACCATTCCAGATGAC
TTGGTGACAGATGTTGAGCAGCTTTTGGAGGACGTCCCGGAAGAACTTCATCAGCTTCTT
CATCCCGCAGAAATTGATGCGCTGCAGCGCCGTGCCTCAAGAATCAGCAGGTTACCGTTC
CTTCCGCAGGCGAAATCGCATCGTCAATTCCCTTGGCCACTTGTT

>RXN02121-downstream
TGAGTAGGCTGGCGGGCAGGTGC

RXN02138-upstream
TCACTCGCCGGAGATCCGTAAAAAGGGGAGTACACTGCAAGCCTATGATGTCCCGGCCTA
AAAGTAATTCAAAGGGCCAACAGTTAAGGAGACTAAAGCG

>RXN02138
ATGACCGCTCCATCAACCAACACCGGTGTTATCTTGACCGAGTCCGCAGCGTCCAAAGCT
AAGGCACTCATCGATCAGGAAGGCCGCGACGACCTCTCTCTGCGTATCGCCGTTCAGCCT
GGCGGCTGCTCTGGCCTTCGTTACCAGCTTTACTTCGACGACCGCACCCTTGATGGCGAT
AAGGAAGACATCGTCGGTGGCGTTCGCCTTGTCGTTGACAAGATGAGCACCCCATACTTG
CTCGGCGCTCAGATCGACTTCGCTGACACCATCGAGCAGCAGGGCTTCACCATCGACAAC
CCAAACGCAGGCAGCTCTTGCGCTTGTGGTGACTCCTTCAAC

>RXN02138-downstream
TAAAGAGATTCCGTTATGTAGGA

>RXN02151-upstream
ATGAGCGCATCGTCTTTTTTAGGAGTTGTCCGCCACCGTGAAAACTGGAAACTTAAACCC
AGCCCCACAGCAGGTGACGGCTCCCCAGAACAAGGCTCGT

>RXN02151
ATGGATTGGCCAGACATCGCCAAGGGAATATCCATCCTAGGTGTCGTGTTACTACACGTG
TCGTTGGCAATTCCAGGTGGCCAGGACACCATGATGTCCCACCTGAACGCACTGCTTGAT
CCACTTCGGATGCCATTATTTTTTATGGTGAGTGGATTTTTTGCAGTTAAAGTTCTGAAT
CAAAGCTTTGGTGAACTTTTCCGCGGGCGACTGTGGTTCTACCTGGTTCCATATTTGCTG
TGGACTCCAGTGAATCTTTATCTACACCGCCTCGAGGGCACAGTTTTTACCGGTAGAGCA
CCGGGAACATGGGAATGGTACAGCGGCTCGATGCTCTCGGCCACCAATATGTACTGGTTC
CTCTACTTCTTGGTCATCTTCAACCTATTTTTATGGGCAACGAGAAAACTCCCAGCTTGG
GCAATTGTGGCGTTGGTGGCCTCACTGTGGCTACTTATGCCGGCTTATAGCGAGATTGAG
ATTCTACGCAAGTCCATTATTTACTTGCCTACATTCCTCATTGGCGCTTACTTCCGCCCA
CTGATTTCGCGTTTTGCAGAAGCCGCAACAAGGCCAAAAGCAATAGTGTTTGCAGCGGTC
CTTTATGTCTCGGGACTTGCTTTGGGCGTGATCTCAAATGGGCTGCGCGACAGCGAAAAC
CATGGCGCAAGCGTGCTGTGGCTGATGAACCTCCGCGATACTTTTGCTCATGCACTCGGC
GGCAACCTCACTGGATTCGATATGGATCACCTTCCTGGAATGATCATTCGGATTGTTTCC
CTGCCTGCAGGAATTGTGTTGTGCGTATGGCTTGGCCGAATAAAGCCAGTAGGGGAGTTT
TTGAAACTTATTGGTAGGCACACCCTTCCCATCTACATTGGGCATGCAACAGGACTATCG
CTGATTTTTGGTTTCGGCTTGCGCTGGAATTTCATGGAGATTGATAACTTCTCTGACAGT
TTGTGGCACCACACCAATACGTGGATGGTCATCGCGTTTGCCTGCGCGATGCTCGGCGGG
TACCTGACCTATCTGATCTCGCGAGTTCCAGTGCTGGGATGGACTCTTGTTCCCCCTAAA
CTGCCAGAACCAGATAAAACTCCAGCTAAAGCACAAGCTGATTCTCACGTTAAAGCTCAG
TCTGCGAAGCCTATGAATGCTTCTACCTCTTCTAAGACGTACGGTATA

>RXN02151-downstream

TAACTGAAGCATAACCTGTGTGA

>RXN02169-upstream
GTTAAAGGTCGAAAAATCCCACCCCTAGCCCTTTTAAATGAGTGTTGTTATTGTTAACCA
CTGTTACTGGTGGGATTAATACTTATTTTTGGGAGAACTT

>RXN02169
TTGGACATGCAAATAAACCGCCGAGGCTTCTTAAAAGCCACCACAGGACTTGCCACTATC
GGCGCTGCCAGCATGTTTATGCCAAAGGCCAACGCCCTTGGAGCAATCAAGGGCACCGTC
ATCGACTACGCAGCAGGCGTCCCCAGCGCAGCATCCATTAAAAATGCAGGGCACCTTGGA
GCTGTCCGTTACGTGTCACAGCGACGCCCCGGCACTGAATCCTGGATGATCGGCAAGCCA
GTCACACTGGCAGAAACCCGAGCTTTTGAACAAAACGGCCTCAAAACCGCATCCGTCTAT
CAATACGGAAAGGCAGAGACCGCCGATTGGAAGAACGGCGCCGCAGGAGCGGCAACCCAC
GCTCCACAGGCAATTGCGCTTCACGTGGCAGCTGGTGGCCCTAAAAATCGCCCCATCTAC
GTGGCGATCGACGACAACCCAAGCTGGTCTGAATACACCAATCAGATTCGCCCCTACCTC
CAGGCATTCAATGTTGCGCTGTCCGCTGCCGGCTACCAGTTAGGTGTCTACGGCAACTAC
AACGTCATTAATTGGGCTATCGCCGACGGCCTTGGAGAATTCTTCTGGATGCACAACTGG
GGATCAGAAGGAAAGATCCACCCACGCACCACCATCCACCAGATCCGCATTGATAAGGAC
ACCCTCGACGGAGTCGGCATCGACATGAACAATGTCTATGCAGACGACTGGGGTCAGTGG
ACCCCAGGCAACGCGGTTGACGATGCCATCCCCACCATTCCTGGAAACTCCAACACGGGA
ACAGGTACTGGAATTGATGCTGACACCATCAACCAAGTAATCAAGATTCTTGGCACCCTA
TCTAGC

>RXN02169-downstream
TAAACTAGCCGTGCTGACTCACA

>RXN02180-upstream
GTTTCAGCTAAAAGAAGAATCCTTGCTAGTGGAATCAGCTGAGTTTTCCACGAGTTTTCC
AGCTTTCTCACAACTTGAATAGAAATTGAGGTATCCGGCA

>RXN02180
ATGACGTCAGGGAAATCAACGAGTACTAGGGGAGCCCTAGACCGGTATTTCAAAATCTCG
GAGCGAGGATCAAGCATTGGCACGGAAATCCGTGCAGGTGTGGTCACATTCTTCGCGATG
GCCTACATCATCATCCTCAACCCCTTGATCCTTGGCACCACCCCTGACGTAGAGGGCAAC
ACCCTAGGCATCGCACAGGTTGCAGCGGCAACAGCGCTTGCCGCTGGTGTCATGACCATC
GCGTTTGGTTTGATTGCGCGTTATCCATTCGGCATTGCTGCTGGCCTGGGAATTAACACC
ATGGTCGCCGTGACACTGGTTTCAGGTGAGGGCCTGACCTGGCCGGAAGCAATGGGACTT
GTGGTCCTTGACGGTGTGGTCATTGTTATTTTGGCTGTGTCCGGCTTCCGTGTTGCTGTG
TTCCGTGCGATCCCAGCATCCATGAAGGCGGCCATCAGCGTGGGTATCGGCCTGTTCATC
GCCATGATCGGCCTCGTGGATGCAGGCTTTGTTCGCCGTATTCCAGATGCTGCCGGTACT
ACTGTGCCAGTGACTTTGGGCATTGATGGTTCCATTGCGTCTTGGCCAACGTTCGTGTTC
GTTGTCGGTGTTCTTCTCTGTGGCATCCTTGTTGTCCGTCGAGTTCGCGGTGGACTGTTT
ATCGGCATTTTGGGAACCACCATTTTGGCGATCATCGCAGAAGCAATCTTTGATTCCGGT
GCGTCCTTTGAAAATGGTGAAGCAAACGCAGAAGGCTGGTCACTCGCCGTTCCTGGTCTC
CCAGACTCCTTCGGTGGCATCCCGGATCTTTCCATCGTCGGCGCAGTTGATTTGATCGGT
GCGTTCAGCCGCATCGGTGTGGTCGCCGCGACCTTGCTGATCTTTACCCTGGTCCTTGCA
AACTTCTTCGACGCCATGGGCACCATGACCGCTCTTGGTAAGCAGGGCAACTTGGTTGAT
GATGAAGGCAACCTTCCAGACATTAAGAAGGCACTGGTTGTGGAAGGCGCAGGTGCCATT
GTCGGTGGTGCTTTCTCTGCATCCTCCAACACCGTGTTCGCTGACTCTTCTGCAGGTGTT
GCAGACGGCGCACGAACCGGCCTTGCCAACGTGGTCACCGGCTCCTTGTTCTTGGCTGCC
ATGTTCTTGACCCCACTGTATGAAATCGTCCCCATCGAAGCAGCAGCACCAGTGCTTGTA
GTTGTTGGCGCGATGATGATGGGGCAGGTTACCGAGATTGATTTCTCCAAGTTCTACATC
GCATTCCCAGCGTTCTTGACCATTGTGATCATGCCTTTCACCTACTCCATTGCAAACGGC
ATTGGCGTTGGATTCATCATGTACGCCATCATGGCTGCAGCGGCAGGCAAAGCAAAGCAA
GTGCACTGGCTGATGTGGCTGGTCGCTGGACTCTTCGTCGTGTTCTTCGCGATTGATCCC
ATCATGGAAGCTGTCGGC

>RXN02180-downstream
TAATGACAACGCGCACGGTAATT

>RXN02185-upstream
CAACTCCTTGGGGTGAAGCCAGACATCCACTGGCAGAGCAACTCCTCCGCTCTAACCCGA
CAGCTAACCTCGACGGCGACAAATGAGAGGAAAACTTTTC

>RXN02185
ATGGGACGTCACTCCACTAAGACTAGCTCCGCGTTCACCAAGCTCGCAGCTTCCACCATC
GCTTTCGGTGCTGCTGCAACCATCATGGCTCCTTCTGCATCTGCTGCACCTGATTCCGAC
TGGGATCGCCTCGCACAGTGCGAGTCCGGTGGTAACTGGGCAATCAACACCGGTAACGGC
TACCACGGTGGTCTGCAGTTCTCCGCTAGCACCTGGGCTGCTTACGGCGGCCAGGAGTTC
GCTACCTACGCATACCAGGCAACCCGTGAGCAGCAGATCGCTGTTGCAGAGCGCACCTTG
GCTGGTCAGGGCTGGGGCGCATGGCCTGCTTGCTCCGCTTCCCTTGGACTGAACTCCGCT
CCAACCCAGCGTGACCTCTCCGCTACCACCTCCACCCCAGAGCCAGCTGCAGCTGCACCA
GCTGTTGCTGAGTACAACGCTCCTGCAGCCAACATCGCAGTTGGCTCCACCGACTTGAAC
ACCATCAAGTCCACCTACGGCGCTGTCACCGGCACCCTCGCTCAGTACGGCATCACCGTT
CCAGCTGAGGTTGAGTCTTACTACAACGCTTTCGTCGGC

>RXN02185-downstream
TAAATCTAGCTGCACTTTTTAAA

>RXN02186-upstream
TCCAACCACCCCTTGAGGGTGGGGATGGGGGAGTCTTTTTTCATGATGTTGTTAAGTTTA
AGCCTTGTTGAGGTGACTTTTGTTCCCAGAGTTTGAAAGA

>RXN02186
ATGTATGACATGGCAAACGTAGAGAAGAAGCACTTCGTCGATCCGGCATGGCCGGAGCAC
AATCCAGCTGACGGACACGTCGTTACTGAACTCATCTCCAAGGTCGCAGGCGCGTCCAGC
CCATGGGGCGATGACAAGGAATTCCCAGTTTCTGCAGAAGAGACCGGATACGTTCACCCG
TACACCCGGATCAACCGC

>RXN02186-downstream
TAAGAAACTTAAAAAAGAGGCAA

>RXN02207-upstream
GAATCGGTGACTTTGCCAACACCAATCACACAAGCCCTTGATGATGTCTCCCTGTGACTT
GGTCCAATTACATTCACTGGTAATCTGAAACCTTGTGAAT

>RXN02207
ATGCGCCGTCGATCCCGTGTGTCCCGTTTGCTTCCCGCCACAGCTTTGCTGGCCTCAACT
GCACTTCTTTTAAGTGCATGTACGCAAGGGGTAACGGACTCCCCGGATATGGGCAAGGCA
ACTCCCGCTGTCTCCCCCGCAGCAAGCAACCCGGATGGCCAAGTAATTGAGTTCGGCAAC
ATCACTGACATGGAAGTCACTGATGGTGACATCCTCGGTGTACGCACCGAAGACGCACTC
GCTATTGGTACAGTCTCCGACTTCGAAGCGGGTAGCCAGGTGGAACTGGACGTCGATAAG
CAATGCGGCGACCTGACCGCAACCGGCGGCACTTTCGTGCTCCCCTGCGCCGATGGCGTT
TATTTGATTGATGCCAAGGACCCGGATCTGGATGAGTTGCGTGCAACTGACAAGCCAGTC
ACGGTGGCAGCCTTGACCAGCGATGATCAGCTTCTGGTGGGCAATGGTGAAGATGAAGAA
CTCACCATCTACCGCGAGGGCGAAGAGCCAGAAACCTTCACCGTCGCGGGTCCCAATACC
CAGCTCATCGCCGTTCCTGTCATTGATCGCCACGACGCCGTTGTGCGCACCTGGAACGAA
AACACCACGATTCAAGATGTGGACTACCCCAACGACCGTGAAGGCGCGACCCTTCGCGTG
GGACTCGGCGTTGGTCAAATGGCTGGTGGCGAAGACGGCCTGCTGGTGGTCTCTGATGAA
ATGGGTGGCCAAATTGCCATCTACAACGCTGATGATGTCATCCGACTTCAAAATGACCGC
CCCCACCGACGAGGAACC

>RXN02223-upstream
CTTGCTTTTGAGGGCCGCTACGCGCAGCTGTATCAACGATGGAGTGCTCAATAGTTCAAA
TCCACCACAAACTCTAGAGATTTGGGGTAGAAACGAAGAC

>RXN02223
ATGAGCACCTACCAAGACGATCGTTTCCCAGGCCCAGACCCCTACGCACCGCTTGGTGAA
AAGCCAAGCTTTACCCTCACCTCCACCGACTTGGAAAACGGTGCAAAGCTGGCCGAAGCC
CAACTCGGTGGCACCGATATTTCCCCACAGCTGTCCTGGTCAGATCTTCCAGAAGGCACC
AAATCCCTCGCGATCACCTGCCTCGACCCAGATGCCCCAACCGGCGCTGGTTTCTGGCAC
TGGGCAGTGTTTAACATCCCCACAACTGTCACGGAGATCCCCACCGGTGCTGGCGATGAA
ACCCTCGGCGGCATCGAAGGCGTAGTTTCCCTCAAGGGTGATTCCGGCAAGCGTGGCTTC
TACGGAGCGCAACCTCCAGCTGGCCACGCACCGCACCGTTACCTCTTCGCAGTTCATGCA
CTTGATGTGGAAAAACTCGACATCGCCCCCGACGCTACCCCCACTGGTCTAGGCTTCAAC
CTGTATTTCCACACTCTTGGC

>RXN02226-upstream
CTGACACCTCCTATGGCACGCGGTATGTTTAATAAACGTAATTCGAGTTTCGGCGGCCGT
GTCGCGCGGCCAGGACGACCCTAGCTTTTAAGGACCCACC

>RXN02226
ATGACTGAGAACCAGACTCCCAGCTCCACCTCTGCACCGAAGCCGGGACCTCGCCCGGGC
CCACGGCCAGGACCCCGACCTGGGGCTCAGGTTGCTGCAAAGAAAGCTGCGGTTGCTACA
CCTGCGCCGATCGCCAAAACTTCTAACGATCCTGCAAAGTTTGGTCGCGTTGAGGCAGAC
GGATCTGCATATGTCACCACCTCTGCTGGCGAGCGTCTGATTGGTTCTTGGCAGGCCGGC
ACCCCTGAGGAAGGTCTTGCTCACTACGGCGCCCGTTTTGATGATCTGGCCACCGAAGTT
GAGCTCATGGAACAGCGCCTAATCTCCCACCCTGATGATGCGACCTCCATCCGCACGAAG
GCTGAAGAACTCAAGGCAACCCTGCCCACCATCGCTGCGATCGGTGACCTTGATGGCGTT
GAAGCTCGCCTGTCCAAGATCATCAACAACTCCGAGGAAGCCAACGAGCGCGCCAAGGAA
CAAAAGGCTAAAAACCGTGAGCGCGCAGTAGCTCGCAAGGAAGAGCTCGCTGTTGAGGCT
GAAACCTTGGCAGAAAACTCCTCCGACTGGAAGGTTGCTGGCGACCGCATCCGCGCCATC
CTGGATGAGTGGAAGTCCATCCACGGCATCGACCGCAAGACCGATGATGAACTGTGGAAA
CGCTACTCCCGTGCGCGTGACTCCTTCAACCGTCGCCGCGGCGCACACTTCGCAGAGCTG
GATCGCACCCGCGCATCTGCACGCAAACTCAAGGAAGAACTCGTTGAGCGCGCCAATGCT
CTCAAGGAATCCACTGAGTGGAACGACACCGCCCGCGCATTCCGCGATCTCATGACCGAA
TGGAAAGCCGCCGGCCGCGCACCACGCGAAATCGACGACAAGCTGTGGGCAGCATTCAAG
GGCGCCCAGGACTACTTCTTTGATAAGCGCAACGCCGTAGCCAAGGAACGCGACCAGGAA
TTCGAAGCCAACGCAACCGCAAAGCAGCAGCTCATCGACGAATACGACGCACAGATCAAC
CCCGAGCAGGGCCTCGATGGAGCGCGCAGCAAGCTC

RXN02238-upstream
GGCGCTTAGCCAAAACATAGAGCGGTAGGGTATGCTTATCCGATTGAGCAACCTTTCCCG
CTCTTAACACTACTGTCCATATACTTTTGAAAAGGTGTCA

>RXN02238
GTGACCAACGTGAGCAACGAGACCAACGCCACCAAGGCCGTCTTCGATCCGCCAGTGGGC
ATTACCGCTCCTCCGATCGATGAACTGCTGGATAAGGTCACTTCCAAGTACGCCCTCGTG
ATCTTCGCAGCCAAGCGTGCGCGCCAGATCAACAGCTTCTACCATCAGGCAGATGAGGGA
GTATTCGAGTTCATCGGACCATTGGTTACTCCGCAGCCAGGCGAAAAGCCACTTTCTATT
GCTCTGCGTGAGATCAATGCAGGTCTGTTGGACCACGAGGAAGGT

>RXN02238-downstream
TAAAAGACCTTATAACTTCACAC

>RXN02254
ATCGCCGTTGCCGAAGAAGGCGGATTGTGGGAAAACCTCCTGCAGCACCGCTTCGGTGGA
CATGGTGCGCTAGCTGGTCACGCCTTGGGAAACCTCGTGATCGCGGCGTTGACCGACATT
TTGGGCACCTCCCAGCATGCGCTTGATCAAATCGCTCAACTCGCTGGAGCCAAAGGACGC
ATCATCCCGGTATGTGCTGAACCTTTGGATCTTGAAGCGGAAGTATCAGGTCTAGACTCT
GATGCTCGAGTCATGCGTCAAGTTCGTGGTCAAGTGGCGGTAGCTGCAACCCCCGGGCAG
GTGCGACGCGTTCGAATCATTCCGGACAATCCAGAACCGAACCCCGCTGCCATCGAGGCC
ATTCTCGATGCAGATTTGGTCACCCTTGGCCCAGGTTCCTGGTTCTCCTCTGTGATTCCA
CACATTTTGGTCCCAGGGATCGTTGATGCCTTGGCGCAGACAAAAGCAACCAAAACCGTG
GTGTTAAACCTGACGTCCGAGCCAGGGGAGACCGCGGGATTCTCTGCAGAACGACACATC

CATGTGCTCCGCCAGCATGCTCGAAACCTTCAGGTTGACCAAGTCATTGTCGATGCCAAG
ACACTGTCCTCACAAACCGAACGCAATCATGTAGAACGAGCTGCTCGCACCCTTGGTGCA
GAAGTCTCCTTCCATGATGTCCAGGCTGAAGATGGCCGTGGTCGATTCACCAGTATTCAC
GATCCAGCAAAGCTGTGTGCAGCGTTGCTGGCAAGTTTTGCTGGAGCACGAAAGCGT

>RXN02254-downstream
TAAGGAGTAGGCGTGTCACTGAC

RXN02271-upstream
CACTCCCCTATCCTAAGCCACATCTCGGTTTATTAAACTGTTAGTGAATTCTCACCCGCA
ACACTGGTGTATTTCAGTTACATCCGTATGGTTATTGGTT

>RXN02271
ATGAGCTTTCTTAACTCTGCAAAAACCAAGACCGTAGCCCTCACCGCAACCTTCGTTGGT
GCAGCAACCCTTGCAACTCCTGCAATCGCATCCGCTGACATCGTCGACAACGCCCTCGCA
GCCCTCCCATCCGGTGAGATCAGCTGCTCCCAGGCTGAAAAGTACTGGACCACCGAAGCT
GATTACAACAGCAAGGTTGCACAGGCCAACGCCTTGGCAATGTTTGACTCCCGCGGCCCA
CAGATCCAGGCAGCTCTCGCACGCGTTGACGAAGCAGCAAACCGCTGCGGACTCAAGGGC
GGCACCGTAGCTGCGCAGGCTGAGGCAACTGAGGCTGCGCCTGCCGCTCCAGCACCTGCA
CCGCAGGATAACACCGGCACTTCTCAGACTGCCCCTGCCCCAGCAGCACCAGCAGCACCA
GCAGCTACCCCTGTGGTTAACCTTGCACCTGCAGGATCACCAACTTTCACCATTGAAGTT
CCAGGAGTTGGCGGGGTTCAGCTGCCAGATCTATACCAAATCGTCCAACAGTTCTTGGCA
CAGTTCGGAATCAAGATC

>RXN02271-downstream
TAAATCTATTCACATCCCTTAAC

>RXN02279-upstream
GGTAAGAGGGCATTTTCCGATGCGCAGCGATTCTTGCTCAACGCCGACGAGCTCGCGGAG
CTTTCTGATTATGAGCGTCTGGCTTATGCCATCACCTTGC

>RXN02279
TTGATCAGCCTGGAAAAGAAGCAGAAGGACGCGAACTTTTTCCTTTCGGAGCTTCGCCGC
CAGGGCTACCGCGCTGTCGATTTCTTGGAATCCCAGACTGTTGACCAGCTGAATAACCCC
GATGTCCAGACTTACCTCACCGAAGCGGAACTGATTCGCGATGACTTGAGGTCTTGGGCA
GTCATCAATCAAATGGCATTGGACAACATCGATCTTGTTCCATACGGCGAGGAAAACGAC
GAGCCACTTGCAATCGCCCGCAAGATCATCGAGGAAACCGCTTCCCATCCTGAGCTGAGA
TTCGAAAACCTCGAGGCCCAGTTCTCCGAGTTCACCATCTTGCTTGCTCAAAGCCCGGAG
AACCTCGACGTAGCCCGCTACCAGGAGCTTCGTACACAGGGAAACTTTGTTCAAGAACTC
GCCTTGGACAGCATTTTCGGCCAACATGCCGTTGTTCAAGACACCGGAAACGGCGAAGCC
ATCCTAGATGAAACTATCGGGTACATGATCGGCGCCGGCATGCGTGAAACCACTGCCCGC
ACCGCCAGCCAGTTCGCGCAGCTTTACTCATTTGTGGGCAGGCAGGAACGCTCCATTGAA
ATGGCACGACTCGCTTTCGAGGAACTTCAAGCGGCAGGACTTCCCCACCGTGAGGAAGAA
CTGCGATTGGGCATGCAACTCGCCCAGGTTGAACCAATTGAAGCCCGCGAAATCCTGGAA
AAGCTGCTGCTGCCTAAATTCGAGCAGAATCTGACACTTGATGAACTTGAAACTGAAGCA
CTCCTTCCTTTGGGTGCTACCGTTGCTATCCACGACCCCCAGGCTGCCGCAGCAATTTTG
CGCCACGCTCGCGAAAACGCCGCAGGGTTCGGCAACTTCGAACTCGCAGTCCAAGCGATG
ACCATGATCACGGATGTCCTCTACACCCAAAACATGCACGAGCAACTGCTGGAGGAGCTC
AACCACTCTCTCCCCTATGCTCAAATGCTTGATGATCAACACCAAGCTGAACTGAAACTG
CTGGACAGCATCGCCATCGTCCAGGCAGACCTCGGTTCCACCGAAGCGCTGGAAACCCTG
GGCACCGCAATGGGACTCGCAGAAACCACAGCTCAGAAGCTATACGTGCAGGAATCCCTC
AACCGCGCATACTTCACTTTTGCCCGCCCTGAAGATTGCATCAGCGGAGCAGCCGACGCT
TCTGCCCTGGCCATGCAAAACGATGACCCTTCCAATGCAGCTGCCCAGTTGGAGCAGTGT
GCACAGTACTTGTTCCAATTGGGCCACGAAACTGACGGCGCAAGCCTGCTGGAATCTGCA
TTCAGGGTTGAAGGCATCCCCACTGAGCAGGCACTGTACTACGCAAATGCACTGTCTTCC
ATCTATGAAGATTTCGGCGATTCCGCGAAGTCGCAGTACTGGGAGCAGCAGGCGCAGGAA
AAGCAGCAGCTTCTGGAG

>RXN02279-downstream

TAACGGCCGTTTAAAGAGTCGAA

>RXN02296-upstream
GCATCATTTGTGTTGTTTAAAGTATATGGCTGTTGAAGTGCCATTTTCGCGGATTAGCAT
GGGAATCACCAGTATTTCTGGACGGTTAAGGATGATTCAT

>RXN02296
ATGCGTAATCAAACAATCGCTGCGGTCGCAGCTTTGGTCCTGCTCACCGCCGCCACGCCC
GCGATCGCTGCCACCCCGGCGACAGCTGGAAACGGACTCTATTCCATTGACATGGGCGAC
GAGCAAAAGCTTACCTGCGTGCTTTTCGATGAGCCCTCCACCGAAGCGCACGTCGTCGCC
AGCTGTGCTGCGACTTTCCCGGTGACCTGGAAGCTTCTCGACGGCGCTCACGAACAAGCC
GCGAAACTTGAAATCACCCAGGCTCAAGACGGTGAACTCTCGGTGACAGCCAGCAAGCAG
CCGTTGATCACCACGATGATTGCGCCCACCAGCATCACTAAGCCCATCACTGTCAATAGG
CTTGTGGTTGTTCCTGGTGAGAATGAGGTTCGCTTTTATGCTACCGATCCTGATGTTTTA
CCAGTGCTGATCACGCCTGACTCCTATGAAGTGTTGACCGATTCCGCTGCTAAAGTGAAA
GCGACATTA

>RXN02296-downstream
TGAAATAAACGTGGATCAAGGAG

RXN02300-upstream
GGGTCATTCCGGTGAACACGGATTTCGCGCCGGTGAATCTGACGGTCAGCCAATTGCGGG
CAATGCTGTCCAAAGCGGAGCGTAAAGATAAGGATCAGAA

>RXN02300
ATGAAAACTTATGCAGTACTAATTGCGGTGGCAGGGTTGGCACTTGCTGGGTGTAGCTCG
TCGGCTCCTGGAATCTGGCGTGCCACTGAACCCGCAGATGCCTACCTTGAAATAGCCGAT
GACGGCACGCTGTCCGGAACCGACGGCTGCAACAGACTTTTTGGTGGCTGGGAAAAAGAC
GGCTCTACCATCACTTTCGGCGCCATCGGTATGACAGAAATGTACTGCGAAGGCGTCAAC
GATTGGCTGTCCCAGATGCACACCGCCACCGTCACCGATGCCACCATGACCATTTTCAAC
GAGGCCGGCAGCAATATTGGCGAGCTAAAACGC

>RXN02300-downstream
TAAATGCTTCTCGACGTCAAAAG

>RXN02301-upstream
GCTTCGCATATGTCTGGATCTTATTGGATGTATGAGTCAGAGATCAGGGAGATCGCGCAC
TAACCGAACCTGGCCAGTGCAACAGGATTATGTTTAAAGC

>RXN02301
ATGGATCTTGCACTGGCTCAGGTTGATTCCACCGTTTCGGGGCTTTATGACGCCCTCGAT
CTCATCGGCGTGCTGCTGAACGGAATAATCGGTGGAACGATCGCCAGGCAACGAGGCTAT
GACATCATTGGCTTTCTGTTCCTGGCGTTATTTTCTGCGCTGGGTGGCGGAATGATCCGT
GACATGCTGATTCAGCAGGGGACTGTCGCGGCGATCGATAATCAGATCTACCTTGCGCTC
GCGTTTTCTGGCGCGCTGATTGCCATGGCGGTGAACTTTAAAGGCAGGGTGTGGGAGCTG
TTTAAAGTTCACGGCGATGCCATTGTGTTGGGCGTCTGGGCGGTGACGGGTTCCGTGAAG
GCGATGAATGCGGGGGTGGCTCCGCTGCCGAGTATTTTCATGGGCGTGCTCACCGCGGTG
GGTGGTGGCATGGTGCGTGATGTGGCTACTGGCCAGACGCCGACGATTTTTGGTGGCGGA
ACTCTTTACGCTGTGCCTGCGACGCTTTCTGCCACGTCAATGGTTATTTTTCATAGCTTT
GACCAGGTAATTCTGGGTATGATTATTTCACCGTTCTTGGGTATCGCGTTGGCGGTTACT
GCGTATTGGTGCGGTTGGGTCATTCCGGTGAACACGGATTTCGCGCCGGTGAATCTGACG
GTCAGCCAATTGCGGGCAATGCTGTCCAAAGCGGAGCGTAAAGATAAGGATCAGAAA

>RXN02301-downstream
TGAAAACTTATGCAGTACTAATT

>RXN02302-upstream
GGCCAGGTTCGGTTAGTGCGCGATCTCCCTGATCTCTGACTCATACATCCAATAAGATCC
AGACATATGCGAAGCTAATGAAGGAAACGAGGAGCTGATA

>RXN02302
GTGGCAACAAATCGTACATCTTCCGCTGGTGTCATCACGTCTGTTCTCGCATCCGCTTTG
TTCGGAGCGATCTTTTTTCATCTCTGGGGCGATTGAGGCAAAGGCGGAAACACTTGTTGCT
TGGCGTGTCCTTCTAACAGCGGCATGCTATTTGCTTGCCCTTCTGCACCCTGCTGGTCGG
AAGGTGTTTAAGGAATTTTGGGACACACTAAGGTCCCAACCTCGTCAAATTCTGTACTTT
ATCTTCCTCGTTGTACTCATCACGCTTCAGCTGTGGCTGTTTTCTTGGTCGCCTAAGAGT
CATGCTTTAGATGCCTCACTTGGTTACCTGTTACTGCCCATTTTCCTAGTAATTGTGGGG
CGGTTTTTCTTCGCTGATTACATCACCAGGCTGCAGTGGATTGCGGTGGGAATCGCGCTG
ATCGCAGTAACCTTGAAATTTGTCATTAGTGCGCAATTATCGTGGGTAACTTTTGCCATC
GCTGCGGGTTATGCACTGTATTTTGCGCTTCGTAAATACTCGGGGCTGAACAACGCTTTT
GCTTACGGCGCAGAAGTTTTAGCGTTAAGTCCCCTGGCATTTTTCATGCTCGCCACTGTC
GAGGATCCGCTGTCTAACGCCATGTTGTCAATGGTTATTCTGGCGGGCCTCGCTGGCGCA
TTAGCTATGGCGTTGTATCTAGCCGCCTCAACTCTGCTTAGTATGCCGATGTTTGGCCTG
CTCAGTTATGGTGAACCAATCTTGCTGTTTGTTGCAGCACTATTACTTGGTGAAACGTTG
AATCTCAGCGACGCCATTGTCTACTCACTACTGGCGTGCGCCCTGGCGTTACTGGGATTT
GATGGGATACGAAGGTCTCGAAAAAACCTCGAGACCGAT

>RXN02302-downstream
TAACTTCTGCTCAACTTCCCACC

RXN02303-upstream
GCCCGGGCCGAAATCATTCCAATCTCACCCCCACCCAAAACACTGTTGATATTTTCACTT
TCCAACCAGCGACGTGAGCGCACGCACTAAGGTTGTGCCC

>RXN02303
ATGGCTGAAAACAACACCCCACAAGAAACTGAACAAGATCAGGAAGCACGCTTCCGTGAG
GAGTTCGAGGTTGGCGGTAAGGATCGTCAGCTTTCTGAAGAAGAACAGCTGGAGCAGCTC
GGATCGTATATTGATGCGCACTACCCTGTTCCAGATTTCACGCCCCCTTGGGCAGGTGGC
GCCGGCGATCCTGATCCAGCAGACCGCTATATTGCACATCTTCCCGATCGCACCACGCAT
ACTGCGATGATCATGTTGGGTTCTGGCCTTGATCATTCCATGCCGGGTGTCGCATTTATC
GGTGGTGTGAGCGTCGATGACGTCCCGGAGGTCGGAGGCGCGATTTTCCACCCGTCGAAT
CCGACGGGCCGCTGGGCTGTATCGTTCCACAGCGGTGGTTGGTGGCGCGGTTCCGGTGAT
GCGTTGGAGTTCCAGTGGCGTCCAGAGGTCGCGGCAGCTGCGGAATTGTCCGGCACAACC
ATCCTTGACCTGGACTATCCGCTGGCCCCAGGCCATAACCTCCACGATATGAATGAGGTT
GTGGGCAAGGCGGTCGGTTACGCCCGCCACCATAATCCGGTGTCGATCACGGGTTGGGGT
TATTCCTCGGGCGCGGCGTTAGCCGCGATTAATGCATCGCTTTTCGACGCCCTGGTCCTC
ACCTTTCCGGACCTGGGTAGCGTCGAGAAGCTCCCTGCCGAAATTCGTGGAGACGCTGTA
GTGCCCGCGGCGGCTGCGTGGCCGACGACCTTTGTGCAGATCGCGGCGCAGGATGAGATC
GCGGAGCGGCCAGGAGAGCTTGGCGACGCGACCGTGAAGGAATACGTTTCCCGCCACCGT
ATTTCCACACCGAAGGTCGCGCGCGAAAAAATCACCGACGTGGCGGAGTTCCTTAAAACT
GTTTGC

>RXN02303-downstream
TAATGTGCCAGCAGGTTGTAAAT

>RXN02307-upstream
TTTTGCATTAACCCCAGGTAGGGGCATTGTCGCAAAGCCCAACTACAGCAAGGTGCGTAC
GCTGGTGGCCAACTGAATACGTTTGAGGAGAAGGTTTTCT

>RXN02307
ATGAGTGGCACCGCCATCATGTACGACACGACAGTTGTTCCATCGAAGAAAGAAATCGCG
CAGGCTTGGACTGGTTATGTGGATCTTCAGGGAAGCTACCGCCTGGTAGATACGGTGGAT
GGGGAAGTTGGCGTTGAGGTGCTGATTTCCAAGGATCGGGAGGGGCGTTTACTCCAGATT
CCGTTTAGTTATCGTTCGGCAGAGATTAACCCAGAGCAGACACTTTCCACATTGGAGCAT
GGTGTGTTGGGCAAGCGTTGGGTGACTAATGCGTTGGGTGACCCGGTGGCAGTGCGGGAG
TTTATTCGCACTATTTTGACGGGCGATGATGGTGCAGCTCGTAGCGATGGCGTGAAGGGC
TATCTGGATATTAAAGGTTCCGGCGATGCTGAGTCGGTGGATTTACAGGATGTAAAGCTT
ACTGAGGTTACAAGGCAGCGTGCGATTGGTTCGGTAACCATCAACGGTGAGCGAAAGCAA
TTCTCGCTGCGGTTGCCTCAGTTGCTGAAGAATTTCAGGGAGACAGCCGCGGGCCATACA

GCTACGACTCTTCGTATTGTGGCGACTCATCCGGAAAAGGACGATGTTGAGCTGCTGGTC
GCTGAGTTCAACTGGATGGAA

>RXN02307-downstream
TAATCCGAGACAGCTCCTGAAAG

RXN02314-upstream
TGATACCACCGAAGTATCCGGATTCACCATTATTGAAGCTTCGACCGTCCGAGATACCCG
CCGTGCACAACAGCAAGCTCTCATGGACACGGTGCACTAA

>RXN02314
ATGGAGTGGTACCAAGTGCGCCGACGGGCCCGACAACTGCTCATTGTCCTTTTTATAGCA
GCGATGCTCGGAGCAGCCTCCATGGTGATCGGGCCATTCCTTAACGACCGCACTATCGAA
GGCAACTCCGGGCGCGCCTTGGCACAAGTAACCAACGTCGGCAGCTACCGCACAACGGTG
GATTTCCAAGATGAAAACGGCATCTATCACTCACCAGCCACCGGCCTGTTGTTCCCCACG
GGACTGGGCGAGGGGCAACGCGTGTGGGTGAACTACGCCAAATCAGATCCAGACCTGGTC
AAAGTAGAAGGCCGCAAGTGGACACTGTCCATCATCCCAGCGCTTAGTGTCGCAGCTGTC
GCCACCGCTACCTGGTCAGTACTATGGCTGGGAGTGGGCAGATTCGGAAGACGATCCGAC
GACGCCAACGAAACCACAGTG

>RXN02314-downstream
TAAAGCTCTATGCCGGGAGCATT

>RXN02337-upstream
CACAAGGTAAAATTTGTGTAATTGTGTCGTGTGGATTTGAAGGTTTTTGTAAATCTAGTT
AAATCATGAGGTCATAAGCTTTTCGGGAGGTTGTCAAAGG

>RXN02337
ATGTCGAAGCTTTACGCGGGGGCAAGGATCAATGCACTGCGCCGAACCCATCAGCTCACC
CAATCAGCATTGGCCGACAAGCTTGATCTCTCCACCAGCTATCTCAACCAGTTGGAAAAT
GACGGACGGCCACTCACTGCCACGGTGCTTCTGCAGCTGATGAAAGTGTTCGATGTTGAG
GCCAGTTACTTCTCCCCTGACCGGGGTACGGCCACTGCTACCCGACTGGCTGAAACCTTG
GCGATGAATCAGGGTCCGACGATGTCGATGGATGATCTTTTAGATTTCGCGGATCGTTTC
CCTCAGTTAGCGCAGCATATTATCCAGCCTGCTGAGGTTGATCCCACGCATAGTTCTGCG
CATGATTTTGTTCGGGATTATTTTGCCACCCACAAAAACTACATTGATTCGCTCGATCGC
CTTGGAGAGGAGTTGGCAACTGCCATTGGTCAGCCGGGACTTCGGGTTACTAGGCTCGCG
CAGTTGCTTGATGCGGAGTACAACATCACGGTGCGTTTCCGGGCGCCGGATATTACTGGC
CGGAGGCACTTTGATCCCCAATCGCGTCAGATTCTGCTGCGGCAAGATCTCAGCGAGGCG
CAGCAGTGTTTCCAGTTGGCGGAGGAATTGACGTTTCTTGCTCATGCAGAGCTCTTGGAT
ACCCTGACCACAGATCAACCGGATCTCCCTTCTGAGGCAGCTATCCGCCTGGCTAAGGTG
GGTCTCTCCCAATATTTCGCGGCTGCTGTTGTCATGCCGTACACCCGCTTTTTGGAATTC
GCCCAGGATAAGCACTATGACATCGAGTTGATCTCTGAGGCGTTTGGAGTGTCTTTCGAG
TCTGCATGCCACCGCCTGTCTACTCTGCAGCGTTCGGGGGCGTCAGGGGTGCCGTTTTTC
TTTGTGCGCTCGGATCGTGCAGGAAATATCTCCAAGCGGCAATCTGCAGCTACGTTCCAC
TTCTCGCGAACAGACGGCACTTGTCCTTTGTGGGCGCTGCATCGTGCTTTTGAACGTCAG
GGAAACATCACCCGCCAGGTTGCTCGCATGCCGGATGGCCGGACCTATTTGTGGCTCGCA
CGCGCGGTGAAAGGTCGAACTCATGGTTTCGGGTATCCTGCTGCGGAATTCGCCATCGGC
CTGGGCTGCGATATCAGCGAGGCACCAGGCTTGGTGTATTCCCAAGGCCTTAATTTGGAT
CCCGAGTCCGCCGCAGAGATCGGCCCTGGTTGTCGGATCTGTCCTCGGGAGAACTGTGTG
CAGCGTGCATTCCCACCATCGGGTCAAGAATCTATCCGCCCAGCCCCTGTCCAACTCCTC
AAC

>RXN02337-downstream
TAAAAAGGCAGCACTTAAAAAAC

>RXN02339
CCCACCGACAACCTCTTTTCATATCCTGCACAACGCTATGATCTTCTCACACTTGCCTTT
GAAGTTAGGATTGGGGACATGGTTCAAATTAATGACATGCTTGCCCCTCCTCCAGTAAAA

CTTCCGGAAGATCCTGCCCTCGGCGCCGATCCAACTTTGACCTCGACAGCGATTGCGCAT
CCTGACAGCCCATTGGTGTGGGCGTACCGAGCTGAAAATCTTATCAAATCTGCATCAAAT
GATGAAGAGAAGATTCAGGCCTACGCTTTTGCGCGCACGGGTTACCACCGCAGTCTCGAT
CGTCTGCGTGCCAATGGTTGGAAGGGTTGGGGTCCTGTCCCCTTCTCTCATGAGCCAAAC
CAGGGAGTGTTGCGGGCTATCGCTTCCCTAGCTCTTGCTGCGAAGCTGATTGGTGAGGAC
AACGAATACGATCGTTGCCGCCAGATGCTCTCTGATGCGGATCCAGAGTCCGTCGCAGTC
CTACTCGACAAA

>RXN02339-downstream
TAAACCACCAAAAATAAAACAAT

>RXN02340-upstream
AAAACGTGTCTAAAAATTCAGTTTTTATTGCTGCTGATCACCTCTTGAAGAACTCAACCC
AAAAGTGCTTCAAGTTATGAGAAAGTGAAATCCAACACCC

>RXN02340
ATGAAAAAGAGCATCGTTGTATTTGAAGTCGAAGGCGGCTCCGACAAGCACTTCGACGGT
CACCGTAAAGACACCATGCCTATCGTCAACTCCATAAATGATGCTGGCTGGCAGGCAGAG
GTTGTGTACTACCGCCCAGAGTGGACCGAAGGTCTCTTTGAGTACGTATCTGAAAACTTC
GACGGCTACATCTCACGTGTCAACCCAGGCAACATCCCAGGCGGCGAGCGCGGCTACTTT
GACCTGCTCACCCGCCTGTCCGAAGCAGGGCTCGTGGGCATGTCCACCCCTGAGGAAATG
ATGGCATACGGCGCGAAAGATGCGCTGGTCAAGCTATCCCAAACCGACCTGGTGCCATCC
GACACCGAGGCGTACTACGACGTGGAGACCTTCCACAAGGTTTTCCCAACCTCCCTGTCC
TTCGGTGAGCGCGTGCTCAAGCAAAACCGTGGCTCCACCGGCTCCGGCATTTGGCGCGTC
CAGTTGGTAGACAAGGAACTGGCTGCATCCATCGAGCCAGGCACCGCACTGCCATTGGAC
ACTGAAATCAAGTGCACCGAAGCAGTCGACAACCACACTGAAGTCCGCAAGCTCGGCGAG
TTCATGGATTTCTGTGACCAGTACATCATCGGCGACAACGGCATGCTCGTTGATATGCGT
TTCATGCCACGCATCGTCGAAGGCGAAATCCGCATCCTTCTCGTCGGACCACACCCAGTG
TTCGTCGTGCACAAGAAGCCAGCAGAAGGCGGCGACAACTTCTCCGCAACCCTGTTCTCC
GGCGCGAAGTACACCTACGACAAGCCAGAGCAGTGGCAGGAACTGATTGACCTCTTCGCA
GACGCTCGCCCAGTCATCGCAGAAAAGCTCGGCGGCGACAACATCCCATTGATCTGGACC
GCAGACTTCATGCTCGGCGATGTCGTTGACGGCAAGGACACCTACGTGCTCGGTGAAATC
AACTGCTCCTGCGTCGGCTTCACCTCCGAGCTGGACATGGGCATCCAGCAGCTTGTGGCA
TCAGAGGCCATCAAGCGCATCGAGGAATTCGCGCAGCTTACTGTT

>RXN02340-downstream
TAAAACTTTGCTTCTCGACGTCT

>RXN02341-upstream
CGCGACTGGCGGAGAAATTCGTGTTCGCGATGCTTCGGGCACCGTTCACACCCTCAACGC
CGGTGAAATTACGCACCTTCGCCTGCAGTAAGGTGACGGT

>RXN02341
ATGGGGAATTCACTTGAGAAACATATTGCAGAGGGAGACCGGATCCACGTCGATCTGACA
TCTCCTTTATCCGCAATGTTGTTCCCCATTTTTGAACTCATTGTGATTACTGGAATCTGT
TGGATGGGCATCGGCTTTTTGGATCAGCTTCCAGGAATCGATGGCACCAACCCCGCCGAT
AGCTTCCCCGAAGGCACCCGCAATCTTCTAGTGGGTGTGTGGGCAGTACTTGCTGCATGG
CGTTTCGGTCTTCCTTTAATAAGGCAACGTCGACTCCGCGTGATCTTGAGCGACCGCAAA
CTGCTGGTCCGACGCGCGGGTCTGCGCACCGGGTTCGATTCCATTCCACTGAGCTACATT
CAGCGAGTCCAACGTCGGCGAAACACCCTGGTCTTAGGTGTTGGTGGACACCACCGACCC
TATGTAATCAACCAGGTTCCCAAGGCTCGAAAAGTGGAAGCGCTGCTCAAAGATCTTACA
TTTTGG

>RXN02341-downstream
TGAAGGCGTTATAGTTAGGACTT

>RXN02360-upstream
AAGTAACTAAAGTTCGAAAGTATTTCCGAACGGTGTCGGCCTCTGCGCATACACTGTATT
TTTAAAGAAAATTCTTCTCAATTCTAAGGGTGAATATCCA

>RXN02360
ATGCGTGGTGACGTTCAAAAAATAACCAAGGTTTATGACGGCAAGCACCGAACCTTGGAA
ATCCCGGTTTATCAACGCAATTACGACTGGACTGAAAAGCAATGTTCACGCCTCTTTGAT
GACCTCAGCGAAGTGGTCAAAGAAAACCACCGTCAACATTTTTTTGGAGCTGTGGTTGGT
AAGCCTCAAGGCAGCTGGACCTGGGTTGTCATCGATGGACAGCAGCGTCTTACAACAATC
AGCTTGTTCATGCTTGCGCTGGTACATTCCTTGCGCGCATCTGAAGTTGAAGAAGGTGAG
TTTAATGCTGGCTACAACATTGATCTAGCCACATTGATTGAGGATGACTACCTCCGATCC
GGCAATGAGGGAAACCTCAAGTTCAAGCTCAAGCCAGTTAAAAACGATAATGAGGCTTAT
CAAAAGCTCTTCGGCCCAGAATCTGAATTCATAGAGTCCTCAAACCTCACTGCTAATTAT
CGCTACTTCCGCAATGTCCTTAAGGCAACCGATCTCACCGCAGCTCAACTATGGGAAGCT
ATCGAGAAACTCAGGGTCATGTATCTTGACCTTGAGGAATTTGATGATCCGCAGCGAATC
TTTGAAAGTCTCAACTCCACGGGATTAGAGCTCAGTGAAGCTGATAAGGTACGCAACTTG
GTTCTTATGGATCAGGAGCTCAAAACCCAAGAAAAGCTCTATGAGCAGCGTTGGAATCCC
ATTGAAGTCTGCGTGAAATTTGATACCGACAATTTCATTCGCTGGTACTTAACTCTCAAA
ACCGCGCGCACCCCAAGAAAGCAAGATGTTTATGAGGAATTCAAGAAATTCATCCGTAAC
TCCAAGCTCCCGGTCGAATTCATCCTCGACGATATGTACGAGTACGCGAAGCTGTACCGA
GATCTCTTAGGTGCCACTACTGGGTTTATAGCTGCCGATAGGTGTCTTAAGCGTTTTGTC
CCTGTCATGGGCGATGTGGTTTTGCCTTTTCTGCTGCCTGTTCTCAAAGATGCTAAAGAC
GGCATCATCACCGAATCAGACTTCCTCGGAGTTCTAAAAGTTCTGGAATCCTATTTATTC
CGCCGTTTTGCAGTCGGGGTTGCTAGTAACGCCTTAAGCAAGATCTTCTCCACTGCTTAT
AGCGACATCAAGAAATTCTGGACTCCAGGGCAAAGTTATAGCTCACTGCTGGCCTACATT
CTGAAACGTCGCGATGGTTCCGGGCGTTTTCCCTCCGACAGTGAATTCCGTGAGAACTTC
GCAACCAAAAATTTCTGGAATATTCATAACGAAAACAGGCGTTACTTATTTGATTGTCTA
GAAAATGCCGATTCCAATGATGTTCGTGACATCCAAACAAGTCTGGATGAAGGATCTCTC
TCCATTGAACACATCATGCCACGTAGCCTAAACGATCAGTGGAGAGCTGAACTCGGCCCT
GAATATGCTCGAATTCATGAGACTTGGATTAATAGAATTGGTAACCTCACCATCACCGGC
TACAACTCCGCCTATTCAAATTCTTCCTATGAGCGCAAGCGGACGATGGAAAATGGATTT
TTGGTATCCCCCTATCGCATCAATAATTTCATCAAAAAGCAGAAGCATTGGTCTGAAGAA
CAGCTAATTGAGCGAACCGAGCTGCTCACTCAAGCAGCGCTGGACTACTGGCCCCTTCCA
AAAGAAACCTTCCAGCCACCACAAGCTGTGCTTCCTACAGAATCCTTAGATAGTGATCTT
TCTTTCCGCGGACGCGAAATTGTCGCCTTTGAATATGAGGACTACAAGGAAACGGTAACG
TCCTGGGCAGACATGCTCCAGAGCGTTCTAAAAGTCTTGAACCAATCCTTCCGCCAGGAA
CTCATAGCTTTGACCAATGAAGAAATCTGCCTGGCAACTTCAAACAACAGTAACAGCAGT
CTCCGTGAAATTGACCACGGGCTTTTTGTAGACACTGGCTCTAGTACGAGTGTAAAGATT
GGCTTCCTCCGCAGAGTTTTTACTCAACTGGGGCTAGAGCAGGAAGCATTGGTTTTCACC
CTTCGACCACTGGCAAATGATGTAGAACCCCGAGATGATGAACTCGAGGTAGAGGTAGAA
AAGAAATATTCCGATTTGACTAAATTCATCCCACAGTTAGAAGAAGCTGAGAATCTCGAG
GGGGCGGATACAGAGGTTATTCCTCTCCTCTCAAAGCTCAAGGAACAACTGACAGCCTTT
AGCCCGGAGAATCCTCAAGCAGCCCTAGGGGGCCTACCTGTTCCAGAATTCCTCAAACAA
AATGTGATTGAACAACTAAGCGCAGAGCACATCCTTGCTGTACTCACTCAACACTTTAAT
ATCGCATCCATGATGGGTGATGACTATTTGCTCGAAGAGCTCAGGTCAGGCCGCTTAAGG
GAATTACTGCAGCGTTTAGAGGAATTGGATAGC

>RXN02360-downstream
TAATAGCCGTAGTCGGTGGTCAA

>RXN02361-upstream
TAGAGGAATTGGATAGCTAATAGCCGTAGTCGGTGGTCAAACTTTGACCACCGGACTCCC
CTTTAAGCACAATCTCTAGCTTTTATTTAGGCTTGGAGTT

>RXN02361
ATGGAACTTCTCTCCCACTTGCTTGCTCTTGATCCTGCCTCCCCTCGTTTGACTGTTTAT
AACGAGTCCACGGGTGCGCGTTTGGATTTCTCCGCCATCACTCTTGATAACTGGGCGTCC
AAGGTTGGCAATATGCTCCTTGAGGAATTGGATCTGGAGGAAGGCTCGCTCATCACTATT
GATTTGCCGGTGAGCTGGCAGGCCGCAATGATTATGCTCGGCGCTTTAGCAACTAGTGTT
GAGGTCTCTTTTGATGATCCCGAGGCAGATGCCATCTTTACCTCCCTCGATAGATTTTCC
CACTACAAGGGCCATAGTGATGTGCTGATTGTCAGCGAGGATCCTTTTGGTCGTGGAGTT
GTTGAAGGTGGCGGTGAACTGCCTAATGGTGCCATCGATTTTGGCCCCACAGTGCGTTTT
TATGGCGATCAATTCTTCCAGCCTACCCGCACATTGCCGGAAATCATCCAGCATTCTGAT
GTTCCGGTTGGCGCCAGAGTTCTTGCAACTGGTTGGTCAGATATCGAGTCCTTCAATCAC

CAGGTTTTAGAACCACTCGCAGTGGGTGGCTCTGCAGTAATTGTGACCGGACTGGCTGAT
ATTGAGCGTTTAAACCAGATTGCAACCAATGAGAAGACAACCCACCGTATC

>RXN02361-downstream
TAGGCAAATTTCGGTTACTACTA

>RXN02367-upstream
GGCACTTGAATCCGGACGCTAAGTTGTTGATACATCAACTTATTTCTTGGCTATACTTGA
GGTCACGTTTCCTCAGCTCAGGAGAAGTTCGGAGAAGTCC

>RXN02367
ATGTCAAACGCAGAAATTAATCCCGTTGAATATGAAATCAACAACCACGCCCCTGGTACC
GCGCTAAACCCACAGTGCGAAGACGGCGCCAACGTAGAAATCATCACCTCCCGTGAAGTC
CCCCTCGGCGGACCACGCGCCATGACCGTGCACCGCACACTCCCCCAACGCCAGCGCTCC
CTCATCGGTGCCTGGTGTTTTGTGGATCATTACGGCCCCGATGATGTCTCACTAACCGGT
GGCATGGATATGGCCTCCCACCCGCACACCGGATTGCAAACAGTCACGTGGCTTTTTGAA
GGCGAAGTCACCCACCATGATTCCGGCGGAAATCACGCAGTCGTGCTTCCTGGCGAAGTC
AACCTCATGACCGCCGGCGCAGGCATCTGTCACACCGAAGTTTCCGCCACCTCCACCACG
ATTCTGCATGGTCTGCAGTTGTGGACAGTTCTTCCCGACAAAGACCGCGAAGGACCACGC
CGCTTTGATCACTACGCTCCAGAAGAAATCACACTCGAAGGCGGAAGTGCACGCGTTTTC
CTAGGTTCGCTATTTGGTCAAACCTCCCCTGTTCATACGTTTACTGGCTCTTCCTGTTTT
AGAGTGCAT

>RXN02367-downstream
TGATCTTATGGACCAACTGCCCT

RXN02368-upstream
CTTAGGTCAAGCTTGCATTTATTGGCTAGTGTCGGAAATCATGGGAGATTTAGCAAAGCA
CATGGGCAGTGAACCACCAGCATGGTGGAAGTTTTTACCG

>RXN02368
ATGATTGTCCTCGCTGGAGCCACTCGAGTTACCTATGAAGTAGAACCTTGGCTGGCGATC
CCATTATTCATTTTGGCTTTTGCATCGATATTGATCCCATTCCCGATCTCTAAGACAAAA
GGACTCCGTGATATCGATGCCTGGAAAATCCACACCACGCAAGGCGATAAAAAGCGTGCC
ATCCGCCAACTGATCATTCCGGCTACGGCTTTGGCCATCGACATCATTGGGCTGCCGACA
TTATTTAATGCCCCTCCCCTTGCTTCCGCTGCACTTTTTGGCGGTGTTTACGGCGCTTCC
CTAGCTTGGGCTGCGTACAGAGCTGATCAGCTTCCACGCATTCGAACGAAGGAACGCCTC
GCAGAACTTTCACAAAATGCATCTCTGGATGATGTGCGCTCAGATGACTTAGATGTTCTA
GAGCAGCCGGAATCCCGTGAATTAGTGCGCTGTCTGCTTGCCCACGGTGCGATGGATGGC
ACTCGGGTGATGGCCAGACAGGTCGCGCGAGTACTGGATACCGAGGTAGACGAAGTACAT
CAGGTAGCACGCTCACTAGAACAGCATGGTTTGGTTAGTCGCTCCACCATCATGCCGGGT
GGGGATCCAGGAAAAGTATTCATCGAAGTTTCCCTGAAAGGGATCTCAGCCATCAAGGCA
CTTGAATCCGGACGC

>RXN02368-downstream
TAAGTTGTTGATACATCAACTTA

RXN02381-upstream
AAGTTTGAAGAAGTAATCAAGCTCCCCTGTGAGGACTCGTTGTAGTCTTTTATTTAGTTA
ATAAAAGATTTCATACCAACTTGTCAGCAGGGGAGCTTTC

>RXN02381
ATGTCTGTCACAAACTTCCGTCGGTTTCTTGCTGGCATAGCGGTCATCGCGGCGTGTGTT
GCTGCGACTCCAACAGCTCAGGCACAAAGCAGTGGCTCTTCTGGATCCTCTGGTTCTTCA
GCGGGATCTAGCGGGCTGTGGGATTTACTTTTTCCAGAATCCCATGAGTCTTTTATCGAG
CGGCTTCTTGATCCTTTGGATGACAGCCATATATCTATTCACCCTGACCTCACCCCAGAC
CTGTATGAAGAGGTGTTTGATCCACCGCAAATTGGTGAATGCCCAGCCGTTGTTGCTGTG
GTCGCACGAGGCAGTGAACAAAACCTTCAAATCCGACCCGCGCGATACAGCGAGGAATCT
CCATGGACATCCAATGGATTTGAGGAAAAAAACTTTCGTAGTTTCTTTGGCCGAATGGAA

AAACACTACCGTGAATCGACTGGCGAGTCGTTGATGAAAGACGTCTACGTGATGGGTCTG
AATAATATCGAATACCCTGCTTCTTTGCCACTGTCTTCGGAGGGAAGCAGCGCCATTGAA
TTGGGCACTTCCATTTCTAGTGGTCGCGACAATGTCATCAGCGCGATTGATCGCTTTGAA
TCAGCGACAGGGTGCACGCCGAAGTACCTGTTGGCGGGTTATTCTCAAGGTGTCCTCATC
GTTGATGGCTATGAAGAGGAGTTGATTGCGAGGGATCAGTACCTCGGCACCCTGCACATC
GCGAATCCAGCGCAACAAGTTGATGATCCAACACTTGTTGGGCATGAAGTAACCACGGGA
GGCTTGGCTAGTTCCGTGGAGCCCGTCGAGGACAATCCTTTCAAGGTGAGCTACTGCCTG
CCTGGAGACATCGTGTGCGATCGTTCTTTTGAACAGTTCTCTGCTGCGGGATCCTCTATA
GCAGCTGCGCAATTGAGCACCGGAAATATCCGTCCAGGTCGAGTACACGTGCAATACTTC
GTTACCACCCAACCGTGGGATGAGCAGATTTTTGACGAAGTCGCATCGTGGATTGAAGCT
GCC

>RXN02381-downstream
TAAAAACTCGCGAGGACGCATGC

>RXN02383-upstream
GGGCAACAATGTGGAAAACGCCCAGTGGTATCTTGACGGCTGGAACATGGGTGTTACGCA
GTAAAGAAGATGGCAATAAAAATGTGGAGGAGTAAAGGCG

>RXN02383
ATGCCAGTTCGGGTAATTGTTGATTCCTCCGCATGCTTGCCAACGCATGTGGCCGAGGAC
CTCGACATCACGGTGATTAACTTGCACGTGATGAATAACGGTGAAGAACGCAGTACATCC
GGGTTGTCGTCGTTGGAACTTGCAGCAAGTTACGCCCGCCAGCTTGAACGCGGTGGCGAT
GACGGTGTGCTTGCGCTGCATATTTCTAAAGAGCTCTCGTCCACGTGGTCCGCAGCGGTG
ACAGCAGCCGCTGTGTTTGATGATGATTCTGTGCGCGTGGTGGATACCAGTTCGCTCGGT
ATGGCTGTGGGTGCTGCCGCGATGGCTGCTGCCCGCATGGCTAAAGATGGCGCGTCTTTG
CAGGAATGCTACGACATCGCGGTGGATACCTTGAAGCGTTCAGAAACCTGGATCTACCTG
CACCGCATTGATGAAATCTGGAAGTCGGGACGGATTTCCACTGCAACCGCCATGGTGTCA
ACGGCTCTGGCAACCCGCCCCATCATGCGTTTCAACGGTGGTCGCATGGAGATCGCCGCT
AAGACCCGCACCCAATCTAAAGCGTTTGCCAAATTGGTGGAATTAGCCCAGATCAGGGCA
GATGGTGAACCCGTATTCATTGCGATTGGCCAAAAC

>RXN02387-upstream
GCTAGCCCCGATTCGCTTCAGGTCACCACCTTGAAGGCCAGCGAAATTACTCAGGGTGAA
TTGTTGGATGCGTTAAGCCCATCCTTGTTTGCTGAAGACC

>RXN02387
GTGTGGTGGTGCTTACCAACATGGATCAAAGCAGGCCAAGATGCTGTAGATCTAGCCTTA
TCCGCAGCAGTTGATCCCAGCCCTGGTACCTACTTGATCGTCATGCACTCTGGCGGTGGA
CGCTCTAAGTCGATGGTGAAGAAGCTGGAAAAAGTCGCGGTGGTGCACGATGCCGCAAAG
CTGAAAGACCGGGATCGTCCAGGTTGGGTAAAACAAGAGTTCAAAAACCACAAAGTCCAG
GTCACCCCAGATGTCATTCATGCTCTTTTAGAGGGCGTGGGTTCAGATCTTAGAGAGCTG
GCGTCCGCCGTATCCCAATTGGTTGAGGACACCCAAGGCAACGTGACGGTGGAAAAAGTC
CGTGCCTATTACGTGGGTGTTGCTGAGGTATCGGGTTTCGACATCGCCGATTCTGCATGC
GCCGGTCAAATGTCAAAGGCCGTGGCCAGCACCAGACGTGCCCTTCAATTGGGTACCAGC
CCGGTTGCATTGGCAGCTGCGTTGAGTATGAAAGTTGGCCAGATCGCCAGGCTGTATTCC
ACCAGGGGACGCATCAACGGTTTTGAGCTGGCCAAAGAATTGGGCATGCCGCCGTTCGTG
GTGGAGAAGACTGCGAAAGTGGCCCGAAACTGGTCGGGAGATGCGGTCAGCGAGGCCGTG
ATTTTGATGGCCGATCTGGATGCCGCTGTAAAAGGACAAAGTGGCGATCCTGAATTTGCC
ATCGAATCTGCCGTGAGAAGAGTTGCAGAGCTGGCGAGGCGG

>RXN02387-downstream
TAACGCTGAACGGCGGCGGGTAA

>RXN02398-upstream
GTGTCCAATGAATGCGTTCAATAAATGCCCTCTTTAAGCATATTCTCTGAGTGCATTCAT
TACAGGCGTTAATTAAATGCGTTCATAGAAGAACTTGAAA

>RXN02398
GTGGTTGAAGTGAAGAAGCGTAATCTCCTCGTAGCTCCCCTCACTGCTTCCCTGGTGTTC
TGTAACTTGGCTGTTGCAGCAAACGCCGTTGAAGTTGAGGCCGAATCACCAGTTGTCATC
AATGAAGTTGAATCCAACAGCGACCCAGTTGGTGACTGGGTGGAGTTGGCTAACACCGAC
AACAACAACTCCATCGACATTTCCGGTTGGTCCTTAGTCGATGACAAGGAAGACCTGGAA
AATGCCCTCGTCCTTCCTGAAGGCACTGAGATTGAGTCCGGTGGATACTTTGTTATCTAC
ACCGACTCTGCTGATTACGTGCCTACCAACAACACCTTTGGTGGCCAGGAATACTTCGGC
CTCGGCAAAGATGACACTGTTACTCTGCGCAACGCTGAAGGCGAAGTAGTTGCTACCTAT
TCCTGGAAGGATCTGGGCGAGCACGCAGAAAACACCTATGGTCGCATCCCAGATATGACT
GGTGATTTCGCAAACACCGGCGTTCCAACCCCAGGTGCAAAGAATGTTGCTGCTGAAGGC
TCCGGCGAAGAAGAAGGCGTTGTTGCAAACGCCCAGCTTCCATTCCACAACGTTGAAATC
ACCCCAATTCACCTCGGTGGAGATTTCACCGGTGAAGATATGTCCGGCGTTGATTTCGAT
GCAAACAGCACCGCATGGATCGCCAACAATGACATTGGAAAGATCTACTCCCTCGCCCAC
GACATAGCTAACAACACCTACAAGCTGACTGGCGAATGGGAAACCGGCTACCCAGAAGGC
GGCGGAGAGCCAGACGCTGAAGGCATCGTCGCAGCTACCAACGGTGACATCTACCTGTCC
ACCGAGCGCAACAACGCTGACAAGAACGTCTCTCGCCCATCCATCCTGCGTTTTGCTACC
CCAACTGGCAAGACTGGCGTACAAAACGCAGTTCAGGAATGGGACCTGTCTGAGTTCGTC
GGCGACATTCAGCCCAATGGTGGTCTTGAGGCAATCGCGCAGCTCGAGGACAACATCTTC
GTTGTCGGTGTCGAAGAGACAGGTGATGTCATCGTTGTTGATCTTTCCGCTGACCAGCCA
GTTCTGGTTCAAAGGTACGAATCTTCCTTCGACGGTGTCATGTCGCTTGATTACAACGCA
GCAACCAAGCAGCTCAGCGTTGTGTGCGACGAAGCATGTGACGGCTTGTCTGAAATCCTC
GAATGGGATGGCGAGAAGCTGTACAAGTCCGACGACAAGATCTACGAGCGTCCAGCAAAC
CTGGGCAACTGGGCTAACGAAGGCTTCGGCACCTACACCTCAGAGCTTAAATGCGAGAAC
GGCAACACCGTTTCTGTCACCAGCTACCTCTGGGCTGACGATGCAGCAACCAACGAAGGC
ACCTCCCTCAACTCCGCACAGGTCATCAACGGAGATTGCGGCGACGTCAACATCCCTGGA
GAGTCCTCTTCCGACAATTCCTCTTCTGACTTTGCAACCGGCAGCATCGCAGGCGCCTTT
GCAACCGCAGTGCTCGCAGTCGTAGGCATTGCGGGCGCACTGGGTGGATTCTTCCAGCAG
ATCCTCGCAGCGTTCCCAGCATTGCAGCAGGTCATCCGTTTC

>RXN02398-downstream
TAAACCCACTGCTTGAAACACTT

>RXN02406-upstream
CACTCTGATAGCCTTTTCTCTGAAATTGTACCGAGCATTTGATTTTGTTCCCCTATCAAT
GCTGGTTTTGGTGACAAAAACTCGGCGGAAGGACCACCGA

>RXN02406
ATGGAAACCCTTGCAGCACAAGCGCGCACCCTGCTAGAAAAATGGGGCGTCGCGCCGACG
CACGCATCTTTCGTCGAATCCATTGCAAAGGCCATCCCGATTCTGTCGATCCTGCTGACG
CTGATTGTCACCGTGAATGGAATTTCAAGCGGAAATCCGGTCCAGCCACCAGCACTGGAA
CAGGTACGGACCGATGTAGTGAACAAGATCAACTACGAACGCAACCTAAAGGGCCTCGTC
TCGATCAGCCCGGAGCTTGAATTACACACGGCAGCCCAAACAATTGCGCAGCGAAATGCA
GACTCAGATTCCGAAGAAAAAGTACCGGATCCAGAGGGCAACCTGGTGGTTCTGCAACAG
AATCTGCCCTATGCAAATGCCAACGCCGATACCATCGTTGATCGGTTCTTAAACTCTCCT
GATCATGTCAAACTACTGCTTGCAAACGATTATGAAGCCATCGGAGTTGGTGTGGCCTAC
AAGGGTGATCATGCGTGGATAGTGGTGGAGTTCACTGTAGCTCCCGCTGATTCCGTAGAA
TCAACAGAG

>RXN02406-downstream
TGAATACCAATCCGTCTGAATTC

>RXN02407-upstream
GGATAAAAATTTGGATGACATATCACCTAAGCTTGCAATTTCTACTGGAATAGCGCGACT
ACTCTGCACCAACGCATAGTTGTTGACTAGGCTATTTGTC

>RXN02407
ATGAATAGGCAAAACCAACTTCACTACCCGCAGGAAGTGAAGGCAGTGGAAAGTGTGGAA
TCAAGCTTGAACATGTCGTCACCTTCTGCACCGCTTGCCACGCCAGATGTTGAGCTTGAT
GTGCACACGTTGTCGAGCGAAAACCTGCCTTGGTTGTGCATCGTGTGGGATGATCCGGTC

AATTTGATGAGCTATGTCACCTACGTTTTTCAGACTGTGTTGGGCTTCAGTAAGAAGAGG
GCCACTGAGCTGATGATGCAGGTGCACACCGAAGGTAAAGCCGTGGTGAGTTCTGGCGAG
AAGGACAAAGTGGAGGGTGATGTGAAGAAACTCCACACCGCAGGGCTGTGGGCGACAATG
CAGCAGGCAGGG

>RXN02407-downstream
TAGGGGAGAATTTTCATGCAGCA

>RXN02408-upstream
GTGATGTACGCGGCGGGGAAGCCGCCGAGGAAGACCGCGAAAACCTCGTGCAGTGGCTTG
CCTACAATCAAGAGTCCTTGCTGGAAGCGATGATGAATTA

>RXN02408
ATGCTTATCGACGTCGCGGGCTTCCTTTTAGGCCACGTCACGAAGGGGGATACGGGTTGC
TCAGTGGTCATTGCACCTAACGGTGCATTTGCGGGCGTCGATGTCCGTGGGGGAGGCCCA
GGCACCAGGGAAACCGACCTTCTAGAACCACACAATTCTGTGCAGCAAGCACATGCCGTG
GTGTTGTGTGGCGGTTCGGCGTTCGGGTTGGCTGCTGCCGATGGAGTGATGACAGCCCTA
GAAAACCGCGGTATTGGTTTCCCTGTCCGTCCCGAAGGGCCTATCGTGCCAATCGTTCCA
GGCGCTGTGATTTTTGATTTGTTGGTGGGCGATCCCAAAAACAGGCCCACGGCAGCTGAT
GGGGAACAAGCAGTTGAAAACGCTTTCGCTGGTACACACAACGGTTCGGGCAGCGTCGGT
GCAGGAACGGGTGCTACAGCAGGTCGGCTGCGTGGCGGTTTTGGCCAAAGCTCGCGCCGG
GTCGGAAAGTACACCATCGCGGCAGGGGTCGTGGCGAATCCTGTTGGGGAAGTCGTGGAC
CTAACAACTGGAGCTTTGTTTGGTAGGCCCGAAGTGATGGGGGTGGGCGTCGATAAGCTA
AAAAGCGCGGCAGAGACGCTGAACACGACCATCGGCGTCGTGGCAACTGACGCGCCGGTG
ACAAAAGCCCAAGCGAAGCGCTTGGCGCTGGTGGCCCATGATGGTTTGGCGAGGGCAGTG
CGGCCGTCGCATTCACCGATGGACGGTGACACATTTTTCGCCATGTCATCGGGTGATGGT
AGTGGCGTTACCCCGGTTGAGCTGGCGGAATTGTCGGCTCATGCTGCAGATTGCGTACAG
GACGCTATCATCGACGCCATACTTACCGCGAGTCCGGGACTCGGGCTCAAAAGCTTCAGG
GAACTTTTACCA

>RXN02408-downstream
TGAGTTACAACAGCCCGTATAAC

>RXN02409-upstream
GAGTTCTGGCGAGAAGGACAAAGTGGAGGGTGATGTGAAGAAACTCCACACCGCAGGGCT
GTGGGCGACAATGCAGCAGGCAGGGTAGGGGAGAATTTTC

>RXN02409
ATGCAGCAGTGGAAGAAGAAAAAAGGGCTGATGCGCCAGGCTCGTTACGCGGTGGTTTTT
GAGCCGATGGAGCGGGAAGTGTTGGGTGATTTGTCAGCTGCGGTCAGTGAGGCGTTGATT
CAGCGTGCACAGTCTGTGCCGAAGGATCCTCTGGCAGAGATGACCGGCATGACAAGTGGA
CACAAAGAAGCACCAACCGATCCGGCGCTTGCGCGTTTGCTCCCTGATTTTCAGCACGAG
GGCGATGAGGAATACGACGGCGATAATTCTTTCCTCCGTTCACTCCATGAAGGCGACATC
ACCCGAGCAAAACTGGAAAATCTGCGCGTGATTAACGATGCGCTGGGACCCGACGGAAAT
GTTGCGGTCACCGCCTCTGAGGAGGAAGCGCACGCTTGGTTGGCTGCGCTCAATGACATC
CGCCTGTACGTTGCCTCCGGTGATGTACGCGGCGGGGAAGCCGCCGAGGAAGACCGCGAA
AACCTCGTGCAGTGGCTTGCCTACAATCAAGAGTCCTTGCTGGAAGCGATGATGAAT

>RXN02409-downstream
TAATGCTTATCGACGTCGCGGGC

>RXN02428-upstream
CGAAAGATATGCATAAAGTGATGATGAAATAGCTTTGTCGAAAGGTTTGCTCCCGGTGCA
TTCAGTTAGCGTGAAGGTGCCATCATCACAAGGGTTGATG

>RXN02428
ATGGCCGCGACGTTAGATCTTCCAGATACAGATCCCATTGCCTATGCAATGTTTGCCCAC
TGTTTCACCGGCTCACGGTTCACGCCAGCCGCCGCGCGAGTCAGTAAAACACTCGCAGAA

TCCGGCGTCGCCTGCCTGCGTTTCGATTTCCCAGGACTGAGCCAATCAGAAGGTGACTTC
TCCAAAACCACCTTCAACTCCAATGTGGACGATATCGTGGCGGCCTCGCAGTGGTTGACG
GAACACTACTCCGCTCCACAGTTGCTCATTGGACACTCCTTGGGTGGTGCAGCATCACTG
AAAGCTGCCACCAAAATCTCCTGCCTCAAAGCAGTAGCAACGATAGGTGCACCTTTTGAT
CCTGCGCACGCAGTCCTGCACTTTGCTGATCGCATATGTGATGTAGATGATCAAGGTGCT
GTCACTCTGCAGCTCGGAGGCCGGGATGTCACCATTTCCCGCGAATTCCTCGAAGACCTT
GCAGAGGTCAACCCCGAAGATCACCTCCGCAGGCTCCGCAAACCACTGCTTTTACTGCAT
TCCCCCACCGACCAAACCGTCGGCGTGGACAACGCGCAGCTCATCTTCAGAGTCACTCGC
TACCCTAAATCCTTGATGACTTTGGACAAGGCAGATCACCTGCTCACCAAAGATGGCACC
GCACAGCGTGCAGCCCGGATCATCGCGAACTGGGTCGAGCCCTACCTGGTTCCAGAAAAC
GTCTGTGAGGATCTTCCGGAGTTTGTCGCCGAAGCCTCAACCATCAAAGCCAGCAAATAC
GGCGCAGCCATCCGCACCGGTGGTCACAATTTCATCACCGACCGCGACAAATCCCAGGGT
GGCAAAAACCTCGGCTTCACCCCTACTTCCCTGCTGGTTTCCGCGCTTGCTGCTGCAAAC
TCTCAAACGATCAAACAAGCAGCCATCGACAACCGCATCAAAGGCCTTGACGATGTCAAA
GTGACGATCTCCCAGGAACAATCAGCCGACCACGGCCAGATCAAACTCCGCCGAAAGATC
TCTTTGATCGGCAACCTCAGCGATGCTGACAGTGCTTCACTTCGGGCCGCATCTAATTCC
TGCTCGATTACCCAACTGCTCGCGCAGGGAATCGTCATCGACGACGAGGTGAAC

>RXN02428-downstream
TAGCGTGGATTTTGAGTTGGGTA

RXN02454-upstream
GGCAAGCGCCTCCCTTAAGCCCGCGTACCGGCTACCCCGAGGCACGTAATGAGTAGGGCA
GTTCTAGCCATAATCAGCAGAAAAGGTGGAGTGATTCGCC

>RXN02454
ATGAAAGAGTCCATGAGCATCACCTCGTCGACGTACGCGTCGGCACTGCTGACACTGCCC
TGGGGTACACCCCTGGAACAGTGGCCCGATAATCTCATCGCCGCGCTGCCCAGGGGTATT
TCCCGGCACATCGTGCGTTTCGTGGGGATCAACCGTGGCATCGTCGCGGTCAAAGAAATT
GGTGCGCGTACCGCCCACCACGAGTACAAGATGCTGCGTGAACTGCAGCGCCTTGGTGCC
CCCAGTGTGCGCCCCGTAGCCGTGATCACCGGACGCCATCCGGCAGAGGAAGACTACGGG
GAGCTCACCGCAGCTTTGGTGACCGAGCACTTGGAGTTTTCCCTGCCCTATCGCGAGATC
TTTTCTCGGCACCTCACGGTCGTGGAATCGGAGAAGCTCATCCGCGCCCTGTCCGTGCTG
TTGGTGCGGATGCATCTGCTCAACTTCTACTGGGGAGATGTGTCACTGTCTAATACTCTC
TTTCGTCGCGATGCTGAAACCTATTCCGCCTATCTCGTCGATGCCGAAACCGGGGAGTTC
CAGCCCAACCTCTCTGAATCACGCAGGCTTTACGACGTCGACATCGCCCGCGTCAACATC
ATTGGCGAACTCATGGACCTACAGGCGGGTGAATGCCTAGATAAGTCCATCGATGTCATC
GCCCTAGGAGGCCTTGTCGAAAGCTCTTATCTTGAATTGTGGACGGAGCTCACCGCGGAG
GAATCCGTCGATGCCAGTGAATATTGGCGCCTCTCTGAGAGAATTGACCGGCTCAATCAA
CTGGGCTTTGACGTAGGGGAGCTCAAGGTCACGAAGGACGATTCGCGGCAGGTTGTGCGC
ATTCGCCCTGTAGTGGTGGATCCGGGCCACTATCGTGCAGAGCTATTGAGCTTAACCGGG
CTGAGCGTCGAGGAACACCAGGCCCAACGCCTATTGGGCTCGATCCAGGCCTATCAGGCC
GTCGAATGCGGACCGCATGTAGGTCTTACCCAAGCCGCGCATCTCTGGATGACGAATGAA
TACGAACCGACTATCGCCGCCGTCCCCGTGGAGATGTTAGACAAGCTGGAGCCAGCACAA
ATCTTCCACGAAATCGTCGACCACCGCTGGTTCCTCGCCCAAGAAAGGGGAGGGGCTGTC
ACCCTCCCAGAGGCCACGGCATCCTATCTTGAATCCGTGCTTCCGGCCCGCCGCGACGAG
GCTCGCCTCCTCAGCACAAACCCTTCAGACGAAGACTTGTCA

>RXN02454-downstream
TAACCTCTCGCGTGCCCCAACGG

>RXN02457-upstream
CTGTAAAGCCACGTGAGCTGTTGCTTAGACTTTACTCTACCCCCGCGTGTCCACCACATC
AGTTAGAACATATGTACCACTTCAAATCTAGGGGGAAACA

>RXN02457
ATGTTCTACTTCACCGTCAATAATCCGCAGGATCCTTTAAGCACCGAAATTGTTGAGACT
AATCGCCGTGACCTCGCATTTTGGCATCGATTACGCCCCAAAGATGACGATGATTTAGCC
ACAGCCATCAACAAAATATGCGTGCGCACAGGCTTATCCCGCAAACTGATCGCCGCTTGT

TTATTTAGCATCTGCTTCCTGCCGTACTTACCCAACTTCCACAAACTCGTCGAAAAGCTT
GGTCATCTCGACATGGCGCGCATCAACGCGATCACTAAAGCTGGCGAAAAAGTGCCAAGC
GAGAAGAGAGAGCTTTTCGACGCCTACCTCGTCGATTACCTGACGCCTCGAGCGGAGGCT
CAGTGCTTGCCCCAGGCAAGCTCAATTTCCGCAATGATGCGGAAATTTATCGCACAACAC
TGCCCCGACGACAAGGCCTCCTCAGCCACCAATGATGGCTCCATCCGCTACCGCAGAAAC
AACAAAGGCGGGATCAGTATCACCGTCGATGCCACCGCCAGCGAAGTAACAGAAATCAAA
GCTGCCCTGGAACAAATGTCCAAAGATAAGGACTGCACACCAGGCACTTCCCTACTCCAC
ATCATTCGTGGCCTGCCGACAAAAGTCGTACTCAACACCTACGGCACCAAAGACAGCCCT
GAATACTTAGAAGGAGGAACCTGGCTGTCAAAGGAACAGTCTGAGTTCTGGAAAACCCGA
ACCACGTCCAGTCGGGATATGGACGCCGCCCACTTCTCTTACACCACCGCCTACGCTCCA
ACCCGAGAAATGCGCGTCTACATCAAAGGTCTACGCACCACCTGTAGCGTCCCTGGCTGC
AGTGTAGCGGTCGAAAACTGCCAACTGGACCACATCATCCCCTGGGGTGAAGGAGGGCCG
ACAACACCGTGGAATATTCATCCCCTGTGTGTCTTCCACCACATCCAGAAGACTGAAGGG
AGGCTCCAGTGCTATCCACTACCGGACGGCACCGTCCTATTCCTAGTGGATGGAATACCG
GTGTTCTCCATCCCCGACGGGCCTTTATCTAAATCGAATAAAACCTGGGGGACAAAGTTC
GGCAAATACATGGAGCGTCGAATCGCCGCC

>RXN02457-downstream
TAATCCAGCAAGCCAGCGTGATC

>RXN02460-upstream
GCGCCGTCGAAGCCGGACTCGTAGGCGTCTACTACCAGCAATTTGACCGTGCAGTCGTCG
AAATCGTCGGACTGTTCGGGCTAGAAGGAGAATTCTAATC

>RXN02460
TTGCGCGTCTACATCCCAGCAACGTTTTCCACACTCCGCGGACTCAATGAATCCCGCGTC
ATCACAGCACGCTCCGGATACGGTTTCGCAGTCACCCCAGCACTCCTTGACTTCTACACC
GACGGTGACGAAGAAGAAATCGCACATGCAGCCTTCCAAGACGCCGCAGAAGCCTCCATC
CGACTCCTCGCAATCGGCGACGAAGAAACATTTCCCTACCGCAGAGTCGTCGTCTCAGTA
GATGTTGACGACTCCGTGGTGACCTACCAGCCTGAAAACGGCGAATCCGTAGTCAAACTC
AGCCCAGCGCACATCAACCTCGACGACGTGGCAGCAATCCACATCGACGTTGAAGCCTCC
GAAGCAGACACCAAAAAAGCTATCGAAGTCATCGACGAATCCGACCTCGGCGAAGAAGAC
GCCGAACTCACCGTCGGAGACGCCCAAGACAACTTCATGGCCTGGTACGACCCAGAAGAG
CTCCCCTTCCTAGTCGAGCTCCTC

>RXN02460-downstream
TAGATCACATATCCCACGCGTCG

>RXN02464-upstream
ACTCGACATCCCAGAAGGTGTCACCGAACGAGTCGGACCACCAACCAAAGTTCTAGGCGG
AACAGCCCCACGACCACCACGCCGCACCCGGAAATAACTT

>RXN02464
ATGGCAGCAAAGCTTCAACCACTCAAACGCACCAAAAAAGACCTCATCGCAACCGGTGTC
ATCACAGCACTAGCAGTCATTGGCGTCGGCACGGTCTGGGCAACCGCACCAATACGAGGA
TCTGAACTCACCCCCGCCGACGAACCATTCATTGGCTCAACCACACTGGACGCCATCCCC
GAAACACTCAGCGAACATTGGCGAGCCACCGACACCTTAACAAACCACAAACCCCTCATC
ACCGGCGGAGTCATCTTCACCGCCGACGGCAACACCATTAAGACCTACACCCCCGACGGC
GCCCTCCTGTGGAGCTACGAACGCGACAAAGAACTCTGCAGCCTCTCCGTAGGATTCGAC
GCCGCCGTCGCCACCTACAAAACCGGAATCGGATGTGGCGACGTCACCGCCATCAACGCC
AACGACGGCCAATACCAAGCAACACGCAGCGCAATCTCCAGCGACCACGTAGCACCGATC
TCCTCGAACGATCGGATCGGTGTTCTCGGGACAGAACGCTTGGAGCTTTGGCGATCCGAT
CTGGTGCGAACCATCGAATACGGCGATGTGGAAGCTCCTCAAGAATCTGGGCAACAACCA
CATCCGGAATGCTCGATTACGTCCGCCATGACACGCAAAGATCTATTGGCTATCACCGAG
GATTGCCCTGACGGATCTTCTTACTTGAGGTTCATGGGCACAACACCAGACGATTCCCGA
ACTCCTGAAATCACCCAAGACATAGAAATAACCGATGGCAGGATCGTTGCCATCGGTCAA
TCAGTGGCTGCGGTGTATACAAACGATCCTTCGCCTCGAATCGTCTCCTACAACGATGAT
GGTGAACTAGTTGGAGAACAAGCAGTCGATGAGGTTGAGTTCCCGGATCCGCCGTTTCAA
AGCGCGACCGCTGATCTTCCACACCATATGAGTTGGTTCAACGGAGACAGCCTCGTACTG
TTCTCTCCCACTCAGCTCAATGTACGACAAAGCTTCAATGATGCTTTAGGAACCGGCATT

GCGTTGAACGGAAGTCTCCTCTACCCCACCGCTGAGGGCATCACGGTAGCTAATTGGGAC
ACCGGAGAGGTGCAGCGCACCATTCCGGTGGACCGTGCGGGCTACGACGGTGAAGTTGCG
CTCGGCGTTGTAGGGCAGGTGATCGTCGAAAAGCGTGGCTCTGAGATCGTTGCTCTAGGC

>RXN02464-downstream
TAGATCTCGTTGTTAGCCCAAAG

>RXN02465-upstream
CTGGTGCAATATAAAAGTTAACCAACCAGTCATCCAATATGTCGCCTAAGTAGTCTTCCC
AAAGTTAACAGCTAGAATCATGGCCGTGACTTCTCCGAAC

>RXN02465
ATGCCTGCATCAATTCGCTGGGGCGGCATCGTCGCCCTCATTCAATCCACCATCGGATTC
GGTTACGCCTTTTTCCTTATTTACAGGGAAGCTACGGGCGAGACGGATCCAAGCATCGTC
TACGAAACCGATAACGCCAACACGTGGGTTGGCTACGGTACCGCTGCATTCTTCATCATT
GTGTTCGGAACGGTTGTTGCAGGCGCAATCAACATGATGAAGGGGCATCGCTGGGGACGC
GGAGCTGTCGTCATGCTGAATATTATTTTGTTGCCGGCTGCGTATTACATGTTTATCGAA
GGCCGATTCTCCTGGGCGATCGTCACAGGAATCTCAGCTCTCTTCGTTTTGGGCGCACTG
TTTAATAAGCGCGCCGTCCTTTGGGCTAACAACGAGATC

>RXN02465-downstream
TAGCCTAGAGCAACGATCTCAGA

>RXN02466-upstream
CGAACCGCAAAGCGTTCCGCTGACGGAACTGCCGCCTGGCGGCAGCTACACCGAAACCGG
TGCTGGCACTTTCCGCCAGGTCGGCGCTGCTCTTCCTCGC

>RXN02466
GTGGGCGAGGGGCAGGAACAAACTTTTACGTACGTCATTGAGATTGAGGATGGCGTCAAC
ACGGCCGCTTATGGTGGCGACGATGCG

RXN02505-upstream
TCGGAAAGCAATCCGGAACATTCAGGTTGTAGACAATGTCATCAGTTCAGTTGACCGTCC
CATTAAGCGCACTGGTCGTTTGCGTATTCCGGGGGTCTTT

>RXN02505
GTGGCTGGCACTCATGCGTATGTCAATGAAACTCTTTCGGAAAATGAGTTCAGCATGTGC
CGAAAGAATGAACCTGGTTTGGTCATTGAGCTGGAGAACATCAGCATCGATCGCATTGTC
ATTTCCACACCAGATGCCCACCGCTATGCGGATGAGCTCATGGCGGCTGTT

>RXN02505-downstream
TAGAACTCAGTTTCCGTCAATAA

RXN02510-upstream
CCCGTCGATGAGGCAATCGCTGTGATTTCTTCCTGGATTGGTGACCGCATCAATGATCAG
CCGAGCGAGGACTCCATTGCAGCTCGCAGGTAGCCCTGAG

>RXN02510
ATGGACTCATCTGACAGCCACGTTGGTCAGGATGTATATGTTGATCAAGGTCTAGGGGAG
CCCGACAGACTGGAACGTCTGTGGGCGCCCTACCGGATGAGCTACATCAACACTCGATCT
GGCGGTAAGCAATCAACTACCGCCAAGCGGGACCCCTTCATTGAGGTTCCCAAAATGAGT
GATGAGGACGGCCTGATCGTTGCGCGGGGTGAGCTGGTGTATTGCGTACTCAACTTGTAT
CCCTACAACGCTGGACACATGATGGTGATCCCATTCCGTAAGGAAAAGAATCTAGAGGAT
TTGAGCTTGGCAGAATCTGCGGAGTTGATGCTCTTTACCCAAACGGCCATCAAGGCGCTG
AAGCAGGTGTCAAACCCTGATGCTGTCAATGTTGGTTTAAACCTTGGCAAAGCATCGGGT
GGCTCAGTGGGAGATCACCTTCATGTCCATGTGGTGCCTAGGTGGTCGGGTGATGCTAAT
TTCATGACTGTGATTGACGGTGTCAAAGTGCTACCGCAGACCCTGCGTCAAACCAGGGCC
ATGCTTGCGCAAGCATGGGGCACCATTGATGGGGCACCAGGCACTGTCGACCCAACGCTG

ACTTCAGCGATCCGTACCGCAGCACCGAAGGAGCAC

>RXN02510-downstream
TGATGCTGGGACTTCATGGACGT

RXN02519-upstream
AAACAGAAAATGGTTTCCTCGGGCACCTCGTCCCCTACGCCAATTTCTCGACACTTTGCC
GCGCATCGGCACCGCTGGTTCCAGATCAGCGACCCTCCAC

>RXN02519
GTGGAAGACGAGCAGAGCCCTTTAGGGGCAACGCTTTTCGACGTCGCGACCGGCGCGAGC
TCCATCAACGACCGCGATACCGACGCCTCAGGGCTTGAGCCTGAAAAGATTCGCCGATTT
GCATGGCTGCGCCTGATCGGCACCATGGGTGCGTTAATGATCGCGTTTGGTGCGCTGGGC
GCGGGTGCACTTCCGGTGGTGAATAATCCGTATGTGGATTTCCCTGGCGGAAACTTCATG
AGCCGAATGCTGCAGACCTCTTCCATGATCGTGCTCATCGGCGTGGGATTTTTGGTGCTG
GCGTGGGTGTTAATGGCACCGCTGGTGGGTATTCCTTTTAAACGCAGCGGAAACAGAACA
GCCAGCGTGAGTTTGTCCATGCTGCGCCGCACATTTGGCGCCTGGGTAGCGCCCATCATG
CTCACCGCCCCACTGTTTACTCAAGACATTTATTCTTATCTGGCACAAGGCTCTGTGACC
GCGCAGGGAATGGATGCCTACGCCGGTGGACCGCTTGAACTATTGGGGCCCGATAATCAT
CTGGCACGGTCCGTGCCCTTTATTTGGGCCCAGTCGCCCTCGCCCTACGGCCCTGTTGCG
CTGAGCATCGCGGCGTCGATAAGCGTTATTACTAATGACAGCATCGTTGGAGGCGTGCTG
GCGCACCGTATTGCGTCGCTGCTGGGCGTTGTGGCTGCAGGCTGGGCGATCACCATGCTG
GCCAGGCGCTGTCGGGTATCTGAAGAAGCGTCCTTTTACCTGGGCGTACTTAATCCGCTG
CTGATTCTGCACCTGATCGGCGGTATTCACAACGAATCCATCCTGCTGGGATTTTTACTT
GTTGGCCTGGAACTCGGACTGCGTGGCACCGACCGGATTCAAACAGGGCTGTGGGGGCCT
GCGTGGACATATATTGCACTGAGTGGCGTATTGATTTCTTGCGCAGGCCTGGTCAAGGTG
ACCGGCTTTATTGGGCTCGGTTTTGTGGGCATGGCCTTGGCCAGGGCGTTTCATGCACGT
GGACATCGACACGTCGTTGCGATCGGCGTTGCAGGCCTCGTTCAAGTAGCAGCCCTGGTG
ATCACCGTGGTTGTTCTCAGTGTGATTACCGGAATCAGTTTGGGGTGGATCACAGGTCAA
GGTGGCGCTGCGACGATCCGAAGCTGGATGTCTATGACCACCAACATTGGCGTTATTTCT
GGATTCATCGGAATGAATTTGGGGCTAGGCGACCACACCGCAGCCATGCTCGTTGTGACC
CGTGCAGCCGGAATCGCGGTAGCTGCCGCCTTCATGGTTCGTATGTTGTTTGCCACATAT
AGAGGTCACATTCACGCTGTGGGCGGACTGGGCGTGGCGACTTTCGTCCTCGTTATCCTC
TTCCCCGTGGTGCATCCGTGGTACATGCTGTGGGCTATCGTGCCGCTAGCTTCCTGGGCA
AATAGACTGTTCTTCCAGCTCGGAGTGATTGCCTACTCCACTGCCTTCAGTTTCTTTGTG
CTGCCTCGCGGGCTTGCACTTCCAGTCGGAACTGTCTTTTCCATCTACTTCGGCGCAGCG
CTCGGATTCAGCATTCTCCTATTAGTTGGATGGTGGAGTTTGAGGCGGAATCCAACCTTT
GGTTTACAC

>RXN02519-downstream
TGATCAACTGTGACTACTGATTT

RXN02520-upstream
TTTGCGCTGGTAGGGGGGAAGGGATTGGACACGGGAATGGAATTAGGGAACACTTGTGTT
GTCTAAAGGTGAAAGCTAAATCAAGCAGGAGGTGACACCA

>RXN02520
GTGGGAGATGTTGTAAAAGGCAACGACGCGCACACCGGAGACGGTGATACGCGCCGAAAA
ATTCTTCTCATCCTGTTGGAACGTGCACCGGTGATCGCTTCAGATATTGCTGAACAGCTT
CAGCTTTCAACTGTGGGAGTGCGCAGGCACCTAGACAACTTGGTTGAAGAAAATCTGGCG
GAGGCGGCAAATCCGCGCCAGAACCCATATGAGCCCAAAATGCGCGGTAGGCCAGCAAAA
ACTTATCGGCTTACTGATAAAGGTCGCTCAATCTTCGGCCACGAATATGATTCCCTTGCT
GCGGCAGCTCTAGCCACTCTTCGAGAGGTCGGCGGAGATGATGCAGTAAGGCAATTTGCT
AGAAAGCGGATCGAAACAATTGTTGAGGGTATTACCCCAGCAGATGTCACAGATCAATCA
ATCGAAGATACAGCCAAATCTTTAGTTGAAGCTTTTAGTCGGCATGGTTATGCAGCAACT
GTCGATGCCACTCGAAACGGGTTGCAACTCTGCCAGCATCACTGTCCAATATCTACAGTC
GCCACGGAATTTCCGGAACTGTGTGAGGCAGAGCATCAAGCAGTCTCAGAACTTTTGGGG
CAGCACACGCAACCATTGGCAACAATCGCGGACGGCCACGGCATCTGCACAACAAATATT
GCATTGACACCCATCAAACACTCC

>RXN02520-downstream
TGATGAAAGGAGCGGATCATGAC

RXN02534-upstream
TTACCAGTAATCTATGCAGATTTACTGTCCGTTGGGGATCCGCGCCTATCGGAAGTTGCC
TACATTATAAAAACTCAGATTCAGGAATACACAGACCATG

>RXN02534
ATGAATTCACCGAACGCGGACATTATTTTAGTAGTTAACAAGCTGTCCAAGTTTATTGAT
ATCGAAAATATTATGCTCGTTGGAGCACGATGTAGAGACATTCACCAGCAAAAATATCGC
GATCAAACAGCGGGTAGAAGAACTAAGGATGTTGACTTCGCTTTAGCTTTAGAAAGCTGG
GACGACTTCAATCTATTAAAGCAACAATTCTCACCGACTGGTAACGCATGGCAAGGAATC
ACCATTGGAAATATTCCAGTAGATCTCGTGCCATTCGGAAATATTGAAAACCCACCCGGT
GAAGTCTTGTCCAGAAAAGGTCATCTACTTAATGTCGCTGGGTTCAAGGAAGTATTCGAG
CAAGCTGAGCTATATCCCCTAAATGATGCGATAGACATTAAGTTGTCTACAGTTCCCGGA
CTTACTGCGCTAAAGCTACATGCATGGCTCGACCGTAAAGAAAATAACATCAAAGATGCA
AGCGATCTAGCATTAATCTTGTCGTGGTACGAAGAGGATGTAGAAACTTTATGGAATCGC
TATTTTGCCCTGGAAAATCAAGGATACATAGGTGAACCAGAGGCAATGGCAGCTGAATTA
CTAGGACTTGACACTGGAAGAATACTCGGCCACAAGGAAACTCAAGCCCTCCTTGATCGA
TTTAATGAACAGTCTCCTCCTGAGCTAAACCAATTTGCTGAATCACTTGAAGCCCCTCCT
GAACACAGTCACCCATTAGAACGGCGTCGTATCCAGGTCGAGGCACTGTTAGGTGGACTT
AGAGATTCCCTCGGTTACGATGAA

>RXN02534-downstream
TAGCTTCCAATCCCGCATTGTTC

RXN02537-upstream
ACCTCCATCTCAACAATCATCTTTCCGATATGCGCACTGTCAGCGAGCAGATGCTCAACA
TAGACGTCGATCTTGGCCACACACTGAATAAGTTGCACTG

>RXN02537
ATGCTCGCCCTCAAAAGTTCAGAATTAGAAGGCATAGCCACATCACTCACCGCCGTGGCG
GGTGCGCTCCACGAATCAAACACTGACCGGTTGCAGTCCTGGCAGCAGCTCGAAACGATG
ACCTCTGCCAGCTCCCTTATCCAGGGCTTTATCAAGCTTGTCGATTACAACCGACCCACA
GTGAATATCGTGGAACAAATGCACAAAACCGCATCCACGCTTTTCAACACCGCTGATTTC
CTACGCACTTTGGAAGGCTATGTTGATGTACTGGAAAAACAAGCCGATAAATCTATAACG
CTCACCGTCATGCTTCGATATATTGCCAGCTTGAGTAGCCTTTTAGACCTCATGTGTGCA
CGCGAGATCAACGCGTTGTGCACAGCGATTACTCCAGAACCATTGAAGCATCTGGGCGAT
TTTGGCACTCTACCGCCTCAGCAATCCACGAGTTTCATTTGG

>RXN02537-downstream
TGAATGCCCCACCAGAAATCCGT

>RXN02538-upstream
GCGAGATCAACGCGTTGTGCACAGCGATTACTCCAGAACCATTGAAGCATCTGGGCGATT
TTGGCACTCTACCGCCTCAGCAATCCACGAGTTTCATTTG

>RXN02538
GTGAATGCCCCACCAGAAATCCGTGCCTTAGCCGAAGCCCATCCCGATATGCAGATCCTA
GAAGCCGGCGATGGTTCATTGGTAGCATCGTTTGGGGATATTGATAGGGCTACGACCGTG
ACCACCATCGTGGCAGGTGTGGGTTCCTCCAACCCAGAAGGGTGGAATACATATGTTGAC
CGTGCCCGCACAGTATCTGCTTCCACCGGTTCCGCAACGGTGTTGTGGCTGGGATATCAA
GCACCCGCTTCGATTCCTGCTGCGGTATCCGGCGCGGCAGCGAATCGCGCTGCCGCGGAT
CTCCAGAGGTTTCAAGCGGCACTACAGTCCCGCAATCCCCACCAAAGAAAAGTAGTGATG
GGCTACAGCTACGGTTCCACAGTGGTGGGAAAAGCTGCGTCTTCCGGCGAGCTCAGTGCC
GATGCGTTGGTATTGGTTGGCAGTCCCGGCGCGGGTGTCTCGCACTCTTCCCAGCTTGGC
GCACCTGTGTATGCGGTAACAGGGTCTGCTGATCCCATCGGTTTTGCCGGCACCCAATAT

GACGGCATCCACGGCACTGATCCCACCGCTGCCCTATTCGGTGCAACAGTGTGGGATTCG
CCCTCAACGCATTCCGGTTATTGGAATGACCAGGAGTTCCTGGGCAATGTGGCGGAGGTG
GTTCGCGGCAAA

>RXN02538-downstream
TAGAAAAGCCGCCGCACACTGGA

RXN02555-upstream
GTTTTATCGCTATTTAATACAGGCCTACCCCCACTACCCCCATTCAGTTCAGGGAATCCC
CGGATTTAAAACAATTAAAAACCCTCTAGAATGAGACATT

>RXN02555
ATGGGCGAACAATTTCCAGGCGATAAAAACATCCGAGTCAGCGACACCGAAAGATCAGCA
GCACTAGCAGCACTCGGCCAGTTCTACGCAGAAGGTCGCCTCTCCCTAGAAGAAACCGAC
GACCGCTGCGAAGCCGTCGCCGACGCCAAAACCCGCGGCGACCTCAACGCCATCTTCTAC
GATCTGCCCAACCAACAAATCGCAGTCGTCGACCGCTCCGAACAAACCTACACAGCCACC
GAAGTTGCCGAACTCCACCGCAAAGGCGCACGCCCACGCGCCGGAATCCTCGGACTCACC
ACAGTTTTAGCCATCACCGGTACCGCTGCTTTCGCCAGCACCACAGCTTTTGCAACAGTA
CTTTTAGCCCTGATTCCGATCGTGTTCATCATGCTGTACGTGATGAAAATTGGTCCTGAA
TCCTGGCACGCACCAACACCTCGCCAACTTCAGCGAAAGCGCATGATCGAACTGCGTGAA
AAGGAAAAACTCCGCGACATGGAGCTCAAAGCCCAGCGCAAGGAACGCACCCACGCATTA
ACCAACCGCGCGTTGGATGCTGCTGAAACTGCTTTCAACACCAAGCCCTGGAAGAAGAAC
AAA

>RXN02555-downstream
TAGGGCTTTTGAAGTGTGTCGCG

>RXN02564-upstream
ACACCACAGTGAAGCGGTGACGTGAATCACCCAAGCACTTAGGCATCAAACATTCAAGAG
CTTGTTGTCCAAAAGTCCGACCGAGAGGGATTCCCCCAAA

>RXN02564
ATGGCCGAAGTAGGAGCAGAACCCGCAGGGTCTGCACAATCCAAAACTAAACAATTTGTT
GTAGGTACCGCAGCGGTGGTCATCACTGCAATCGCTGCGTTTTTCTCCATCCAGTCTGCA
TCCGGTGGCGAGGATATTCGTTCCAACATGACGCTGATTGCTCCTGCAGCTGCAGGTGGA
GGTTGGGATACTTTCCAACGTGAGCAGCAGCAGTCTATGCGCGTGAATAAGATCGTGAAC
AATATTCAGGTGGTCAACATCCCTGGAGCTGGTGGAACCATTGCACTTGGCAAACTGTCT
ACCATGACTGCACCGAACACCTTGATGGTGGGTGGAACGGGGCATATCGCAGCACAAATT
CAATTCGATACCCCTGCGAAAATCCAGGATGTCACCCCAATTGCTCGTGTGGTGGAAGAG
TTCGACATCATCACCGTGCCAGCGGATTCTCCATACAACACCCTTGAAGAGCTCATTGAA
GGTTGGAAGGCAGATCCAGCAGGAGTGTCCTGGACCGGTGGTGGTTCCTTTGACCAGCTT
GTTATGACAGAAATTGCACTGTCTGCAGGTATAGATCCTAAGCAAACCACCTTTATTCCT
TCTGATGGTGGTGGCGAAGCGATTCAGGCGCTACTGAACGGAACCGCAAAGGCATCAACT
GGTGGTTTTGCTGATATGTATCCGCAGGTAGAAGCCGGTCGATTGAAGGTTTTGGGAATT
GCTGCAGAAGAACGCCTTCCAGGTTCTGACATTCCAACGCTAGTGGAACAAGGCTATGAC
GTGACCTTGACCAACTGGCGTGCCATGTTCGCTCCTCCTGGTTTGAGCGATGATCAAATT
GCGGAACTTCGAGCAATCGTTGCGGAGTCTGTGGAGACTGCTGAATGGCAGTCCGCGGTG
GAACGAAACTACTGGATGAACGCCTCACTTGAAGGCGAAGAACTCGACCAGTTTGTTGAA
GATGAAATTGACCGAATTGATCAGCTATTCAAGGAGATGGGC

>RXN02564-downstream
TAGTGAACGTCACTGAACAATCC

RXN02568-upstream
CCAGCTACGATATGGAATTTCACCAAATGCGAACTACCCTAAATACCAAAGACAGACAGT
GACAGCCCCTTCGAGAATGCAGCAAGAGACGACACCTCCT

>RXN02568
ATGGACGGCACCTCGCCACAGAACAAAATTTCCACCACTCCCCCAGCGCCAGGAAATGCT

ATTCCTGCACCTGGAGGCGCCATTCCTACACCAGCGAAAACTGAGCAGGACGCAGTACCT
CCAACTGTGGCGGCGAAACTACCCGTACCTGGAAGTTCTATTCCAGCACCCGGTAGAGCA
TTGCCAACTCCAGTGGCTCCGGGAGGTTCCGTCCCAGCTCCGAGAGCGTCCGCACCTGCG
GTTCCTAACGTTCCTGCAGCTCCCGGCGCTGCTGTTCCAGCTCCGGGAATCTCGATCCCG
GCAGCACCTAGTGCCCCAGGCAGTGCAATTCCAACACCAGGCACAGCAATCCCTGTGCCT
GGAAGTGCAACTCCTGTCCCAGCACCTGGGGTTAGTGCACCTGGCGCAAGCGTTCCAAGC
ATTCCAGTACCAGGATCTGTCACCCCACCTGCACCAGGAATTTCCGCACCTGGCGGTGCA
CTTCCGACTCCTGGCAGTGCGCCCCCAACACCTGGCGGTGCCCTTCCGACTCCAGGTGAG
GCACTTCCCGTTCCCGGAGCACCTGGTGCACCCGGAGCATCCGGAATCCCAAGTCCTGGC
CTTCCAACCCCAGGTGTCCCAACTCCCGGAGCTTCCTTACCAGTCCCAGGAGCACCAGAC
GCACCTGGAACCCCAAGCATTCCCGCAGCTCCCGGCATTCAAGCACCAGGAATTCCAGCA
GCACCAGGAGCCCCTGCCCAAGCTGCTGCTCACGCAAAGCCAGTATTCCAAGATGCAGAG
AAACGACCTCGCACAGATGAAGCTGGAAATGCGAAGAAGGAACTGCCGCTGAGAGTTCGG
TTGGCGCAGCCAATTACACGTAAGCAGTGGGCAATGACTCTTGGTGTCCTGGTTCTCGGA
GCAATTGTCGTGGCTGCAATCGCGGTGGTCCTTGCCAAATGGGCGTTTACCACGGAGTGG
TTGCAGGACTTCGTCGAGAAGTATCCGGGTAAATATGACAACCCCGAAGGTGCGCCAGTA
GGAATTCCAACGTGGCTGAGTTGGCAGCACTTCTTCAACATGTTCTTCATGGTGTTGATT
ATCAAGACGGGCATTGAGATCAATAGAACCCGCAGGCCAAAGGGTTATTGGACGCCGAAA
AAGGGTGGCAAGAAGATCTCCTTGACGTTGTGGATCCACCTGGTTTTGGATTTGTTGTGG
ATCATCAACGGTGCGGTGTTCATCATTTTGTTGTTCGCGACGGGTCAGTGGATGCGCATT
GTTCCAACCAGTTGGGATGTGTTCCCGAACGCGCTGAGTGCTGGTTTGCAGTATGTGTCG
TTGGATTGGCCGACTGAGAATGGTTGGGCGAATTACAACAGTTTGCAGGAGCTGACGTAC
TTCTTCACTGTCTTTATTGCGGCACCGTTGTCGATTGTGTCTGGTTTCCGGATGTCGAGT
TACTGGCCTAAGAACAATGCGACGATGAATAAGTTGATCCCCATCGGGTTTGCTCGTGCG
CTGCACATGCCAGTGATGGTGTATTACATCGTGTTCATTTGTATCCACGTGTTCTTGGTG
TTGGCGACCGGCGCGTTGCGCAATTTCAACCATATGTATGCAGGTCAAGACGTTGTGAAC
TGGGTTGGTTTTGGTTGGTTCGTGGCGTCGTTG

RXN02593-upstream
GCGTTCACTTCCGCCACCTTGAGGATGAGTGGTATCACGCCAGCACAACAAAAGGATCTT
CATAGGGTTATTCAGTCTAGCTGCTTTTAAACAAGCCATA

>RXN02593
ATGGAAGCCATGGCCACAACGATCACCGTTTTCTCTCCCACCCACTCCCCCGCACAAATC
CGCGAAACCATCCTCAGCGCCGCGAAAGAAGACGACGTGGACTTCCTCGGAGTCCCCTTT
ACCCACCCCAGAAACGTCACCATCGAAGTCGACGACGAACTGATCAACGACTGCTTAGGC
TGGCTCGACGACGTGGCACTCGCCTCCGGCCTGGGCATCCAATACAACGACGAAGTGCTC
CGCTACGGCGACGAAGACATTTCCTTTACCGTCCAAACCAAAAATGACGATGACGCCCGC
ATCGGCGCCTCCCGCCTTGGACTCGAGCACCAGTTGAACGTCATTGCCGGGGGCTCTGGA
GATTCCGGGGATTCCGGGGATTATTTGAAGATTGCACACTTCGACCTAGACAACCCCGCC
GACGAGTCCTCCTACATCTTCGCGCGCAGCCTCGCAGAAGTAGACGGCTGGACCCTAGAA
TTCGGCGTCGCAGGAGTAAAAAACACCACCATTGTTTCCTCCATCGACGATGCCATCACC
ACCATTTTGCGATGGATGAACGGCGAAGACATCCGCGACCTCAACTGGACCCGCGCA

>RXN02593-downstream
TAAATGGCCTCATTTCCGGAGCT

RXN02606-upstream
AGGGCGCGGATCACTTCGGATCTGTGGATAACTTTTAAGGCCCTTGTTTTCCCCTTGAAG
CTTCGGTTGTGTGGAAAACAGAAAAGGAGGGGAAAACAAA

>RXN02606
ATGCAAGAAATCCACACCATCATGAAACACATGGACGCGCTCATCGCCGACCCGTCCGCC
GCCGCATTCAAAGCAACACTCCCCTTCGCCGAACTCCTCGAAAAGCTCCACAACAAAAAA
GCGCTTTTCGACGCCGCCCTCGCCAAATCCGCCGAGCGCGCCGATGCCGGACGCATCATC
GGAAAAACCTCCCACATCGATGCCCTCGCGTACCTTCTCGACATCTCCAAATCCGAAGCA
TTCCGACGCACAAAACGCGCCGAAGAACACTACGGCAACCCAAGCCCGGAACCCAGTTCA
GAAGAACTCGCGAAAGAAACCCCCGAAGAGAAGCTAGCCAGAGAAGAAAAAGAGAAACAA
GACCTAGCCGAACAAGCAGAAGCCAACCGCATCGCCCGCGAACACGGCATCTCCGCCGAA

AAACAAGACACCATCCGCTACGAACTAGAAAAACTCAACGACAACACATCCCTATCCCGA
GCCTCACTCCGCAAACTAGCAATGCAGGAAGCCACCAGCCGAACCCCCGAAGACCTACGC
AACTGGACCCGCAACAAAGTTATCCGCATAAACCCCACCGCCAAAGACCCACTCGCCGCA
GTAAAGAAACGCTCCTTAAGCATCGGACGCCAAGACCACGACGGCGGAGCCAAAGCATCC
CTCTATTTAGATGCCAAAGGTCTAGCCCTGCTCAAATCACTGATGTCTAAAGCCAAGCCG
GGGCATTTGCTTGAAGACTCTTTGGCGGAGGATAAACGTACGAAACCGCAACGCCAATAC
GATGCCTTCGCCGACATCCTCCACCGCGCACACAGCGATCTCCTCCCCGCACGATCCGGA
GTGGGCACCATCCTCGTCTCCCTCTCCGCCAAAGACGTAACAAACCTCAAAGCATCGGGC
CCCGACCACCGCTACCCCACCAGCACCGGCATAAAACTCACACCGCTTGAGATCCTGCGA
CTCGGTGCAGCCAAATATGACTTCGTGACCGTCCTCGACTCCGAATCCGGCCGTCCGCTG
CACCTGGCACGCACTCAACGCACCGCCAGCCTGTATCAACGCCTAGCCCTCTTCGCCTCC
GAACTCGTCTGCACCCGCGAAGGCTGCGACTCCCCCTTCGAAGACAACGAAATACACCAC
ATCAGATCCTGGCTAGACGGCGGCCCCACAGACATAGAAAACATCACCAACATCTGCCCC
CACGACCACGGAAACAACAACGACCAACGCGACGGCAAAGACAACATGGGGCACATGAAC
ATAGATCCCACAACCGGGCGCGTCGGATATCAACCCGCCGACCGCCGAAAACCCATGCGG
TTTAACAACACCGCAGCCGCAGCAGAATCAGGAGGAGCACAGGCCAGGACC

>RXN02606-downstream
TAAGTTTTTAGCGCGCCAAAAAG

RXN02610-upstream
CCAGCTCATCGTGCAGGGACGCACCAGCGTGAAGGAAGATCAAGCAGCGGAAATTTCTAC
GCTGCTGAAGGAATCTGCGGATCGGACGTATTGTTAACCG

>RXN02610
ATGAGGAAAACCATCACCGTTATTGCTGTATTGATCGTCCTCGCCTTAATCGGCGTGGGC
ATCGTGCAGTATGTGAACACATCCGATGACTCAGATTTCATTGGCCAGCCTGGCGAGCCA
ACCGGTACCGAAACCACGGAACCACCGGTTCAACCTGATTGGTGCCCTGCGGTAGAAGTC
ATTGCCGCGCCGGGTACGTGGGAGTCGGCTGCTAATGATGATCCGATCAACCCGACCGCT
AATCCGCTGTCATTCATGTTGAGCATCACTCAGCCACTGCAGGAGCGTTATTCTGCGGAT
GACGTCAAGGTGTGGACGCTGCCGTACACTGCGCAGTTCCGCAACATCAACTCGCAAAAT
GAGATGTCCTATGATGATTCGCGCAATGAAGGCACCGCGAAGATGAATGAGGAACTGATC
AACACTCACAATGAGTGCCCTGCCACGGAGTTCATCATCGTTGGTTTCTCCCAGGGTGCG
GTCATTGCGGGCGATGTGGCTGCTCAGATCGGTTCAGAGCAAGGTGTTATTCCAGCTGAC
AGCGTCAGGGGTGTCGCCCTGATCGCTGACGGTCGCCGGGAGCCTGGTGTGGGCCAGTTC
CCAGGCACGTTTGTGGATGGCATCGGCGCGGAGGTTACTCTGCAGCCTTTGAACTTGCTG
GTGCAGCCGATTGTTCCGGGCGCAACCATGCGTGGCGGGCGCGCGGGCGGTTTCGGTGTG
CTCAACGACCGGGTGCAGGATATTTGTGCTCCAAATGATGCGATCTGTGATGCTCCGGTG
AATGTCGGCAACGCCCTTGATCGTGCGTTGGCCATGGTCTCCGCCAACGGTGTGCACGCG
CTCTACGCCACCAATCCGGATGTTTTCCCAGGCACAACCACCAATGCGTGGGTTGTGGAT
TGGGCGACCAACCTCATCGACAACGGA

>RXN02610-downstream
TAAAGCTTTTTCGCTTTTCGACG

RXN02624-upstream
ACCCGGTCAGATCCGACGTCGCCGGCCAAAACCGCAAGCACCTGCGCAAACGCCACAGAA
GGCAGCTCAGCAATCAAAGTTGCTGCGTTTCCTTCCAACC

>RXN02624
GTGCTGATTCCGCATGGCGTGGCGGTGCTTTTGGTTATTATTCTCGCCGTAGCCTCCCTA
ATGTTCACCAATTCTTCAATGGTGAATCTTTCGGCAACGATTGCACAGCTGTGGCTTTCC
CTAAATCTCGGTGCGGTGGACGGCAGTGGGGAAGTGATCTCAGTACTGCCCACGCTTCCC
GGCTTTATATTCCTCTGGGCCATCGCCGCGCGCATCCACCGCGCAGTCAAAGATCGTGTC
AGCATCGCCGACTTAGGCGTCCTCGCAGCACTCGTCCTCGGCATCCCGCTTGCGCTCACC
GCCATCGCAGCGTTCATGCTTTTCGACGCCTCCAGCGTCCTCAACGTCGAGGTCCCGCCA
ATCACGCGCCTCCTACGCGTGATGTTGTTCCACCTCAGCGCCCTCTTCCTCGGCATGGGG
CCACGCCTGTGGCAGGCGTTGGCGCGCCGCTACGGTGCTCCAGAATGGCTTATCGACGCC
ATCACCCAAGCTTTCCGCTTCCTCATCGCATTTGGAACAGTCTCCTTGGTTTCCGTGCTC

GTGATGACCGCGATCAACCACAGTGCATTCACCGCGACCATGCAGGGTTACGACGACTCC
GCCTCTGTTGTGGCCTTGATCGTCCTGAGCATTCTGTATCTGCCCAACATGATGATCTTT
GCGATGGGCAATCTGATCGGCTCACCCCTTTACTTCGGTGACGCCTCCATCAGCGTCTTC
AGCGTGCATTCCGTTCCATTGCCACCGCTTCCCATCCTCGCAGCTCTCCCCAGCGAAGCC
CTCTCATGGGCAGTGGCCTTACTGGTCATCCCTGCAATTATTGCCACCTGGGTCTGCGTG
AGAAACCCCATGCGCCTTGCCGTGAACACAACAGCAGCAGTCATTTCAGCACTGTGTTTC
CTCGTCCTGGCAGTTTTCGCCGGCGGAACCTTGGGCGTATACAACTACGTCGGACTCAAC
CTCCTGGCGTCAGTTGGCCTAGTTTTCGTCTATTTCGCCCTCGTTGGACTCCTCATCGCC
GGAATCGACAAGCTGCGCAACCCTGTAGAAGTTAAGTCTGTTAAGGCTGTGGCTGTTGTG
GAGCCCGAGCCTGAAGAAGTTGAAGAGGACGAAGAGGAGCATGTTGAAGAAGAAGTAGAT
GAGGAGGAAGAGGAAGTTGAGGAAGGGGTAGAAGAGGTCGAAGAAGACGACGCAGAGGAT
CCTGAAGAGAATCCTGAAGAGGAAGAATCCGACGAAGAAATTGAGACAGAAACTGAGGCT
GAAGAAACCAATGATGGTTCCGAGGCCGAAGACCGT

>RXN02624-downstream
TAACATATCTGTTGTGAATTCTG

RXN02626-upstream
GTAGCGGTCGAATTATTTGCCTGTGGGCATAATTTTGAGACAAAATAATAGAAACGTCTC
AGATGTTGGGAAGTTCTTCACGCTATCAGTTAGGGAGCAC

>RXN02626
ATGAGTACTCAAGTTGAACTCAAAACACCGAAATCGGAAGACCGGGCAGCATATATCGCT
GCATTGGGATTCCCGGTCTTGGTCATCATTGGCGGCATCATCGGATTCACAGCCTCGGAT
GTTGTGCTCAATATTTCTTCGTGGGTCAATCCTTTGCTGGGCATCATCATGTTCTCCATG
GGCCTGACCTTGAAGCCAGTTGACTTCGCCCTTGTTGCTAAACGCCCACTCCCAGTTCTT
ATCGGCGTGATCGCCCAGTTTGTCATCATGCCCCTGATCGCATTGCTGGTGGTCTGGGTT
TTGCAGCTGCCTGCGGAAATTGCGGCCGGTGTCATCTTGGTTGGTTGTGCACCTGGCGGA
ACTTCCTCCAACGTGGTGTCTTACCTGTCCCGTGGTGATGTTGCGCTGTCTGTCACCATG
ACTTCCATCTCCACGCTGCTTGCTCCAATTTTCACTCCACTGCTTACCCTGTGGCTGGCG
GGGCAATACATGCCACTTAATGCCGCTGATATGGCTGTATCCATCGTCCAAGTTGTGCTG
ATCCCAGTCGTGGGCGGACTTGTTGTGCGGTTGATCTTCCCGACACTCATTGGCAAGGTT
TTGCCTCTTTTGCCATGGATTTCAGTCATTGCGATTTCATTGATCGTTGCCATCGTGGTC
GCTGGTTCAAGGGATAAAATCCTCGAAGCAGGACTGCTCGTGCTGGCTGCCGTGATTATT
CACAACACCCTCGGCTACTCCCTGGGATACCTCGCTGCGAAATTCACTGGGCAGCCTGCT
GCAGCTCGACGCACTACCGCGATTGAGGTCGGTATGCAAAACTCCGGCCTCGCAGATGGA
CTCGCATCCCAGTACATGTCACCAATGTCTGCTCTGCCAGGCGCTATCTTCTCTGTCTGG
CACAACCTTTCCGGAGCACTTCTTGCTGCATTGTGCAGGGCGTCCGATAAGAGGGCTGCG
GAGAAGGTGGCTTCAGAAAAGGCTGCCTCGGAGAAGGCCGCTTCC

>RXN02626-downstream
TAAAAGGCTTCGCTCCTAAAACT

RXN02656-upstream
GCCATGTGGGACAGTCTAGCCATCTCCTTACACCCGTGAAACTCCTATTTCATTAACGCA
TTGATCTCGGCTTTTCTAACCTAGGTATAAGGTAACAGCT

>RXN02656
ATGATTTTCGGCGTACTCGCATACTTGGGATGGGGCATGTTCCCGGCCTTTTTCCCACTA
CTTCTTCCGGCAGGACCGTTCGAAATTTTAGCGCATCGGATCCTATGGACTGCTGTATTA
ATGATGATTATCATTAGTTTCACGTCGGGATGGAAAGAGCTTAAGTCCGCTGATCGCGGT
ACATGGTTACGCATTATATTGTCATCGTTGTTTATTGCCGGGAACTGGCTGATCTATGTC
ATCGCTGTCAATTCTGGGCAAGTTACTGAAGCCGCTCTCGGATACTTTATTAACCCCCTG
TTAAGTGTCGTGCTTGGCATTGTGTTCTTCAAAGAACAGTTACGAAAACTGCAAATTAGT
GCGGTGGTTATTGCTGCTGCGGGGGTTTTGGTACTAACATTTCTAGGTGATAAGCCACCG
TATTTAGCGATAACACTAGCATTTACATTCGGCATCTATGGAGCGTTGAAAAAACAAGTC
AAGATGTCTGCTGCTAGTTCTTTGTGCGCTGAAACTTTAGTACTGCTGCCCATCGCAGTC
ATATACCTGATTGGGCTCGAAGCTTCCGGTCACAGTACCTTTTTCAACAATGGCAGTGGG
CACATGGCGTTATTAATCTGCTCGGGTTTGGTCACAGCCGTCCCGCTGTTGATGTTTGCA
TTGGCCGCCAAGGCAATACCTCTTTCCACTGTCGGCATGCTGCAATATCTGACCCCAACG

ATGCAGATGCTGTGGGCATTGTTTGTGGTCAACGAATCAGTAGAACCAATGCGTTGGTTC
GGATTCGTTTTCATTTGGATCGCAGTTACTATTTACATCACAGATAGCCTACTTAAGAAG

>RXN02656-downstream
TAGGTAATAGCAGTATTGATATG

RXN02673-upstream
ACGCCCAAAACGCTAATCCGCTGAACAGGCCGATGAAAGTAATAGAGTGTTCTGTGTGGG
AACGCCGAGACATAATGAAGTCATTTACAAGCGCCGCCGC

>RXN02673
ATGGCAGCGCTCCTAGTTCTGCTCGTCGTGATTGCCTTGATTATCTGGGCAGTCGTCGCG
CTTCGAGGTGGATCATCGGAGCCTGAGGAAGAGCAGCCAAATAATGCTGTAGTGACCTCC
TCAATGGAATCTTCCGCGACGTCTAGTTCTTCTTCTAAAGAATCCACGACTGAAGCCACC
ACAGAAGAAGAGACTTCCAGTGCTGAACCAACCGCAACATCCTCCGTTGCAGCAGATGCA
AAAAAGACCTGTGAGCTTAGTGACTTGGTGATTTCCGCAAGCACTAATCAGCCGACTTTC
TCAGGTTCTGCGCAGCCAGAATTATTTATGGCTGTGCATAATCCGACTGCTGTTGATTGC
GAAATTGACCTCGAGGAGAACAAACTCCGTTTCGAGGTATACAATCTCGCGACCAACGCA
CGAATCTGGTCTGATGTCGACTGCAACCCTGCAGTTGAAGACGGCACGAGCGTGTTCCCT
GCCGGCGAGGATCGCTACTTCCAGGCAACATGGTCTCGTACCACTTCAGCGCCAAACCAG
TGCAACAACCGCACTGATGTCCCCGCCGGTGGCTACTACTTGCACACTGTGGTCGGTAAT
AACCCTTCACCAGCGGTGACCTTTAACCTAACT

>RXN02673-downstream
TAAACGGCCAAGTCCGTCGGTGA

RXN02680-upstream
AATACCAGGTCAACACACACAGGAACCGTTCAGAAACCTTCCAGATTGCTCACTTTTTAA
TTTCACTTTTTTGAGAAGTTTTACTTTTATATTAGTTCTC

>RXN02680
ATGCGCCTCAACAAACGACTCCCAGCGGCACTCTCCGGACTGCTGCTCTCTGCTGCCCTT
CTTGCCGGATGCTCCACTTCTGGAACCGCCGAGACCACGACAACAACCGTTTCATCTGCT
GCGGCATCAACAACCACTTCCACCTCCTCTGCTTCGTCTTCCTCTTCCTCCTCCTCTTCC
TCCTCTTCCTCCGACTCAAGCACCACCGCCGAAACCATCTCCAACACCGCGGAAGCTGCC
CAAGCTTTCTTGTCCACCCTGTCCACCGAAGAACAAGACGCCGTACTCTACGACTACGAC
GCCGAAGAAAAGTCCACCGGCTGGTCTAACTTCCCAGTCACCTTCGTGCAGCGTTCCGGC
GTGAACCTCACCGACCTCACTGAGGAACAGCAAGCAGCTGCCCTCAACGTGCTGAAGAAC
CTGCTCAACGACGACGCCTACCAAATGATCGAAGACATCATGGCTAGCGATCAGTACCTC
AACGACGAAAGCAACACCACCGAGGATTCCCTCGGCCAGTACTACATCGCATTCTTCGGC
GATCCAAGCAGCGACTCCGACTGGTCCATCCAATTCGGCGGACACCACATCGGCATCAAC
ACCACCTTCTCCGACGGTGCCATCACCTTCGCCCCAACCCACCTTGGCACCCAGCCTTCC
GAGTGGACCAACGAGGACGGCGAAACCGTTGCAGCACTAAGCAACATGTACGAAACCGCC
TTCGCCTTCTACGACAGCCTCGCCGAAGAGCAGCAAGCACAGCTCTACCAGGGTGAAGAG
TTGGATTCCATGGTGTGCGCACCGGGCAGCACGTGCGACTACCCAACCGGCACCGGCTTG
AAAGGCTCTGACCTCACCGATGAGCAAAAAGAATTGCTCATCGATGTCATCGCAAACTGG
GTTGGCCTCGCCGATGAGGAAACCACCGAAACTGAACTCGATGCCATCCGCGAAACCCTG
GATGACACCTACATCAACTGGTCCGGCGCCACCGAGTACGACACCTCCACCGGCGACGGC
ATCTACTTCCAGATCAGTGGCCCAAAGGTCTACATTGAGTTCGCTAACCAGCAAGGTTCT
GCAGGTGCCGACATCGACGGTGTCATCACCGCTGGATGGGGCCACATTCACACCATCTAC
CGCGACCCAACCAATGACTACGCTAACTCCGTAACTCAGGAAGCAGCCAGCGGAATGATG
GGCGGCGGCCCTGGTGGTAATGGTGGCGAGATGCCTAGCGGTGACATGCCTACTGGTGAG
ATGCCTTCTGGCGCTCCATCAAAC

>RXN02680-downstream
TAACGCCATTTAAGAGGCCGAAC

RXN02693-upstream

CAGACCAAGTGTTATTTTTGTTGAAAAAATCACATTGTAAATCGAGCAAAACCAACCTAT
GCCCTGCAGAATTGTGCATGCTCTGCCAAGATGACTCAAT

>RXN02693
ATGGTTTCGCTCCCCAGACTAGCGTCTCTGCTCACCACTCGCCTGGCAACGCTTAAACCC
GCACTAAAACCTGCCACCCACCTCGCCTCCCTCGGCGCGCAGGTCATTGCAGAGCTAGTT
CCGGGGATCCGAATGTCGCCAAACCGCAGGCGAATCCTCCCTGCAAATATGGGCGCTGGC
TTTATCGGAGCGGAAATCGCAATGTGGTGGGCTCTCTCGCCGTCATTGTTGCCGAAACCG
TGGTGGGTTACGGCTGCTAACCTGGCTGTTTTACAAGCGGTGGGGCATGCGGCAGCGACG
GGAATCCACTCGATCCTCCCCAGAACCAACCGGCGGGTATCCAGGAAAATTTACAACGCC
ACCCACATCGCAACTGGTGCCATCACGTTGACCACCACGGTTGTGGGATTGATCAGGCAT
CGCACCCAAATCCGGCTGATTGGGCAGAAGAATTTTGGACCGAAGGAGACGATCGCGGGC
ATTAGTGTCGGCACCTTGGGGTACGGCGCGCTGCTGATCACCGGCGAATTAACCCAGCAC
AGTATTAATGAGGTCAAGCTCCTAATTGAGAGGTTTTTACCGCCGTGGATAAGTTTCATC
GCAGCGGTTTCGGTCATTACATTGACCACTTTGACCTTGGCCGATCGCGTTTTGTTGCGG
CGCATCTTGCATAATTCTGCAATTCAAGCAGCGCACCTTAATCGCATGGTGTTCCCAGGA
ACTGAGCAGCCGTGGGAGCCGGAGCGTTCGGGTAGCCCGTGGTCGTATGAAAAATGGGGT
GCGGTGGGTTCGCAGGGCCGTGCAGTGTTGTCGGGAGGCCCACGCAAAGATGACATCATC
ACGGTAACCAGGCTTTCTGACACGGAAACACATGAACCGATTCGTATTTTTATCGGTATG
GTTCCGGGACGATCCTTAAGCGATCAGGTGGATCTTGTCATTCATGAAATGCGCCGCACG
GGAGCCCTGCGCCGCGACCACATCGTGATCAACAATTCCACGGGCACCGGCTGGATCACC
GATTGGTCCGCCCACACCTTTGAGTTCCTCACCGGCGGAAACTGCGTGACAATTTCCATG
CAATATTCTTATCTTCCCAGTGCACTGAGCTGGTACAAGGACAACGACGGCCCCATTAAT
GCGGCGAGAATGCTTATCGACGCCGTCCTCCACGAGCTAGACCAGCTTCCCACCGGGAGT
CGCCCAAAGCTGTTCCTCGCGGGAGAGTCACTGGGGGCGTATGGGTTGGCTGAGGTGTGG
GGAGACGTCGAAAAGCTTCTTGGAACCGCTGACGGCGTGCTGCTCAGTGGGGCGCCGCGT
TTTTCGGACGCCATGAATGCGTTGCGCACCCGGCGCGATGCGAGCAGCTCCGAGCGGCTG
CCCGTGATTGATAGCGGGCGGCACATCCGTTTTGCGGGCGAGCCTGAGCACCTTGATATG
CCGGCTACCTGGCAGTTTCCGCGCATGATCGTGGCGCAGCACGCCTCTGATCCAATTGTG
TGGTGGAACGCGGAGCTGTTTATTCGGCGGCCGGAATGGTTGAAAACTCCCAAGCAAGAC
CACCAAGATGTCTTTCCCCGCTTGCGATGGATGCCGTTTGTAACCGGCTGGCAGGTGGCT
TTGGATTTGTTCACTTCAACCTCCGTTCCCGGCGGGCACGGGCACAATTATCACGAGGAG
TTTATTGATTATTGGGCAGCTCTTTTGGACCGCGAAGTCACCCCCGAGCTGCGCCACAGC
ATTGCTTATTGGATCCGCGCGAACCACATCAAACGC

>RXN02693-downstream
TAGAGTGATTCCATGACGCATGC

RXN02696-upstream
CTTGGGAACCGACCGCTAGCGTAGAAAATCAAGTTAAGGGTGTGACGAGCACCCCAGCTG
CACATGAAATTTAAGACATTCCAGGTGAAGGGAAACTGCC

>RXN02696
ATGTCCATGCTCAAGAAGACTAAAGAATTCTTCGGACTCGCTCCATACGAAGCGGAGCAC
GAGGATGCTTACTATGCAGATGAACCACGTTACGAGGGCACCGCTGCGTACGCACCTGAA
TACCGTGAGCGTGACTACGGCTATGCACCAGAGGCACCAGCCCCTGTTGCTCCATCGCCA
GCACCTCGCTCTTACCAGTCCACCATCGTTCCAGTAGAGCTTCATTCCTTTGAAGACGCT
CAGGTTATTGGTGGAGCATTTCGCGACGGCGACGCAGTTGTTTTCGACATGAGCTTGCTT
TCCCGTGAGGAAGCACGCCGCATTGTGGACTTCGCTGCAGGCCTGTGCTTCGCATTGCGT
GGCAAGATGCAGAAGATTGACAGCGTCACCTTCGCTGTCGTTCCAGAGCTGTCCAACATC
AGCACTTCCGAGCTCGAGCGCGCCGCACGCATCCGC

>RXN02696-downstream
TAAACACACCCTCGTGGTGTGGA

RXN02697-upstream
TTTGGCTCACCTCGATGATGTAGACATCCCCGATGAGGTGCGCGCACAGTTGCGGGCACT
GGCTATCCGCTCAACCGAACGTCGGATGTAGTAGACGCGT

>RXN02697
ATGACACTTTTTCAACGTTTAACCAACCCTGTAGTGCTCGGCGGCCTAGCAGGTGTTTTG
CTTCTGCTCGGCTCTTTCGGTGGCGGTGCCATTCGGTACCGTGGCGGAGTGCTCGATGCG
TTGGGGCTTAACTTCCTTGCTTTTGGCCACGCGCAGGGTATTTCCAATACCGTGTTGTGG
GTTGGGCAGCTGCTGCTGATTGGCGCGTGGGTTCACCTTGGACGTCGGTTGTTCAAGAAA
AAAGTCGCTGATGACACCGCAGACGCTGCTGACTTAGGTCTTGTAAAGCGCACGTTGTAT
GCCATGGTGGTGCCCCTCATTTTTGCGGCACCAATGATGTCGCGTGATGTTTATTCCTAT
CTCATGCAGGGCGCGATGCTGCGTGATGGCTTCGATCCCTACACTGAGGGCGCTGCGGTA
AACCCTGGCCCCATGTTGCTTGAGGTCTCTCATGATTGGCGCAACACCACGACGCCGTAT
GGTCCACTACACCTGTGGATTGGAGACATGATCACCACGGTTGTGGGCGATAATGTCACC
TTGGGCGTCGTCGCTTACAAGATCTTGTCGATCATTGGCCTTGCTGTGACAGGCTGGAGC
ATTGTCCGCATTGCACAACATTTTGGAGCCAACCCAGCAATTGCATTGTGGATTGGTGTG
GCCAATCCTGTGATGATCATCCACATGATCGGCGGCATGCACAATGAATCCCTCATGGTG
GGATTGGTCAGCGTCGGCTTGTTGCTAGCACTGAAGAAGCGTTTCGTGGCAGGTGTGGCA
CTCATTGCAGTGGCTGTGTCGCTGAAAGCTACAGCGGCGATTGCACTTCCTTTTGTGGTG
TGGATCGGCATGCATCATTTCGCAGGATTCTTAGCCACCAAAAAGGGCAAAGACTCCCCT
ACCCTTAAGCAACAGGTCCCCGCGTTCTTTGCCACTGGAGCTGCAGGTGTTGCTGTCACT
GGTGTTGTTGTCAGTGCGATCACTTGGGCGTCTGGCGCTTCGTGGGGCTGGATCAGTGAG
ATCAGTGGCAACAGCAAGGTAATCAACCCGCTGGCTTTCCCTTCTTTGGTGGCCAGTGTG
ATCACCATGGTGGCTGAAGTGTTCGTTGACGATTTCGACTACAACGCAGTGGTTAATGTT
GTGCGCTCAATCTCCATGCTGATCATGCTTGGCGGGTTGGTCGTATGTTGGTGGCTGTTC
CGCCAGAACGAACGCAGGGCGGTCACTGGTACAGCAGCGGCTTATGCCGTGGCTTTTGTG
TTCAATTCTGTGACCTTGCCGTGGTACTACGCCAGCTTGATCTCTTTGCTCGGCACATTT
AAACCACCGATGTGGTTGATTCGCTTCGCAGCGGGTGCTTCGGTGTTTATCGCGCTGATG
TTTACCGGAAGTGGAAACCACCAGCTGTACAACATCGTTACGGTGATCATCGCAGCAATT
ATCGCGTGGCTTGCCACCGTGGTGATCTTTGATGACACTGACCCTGCAACAACGGCCACG
GAGAAACCCTCCCCGCATACCGTTTCC

>RXN02697-downstream
TAGTTGCATAAGGTAAACCGCCA

RXN02720-upstream
CCACGCTGCACCATCGAAGACGAAGATCTGTTTTCTTACCGCCGCGAAGGCACGACAGGC
CGCCAGGCCGGCGTGGTGTGGCTGCCAAAGGAGGCATAAA

>RXN02720
TTGGAGCGCCGCGAAGAGCTGCAGGTACGACTGCAGCAGGTGCAAGCGCGTATCGACGCG
ACCCTCAACGAACACAACCGCCCCGAGGGCAGTGTACGTCTGTTGCCGGTCACCAAATTC
CACCCCGTGGAAGACATCAAGATCTTACAAGAGTTTGGTGTCACCGCAGTGGGAGAGAAC
CGCGAACAAGAAGCACGCGCCAAAGCACTCGAACTTCCCGACATGGACTTTCATATGATT
GGCCAAATCCAATCAAAGAAAGCCAACTCGATCGCCAGGTGGGCAGCTGCAGTGCACTCC
GTTGATAGCGAGAAAATCGCCGAAGCATTGGGCAGGGGAGTAGCCCTTGCATTGGATAGA
GGCGACCGCACCAGTGACGAGCTTCCGTGTTTTATTCAACTGAGTTTGGATGGTGACCCG
AGCCGAGGTGGAACTCCATTGAGCCAGGTCACACAACTTGCCGATTGCATCAGTGACACC
ACACATCTGCGTTTTGAGGGCCTCATGTGCGTCCCACCGCTTGGTTGGGGCCCTGAAAAA
GCTTTTTCCCAGGCAAGAGACGTACTTTCAGGTTTAGAGGAACACTTTGACAGGTCTTTG
GAATTTTCGGCAGGTATGTCTGGAGACCTAGTTGCTGCGATTAAACACGGCTCAACAATC
GTGCGTGTCGGAACTGAAATTCTTGGGAACCGACCGCTAGCG

>RXN02720-downstream
TAGAAAATCAAGTTAAGGGTGTG

RXN02744-upstream
GCCAAAACGTCATGATTCGCTCTTTGGATACGGGACACCGCTCATTGGAAGATGTCTTCC
TGGACATCACCGGAAAAGAACTGAGGAGTTAACGCACACC

>RXN02744
ATGTCTAAACCTTTTGAAAACTCTGCGCTCCGCGGTTCTTCTCGATTCCCAGCTGGAACG
TTCACCCCTGCTCCCAAACGAGCCACCCCGGCAAAAATGTTGGCTGCTCAGGGCAAGATG

GAATCCCTGCTGTTTCTTCGCCACGGCGAACAGCAACTGCTCAGCATCATCATTCCCTTG
GTCGCGCTCATCGCACTAGCGAATTTTGATTTCATCCCTGGTGAGAACTCCCTCGACAAG
ACTTTCCCCTTCGCGCTGGCCACAGCAGCCATGAGCGCTGGTTTTACAGGTCAAGCCATC
AGCCTAGCTTTTGACCGCCGCTATGGTGCCCTCAAGCGCACCGGCGCCAGCGGTGTTCCC
GCCTGGACGATTATTTTTGGCAAAGTCATCGCAGTCATTGCAGTCACCATTGTGCAGATC
ATCTTTCTCGGTGTGACTGCACTGCTGTTGGGCTGGTCCGCACCTGTCGGTGGTGTGCTC
TTTGGCATCGTGACCCTATTTGTGGGTGTTTCCAGCTTCACCGCGCTCGGCATGCTGATG
GGCGGAACGTTGTCCTCCGAATTGGTATTGGCACTGGCTAACTTGATTTGGATTGTACTG
TCCGGCCTTGCAGCATGGGCGGTCTTTTCCCCTTCCGTCAACGCTGAAGGAGTGCTGTCC
ATCATCCCATCCGTTGCGCTGTCCCAAGGTATGGTTGACGCATTCAACGGCGAACTTCCG
TGGCTCCAGCTAGGAATTTTGGTGGGCTGGCTAATTATCACCGGCGTGGCCGCAAACAAG
CTATTTAACTTCTCTGCGAGCCGC

>RXN02744-downstream
TAGATATACCCTTAGTCGGAAAA

RXN02770-upstream
TCGCCGGGGCAAAAACCGTATAATTACAGTCCTATTACGATTCGGGGAAAGGCTGGGTAC
TTCACACATGTTGTTTCGGAAGTCACGCAGCGCGGTAATC

>RXN02770
ATGTTGGTTGCAGCGTTAGTGATGACAAGCTGTGGTGATGGGGAACCGGAACCAACCAGC
CACCAAACAAGCCTTTTCGGCTACGCAGTTAACTCTTCGCTGGCTACAACCAACGCGGCG
TCGCTGTTGGGAGTGGCTAATGATGCTGGTCTTTTGGCTGCCAGAGTGTATCCGGGTGTG
TATGTTCAGGGTCCTTCTGGGCAGATGATTCCCAACACTGATCTTGCTTCCACGCAGGTA
TTGCCGGGTATTAACCGCCAGGTGATTTACACTATCAATGAAGATGCCACCTACTCAGAT
GGTCAGCCTGTGGTGTGTGATGATTTTCTGCTCTCTGCGACAGCTGGGCAGATGCCGGAA
CTGTTCCAGTCCCATGTGCCATTGACCTCGCAGATTGAGCGAGTGGACTGTGTATCTGGT
TCTAAAGTAGCCACCGTGGTGTTCAAGGAAGACCTCGGTGAGCGTTGGCGTTATCTTTTT
GAGCAGGGCGATTTGTTGCCAGCCCATGCCGTTGCTTCCAAAGCAGGTATGACCTTGGAG
GAGCTTAATCAGGCGTTGAAGGATAAGGATCCTGAAGCGTTGACTGAACCTGCTCGTGTG
TGGAGCGAAGGTTTCCAGCTGTCCCAGTTTGATCCAGAGCTGCAGACGGCTTTTGGCCCG
TACAAGGTGGATTCTGTGGGTGAATTCGGCGAAGTCAAGCTGGTACGCAATGAGTTTTAC
AGTGGCGACCAGGCGGTTGAAGCAGAAATCACGATGTGGCCTAAAGGCTCGGATCTCAGC
GCCATTGCGGATAATGGAAACCTTCAGATCGCACATGTTGTGGCGTGGGAGAGCGAGCCG
TGGGTAAATCGCGATGACCCATTGAATCCTTATGACATTAAGGAAGAGGTCGGTGTTTTG
ACTGAGCAGCTCACCTTGGCCAGTGCCGGTGTGTTTTACGCTGCGGAGGCCCGGCAGGCG
TTTGCGGCCTGCGTTGACCAGGAAGCGGTGGCTGCGGCGTCGTCAAGCATCTCTGGAATC
GATGTGCCTGCCGTAGGTGTGCACTCGGTGCGTCACCAAAATCCGGTCGTGCACCAAATC
GGTGATCTGCCAGCACAGCACATGGCGGTGGATATTAATGCCGCATCAGCGTTGGCGGGT
CAATCCATCCGCATTGGCTACGACGGACCCGATGAGCGCAAGGCTGCAATGGTGGAGGCG
ATTCGCCAAAGTTGTGAGCCTGCCGGTATCACCGTTATCGATGCGTCGCAGGAGGCTGTT
AGTCTTAATGATCTCAGTCGAACCGAAGTCAGTGAATGGGGCTATGAGCAGTACTTCGAA
GGGACACTTGACGCTGTTCTGCGTACAGTGGATCCACATCGGGAGTATGAAAATGCCAAT
ACCATTGGAACTGATGCGGAGTCGACGAGGCGCACTGAAGAACAATTGTGGGCTGAAGTC
CCATCAATTCCACTAGCAGCGCAACCCCGAGTGTTTGTGATAGATCGCACAGTCGGTAAC
GTTGTTGTTAATACAGACCTAGCCGGTATCGGATGGAACATGGACCGTTGGTCCAGAAGT
GAGGAA

>RXN02770-downstream
TAAGTAGTGAGCGAACAAGCTCT

RXN02781-upstream
CTCCGAGAGTTTCCGCATCCGCGGTTCGATCCCGGACGTTCCCCGGGAGACGCGGTGGGA
CCGGCTGTGGCGGCCCTTCTGGGCGATACCGGCTGCCAGC

>RXN02781
GTGGTCGCGGCCCTGGTTTTCGGTTTCCTGCTTCCCACGTGGGAACGTGGGTTGTCCGAC
GCCGCGCTCAAATTCGTTTTTGAGGGTGGGCCTGATGCCGCCCGCGAGGTGCTGGGCACC
ATCGCCGCCTCCACGATCTCAGTGACCGGTCTCATCTTCTCCATCACTCTCGTTGTTCTG

CAGCTGGTGAGCAGCCAGTTCAGCCCGCGAATGCTCAACGGCTTTCTGCGCAACCGCATC
GTGCAGGCCACCCTGGCGATGTTCCTGGGGACGTTCGTGTTCTCCCTGACGGTCATCCGG
TACGTGTGGAGCGAGGACGAGGACATCACCGGATTCGTCCCCCGTGCTTCAGTGTCGGTT
GCCTTCCTGCTGGTGCTCGGGTGTCTGGGACTGTTCCTGGCGTTCATCCGGCTCATCACC
TTCTCGATGCGGGTGGCCAACGCCATCTCCGAGATCGGGGAGGAGACGATGGCTCTGGCC
GCACGTATCTATCCCGTGCAGAGCGACGACGCAGGCCCAGTCCAGGGGCCGGGCTGGTCA
CCGCGGCCCGGTGACCCCCGGGAAGAAATCCGGGTGGGCAACCATGGTTCGCTGGTGTGG
ATCGACTACCGGAAGCTGGTGTCCTGGTCGACGGAACACCAGGCGGTGATCACGGTCGAC
CGGCCGGTGGGGGACTTCCTCGTCGAGGGCCAGCCGCTGCTGCGGGTCTGGTGGGACGGG
GAACTCAGCGACCGGGACCGACGCGTTCTGCACTCGGCCATCGAGGTGCGGACCGAGCGG
GAACTTCACCAGGATGTGGCGTTCGGACTGCGTCAACTGGTCGACATTGCCGATCGTGCG
TTGTCCCCGGGCATCAATGATCCGGCCACGGCGGCCCAGTGTGTCCAGGAGATCCACCGG
ATCTTCCGCTATTTGGTCACCGTCATCGAGCCCAGCCCCTACATCGCCGATGACGACGGT
CGGGTCCGTGTGGTGCACCAGCCGCAACGTATCGCGGACATGCTCTATGAGGTGATCCGT
GAGATCCATCTCTACGGGGCGGATTCTGCGATGATTCCGAGGCTGCTGCGCACCATGGTC
GAGGACCTGGTGACGGCCGCTGCCGATCATTCCCTGCCTGCCGTCGAGCGTGCCCGCGGC
ATCCTGGACGATGAGACGGACGAGGACCGCGACAGTGACACCGCGAACGTC

>RXN02781-downstream
TGATCCGGGATCAGGTGGCGGTG

RXN02782-upstream
ACCCCACCCGGTCCCCCTTTTTTCCTCACTGACACCGGAGCCGCCTCAAGCACCACGCTG
CAATCACAGAAGCTAGTTGAGCATATTGTAGAATATAACT

>RXN02782
ATGCCAACACTGCTTATTGACACCCATCCGCATCTTGCAGCGCAACTTCTTGACCCTGGT
TTAGGTGAACTTCTTACAGCCGGTTCCAACAAAAAAGTGCAGTGGCAGTGCCCTAAGCAC
TCCAATCACATCTGGACGGCCTCGGTTAATAACCGCACCAATGCAAAGAACCCGCGCTGC
CCCTATTGTGCCGGAACACGAGTGTTGGCAGGTTTTAATGATCTCGCCACCACTCACCCG
CATCTTGCTGTACAGCTGGTTGACCAAGATATTGCCGTCACCATTTCCGCTGGTTCTGGC
AAAAGACAACTGTGGCAGTGTGTAGTAAACCCAAAACACCAGTGGTTGGCTACGCCAAAT
AATCGCACGAGTACTAAATCTGCGAGTTCTGGTTGCCCCTACTGTGCCAACCGAGCGGTA
TTAGTCGGTGACAATGACTTTGCAACAACCTACCCCGAACTTGCAGCGCAATTAGTAGAT
CAATCTGCAGCGACAACCTTTACAGCCGGCCACAACAAGCCTGTTGAGTGGATCTGTTGC
AAGCATGAACCACCATTTATCTGGAAAACCTCACCAATTTTGCGTGTACGACAGAACACC
CAGTGCCCTGTGTGCTCAGAGCGAACTGTGGCGCCGGCGCTTAATGATCTTGCAACCACT
CACCCTAAACTTGCCGAGCAAATTGCAGATCCTCAACCAAGTGGTGTGAGCGCCGCGGCC
ATTATCCCCACCATTAGCAGGGGTTCCCATACGCAATTAACATGGCAATGTTCTAAAAAT
CATGACCACCAATGGGTCGCCACAGTAAAGGATCGTGTTCGCGGAACAGACTGCCCCACC
TGCGCAAATACAGGAACTTCACGCAAAGAGGCTGAACTTATTGAGGTCATCCGTGCATTA
TTCCCAAACACTGATGTCCAGCAAGGTGCGCTCATTAATGGACGTACCGGTAATCAAGGT
GCATCGCCGTCAACCGATGTACTCATACCGTCCAAAAATCTCGCTATCGAGTTCAACGGC
CTGTACTGGCACTCTGAGCTTTTCATCAAAGATAAGCATTATCATGCGAACAAATCAGCT
CTCGCAGAACAAGCCGGTGTGCAGCTCATTCATGTGTGGGAGGACGACTGGAATCTTCGC
CGCGACATTGTGATCCGCATGATCGCACACAAGCTTCATGCAACCCATAACCTCAGTGCT
GTTTTGCCTACCGAAACTACTGACTCACGTGTGGCAACCACCGCTTTCGCCGTACACTCA
CACTGTCGGTGGTCTCTGGTTCACGCGCTGCTGCATTCT

>RXN02782-downstream
TGAACAGCAACCATATTCAGGGT

RXN02812-upstream
CGCAACTGGAGCTGCCGACTCCCCTGCGTTTGCCACCGTTGAAGGAGCAGAACTTCCAGA
GGGCTACACCTTTGAAGCAGTAGACAGCGCAGAAGTACCT

>RXN02812
GTGTGGGCTGTTGCCATCAACGCTGGAAACGGTATCTCTGAAGACCAAGCCCGCGCCGCC
TCTGATTTCAGTAGCTTCAGCTTCGACACCGGCAACGCCGATAACTCCGCGCTTGAAAGT

GTTCTCACCCAAGCTTCAAGCGAATCCGCGGCAGAAACTACTGAGGCGCAACCAAGCGAG
ACCCCGGTCGAGCCCGCCGCTGCTTCCCCATCCGATACCATCATCAACCTGGATACCTCA
TCCAACATGGATCGAGTTGTTGACGGCAGCCAGGAAACCTACCACACGGTTACTTCCCGG
ACTCTGGCCAACCTCGCCCGCGAAACTGGTGCACAGGGC

RXN02817-upstream
AAAATTCCCACCCCCAAAACTCCCCCACTTCGGTTAAGGAATCAGGATTCTCACAAAGTT
CAGGCAGGCTCCCGCTACTTTTCAGCGCTAATCTTGGCTC

>RXN02817
ATGATTTTAGGCGTACCCATTCAATATTTGCTCTATTCATTGTGGAATTGGATTGTCGAT
ACCGGTTTTGATGTAGCAATTATCCTGGTCTTGGCGTTTTTGATTCCACGTATCGGCCGA
CTGGCCATGCGTATTATCAAGCGCCGAGTGGAGTCTGCAGCCGATGCGGACACCACTAAG
AACCAGCTCGCGTTCGCCGGCGTTGGCGTTTATATCGCGCAAATTGTGGCGTTTTTCATG
CTTGCCGTCTCCGCGATGCAGGCTTTTGGTTTCTCTCTCGCGGGCGCTGCGATTCCGGCA
ACCATTGCGTCAGCTGCCATTGGCCTTGGTGCGCAGTCGATTGTTGCGGACTTCTTGGCC
GGATTTTTCATCCTGACGGAAAAGCAATTCGGCGTGGGT

>RXN02818
TCCTATTCCCGGAAGTTTTTGACCCAGGTGTGGATTCGAGACAATGTCGGCGATTATAAA
GGCCTTACCGATACGGCGTTCCGTAAGAAGCTGCAGCGCGATCTTGCCTACCTGCGCAGA
GTTGGCGTTCCGATTGAGCAGTTCACGGTCACCTCAGGCATAGCTGAAGGCCAGCAGGCG
TACCGTCTGGCCCAGGATTCTTATAAGCTCCCCGAGGTCGAATTCACCCCAGATGAGGCC
GCCGTGCTGGGCATGGCAGGGGAGATGGGCCATAATCAGGAACTCGGCGCCTTCGCGCGT
TCGGGGTGGACCAAATTGGCGGCCGGCGGCGCGCAGCGTGATCTGTCCACGTCCACAGCC
TTGACCAATGCGGGCGATTTAGGTTCCTTGTCTGCAAAAACCCTCGATGCGATCATCAAA
GCCCGCCAATTGGGCAAGCAAATCAGCTTCGAATACCGGCGCGCCCCCAAAGACGCCCCC
TCGCTTCGACACATGGATCCTTGGGGTCTGGTCCCTGAGCGCGACCGCATCTACCTGGTC
GGATTCGACCTCGACCGCCAAGAAGCACGCACCTTCCGCATCACCCGCGTCCGCAACATC
AAACTC

RXN02825-upstream
TGGCCTGCCCCTGAAACTTTTACGGCTTTCAGAGCGCAGGGCATCATTTTCTTGTGTCGC
CAACACTTGAGAAAAATTGCGGAAAAGGACACTGCTGTTC

>RXN02825
ATGAAACTTGCACCTCGTATGCGGATGAGGAGCCCCAAAACTTTCGCGGCCCTCGCCTCA
CTTGCTTTAGTCATAGGTCTCGGCCAGGTACCGATCGCCCAAGCTCAAACCGAGTATCGA
ACCGCCTCCGACGGTTCCCTGAACTGGGGATTTAGGCAATCGTTCCGCAATTACATCCAA
ACCGGCGTGGCCAAAGGTTCCATCACGCTTGGCGACGGCGCATCCGACAACGGTGGCAAC
TTCGCATTCACCCCACGCACCAACGGCACCACCGTGACCAGCGATTCCCAAGGCACCGTG
GAATTCAACGGCTCCGTGCACTTCCTCGGACACCAGGCAGAGGACAAATGGATCCTGGAC
ACCACCATGTCTGACATCAAAATGGTGTTCAACGGATCCTCCGCGCAGCTAGTTGTGGAT
TTGGTTGCCCGCGAATTCAAGGGCACCACCTACGATGACATCGGCGAATACATCATCTCC
GACGACATCGTGCTTGCCGACGTCTCCCTCAACTCCGCCGCCGACTTCTCCCAAGATTCC
ATCGACCTGTCCGGCACCACCGACCTCACCGCAGCTGGCGCCCAAGCTTTCGGAGGATTC
TACGAAACCGGCGAAGCCCTCGACCCGACCGGCGGCAGCCTGACCATTTCCTCCACCACC
ACCGCGCCATCGACCAGCACGACCTCCACCTCTGCCTCAACTTCCGGTGGAACCGCCGAC
TGTTCCTCCGGCGCATTGGGTGTTGTCACCACCGGAACCAACGACGGCATGCTGGGCACC
ATCCAGGAAGTAAACAACACCTTCGCGATTTGGAACAACCTCATCGTCAACACCGAGCGC
ATGTTCTGCAACATTGATACCCTCAAGGCGCGCTTCGACACGGATGATTCCAGCGATTCA
GCGACCTCTGCGACTTCTGGGACTACTGCGTCCACCGGCACCACCGCTGCAACTACCGCG
GGAACCACGGGTACCACTGGAACTGCCAGCACCGCTTCCGGAACTTCCGGAACTTCCGGA
ACCTCCGGCACCGCAGCAACTGTCGCTGGCACCACCCCAACTGACAATGGCGTTTGCACC
GCTTCCGGATCTTTGGGCGTGACCCAAGCATCTGCGCAGTGGGGTGTGAAGGCGTCCTTC
CAGAACTACATTCGCGGATCGATCGCCAACGGTAGCTGGACTCTCAACGGCGTTGGTTTT
GATAATCAGCAGTTCCAATTCTCTGGAAATTCCGGAGCAGTCGACGCGGAAAACAAGACC
GGCAGCATCAATTTCCCTGGTTCCATCCACTTCACGGGTCACGGCGGAATCTTGGACATG

CAGATCGCAAACATTGAGATCAGCTTCAACGGCAACTCCGGCGAGCTGATTGCGGATGTC
GTTTCCTCTGACATGGATGGAAATTCCACCAACTACGGTCGCACTGTCGTGGGCACCCTG
AACTTCTCTGCGTTGAATGTTTCTGCAACGGAAGCTTCCGGTTCCGCTTCGGTGTCCCTG
TCACAGTCGGGTTCGCAGGCGTTCGCTGATTTCTACACCCCAGGCACCCAGTTGGATCCG
ATCAGTTTCAGCGCAACTTTGGGCGGCGACGCCAGCTGCGCCACCGGATCCACCTCGACC
ACAGGCGCTGCTGCCACCGCGAACACTGACAACACCGAAGGTGTTGCCGGCGAGGAATCC
ACCACCCCCGCTAACCAAAACAGCCAGTTCCAAATCCGCCAGGCCGCTGCAGATTCCACC
GGACTGGATACCACCACCACAATGTTGCTCATCCTCGCGGCGTTCGTTGTCGCAGGTGGC
TCCATGACTCGCTTCACCGTCGGCAACCCGACTGGAAAA

>RXN02825-downstream
TAAGGCTTCACATGAATAACGCT

RXN02838
AACACGGGCAAGGGCGGGGGGCTGACGGTGCCGCTGGGCGACGGGCAGGGGCGGTATATC
GCGAAGTTCCCCTCGACCGCGTTTGTGGGGGTGTCGGAGAACGAATTTGCCAATCTGGCT
TTGGCCGAGGCGATCGGGATGGAGGTGCCCGCGCGCGAGTTGGTGGGGCGTGCGCAGTTT
GAAGGCGTGCCCCCCGAGTTTGAGGCCATGACCGACGGGTTGGTTTTGCTGGTGCGGCGG
TTTGATCGCGCGGGCGATGGCGTGCGCGTGCATATGGAGGATTTCGCACAGGTGTTCGGC
CTATACCCCGCGCGCAAGTATGATGGGGCGGCCAGTCACGATATTGCGGCGGTGCTGGGC
AGTGCGGTGTCGATCGCGGCGGGGTTGGAGTTCGTGCGGCGGCTGGCGCTCTCGGTTGTG
ATGGGCAACGGCGATATGCATTTGAAGAACTGGTCGCTGATCTATCGCGGGCGGGGCGAT
GTGCCGGCGTTGGCGCCTGTGTATTATATGATGTCGACCGTGACCTAT

>RXN02840-upstream
AAGTGAAATCAATCGGCTTTTCCAGCAGCAGCACTGGTCGCGCCAGCGTGGGTGTTATGG
TGAAGGCGAATACACCTTCAGCACCGCTGAGCCGGAAGAG

>RXN02840
ATGACGGTAATCAGTGGCGCGCTGAATGTGTTACTGCCTGACGCGACCGACTGGCAGGTG
TATGAAGCCGGTTCGGTGTTTAATGTTCCCGGTCACAGTGAGTTTCATCTGCAAGTTGCC
GAACCCACCTCTTATCTGTGCCGCTATCTG

>RXN02840-downstream
TAATTCCTCGCCTTCCCCTTGAA

RXN02841-upstream
CTCACATAACTTTACGCCACCCCATACCCTTTAACCCCTGCACTGCTCATCCACAAGCAC
TGTGCAGGGGTTGTGTTTTCTAACAAGAAAAGAGACCACC

>RXN02841
ATGTTCACAGCTTTTAAAAGCAATCCTACGACCATTAAAAAGCTGGTTTCTGAGCTCATT
AATGGCGACGATGCAGCGCTCAACGAACTAGAGCGACACGTCACTAATGAATCAGTCCGT
GCTCGCGAACTCCCTAATGTCCAGTACAAAGCCACTGCGGGGCGCAACTTCGCCATATCC
AAGCTGGTCCAAAATTTGCGTCGCATCAACAAGGCACAAAACAATCCACGTGGTGTGCCC
ACTCATGCCACCGTGATTCTGCTTAAGGAAGACGGCAGCTACGACGGTGAAGAACAGTGG
CGCATTCCAGAAAAGGCGATCACTCCGTTCGACATGCTACGTTCGCCTGACTTCAACCAC
AACAGGCTGAAGAACCGGCCGCTCATGGTCGAGTCCCAATACCCCTGGGGCGTCCCCGGA
CTCATTAAAATGAAC

>RXN02841-downstream
TGATCAATCCCTGACACAGCCAT

RXN02846-upstream
TACAAGCGCTGAACGTTGAGTTTGAGTTTGGTCCATTGAGGGGTAAAGGCTTACCTCTCG
ACTAGGTGGGGTGGGCGTAGAGCGCCTATTCTGATTGATC

>RXN02846
GTGTTAACCATCGCTATTGTACTTCTCGCGTCAGTCCTCATCGGTGCTCTTCTCCAACGC
ATGACAGGATTGGGCGTCGGTCTAGTTACCGGCCCAGTCCTGACTTCTTTGTTAGGGCCG
CTAGCAGGCGTGACCATGGTGAATGGTCTGTCCATCATCAACGCGGTGAATAATGCGTGG
TCGGTGCGCAAACGCACTGACTGGGCCAAATTCCGAATTCTTGCCGGCGCTTTGGTGCTT
GGTTCTGTTCCTGCTGTTGCAGTGGTGTATTTCCTTAACGGACCATGGCTGTTGATTTTC
GTTGGTGCGATGGTGCTGCTCGCGTTGGGTGTTTCCCTGTTCCCAACAGAGAAATTCGCA
CTCAAGCAAGAAGCTAAACTGCCTATGGTCATCTTCGGCATGATTGGTGGATTCATGTCC
ACTGTTGCAGGCATCGCAGGGCCATCCCTGACTGTTTATGCGCGCCTGAGCCGCTGGGAT
TACCGCGACTTTGTGGCCACCTTGCACCCAGTTCTACTCGTGGCCAACACCGTATCGTTC
CTGCTCAAGGTTATCTTGATCGGTGGACTCGATTTCGGTGGCGCACCCGCATGGCTCTGG
ATCGGTGCCGTAGCGATGATCTTTGTCGGTGCTTGGTTGGGTGAAATCGTCAACGCTAAG
GTGTCCACCCCAATGGCCAAGCGCATCGCTACGCTCCTGGCAGCAGCTGGTGCCGCAGTG
GTGTTGTTCCGAGGCATCATGGAATTGGTT

>RXN02846-downstream
TAGCGGTCTTAATTGGTGGGAAG

RXN02847-upstream
ATATCGCAGCAGCCTCGATGGTCAACGCCCATATGATGGGAAGTTG

>RXN02847
TTGGCGCTAACCGCCAGAGGCTTTCTCAATTCTGAAAGAAGCCAGACAAGGTGGAAAACC
CACTTCACCACCCAGAAAGTTCCACGCTCCGGCTACAGATATGACCTCGATGGGCTCCGC
GGCATCGCGATCGCCTTCGTAGTTTTGTTCCATGTTTTCGTCGGAAAAGTCTCCGGCGGT
GTGGATGTCTTCCTGCTGCTGTCTGGCTATTTCTTCTTAGGGTCGCAATTGCGTTATGCA
GATCGTCCAGATTCTTCCATCAACCCCTGGTGGCCGATTTGGCGCACGCTACGCAGATTA
CTTCCTGCGTTAGTGCTGGTGTTGGGCGTTTCCATGGTCCTCATCTTGGCGTGGGTGCCC
AGACTGCAACCAATAGAAATAGCCAACCAAGCAGTAGCCAGCCTCTTCTATGTCCAAAAC
TGGGAGCTCGCATCCCAAGGTGCTGCCTACGGAGCAGCCTCTGCAGAAGTCAGTCCTTTC
CAGCACTTGTGGTCCATGGCTGTGCAAGGGCAGTTCTACCTCTTTGCCATCTTGTTGAGC
ATGGCGATCATCCTGATTCGTCGATACCGCCCCGAATACTCCGCAGTGCGACTAGCGACT
CCTGTGCTGGCAGTGCTCACATCCGTATCATTTTTCAGTGCAATCCTGTGGCATTTCATT
GATCAATCAGTCAACTACTATTCCACCTTCACCAGGTTCTGGGAGCTCGGCCTTGGTGCA
CTATTGGTGCTGCATGCGCCTCGAATTTTGATTTCTGCGAAGACTAAATCAATACTCGCA
GCCGTCGGTTTGTTTATGGTGCTATCCACTGGATTCTTCATGGATGGCGCAGAGACTTTC
CCTGGATTCCCCGCGCTGTATCCCATCTTGGGTGCTTGCTTAGTCATCCTTGGCGACGGT
AAAATCTCGGTCTTTCTCTCCCGAAAATGGATGCTTTGGCTCGGCGATATCGCCTACCCG
CTCTACTTGTGGCACTGGCCTCTGCTGATCATTTTCACCGCTTTGTTCAACCAAGAAGAG
CCATCCATCTGGCTGGGTATCGCCGTGATTATGCTGTCCCTTGGCTTGGCGCAGCTGACT
AACAAATAC

RXN02849
TCCCCATACCCCGTCATGATCAGCACCTCTGCCGACGCCTCAAACGTGACCGTGCGCATC
ATGGGTGTGGACACCACCTCCGTGGAATCCATCAACAACGGACGTTGGTCCACCACCCAG
CCCAACACAGTTCGAGTATCGGGTTCAGATTGTGTGCCATCAACCGGTGCACCAGGATTT
ACCACCTCAGACACCCGAATCATCAGCGATCTTTCTGGCAACGAAATCACCAGAGAAACC
GTCACCACGGTTTACGATCCTTCACCAAACGTGGTCTGCTCC

>RXN02849-downstream
TAAAACAAAATGCCCCACCAGAT

RXN02911-upstream
ACCGCATACATTAACGTGTTGATCATTGCCCTAGTATGCGCAGTAGCGGCTGCTCTGATC
AGCAGTTACCTTTTCCGCGGAAATCCGAAGGGAGCCAATA

>RXN02911
ATGCGCACTAGTAAAAAAGAGATGATTCTGCGCACGGCCATCGATTATATCGGCGAGTAC
AGCCTCGAGACGCTGAGTTACGATTCGCTCGCCGAGGCGACCGGTCTGTCCAAGTCGGGC

TTGATTTATCATTTCCCCAGCCGCCATGCGCTGCTTTTAGGCATGCACGAGTTGCTTGCC
GACGACTGGGACAAGGAATTGCGCGACATAACCCGCGACCCAGAGGATCCACTTGAGCGA
TTGCGCGCCGTCGTGGTTACGCTTGCTGAAAACGTTTCGCGCCCCGAGCTGGTTTTGCTT
ATGGACGCCCCCTCCCACCCGGGATTTCTTAACGCCTGGCGCACTGTAAATCATCAATGG
ATCCCCGACACCGATGATCTGGAAAACGATGCCCACAAACGCGCCGTCTACTCTGGTGCA
GCTCGCAGCCGATGGCCTCTTCGTGCACGATTACATTCA

>RXN02911-downstream
TGATGATGTCCTCAGCAAGTCCA

>RXN02914-upstream
TGTGGATCGCAGCAATTGCATCCCCTGGGCCAGACCTTTTCAGATCATCAGGCTAAGTGC
CAAAAACCGCCGTGATGGCGTACTGACTGCCGTAGGCATC

>RXN02914
ATGGTGGGAAACTCCATCTGGATCATAGCCAGCCTCCTTGGGCTCTCGGCACTGATCTCC
ACGTATCCAGCAATTTTGAACCTGTTGCAGCTCGTCGGTGGCGGTTATTTGACCTGGATG
GGCATCGGGGCGGTGAGGTCATGGTGGACGAAACGCTCCACACAGCAAGCTGCAGCGGAT
TCTCAAGCTGTAGAGAATACGTTGGTGACAGCCACGGCTGCATCTGTCGGAGTGTGGCCA
GCTATTCGATCTGGCATTGCTACCAACTTGTCCAACCCCAAAGCTGTGCTGTTTTTTGGT
TCCGTTTTCGCCCAATTTGTTAGACCTGACATGGGAATCGGGTGGAGTATTTTCATTGGA
GTCTTCCTCACCCTCACTGGCCTGCTGTGGTTTGTGGGGTTCGCCGTCTTGGTCCGCAAA
CTAGCCGCTGGCCTCACCCGAAATGGAGCCATCATCGACCTGCTAACGGGGGTGATTTTC
ATCGGGCTGGGAATGTTCATGATCTTCGAGGGGGTTGTAGGAATCGGTGGCAGGGTAGTG
GGT

>RXN02914-downstream
TAGCCCCGCCCCCAGGACGTCAC

>RXN02921-upstream
TGGAAAACTGGGAAGGGTTGACGTTGCGGAATCTCTCCGCAGCGTCGGTTCGGACCCTAA
AAAAGGGTGAGGAACCACATGAGCTGTTTTAAGGAATTTT

>RXN02921
GTGTCTGCACTTGAAGAGTCGATCCGCATCGCGACCATCGCGGCGAAAGCAGCGGATGAA
AAGAAGGCCGATGACATCGCTGTCATCGATGTCTCTGACATGATCGCAATCACCGATTGC
TTTGTTGTTGCATCTGCTGACAATGAGCGCCAGGTGGGCGCCATTGTTGAGGAGATCGAA
GATGAGATGACCAAGGCTGGTTTCGAGCCTAAGCGCCGTGAAGGCAACCGCGAAAACCGT
TGGGTTCTCCTTGACTACGGATTGGTTGTTATCCACGTTCAGCGACAGGCAGAGCGCGAG
TTCTACGGACTGGATCGTCTGTACCGCGACTGCCCACTCATTGAAATTGAAGGACTTGAA
ACCTTCAAGCGTGAATCCTCCTGGTCTGATGAGGCGGATATCCGCAACATCGACAGCATT
GATGAACTCCCACCTTTGCCAGCTGAATACGAGCCTGGCTACGAGGACGAT

>RXN02921-downstream
TAAGAGGTAGTCCTGTGACTCGT

RXN02924-upstream
CTAGGCAGGTGTGCGATCAAACCACACTGTCAGAATCAAATCTGCTGGACGCTATGCCAG
CGGATTGTTGATCACGAAAAAGCATGTCACAGACACCTTT

>RXN02924
GTGCCTTCTGTAGCATCCATCTCAGAGCGCGCCACGTTTATTCTCACCGCCGATCACTTT
TTGCGCAGCTGCTCGAAAGTAATTTATGTCCGGGGCGAAAATTTCACCGCCACAGCAACC
ACCAGCCTGTCTGTATTTGGCACAGATCTGGGTTTGATCAAATTAGACGGCAAAGCCCCC
ACCATGCCACTTCCACTTTTCGCAGATAAGCCACTTCGCGTGGGCATGAAAACCACCACG
TTCGGATTCGGCGGTCTGCCATCAGCCACCGTTGCTAAAGAAATCCACGGGCGCGTTATC
TCTGCCATCCCCCATGGCGTATCAAGAAACCGCATCACCCGAGTCCATCACGGTGCCTTG
ATCTTTAACTCCCCAGAAAAGGCAGTAAAGGGAGACTCCGGCGGACCTGTGCTGGTTAAT

GGACGAGTAGCCGGAATCCAATCAATGATCTCTGACCCCGGTGGATTTAACACCGGGGTC
GCCACTGCCGCATCCCTTATCCAGCACATGCCTGCCCTAGCTCAAGCGCTTGAACTGCTC
GAACATAGC

>RXN02924-downstream
TAGCTCGCTAGGAACCGATCGCC

RXN02927-upstream
TCCGCAGTTGGGCCTGCTTGACGCCAGATCTCAAGTGTAAGTTTCATTACTTGTAGTTCC
TTGTCTGCAGTGGGACAGATTCGAAGAACAGTGGTTCTGC

>RXN02927
GTGGCAGACGAAGGTTCCATTCTCGCCTGGTTCCCATGCGGAGACGAAGCACCAGTTTTG
GTCGTCACGTTGTGCTTCGCCATCTTCGGAGAGGTGGTCGTCGCGGAAGTGAGCGCCACA
GGACTCGTCGCGGTCGAGGGCGTCGACACACATGAGTTCGCCGAGGTCGATGTAGTCGGC
TACGCGTGCTGCGTATTCGAGAACCTGGTTCATCTCATCGGTGCTGCCGGTGATGCGCAT
GTTCTTCCAGAAGTCATCGCGGAGGGCACGGATCTTGTTGATGCCATCCTGGAGGTCTTC
TACGTTTCGGGAAACGCCACAGGAGAAGTACAGGATATCGCCAAGCTGGCGGTGGTAGTA
CTCAGGTCCGTGAACGTTGTCACCGACCCACTCTGGGCGGTTGCCCATGAGGCGGTCAAT
GCGAGCCTGTGCACGCGCAATCGCTGCCTGTGCTTCTGGTGCATCCTC

>RXN02927-downstream
TGACAGACGCTCGGAGCCAAGCA

RXN02928-upstream
GGTTTGCACCGTGGTAGGTCCAGGATGCTTCGCCTGCGCAGAACAGACCTGGGAGTGACG
TCATTTCGTTGAAGTCAGTCCAGAGGCCACCCATGGTGAA

>RXN02928
GTGGCAGGTCGGTGCAATACGCATTGGGCTGGAGTATGGGTCCTCGCCAATTGCCTCTTC
GTACATGGTGAAGAGGTTGGAGTAACGCTCGCGGATGGTGTCCTGTCCGAGGCGCTCGGT
GGCGTCGCGGAAGTCCAGGTATGCAGCGTTGTTCAGAGGTCCAACACCGAGACCAGCATT
GATCTGCTGGGAGATCGCACGGGAAGCAACGTCACGTGGGACGAGGTTACCGAATGCTGG
GTAGCGGCGCTCCAGGAAGTAGTCGCGCTCATCCTCAGGGATGGTGTTTGGATCGCGGTT
ATCGTTCGGTTCCTTAGGGGACCAGATGCGGCCGTCGTTACGCAGCGACTCGGACATCAG
AATGGTCTTGGACTGCCAGGTGGAGTTCACAGGCAGGCCGGTTGGGTGGAACTGGATGAA
CGATGGGGACGCGAAGTATGCGCCGGCTTCGTATGCACGCATGATGGCCGAGGCGTTGGA
GTTCTTGGCCAGGGTGGACATGTGGTACACGTTGCCGTAGCCACCGGTTGCCAGGATAAC
GGCATGGCCGGTGTGTGCGGTGAGCTCGCCGGTGATCAGGTTGCGCATGATCAGGCCTTC
GCAGCGCTTTTCACCGTTACGTTCGGTGACAATGACGTCAACCATTTCGTTATGGGTGAA
GATTTCTACGGAGCCGAGGTGGATCTGGCGCTG

>RXN02928-downstream
TAGTGCGGATGCGGTGGAGAACT

RXN02931-upstream
GATGGGTGCAGAAATTGAATTGAAAGAATCCGGGCACATGTGGGTGGAATCCCCGAGTGA
CTAGTGCGGTGTAAGAGCACTAGACTGTTCAACTATGAGC

>RXN02931
ATGCAACCATACCCCCGCAACCCAATCGAAAAACGTAAGCAAGAAGTACGCAAGAACTCC
CGCAACGCAGTTGTCAGTGTTGGCGGTGGCATCGTAGGCGGTGCGGCTCTGTGGCTAGTG
TTCGGCTCTGCATTCTTTATGGGACTTGGATTGATCATCGCCGTGGTCGGCGGTTTTTAT
TACTACAACAAGGTCCAAAAGATCATTAACGAAAAAGACCGTTAC

>RXN02931-downstream
TAGTTAGAAATCTATGTCAGACA

RXN02932-upstream
CACTACTGCGTTAAGGTATGAAAGTTCGCACACCAGCGATTTAATTCTGTGCCCACCACT
AGCACGACCATTTCAGTTTTAACTTTCTTGGAGTTTTCTA

>RXN02932
GTGTCCAAAACAGAAGAAGGCCGTTCAGCGGCCATAATTATTTACGCGTTTCCAACTTTC
ATTCTGCTGGGCGCGATCATTGCGTTTATCTTCCCGGAACCATTCATTCCGCTGACAAAC
TACATTAATATCTTCCTCACGATCATCATGTTCACCATGGGTTTGACCTTGACGGTGCCC
GATTTTCAGATGGTGCTTAAACGTCCACTGCCTATCTTGATCGGTGTAGTAGCGCAGTTT
GTCATCATGCCATTCCTGGCGATCGTGGTTGCGAAAATGTTCAACCTCAACCCAGCACTC
GCCGTTGGCCTTCTCATGCTGGGATCCGTTCCGGGTGGCACCTCCTCCAATGTGATTGCG
TTTCTCGCCCGAGGAGATGTCGCGCTATCGGTCACCATGACCTCTGTGTCCACCATTGTT
TCCCCAATCATGACGCCTTTCCTCATGCTCATGCTGGCAGGTACTGAAACCGCCGTCGAT
GGTGGAGGCATGGCGTGGACTTTGGTACAAACAGTGCTGCTGCCTGTGATCATCGGCCTA
GTTCTGCGTGTCTTCTTGAACAAGTGGATCGACAAGATTTTGCCGATCCTTCCTTATCTC
TCCATCCTCGGTATCGGTGGCGTGGTGTTCGGCGCAGTCGCAGCCAACGCGGAACGACTC
GTGTCTGTCGGACTCATCGTGTTCGTTGCAGTTATCGTGCACAACGTACTTGGATACGTT
GTGGGATACCTCACCGGCCGTGTATTCAAATTCCCAGAAGCAGCAAACCGCACCATGGCG
ATTGAAATCGGAACCCAATCCGCAGGCCTCGCATCGGGAATGGCAGGACGATTCTTCACC
CCAGAAGCAGCCCTTCCAGGTGCTGTCGCTGCCTTGGTCCACAACATCACCGGCGCAGTT
TATGTTGGGCTGGTACGAAACAGGCCTTTGACTAAGGCATCAAGGAAGAAGGAATCCGTC
GCGGTTTCCAGC

>RXN02932-downstream
TAACTTATTTGCTGCCCGTTAGA

RXN02934-upstream
TGGATGGGCCGGTGGCGGTGACCATGGTAGATGCGGATTCAAGCTGCCAGGCGCGCTCAT
TGAGTGGCTGGCCGTAGTAGATTTCTACAACTCCGCCGGC

>RXN02934
GTGGGTGCAGACGAATTCGATTTCATCTTTGAGATTGATGCGCCAGAAGCCGGATTCGCG
CTGGTCGACGCCGGTGGGGTTTCCTTCTTCGTCGAGTTTCCACATGCGGGATTCGAAGGA
GAGGTAGTTTTCACCGTCGTGGGCGAAGGTGATTTGCTGGCCGAATGCGTATTGTCCGTC
TTCTGCGGTGTCGGCTTGGCCTTCGCCGCGCCAGACGCCGACGAGAGGGAGGAGCGCGAG
GAGTCCGTCGTGGAGGTTGGGGCCTTCGCGGAGGTTAGCGGTGTCGTCAGGGATAGGAAG
GTCACC

>RXN02934-downstream
TAGGCCTGGGATGTTGCGGTGAG

RXN02936-upstream
ACCAAGTTCAGACAGCTCTGGGTTGGACCTACCGGAGTAAAGGCGTGCCACTGACATAGC
AGTTTGGCCGTGGCGAAGCAACAAGAAACGAGTGGGATCT

>RXN02936
GTGGTTGCGCCGTTCCAGTTGGTGGGTTTGGTTTCGGTGCAGTTGAGGTCTTCTTTCTCT
GAGCCCGCAACCGAAGAAGCAGAAGATACAGAAGCAGAATCCCCTACAACACCTACCGGC
TTACCTGCCGCTGCAGCATCCATCGCCACGTTGGACAATGCGTCAGCTCGTTTGTTTTTC
TCACGCGGAATCCACGTA

>RXN02936-downstream
TAAGAAACGGACCCGATTTCGGA

RXN02939-upstream
CTTCGAAGAAGACGATATCCCCTACGAAGTCGACGTGGATGACTTATTTATCCTCGGTGG
CTTAGACAACTTCATAAATCCCCTTGGAGTGATTGAGATA

>RXN02939
ATGAATCTCCACTCCTTAGAGATTCGCCAAATTTCATCCGGCACAATTTCAGAACGAAAA
ACTTGGATCTTTCCCACTGCTGCTCGCTCATTCAATCAAAATCTAGTACACCCGCAAAGC
ATTGAAATCGATGCACAAACCGGCGTTATTTTGGCTATGGAAAACCGACTACAACGTACC
GAAGTTGAATCAGTAGAGTACCCAACGGATCTTCCTAATCCTGCATGGACAGGTCCAGCC
ATTTCTTGGCCACTAAAAGACCCATCAATCGATTTCCCTGACCCGCTCCCCCACAGCATT
TCCGAATTACCACCTCAATCCGATAATCCTCGGCATTTGCGAGTATCCATCAGCTTAGAT
GCAGTGGAAGGTGCTTTTCCGCGCTACCGGATCGGAGATTCAATACGTATTCCGCTTGTC
TTTGCCCGGGACACGCCCTTCATGTCCGGCTTAGAAACAACACGTCGCGCCTGGATTGAG
GCGGCCACGGAAATGGACATCCATAACACATGGCCCATAATCCTCACCGGTGACGGCTGG
ACTGCACTCTCTCATTCAGACAAACCAATACGCCACGAAGCCGAGTTAAAGGGATGGTTT
TTCCACAGTTTGTTCGGCAGTGAAATGCCCTTGACTGATCTGAAGATTGAACGAATCTAC
GGAGGCCTGGGTACTTTCGACAGCGGAGCCACCCGGTGGCAAGAACTCACAGACACAGAT
GATGCCTACACAGAAAATGGCAGCTGGCTGTTGGAAGTTATCGTCGATGCCACCCTTGAC
GGTGCAATTCCACCACCACTTCAGCCACAACAGTTTGAAGCATCCATCACTCACATCGTC
GATGAGCAACTATGGGTCCTTGGGCAGATGCTTCCAGTTCTACGATGCTGGGATCTTGAA
ACCGGAAAATACCTGGGGCAAACCTATGTACCTATTTCGGTTTCTCATAGTTCTCGGCTT
CAGTTTTCGGAAGGGTTGATTCACGATTATGAAAATGCCTGGTCGCTGAATCCTGGGGTG
CGCATGCTTGCGGAGCCACAGCCGTGGATAGAGCCTGTCATTGAACTCGACGTTCCAGCG
CCATGGGAATTACAAGAAAGCTTCCCCGATGGGCTTTACTCCCTAACTGATGGAGAGCAA
ACAGCACTGGGTCGAAGCACTCCAGCAGGACAATTGGAAATCTGTGTAATCAGCAATGAC
GGATCCAGGATCTTAAACGCAGGCCGAGTAGAAGACCTGTACTTTGTGCAATTCTGGGGC
ATGACCGTCTTTTTGAATTCCAACTTTCAAGTGCAAAGTGCCGAAGAACATCAGCTTGGT
GCGAAACGTGAACGCTGGATTACACAAGAAGGCGTAGCTGCCAAGTTCACCGAAGAAGAT
GAAATCGTATTCCTCGATCAGATATCTGAAAGCGAAATAACCAGGTGGAAAACACCAGAA
GGATACTTCACTGAGGTCAGAATTCTGTCACCAAACCACTTCAACATACTGGTTACTCCG
CCTACTGGTTCTGACTATCTCAAACCAGTACCTTCCTCTGTCTCAGTGTTTAGAGACGGT
CAATGGAGCAACATTAAATTCGAGGACGTCTCTGTAGAAATC

>RXN02939-downstream
TAGGGCTTTCGACGCTTGAGCCC

RXN02950-upstream
TCCGCCCTATTTCAGCAATGTTTAATACCGGTGGAATCGTTTTTATTAGGATGGGTGGAT
ACCTATCTTTAGTGAGCCGTACTAGCGAGAAAGCTGCCCC

>RXN02950
ATGACTGTTTTCAATGTTCTCCATGACGCACCCGCACCACAGCCGGATAAAAACCGCCCC
GGTGTCAAACGTCTCCTCCAAGGTGATGGCGCAAACCTCATCGCCTTCACTTTCAGCCCT
GGACAGTCACTTCCCGACCACCGCGCCGCACATCCCATCACCGTGACCGCATTTTCTGGC
CAGCTCACCTTCAGCTATGGCGAGGAAACCTTTGAGCTCTCCCCCGGTGTGACAGTGCAC
TTGGAAGCAGGAGTTACCCACCGCGTGGACTGCCCGCCAGAAGCACCAGGCGATGCAAGT
AATGCTGTTAACTATGCTCACTGG

>RXN02950-downstream
TGAAAAACACTCAGTCAACCAGG

RXN02951-upstream
GATAATGAGTCAGAAAATGAAGGTAGCACTACTTGCTGGATTAATTTTCAAGGTTTTCTT
TCAGAAATTAATCCATAGCCGATATTTAAGGTGAGAACAC

>RXN02951
ATGAGCTCCACGCTCGCACGAAAAGCTTCAGGCGACGGTTCCGAAAAGAAGAAGCCTGGC
TTGTTTAGACGTGCGCTTCGTTTCCTCACCCACCCACCTCACAAACAGGTAGACAACAGC
CTTGCGGATATCCGTGAAGGATTAGGCCTCGGGGTGGACGATTCCCACGAAGGATCCAAA
CCCAGCAACGATCATTCTTTGCTGCATGAAAAGCCTGAAATTTCCGTCATGCCGACCGAA
TCAATGGCACGGCTGATCTTTTATGCGCCTGATATGGATGGGCAAACAGACCCCGGTGAA
GTAGTGTGGATTTGGGCACCAGCCGATGGCCCCCAGCAACCACCCCGTAAACGTGCCATC

GTTGTTGTTGGAAGAAACCGAAACGCCATTTTAGGTCTGCTCATTTCCTGCAACCCCGAG
CACCGCACTGATGAAGACTGGATCGACATTGGATCTGGCAGCTGGGACCCTCGAGGTCGC
CAAAGTTGGGTACGACTCGACCGCGTTCTGGAGGTACCCGAATTGGGTATCCGGCGCCAA
GGAACAGTCGTCCCCCCGGGGCGCTTTGAGCGTATCGCCAACCGCCTCCGCAACGATTTC
AACTGGGTC

>RXN02951-downstream
TAACATTTATTTGGTAATTGGGC

RXN02957-upstream
GCATGCTATTGCGCTCCGGGTGGGAGATTCTGTCGTCCATGCCGCGGTTGTGGTGGCGCA
ATGACTGCGCCCCGGGCACGGAATGGCTCCGGGTCACCAA

>RXN02957
ATGCAAACTGCCCAAGGAGGAAGGGTCTACACCTCACTGATGGACGAGAAGTCCCTTTCC
CCGTTGATCGGTCTGCCGGGTCGGGAGAACATCGGCCTGGGCCGACACTGGCACGGTCTG
TCGACGATGTTGCGGGTGCTCAACGGCATCGTCTACGTCGTTCTGCTGTTCGCCACCGGG
CTGTGGCAAGGCATTATCCCCACCTCCTGGGACGTCTTCCCCGAGGCGTGGGAGACATTG
AAGGTTTACCTGGGCTTTCGTGCCCCAGGCATCGAGCACTTCACCCCCCTA

>RXN02957-downstream
TGACGCCTTGCAAATGCTGGGCT

RXN02967-upstream
GGGAATCTAGTCGGCCTTCACCGGTGATCAACAAGTCAGTTTCTGGCAGCGCATCCTCGA
TTCCGTTGGAGCGGGCAATCAGTGGCGCGCCGGGGAGGAT

>RXN02967
ATGGATCTGTTGGTCGTTGCCGTGCATGAGGGTGGACAGCCACGTCAGTCCGATTGCAAT
GCCCCCGGCTGCGCCCATACCTGGCTTTGTGCCATCAACTTCCAGTTGGGCGCAGGCGTG
GTGGAGGGCGGCGTCGAGAAGCGAAATGTCTTTTTCGGTGGCACCTTTTTGGGGCCCGAA
TACGGTGGCCGCGCCCTGCGGGCCGGTGGCGGGGGCGTCGACATCGGTGAGCAGGATCCA
TTCGACGGCGGCTGCGGGGATGTTGAGTTCGGCGGTATCGATGTAATCGAGGTTGATGAG
GTCGGCGCCACCGGTTCG

>RXN02967-downstream
TAGTGCGTAGCCCTCTTTGTTGC

RXN02971-upstream
TTCTGGTCCGGATTTTCGGGGAATACAGCGAGGGAGAAACGTGGCACGCCATTCAAGTGG
GAATTCAAACTTAAGGTTATCTAAATCGCTAACCATTGCG

>RXN02971
TTGATTGCCATCGTCGCTCTCATCGTGGCACTTGTGGTGTGGCTTTTTAACCGTTCAGAT
GATTCTGGCTCCACCACGACCACCTCACAAGAGTGCATCTCCGGAAACTTGAGTCTGCCC
GTTGGTGGCGATTCCACCGCAGCCGAAGAATTAGTGAACAAATTTAATGACTCATCACCT
GTCAGCCGTGATTTCTGTGTTGAGGCGGAAGCTGTGGACGGTAACGTCCCCGCTGCCACG
TACCTGTTCGCTGGTTCTCGTTCTGATGCTGCCACCGCACTTGCTGAAACCGGTGCCGTA
GCAAGCAGCTCT

>RXN02971-downstream
TAAAGCTCTTGGCCCTAGGTTGG

RXN02978-upstream
GCCTCTTAAAATCAGACAATTTCAGTGTTGGAATAGCTACAAGGGTCTACTGTAAACGAA
GAACGCTCGATAGGGCTGTGTACCTCAACGGAGGTAAAAC

>RXN02978
GTGATTGATCGACCTGTATGGTTGTTTGAACTTTATAACACCGCGAAAGAAGTAGTATAT
TCGCTACTCATTGATCAAGTAACTGGGGAAAATACAATACTCAAGAAGGATGATGGTTGG
CGAGATCAATTCATGATTGAGTCTTTCTTTGCTTATGATTCAGAAGCTGACGCGACCTCG
TGGAGCGGTAAGAACATGAATAGCTACTGGTTCGTTAGCGATCTAATCAGCAATATATCC
TTCGCTGAGCGATCCTTGGAAAGCTTTTCTTGGGCTCTTCGAGATCTTGAGGATCTTTCT
TCTAGTGAAACTGAATTTGAAGGGCTTGAAGAGCTGAATCTAAAGTTTAGTGAGCTCCAA
GAATGGTATACGAACCTGGAACTTCCTTTTCAGCCGTCGGCTGCTGATGTTGATGAGGTG
GAGCAGTATCTGCAAGCTGAAGTGACAAGGCAACGGGGTGACTATCAATGGTCTCCTGAG
TTTTGGATACCAAAGCCGGATTCATACTATATCGACCATGCACTAGCGGTTGTCACAGAT
GTTTTGGGAGCTATTGAACAAGGGGAGCTGCGTGAAGAAGTAGAGGTGCAGCAGGCTTTA
GACGAGGTATCTGAAAATTGGAATCCTTTGGAAGATTCTGATTACTACTTACAGGATCAC
CGTGGGCGCCCTGTACAAGATCTTTCCCGGGAAATGGAGGAGTTGGTCAGATGTCTAATG
CTTGACCAAGAGTGGTGGGGTGCAGAGGCAAGGATTAGAAAGCTTGTTGAATCAGTTGAG
TGGGAGGATACTCAGGCGATCAGCTCTTTAATTGAACACGAGCAATATTGGGAGGATGGT
CGTTTTCGCCCACCTCTACATAAGTTTTCGGAAGGACTAGACGAGCCAGAGCCCTTGCCG
ATGACGAGAAAAATGATACTTGCGACGAATCACCCTGATGTTTTACGCGTAAACATTGCT
GATTATTATCAGCAGCATAGGCGCATTGCTACTCAGAAGGTGGAATGTTATAAGGAAGTT
TTGGCATTGTATCCAGAGATTCTTAAGAAATTTGATGATTCATCTTTCGTCAATCGACAT
TGGATCTATAGGGCGTTTGATCGCGAAGGTCAGCTTTTGTATATCGGGGAGACAATAAAC
CCTCTTGTACGGTTGAGGGAGCATGCCGGCTTAGGGTCTATTAACCACGCACATCATAGG
CTAGTATCGCCGTGGTTTTCTACGATGGCTACATTTCATCTTGAATCTTGCTTTACCCAG
GCTGAGGCAAAAGAGAAGGAGGCTTTATATATTAAGCTGGAACAGCCAAGATATAATAAG
ACGCATAATTCTGCTAGATTGGCGGTTTCTGAAGAAGGGGTGCCGGTGAACGAGGTGCCG
TCAAGAAATGATCCGAGGAATGTCGGTTGGAAGGGTCATAGGCACGTGCCACCAATGTTG
CCGATTGTTGCACGTGTTGTCGATGAATCGACAACACGTGAGGGATATGCGTTTTACGAG
GACAACCGG

>RXN02978-downstream
TAGCGTTGCGATCTCTCGTGGAA

RXN02995-upstream
AAGGCAAGGTCGGAGACGAGCCTTGTTAGTTCAGAGTCCTAAATAGGCGTTTATGTCAGC
TCGCGCAACAGGGATACAATGAGCAACCGTGACGCAGCAA

>RXN02995
TTGAACCACGCAAAGGTAAATCAACATCCCGGTCAAGCCACCCTCCCAGAAACCGCAGAG
GGGCAGGTTCGCACCTACGAGGTAAAAACCTACGGCTGTCAGATGAATGTGCACGATTCT
GAGCGCCTTTCGGGCCTGCTCGAGGAGGCTGGATACGTTGCTGCTCCGGAGGACACCACT
CCGGATCTTGTCGTATTTAATACGTGCGCCGTGCGTGAAAACGCCGATATGCGCCTCTAT
GGCACTTTGGGCAACCTGCGCAGCGTGAAAGAAAAGAACCCAGGCATGCAAATCGCTGTC
GGTGGTTGTTTGGCTCAAAAAGACAAAGATACCGTGGTGAAAAAAGCACCGTGGGTGGAC
GTGGTGTTTGGTACCCACAACATTGGTTCCTTGCCAACCTTGCTTCAGCGCGCGGAGCAC
AATGCCCAAGCGGAAGTCGAAATTGTCGATTCCCTCGAGCAGTTCCCGTCAGTACTTCCT
GCAAAGCGCGAGTCTGCTTACGCTGGTTGGGTGTCCGTATCAGTCGGATGTAACAACACC
TGTACTTTCTGCATCGTTCCGTCGCTGCGCGGTAAAGAGCAGGACCGTCGACCAGGAGAC
ATCCTCGCAGAGGTACAAGCACTGGTGGATCAGGGAGTTACCGAGGTAACTCTACTTGGC
CAAAACGTAAATGCTTACGGCGTGAACTTTGTTGATCCTGAGCTAGAGCGCGATCGCAGT
GCATTTTCCAAGCTGCTTCGTGCCTGTGGTGAGATCGAAGGCCTCGAGCGGGTTCGCTTC
ACCAGCCCTCACCCTGCAGAATTCACCTCTGATGTCATTGACGCCATGGCAGAGACCCCA
AACATCTGCCCGCAGCTGCACATGCCACTGCAGTCCGGATCTGACAAGGTGCTCAAAGAG
ATGCGCCGTTCCTACCGATCCAAGAAGTTCCTCTCCATCTTGGATGAGGTCCGTGCGAAG
ATCCCTCACGCCTCTATCACCACCGATATTATTGTCGGATTCCCTGGCGAAACAGAGGAG
GATTTCCAAGCAACCCTCGACGTTGTCAAGAAGGCACGCTTTACTTCTGCTTACACCTTC
CAATACAGCCCACGCCCTGGCACCCCTGCAGCGGAATATGAAAACCAGCTTCCAAAAGAA
GTTGTGCAGGAACGCTACGAGCGCCTCATGGTCGTTCAGGAACAAGTCTGCGAAGAAGAA
AACCAAAAGCTCATCGGCACCACCGTCGAATTGCTGGTCCAGGCTGGCGGAGGCCGCAAG
AACGATGCCACCAAGCGCATGAGTGGTCGCGCACGCGATGGACGCCTCGTGCACTTTGCG
CCAGAGGGCGACATTGATGGTGAGATCCGCCCCGGCGATTTTGTCACTGTCACGGTGACT
GAGGCCAAGCCTTTCTTCCTCATCGCAGACTCCGGTGTGCAGACCCACCGCCGCACCAAA

GCTGGTGACAACTCTGCAGTTGGTCAAGTTCCAACCACAGCACCGATCGGTGTGGGCTTG
GGACTGCCACAAATCGGCGCACCAAAGGTGGCTCCTGCCACAGAATCTGCCTGCTGCTCC
ATTAAC

>RXN02995-downstream
TAAAAATTGCAGGCTAGAATAGA

RXN02997
CCCCTACCGGGCCAGCCCTTTGAGGGCGAGGCTTTAACGCTTATAAACGCCCTCCTCCAC
CACGCCGAAAACGTCGCAGCCTCCAACCCCTGGAAGCGCACCACCTTCCACACCGCTCAC
ATGCACCCTCCAGGGAGTAATGCGGATTGTGACTACTGCCTGGTGCTGCAACGCCGCGGA
TACGTTAAAGCCCACGAAGAAATCCAACAAACCATCCCGCTTCCTTCAGGTGACTGGTCC
GCTGGAGAATTCACCGTGGTGGACGTTGAAGGCACCGCCTTCCCAAGCGCGCTGATCCCC
AGCATCGTGGAACTCCAACACCGCGCAGCCCTCGATGTGCCCCACGGAAACTTAAGTGTT
GCGCCTGCACAGTGGGATGAACACCGCTTGGCGCAGCAATCTGAAAGAATCCTTAAAACA
GGAACGAAACTGTTCACCGTACTGTTTGCCGAAGGATCCACAGTCGCTGCCATGTCCTCC
ATCGCGATTCCCCCAGGCTCCAACCCTGACATCGCCGAACAGGGACTGACCATCGTGCAC
CCAGATTTCAGAGGCCGTGGTCTTGGAACCGCTGTGAAATTAGCGGGACTGTCACTACTT
TCGAGGTGCCACCCAGAAATTCAACGCGTAGCCACCTCAAATGCAGTAGACAACCATGCG
ATGCTGGCGATTAACCGCTCCATAGGGGCAACAGAGATCGCCCGAACCACCCTGTGGGAG
AAGAAACTC

>RXN02997-downstream
TAGGTGATGGAATTCGAGACCAA

>RXN03001-upstream
CCCGGTTCACGTGATCAATGACTTCACGAGCACCGATGAAATCGATGCTGCGCTTCGTGA
ACGCTACGACATCTAACTACTTTAAAAGGACGAAAATATT

>RXN03001
ATGGACTGGTTAACCATTCCTCTTTTCCTCGTTAATGAAATCCTTGCGGTTCCGGCTTTC
CTCATCGGTATCATCACCGCCGTGGGATTGGGTGCCATGGGGCGTTCCGTCGGTCAGGTT
ATCGGTGGAGCAATCAAAGCAACGTTGGGCTTTTTGCTCATTGGTGCGGGTGCCACGTTG
GTCACTGCCTCCCTGGAGCCACTGGGTGCGATGATCATGGGTGCCACAGGCATGCGTGGT
GTTGTCCCAACGAATGAAGCCATCGCCGGAATCGCACAGGCTGAATACGGCGCGCAGGTG
GCGTGGCTGATGATTCTGGGCTTCGCCATCTCTTTGGTGTTGGCTCGTTTCACCAACCTG
CGTTATGTCTTGCTCAACGGACACCACGTGCTGTTGATGTGCACCATGCTCACCATGGTC
TTGGCCACCGGAAGAGTTGATGCGTGGATCTTC

RXN03005-upstream
TAGGTAAACCTTAAACAGTCGCCATTGAAGAATTTTAAAAACAAACAACCTTCAACGCGC
TAACAAGCATCTTCCCACTCTCGTTACCGGAGTTTCTCAC

>RXN03005
ATGTCTCACAAGTTTTCCCGCCGTGCTTTCGCAGTACTGACCGCTGCCGCAATTTCCACT
TCCGCTTTCGCAACCACTGCTCCGTCTGCGATTGCAGAGCCAGTTCTAATGTCGCACTGC
AGACGATTCCAGCGTCGCAACTTCAGAAAACTCCCTCGACTGGGGCTTCAAGGCTTCCTG
GCGCACCTATGTCACCGGACCTTGGACTGGTGGAACCGTGACGCAACTGGCGGTGCAACT
GTCAACGAAGATGGAACCTACAACTTCACCCTCGGAACTGGCTCCAATTACGACGTCGAC
ACCGAGAAGGGCCAGCTGAACTACGAAGGAACTGTTGCCTTCGCCAGTGACGCTCACGGC
TTCAACATCACCTTGTCCAACCCGCAGATCACCGTCGAGGGCGACACTGCAACTTTGAGC
GCCGAGCTGTCTGACAATGCCGCTCCCGAAGAGACCTCCACTACTCGCGTTGATGTTGCT
GAGTTCGAACTGACCGCTCCTGAGGTTTCAGAAACCGATGCGGACATTACCTACACCTGG
ACCGATGCTTCCGGCACTTTCTTGGAGACCCTGCAGCCTGAAGAATTGAGCCGTTACGCA
GGCCAGGAAGCGGATGCGCTGAGCTTCTCCATCACCGTGGACAAGGCTTCAGAGAACCCT
TCCGATGATGTTGCTACCGGATCTTCCTCCAGCTTCCTCTCCACCATCTTGAACTTCCTT
CAGCAGCTGGCGAGCCCACTGCTCAAGCTCTTCGGTTCGCTTTCTTCC

>RXN03005-downstream
TAAATAATCAGTAATGCCCCACC

RXN03009-upstream
ATGTGAACCTGATGCTGGCACCTGAAGATAGCCACAGCCCAGGCACCGCAACAGTGACCT
ACCGTCATGGTTTCAGCGATCACCGTTTACCCTGCACTGC

>RXN03009
GTGGCTAATATCGCCAGCTTGTACGGACTGTGGGAAGGCAGCACATCCACACCAATCGAA
CAGCTCGTACCTGCGAAAGGTTCCAGCTTTCGTTTGGTGAGGTCTTTTTACAGGCGAATT
GACGGCCAAGCAGTTCAGGCTCGTCTCAAGGAGAAGATTCTCAACACCGCGGAAAACCCG
CTTCCTCGCTTGGACATTCCAGGTAAGGAGCGCACTGCGCAGTACCCAGAAAATCCGGAT
ACCTTCGCCCAAAAAGCAGCTCAAGAAATTCTTGATGAGTTCAGAACTCCACTGATCGGT
GAAGAAGCTGCAGCTCATGTTGAGAAAACGAAGACGATTTTCTGGAAG

RXN03010-upstream
TGGGCGCCTTCAATCGGCACCCACTGAATGGATTCTTCCGGGCCTAGTTTTAGGGCTGAT
CAGCCTGGGACTCAATGCGTGGATTACCTTCGGTGCGCCA

>RXN03010
GTGCCCACCGATAATCTTTTTCTCATCGTTGCTGGAATTGCGTGGGTGTTGGCAGGAATT
TTGAGCGTGCTGTCCATCGGCAAGTACATGTCAGCAGTAAATGAGCGAAAGTCGACAGGC
TTTTATACAGAAGTGCCGTGGAAGAAAGCGCTCTTTACTGCGACAGCCGTCCTATTGGTG
TTTGCTGTTGTGTGGTCGGCCTTGGATATTGCCCTGTGGGTAGGAAAGCAGTCATGG

>RXN03010-downstream
TGAACACGTTGAACTCTAAAACC

RXN03011-upstream
CCGACGTACCAGTTTTTGTCGTTCCACCCCTGGACTAAAACCGAGACGAGAACCAAGAAG
ATGAAACCAAGGGGTAAAAACTGGTAGTCTCTTCCACGTC

>RXN03011
ATGGCATACGAAACTGATTCCCTCAACCGACGCACCCTCGGGCCCGCGATTGCAAGCGCA
GTCGTGGGAATCGCCGTCGGCGCAGTCGCAGTAGTTGGGGTTTCAATGATCTCAGGGCAG
GACACTGTTCCCACTGGTAACGCCGTAACTGCAGACGATGCCCTGCTCGGTGGCCCTGAG
TATGGTTCACGCGAAGCAGAC

>RXN03011-downstream
TAAGAAGCCACTTCCCCGTTTTC

RXN03012
ACCACTATCAACATCATCATCACCAATGGCGCTGCACCACACCCAACTAATCTCAATCGC
GCAGAAATTCATGATCACCTACCCCTCACTGCCTCTGATTCGGAGCTAACCCGCCCCTCC
CAGGAATCAGTTCTCTATGACCATGAATCCGAAACTGTCTTGCGCACCATGGTCATCCCT
GCAGACCTGCACGTCGCTATGAAGCATCTAGCTAAAAAACACAACCTCACGGTCACAGAG
ATCTCGCGCATCCTTCTGCAGCGCTACATCGACCGCAATATTAACCATGTAGAGCAAAAC
CAGGCTGAATCCGACATGGTGGAAGTCTTTGCCAGCCAACCAACCAATGCAACCGCAATG
ATCCCTGTACCTGGAACCAGCTTCAGGCAAATATTTATCAAGCACAGCACTGGTTTCTGG
AAAAACATTGATCATGATCTTGTCGATCTCGACGCCTCTAAGACCCCGCGTGTACGCGAC
CGCAGTGTCTTACCACAACCTCAACTCCACAGAGCGTTGTTATCAGATGCTGATATGGCT
CGCCTTGCAGCACAACTGACCGACAAACAC

>RXN03012-downstream
TAAAACCTCCACAACAAGGACAT

RXN03017-upstream
AACTCAATATTAAAGTCGCGTAATTAGTGTTATATTAATTACGCGACTTTAATAGTTTTC
GAATACGTAGATTCTCGAAATACAGCAGAAAGCAGGGGTT

>RXN03017
ATGCTCGATTCATTGAAAAATCGCTTCACCAAAGCGAAAGGTTCTCATGGAGTGGGGGAG
GGGGCTGTTTCTGGCGATGCAGCAGTAAAGCCACTGCGCAAAGAAGAACGACTCGCCTCA
GTCATTCAGGAAACCGAACCAGGTGCTGCAGTCGAGGTCATGCGTCGCAATGACGCATTC
GCTTTGCCAGGTGAGACCGGTTGGGTAGTCATGCTGTTGCCAACTCACGATTCACAATTC
GGTGGGCTCAACGCTAAGGAAAAGAACCGCGAGGATAAAGGCACGATCATCAACCTGGTG
GTCAACGATGATATTCATTCCGTTGTCACTCCAGAACTTCTTGACAGCGATGTGCTTGGT
GTCATTCCTGATGCAGATTCTTTCGATCGCATGGATGAGTTTGATTTACTGCGTAACAAA
GCACGCTGGCACTACGGAGTGGCTGCAATTGAACCTGACACGGGTGAGCTGGTGGTGTTT
AAGGTGCCCGCGAAAAATAGCGCTTCGGCACGCGGTGACATTTTTTCCGAGGTCGGCGAT
GTGCTTAGCGGTGCTGCTGACCTCGAAGACGTGGTTGATTTTGAGGTCATTGCCACCTTC
CTAGAGGTGCTGAATGAGACCTCTGAGGTGGATATTGATGACGAAGATGGCGACGTGCCT
TATGGTCTTGAGGGTGTCAATGCAGCGGGAGTTATCACGGATGACCTCATTCGCGAGAAG
CTTGATGTGGATTCCTATCCGAGCAGTGCAGAGATCATTGACAATATTGTGCATGTGTTC
ACCAAGTTGCAGGGCAAGCATCATGTGGCACCACAGCCGGTGCTTCACAGCGCAGACGTA
GTGGATGTTGATGCACAGGAGTCCCATGACACAGTGGTTATTGAGAGCCCTGATGATGTC
GCACTAGCAGAACAGGTGGATGTACCGGATTTCAGTGATGGATTTGGTATTGACGATGCC
GAGGTTACTGAGCCAGAGGATGAGGAGGTTGTCGAAGCAACAGCTGATGCAGATCCTTTT
GGTGATGTAGCAGAAGACGATCCTTTCGGCAGTGATGATGAACCAGATTTTGGTGCATCC
GATGTTGTTGCTGCACCGGCACCTGTAGCCGGCATGTCCGATGAGCAGATCCAGGCGCTG
ATTCGTGGTGTGTCTGAGTCCGTGCAAGCAAAGACTGGTTCAGAACTTAATGCTTTGCGA
GAAGAACTTGCACAAGCACTGGCTTACAATCCGGTTCAGGATTCACAGGCAGCATTGGCA
CAGGTGCACGCAGCTGATGCCCGCAGCTTTGATGCCGATCAAGTGGGTGATGCTGTCACC
AAACGTTATGTTAATGACGACTTGGGGCTGTATGTCGATGAGGCAAACTTCAATAATGCT
TTGACCAGGGCACCGTTCCAGGTGGCGATGCCGCAATTCCAGGAGACTACACCGTGGTTA
GGTGATCAGCTTCGTACATTGGTGGCTGTGTTTAATGGTCAGCTGCTTGATCAGCATCAG
CGTGACTACCGAAGAAGTGCGCGCGATGTACATTGCGCT

>RXN03017-downstream
TAATGATCGCTCTAATCTTGAGA

>RXN03018-upstream
GTGGCGATGCCGCAATTCCAGGAGACTACACCGTGGTTAGGTGATCAGCTTCGTACATTG
GTGGCTGTGTTTAATGGTCAGCTGCTTGATCAGCATCAGC

>RXN03018
GTGACTACCGAAGAAGTGCGCGCGATGTACATTGCGCTTAATGATCGCTCTAATCTTGAG
ATCGCTCGTGATCTTGGACTGGATAATAAGGATTCCGAATTCTACGAGGTTTACCGTGCC
ATTGAGCGTGACCGCGATGTTATGGCTGGTGATCAACAGCGTGTGGAGTCAGAGCGTCGT
CAGCAATTGCAGCAGGAGTATGAGGCGAACCGTGAAGAATATGTCATGGCAAAGATCGCG
GAGCAGCGCGTGGAGTATGATCGCCGTCATATGCCTCGCCATACCGCATCACTAGAAGCG
GTAGGTCGAGAGCTGACGAGCCTGCGGGATCGCACCATTGAGGATTACACCGCACGCATG
AACACGCTGCGTCGTGCACGTGCTGGTGAACGGGCTAACGCTGCAGAATCTCGCATTATT
GACGAATTGCGCCCGATTGTGGAGCGCCAGGCAGAACTGCAACGAGCAGCTTTCGATGGT
TTCATTGTTGATCTTGACAAGTTTATTGCTGATCACCGCGAAGATGACCTGCGTTTGGCA
TCGGTGAATGAGCAGAAGCTTGCTGCAGATAATCGTGTGGCACAGTTGACCAAGGAAGCC
GAAGAGCGCATCGAGGGTATCCGCGTCGAGACCGATAAGATGATCGCCTCCCAGCGCAAG
GCACTTGAGCGTCAGGAAGCGGAATTCGCAGCAGAGCTTAAGCGTCGCGACACTATTGTC
GCTGCATCGGAGGAACGTGCTGAGCGGGAAATTACCACAGCACGTCTTGATGCTGAGGCG
GCGCTCAAGCGCATGGAAGAGCAAATTCGTGTAAATAATGAGGCGCATGAGGCGGAGATT
GTTATTGAGCGCGATCGAGCCACCCAAGCAGAGGCGAACTCCATGACGTTTGTTGAGTCA
GTCAAGCAGCAGGATCGCAGCAACAACATCATTTTGATTGCCGTCCTCATTGTGGGGCTG
ATTGCCGGCATGGTCGCTGGCGCAGCCTTCTTC

>RXN03018-downstream
TAAAAGATCGTTGCGCGGGCTGT

RXN03024-upstream
CTCTACCCACTTAAAATGGACGCATATTCGCAAGATAAGGCATGCTTGGATGAATAGATT
TTAACTCAACGTTTACTAAACAGAATCGGAATTAGGAGCC

>RXN03024
ATGCTTGAACGCACACAGGTATTCGTGGATACGTCCTACCTGCTCGCAAGCTTTTACAAC
TCTTGGGAGACAGGGGCACGTGCCCAATTAGAAATCGACCTCCCCGAAGTAGTCGGGGTA
TTAGGAAGGATGATTGAACAACAACTTAAACAGCCAGTACAACGCCAAATGTGGTACGAC
GGAATCCCCGATTCCGGCCCCCACCGCTATCAACGAGCACTACGCACCTGCGATGGTGTG
CAACTTCGTGCTGGCCAATTAATTGAATGGGGCGAACGCCGCACACAAAAGGCAGTAGAT
ACCCGCCTTGTTGCAGACCTCGTTCTCGCAGGTGTTCGCGGACAATGCTCCGATATCGTG
CTCGTCAGTGGCGACGCCGACATGATCCCCGGTGTTCAAGAAGCTGCCAATGCAGGCCTT
CGCGTTCACCTCTACGGCTTCGGCTGGGATTCCATGTCCTCCCAACTGCGCCACTGCTGT
GACACCACCACCATTTTGGATCCTCGAGAAGATTTTGCTGAATGCATGCAGCTGCAGGTT
CTCGAAGGTCCACTACCCCCTGTCGTTCGGGTAAAGCCCATCAACGATGCAGAACCCATC
GAGGATTTGGATTTCACTCCAGTTCCAGGCGTCGCCTCACCATTTGAAGAGGTCAGCGCG
AAAGATGAGAAATTCTCTCCACGCCCAAGTGAACCTGCCGAAGCTTTGTCGGAACAGGTC
TGTGAAGCGCAGTATGAGATCTCCAAACACGAAGGTCAAACCGCTGATTCAGGAGAAATC
ACCGAGTCTTTCGAGGCCGCTGAAATCAAGGTAACTGAGTTTTTTGGAGAACCAGCTGCT
CCAGTAGCGGAATCAGGCGTAGAAGCTCCCACTCCGGAAGCTCCCACGGTTCCTGAAGCA
GCTAAGCCCACTCCGGCGAAACCTAAGACTCCAAAGGCAGAGCCCCAAAAGCAAGAATCC
CCCAAGCCGGGAACTCCAAAACCAAAAGCTCCAAGCCCTGCGGATATTCCACCGAAAGCC
CCAGCTGACACTGAGGAACATTCGGAAGTCGAAGCTGAAATCGAGGACTCACGTCCAAAG
ATCCCCAGCCCTTCGATGATGGCTCCCCGCCGCAAGCTTCGTTCCCGCTACGTTCCGCTT
CCCAACGAAGTGTGGGCAACAGCAGGATTCCAAACTCCTTACGATGTCGGGCAACAGTAC
GCATCGTGGTGGTTTGAAAACGCAGCTACCAGCACTCAAAGAGATCAGGCTCATCTATTG
TCTGGTGGCGGACTTCCACCAGAGATCGATCGCCCGCTTCTGCAGTTTGCTTGTGAAACT
CTCCACGAATACACCCTGACTGAAGCGCAGCGCGTAGCTTTACGCGATGGCTTTCACTCC
GGAATCCGTGGTGTATTGCTCAACCAGCGAGATAGC

>RXN03024-downstream
TAGAATCACAAAAAACTGGGGCT

>RXN03025-upstream
AGCGAATCGGATTCAGTGATTTGCTTGCGGGCGCAGAAATGATTTTTCAATTAGACACAC
TTAGACACACGTAACTAAAACCTCAGGGAAGTGACTGATA

>RXN03025
ATGGCTAATCCGCTCAGCAAGGGCTGGAAGTATCTCATGGCATCGTTCGACAACAAGATC
GATGAGAATGCAGATCCAAAGATCCAAATTCAGCAAGCTACAGAAGCTGCCCAGAAGCAG
CACCAGCAGATTATGCAGCACGCTTCTCAGATTATCGGTCAGCAGAAGCAGCTTGAGATG
AAATTGAACCGCTTGGTTACTGACCGCGATAAGTTGCAGGAACAGGCTCGTCAGGCAATT
CAGTTGGCAGATAAGTCCGCAAACGAAGGCGACAGTGTTAAGGCTCAGGAGTTCAACAAC
ACTGCTGAGGTTTTTGCTTCCCAGTTGGTAGCTGTGGAACAGCAGTTGGAGCAGACTACT
GCGCTTCATCAGCAGGCTGAGGTTGCGGCGAAGGATGCTGTTGCGAAGTCTAAAGAGTCT
GAGATGCGCCTGAAAGAGCAGATGTCTCAGATTGATGCTCTACGTGCGCAGGCTGATCAG
GCGAAGATGCAGGAAAGTGTCACTAAGTCTATGGATTCTTTGAATCAGTTTGGCACTCAG
GATTCTTCTGTTCCTACCCTTGATGCGGTGCGTGAGAAGATCGAGCGTCGATACGCAGAT
GCTTTGGGCGCGCAGGAACTTACCCAGAACACTGTTAGTGATCGCATGGCTGAGATTGCG
CAGTCCGGCACCGATATGCGGGCGTCAGCTCGTTTGGCTGAACTTCGCGCGGAGGCGCTG
GGCACGTCCGCAACGCCTAAGGGCCAGCTAGAGGCAGGTGTCGAGGATGCGGAAGAACTT
ATCGACGAAACCTCCACCCCTTCAGCTACCCCAGAAACCGCAAGCCCAGAAGCTGATGCT
CCAGAAGCATCCGCAGACGAGTCCGAGAAGAAA

>RXN03025-downstream
TAACCTAAACACAAAAAACTGGG

RXN03027-upstream

AATAGGAGAATTTAAA

>RXN03027
ATGGAAAACGTTTACGAGTTCCTTGGAAACCTTGATGTCCTTTCCGGCTCCGGCCTCATC
GGCTACGTCTTCGACTTCCTCGGCGCTTCCAGCAAGTGGGCTGGCGCAGTTGCTGACCTC
ATCGGTCTGCTTGGC

>RXN03027-downstream
TAATTAACTTCGCCCACGGGCAA

RXN03029-upstream
GGTGTGGCTTCCTATTCGCTGCATCCTGAATATGCCATCAAAATCTTCACTCTGAGGCCG
AAAAATCCGGTTATGACATTAAGTACCTAGGACA

>RXN03029
ATGTTTGGAGTGGGCTATTATACAACCGCCCACCGATTGTCCACCCTGCAGCGCCCCAAC
TTGCGCGGCATCCCCTTAACCTTCGTGAGCGTCGACCGAGCCGGCAACATGTCCAAACGC
CAATCCGCCACGGGCTTCCACTTCACCCATTACGGCGGCACCTGCCCCCTGTGGAACGTG
TTTGAAACCTTCACCAACCCCGGCCAAGTGCTCCGCCAATTCGCGCAAATGCCCGACGGA
CGCAACTACCTGTGGATCTCACGCACCGTGCGACACCACGAAGCCCGGTTCGGCGAAGTA
GACAAAATGTTCGCCATCGGCTTGGGCTGCGAAGCGCGCCACGCCGACCGCACTGTGTAC
TCCCGCGGTTTCAACCTCCAGGACCTCTCCACCGCCACCCCCATCGGGTCCGGCTGCCGA
GTGTGCACCCGCGAGAACTGCGCGCAGCGCGCATTCCCATCCGTCCACGGCCGCATCAAC
ATCGACGCGCACGAATCCACTATCGCGCCGTAC

>RXN03029-downstream
TAAGAAAAGGAGCTTGCTTTACG

RXN03031
AACAACGGCCTTAACGCCATGGCCGCGATGACCAACCTCCCACACCTGCGCGCCATCCAA
GAACGCTACTACTTCCTGAGCATCCGCTACCTCGCCTCCATCATGATCGCCGTGGCCAAA
GCAGACCCCACCCTGTGGGAAGAACTCGACCTGCGCATCACCGACGCCTTAACACCAGTC
ACCGCAGGGGAAGTGATGATCCAATCCTCCACCCTGTCCAAACGCATCGCCGCCTGGATC
AAAGAACTCGACCCCGAACCCACACCAGAGCCCATACCGAAAGAGGACTATGTTCACGTC
CACACCACTGATGAGGCGACCTATGTCCGCATCAAAATCAGCGGCCCCAACCGCCTGATC
CTCAATGACATCATCACCCAACTCAAAGACACAGACACCGAGGACAGCCTGCCTGAAGCG
CTCATGGCGTTCCTGATGGAGAAAATCCAGTTAAAGATCACCAAGTACCTTTTCACCCCA
CATAAGCACCCTGAGCAGGTGTGGTCACCGGACTACGGTGACATTGGTCCCGAAGCCTAT
GCCAATGCCACCCTCGTGTGCGCCAAGGACTTAGATGAGGTCGCTGGAGCCACGGAGAAG
AGCTACACCCCGAGTGAGAAGATGAAAGCCCTGATCAGAGCTCGGGATGGGCATTGCCGC
TTCCCAGGGTGTTGCGTCCCGGCGAGTAAATGCCAGGTCGATCACATTATCCCGTGGGCG
GAGGGCGGCCCGACAGCGGCGTGGAACCTGCAGTTGTTGTGCCAGCGGCATCACAATATG
AAAACCGAT

RXN03032-upstream
CCTGGTCATAGGATACTTAGCTCAACCACACGGTCAGGGCCAGCAATTCCTCACGTTTTA
CCAACTCCGTAAGCACACCATCATGGCCTGGTGCGCCGCT

>RXN03032
ATGACCGACGGGGACTTAGACGCTGATATCTCACCCCGCCAGATCGGGTTGATGACCACC
CGAACCGTGGTCGAAATCGTTCGACTACGCCACATGATTGCCCAACAACTAGAAAGAGCC
ACGATCATGGAAAACGAGTACCTCAAAGAAATCGCAGCGCTGAAGAAAGAACTCGCGCAC
TACAAGCAAAAAGACCATCAGAATCAAATGGTGATCGATATCTTGGGAAAAGCTATTGGG
ACCAGGCCCAATCCTGGCGAGGGCTTAGACGAGGAGGACGCCACC

>RXN03032-downstream
TAAACGTGGATGAGCAACGCGCC

RXN03034
TTCCCACCAGATCGAATCTCCGCCAACGGGCGACGCTATTACGAGCCACAAACACGACTC
GAGTTCATGCGGATCTACACCACCCTGCCGCACGGCTACCGCCAGCCCTTCCTTAAAGCC
AACAACATCGGCCACTGCACCGTTCGAACCTGGCTAGCAGCAATAAGCACCTTCAGCCGA
CTTCCCCATGCTTTTGATGATGCCCACCGCTTCGGGATCGAACGCACCACCCCAGTCGAC
GATGTCACCACACTAACGGCTGATGACAAACGTGACCTGGTCATAGGATACTTAGCTCAA
CCACACGGTCAGGGCCAGCAATTCCTCACGTTTTACCAACTCCGTAAGCACACCATCATG
GCCTGGTGCGCCGCTATGACCGACGGGGACTTAGACGCTGATATCTCACCCCGCCAGATC
GGGTTGATGACCACCCGAACCGTGGTCGAAATCGTTCGACTACGCCACATGATTGCCCAA
CAACTAGAAAGAGCCACGATCATGGAAAACGAGTACCTCAAAGAAATCGCAGCGCTGAAG
AAAGAACTCGCGCACTACAAGCAAAAAGACCATCAGAATCAAATGGTGATCGATATCTTG
GGAAAAGCTATTGGGACCAGGCCCAATCCTGGCGAGGGCTTAGACGAGGAGGACGCCACC

>RXN03034-downstream
TAAACGTGGATGAGCAACGCGCC

RXN03037-upstream
CGCTAAAAGACAAATGACAGCGAAGCTGCATTCGGATACACACCTGAAGAACACTCTTCA
CCACTAGCATTCCACCAACGCCTCGGAAAGGGCTATCTCC

>RXN03037
ATGTCTGTTGACGATCTTTACGCTGTTGCTCTCGATACTCACACCGGTAAGCCTATCCCC
TGCGTACTCTGTGAAAATGCTCCACAGATTGTTATCTACGATGGTTGCTGCTCGCTTGCA
TATACCCAAGCACTTGGCGATCTCGCCGAAGCGGAATACTACGGCGCCGATCTTGCTGCA
GCTGCC

>RXN03037-downstream
TAAACAAACTTCATAGAACGACA

RXN03041-upstream
ACCGAGGAACTGAAGGAAAATGTAGGTGTCGGGGCTTAGAGAAACAAAAAAGGCTGCTAC
GCGGACAGCATTGTCACGTGCTGCTGCGGAGATCGCCTTG

>RXN03041
ATGGAAGGCCCTGAGGCGTTCACGGTTGCGGCCATTGCAGCTGCAGCCGGGGTCTCCCCC
AGGACTTTTCATAACTACTTCCCTTCTCGGGAAGACGCATTGGTGCAATTTGTGGTCATT
CGCGTTCAGGAACTCACGGATCAGCTATACGAGTTTCCTACAAGCGTGCCCCCACGAGAT
GCCATTGAACAATTGGTGATAAACCAATTGCGGGATGGCGATGACGCTATGGATTCTTTC
AGCGCAATGTTTCGAATCGGTGAGATCCTTGAAAATCTTGACCCCATCAAGTGTGTTATC
GATAAGGAGCGACTCATTGCTCCGTTGCTTGAGTTCATGGTTGAACGTGACAAAGACCTT
GACAAGTTCGATNGCGGCAACTCTGATCCATTTGCATGCAGCGGCAATTGCAACCTCGCT
GCATACGTTTTACCAAGCTTCCGAGCCCCGGGACATAGAAGATGGAGTCGCATTGATCCG
TCGGGCATGCGCCTGGAT

>RXN03041-downstream
TAAGAAANTAAAAATCTSTGACA

RXN03045-upstream
AGCTTTTCTATTTCGAAAAATAGCCTTGTATTCGAAAATTTGATCGGGTATGGTGGTTGG
TATTAGCACAGGGAACTAAACGGGAAAGGGGGAAGACACC

>RXN03045
ATGAGCATCACCACACACGTCCAAGCACTCACCACAGCACTCAACGCCATCGACAACCAT
TTGGCCAGCATGCTTGACCATGGTGTCACCCCAGACCAATACAAGGCCATCGAGCCCGAC
CTCATCGCCCTAGAACACACCATCAACCACCACGCCACCATCGCCGCCCAAACCACCGCC
CTCGCCGAACGCACCAATGCTGCGCAGTCGATTGGCTCCACCCACCTCATCGACTACCTC
ACCACCACCTTCGGCCTATCTAAAGCACGCGCCCACCACCGCATCAATCTCGCCCACTCC

CTCTACCCCATACCGAAGCCAAACTCTGGATCTGGCAACGGCGGTAATGGTGGCAATCCC
GACGGTGGTCCTGATGGTGGCGACTCGGGTGATGACGACTCCGGCGATGATGACCCCGAC
CCCGAACCGGACAAGCCTGAAGACGGCAAACCTGATAGTGATAAGCCCCGTAGGCCACGG
ATCAGCGCGGAAAAACACGCCATCATCACCGACGAACTCGCCCGCCTCAACCCGAATACC
ACACCCAGCGCCGAGGAACTGCGCAACCAAGCCCTGAGTCAGGCGATCTGGCGCACCCCA
GAAGACCTCCGCACGTGGCTACGCCACCAGGTCACCACCGCGAACAAAAACAACCCCAAC
CCCATCACCGCCATGAAAAGGCGCTACCTCTCAGTAGGTAAACCCGATGCCGACAACATG
GTCCGCATCAGCGGCCTCGTGCCCGCAGCCACCGCAGCACTGATCACCGCGAACACCGCA
CCGTTAACCAAACGCGGCAACCTCGTGGATCTACCAGCAGCAGAAGATATGCGCACCCGC
GGGCAACGCCATGCGGACGCGTTGCATCACATCATGGAGATCTACAACCACGGTATTGTC
ACCCCAGCTCGTGGTGGAACAGCCAGCATCATCATCTCCATGACCACCGATGATCTTGAC
GAGATCAACCACGCCAACAGCAGTGGTGAAAGTCTG

>RXN03046
GCCTCAATTGCTAATTCCACCCTGAATATTCCAGTGGGATTGGGCGGCTCCAATTTGCTG
CTCAAGGCGCAAACCGCGACCCCATCTGAGCCTGCGAATGCTCAGGACAAACTGTACCGT
TTCTGCATCGCCAATGGTAAGAGGGCATTTTCCGATGCGCAGCGATTCTTGCTCAACGCC
GACGAGCTCGCGGAGCTTTCTGATTATGAGCGTCTGGCTTATGCCATCACCTTGCTTGAT
CAGCCTGGAAAAGAAGCAGAAGGACGCGAACTTTTTCCTTTCGGAGCTTCGCCGCCAGGG
CTACCGCGCTGTCGATTTCTTGGAATCCCAGACTGT

>RXN03046-downstream
TGACCAGCTGAATAACCCCGATG

RXN03047-upstream
CTCTACCCACTTAAAATGGACGCATATTCGCAAGATAAGGCATGCTTGGATGAATAGATT
TTAACTCAACGTTTACTAAACAGAATCGGAATTAGGAGCC

>RXN03047
ATGCTTGAACGCACACAGGTATTCGTGGATACGTCCTACCTGCTCGCAAGCTTTTACAAC
TCTTGGGAGACAGGGGCACGTGCCCAATTAGAAATCGACCTCCCCGAAGTAGTCGGGGTA
TTAGGAAGGATGATTGAACAACAACTTAAACAGCCAGTACAACGCCAAATGTGGTACGAC
GGAATCCCCGATTCCGGCCCCCACCGCTATCAACGAGCACTACGCACCTGCGATGGTGTG
CAACTTCGTGCTGGCCAATTAATTGAATGGGGCGAACGCCGCACACAAAAGGCAGTAGAT
ACCCGCCTTGTTGCAGACCTCGTTCTCGCAGGTGTTCGCGGACAATGCTCCGATATCGTG
CTCGTCAGTGGCGACGCCGACATGATCCCCGGTGTTCAAGAAGCTGCCAATGCAGGCCTT
CGCGTTCACCTCTACGGCTTCGGCTGGGATTCCATGTCCTCCCAACTGCGCCACTGCTGT
GACACCACCACCATTTTGGATCCTCGAGAAGATTTTGCTGAATGCATGCAGCTGCAGGTT
CTCGAAGGTCCACTACCCCCTGTCGTTCGGGTAAAGCCCATCAACGATGCAGAACCCATC
GAGGATTTGGATTTCACTCCAGTTCCAGGCGTCGCCTCACCATTTGAAGAGGTCAGCGCG
AAAGATGAGAAATTCTCTCCACGCCCAAGTGAACCTGCCGAAGCTTTGTCGGAACAGGTC
TGTGAAGCGCAGTATGAGATCTCCAAACACGAAGGTCAAACCGCTGATTCAGGAGAAATC
ACCGAGTCTTTCGAGGCCGCTGAAATCAAGGTAACTGAGTTTTTTGGAGAACCAGCTGCT
CCAGTAGCGGAATCAGGCGTAGAAGCTCCCACTCCGGAAGCTCCCACGGTTCCTGAAGCA
GCTAAGCCCACTCCGGCGAAACCTAAGACTCCAAAGGCAGAGCCCCAAAAGCAAGAATCC
CCCAAGCCGGGAACTCCAAAACCAAAAGCTCCAAGCCCTGCGGATATTCCACCGAAAGCC
CCAGCTGACACTGAGGAACATTCGGAAGTCGAAGCTGAAATCGAGGACTCACGTCCAAAG
ATCCCCAGCCCTTCGATGATGGCTCCCCGCCGCAAGCTTCGTTCCCGCTACGTTCCGCTT
CCCAACGAAGTGTGGGCAACAGCAGGATTCCAAACTCCTTACGATGTCGGGCAACAGTAC
GCATCGTGGTGGTTTGAAAACGCAGCTACCAGCACTCAAAGAGATCAGGCTCATCTATTG
TCTGGTGGCGGACTTCCACCAGAGATCGATCGCCCGCTTCTGCAGTTTGCTTGTGAAACT
CTCCACGAATACACCCTGACTGAAGCGCAGCGCGTAGCTTTACGCGATGGCTTTCACTCC
GGAATCCGTGGTGTATTGCTCAACCAGCGAGATAGC

>RXN03047-downstream
TAGAATCACAAAAAACTGGGGCT

>RXN03048-upstream

AGCGAATCGGATTCAGTGATTTGCTTGCGGGCGCAGAAATGATTTTTCAATTAGACACAC
TTAGACACACGTAACTAAAACCTCAGGGAAGTGACTGATA

>RXN03048
ATGGCTAATCCGCTCAGCAAGGGCTGGAAGTATCTCATGGCATCGTTCGACAACAAGATC
GATGAGAATGCAGATCCAAAGATCCAAATTCAGCAAGCTACAGAAGCTGCCCAGAAGCAG
CACCAGCAGATTATGCAGCACGCTTCTCAGATTATCGGTCAGCAGAAGCAGCTTGAGATG
AAATTGAACCGCTTGGTTACTGACCGCGATAAGTTGCAGGAACAGGCTCGTCAGGCAATT
CAGTTGGCAGATAAGTCCGCAAACGAAGGCGACAGTGTTAAGGCTCAGGAGTTCAACAAC
ACTGCTGAGGTTTTTGCTTCCCAGTTGGTAGCTGTGGAACAGCAGTTGGAGCAGACTACT
GCGCTTCATCAGCAGGCTGAGGTTGCGGCGAAGGATGCTGTTGCGAAGTCTAAAGAGTCT
GAGATGCGCCTGAAAGAGCAGATGTCTCAGATTGATGCTCTACGTGCGCAGGCTGATCAG
GCGAAGATGCAGGAAAGTGTCACTAAGTCTATGGATTCTTTGAATCAGTTTGGCACTCAG
GATTCTTCTGTTCCTACCCTTGATGCGGTGCGTGAGAAGATCGAGCGTCGATACGCAGAT
GCTTTGGGCGCGCAGGAACTTACCCAGAACACTGTTAGTGATCGCATGGCTGAGATTGCG
CAGTCCGGCACCGATATGCGGGCGTCAGCTCGTTTGGCTGAACTTCGCGCGGAGGCGCTG
GGCACGTCCGCAACGCCTAAGGGCCAGCTAGAGGCAGGTGTCGAGGATGCGGAAGAACTT
ATCGACGAAACCTCCACCCCTTCAGCTACCCCAGAAACCGCAAGCCCAGAAGCTGATGCT
CCAGAAGCATCCGCAGACGAGTCCGAGAAGAAA

>RXN03048-downstream
TAACCTAAACACAAAAAACTGGG

RXN03050-upstream
GTTAAGCCTATAGGAAAAAGTGTTTGCATATCACCCTTGTATTCGAACACGTGAGCGGGT
AGAGTGGGTGGTAACAACACGGGGAAAGGGGGAAGACACC

>RXN03050
ATGAGCATCACCACACACGTCCAAGCACTCACCACAGCACTCAACGCCATCGACAACCAT
TTGGCCAGCATGCTCGACCATGGTGTCACCCCAGACCAATACAAGGCCATCGAGCCCGAC
CTCATCGCCCTAGAACACACCATCAACCACCACGCCACCATCGCCGCCCAAACCACAGCC
CTCGCCGAACGCACCAACGCCGCCCACACCATTGGCTCCACCCACCTCATCGACTACCTC
ACCACCACCTTCGGACTATCCAAAGCACGCGCCCACCACCGCATCAATCTCGCCCACTCC
CTCTACCCCATACCGAAGCCAAACCCTGGATCTGGCAACGGCGGTAATGGTGGCAATCCC
GACGGCGGTCCTGATGGTGGCGACTCGGGTGATGACGACTCCGGCGACGATGACCCCGAC
CCCGAACCGGACAAGCCTGAAGACGGCAAACCTGATGGTGATAAGCCTCGTGGGCCACGG
ATCAGCGCGGAAAAACACGCCATCATCACCGACGAACTCGCCCGCCTCAACCCGAATACC
ACACCCAGCGCCGAGGAGCTACGCACCCAAGCCCTGAGTCAAGCGATCTGGCGCACCCCA
GAAGACCTCCGCACGTGGCTACGCCACCACGTCACCACCGCCAATAAAAACAACCCCAAC
CCCATCACCGCCATGAAAAGGCGCTACCTCGCTGTAGGTAAACCCGATGCCGACAACATG
GTCCGCATCAGCGGCCTCGTGCCCGCAGCCACCGCAGCACTGATCACCGCGAACACCGCA
CCGTTAACCAAACGCGGCAACCTCGTGGATCTACCCGCAGCAGAAGATATGCGCACCCGC
GGGCAACGCCATGCGGACGCGTTGCATCACATCATGGAGATCTACAACCACGGTATTGTC
ACCCCAGCTCGTGGTGGAACAGCCAGCATCATCATCTCCATGACCACCGATGATCTTGAT
GAGATC

>RXN03053-upstream
GAGGTAAAGGA

>RXN03053
TTCCACTTCACCTCGACTGAGTTTGCCGGTTCTTATTCTTTGGTCACCAATGGTCTTAAC
GATGTTGCTGGCGAATACGTCGGTGTCATGCGTGGCGATGTCAACAACTCCGCTGTGCTT
TTTGATGTGGATCGCTGGTCGGGACATGTCGTATGCGCAGATAGCTCGATTAATACATCA
CCACTACTTAAGCGTCCCCGTGTCGTTGACATGTGGGGGTCGAAGATTTCTCAGGCAGCG
CTACTGAATAACCGTCGCGTAGTGCACCTGGTGCTCAATGGTGCCAAGCTCGATGAAATG
GGACCAAAGCTAGAATCCATGACCGCTCATGTGGATATGACTAGCGGAGATCTCAACATG
TTCGAGCTGTTTGGTAAGCAAGAAGATGAGCTGTCGCTGTATTCCACACACATGGACAAA
ATCGTGTTTATGACCGAGCAGGCATTGGGCGATAAGACCTCTGAGCTGGCGCTATTGCGC
GGAAAGCTCAAAGAAATTATTACAGCCTTTTATGTGGATATGAAAATGTGGGCTCTTAAT

GCCGGTGAAAACCGTGACAAGCTGCGTCTTGTTGGTGTGCCTCATGAGCAGATCCCGTTG
CTCTCTGTCTTCGTGTCCTATTTGGATCAAGAATATGAGCGCCAGAAATATGAGGGAACC
AAAGACCCTGAAATGTTTCGTGCCATTTCTGTGCTGCGACTGACCTATAAGGATTTGCTC
GATACTCATGGCGATCTGTTTAATCAGCACACGGCAGATGGCATTGATTCTGTGAACTCT
GCACGCCGCGTGATCTATGATTTTTCTGGAGTGCTGCGACGTGGCGCAGGTGTCGCGATG
GCACAGCTGGTTAACGTGATTGGTTTTGCTGTGGAGACGCTTGGTCAAGGCGATGTGGTC
ATCATTCACGGTGCTGATGGCATTGTCGATGTTGATGTTCAGGATTATTTGGCTAATCAG
TTCGCATATATGGCTGAGCGTGGTGGGCGAGTGGCGTATCTCTACAGCTCGATGGACGCG
ATGCTTGGCACTGTTGGCTTCAATCAATTCCAACGTGCTGCGTACACCATTTTGGGCCCG
ATGAACGTTGACTCGGTGGATACTTATCAATCTCTGATTAATAGTCAGATCCCGATGGAC
TTGGCACGGTTGGTGACAACGCAGAATTCTGGTGCGAGCTATTTGCGCCGAGGATCTACC
AATGTGGTGTTTGAAACCAACCTTGCGTTGGGCGTTAATCCTTATATGGAGCAGCGTCGC
AAGATTGAAGCACAGCGAGGTCAGCGACGATCCAAGCGAGACAAGCACTACGGTGGTGGC
ACGACGATGGTGGGCACAGCGGATCTTGATGTTGTCGCAATTCAGGCGAAGGCCGAGCAC
CGCGAAGAGCGCTTTGATGAGAAATCTGCGCGCAAGATGAAGGAGCTTGATGATGTAGAA
GCGAAAGAACTAGCTTTGAAAACTGGGCCGAAGAATCTTGATGATGCGCTTGCACAGGTG
GAGAAGAAGCGCCTGGCGAAGCGG

>RXN03053-downstream
TAGTTGTTGGCTGTGGTGAATAA

RXN03055-upstream
AAGGTCAGCCGTATTTCGGTCAGTCAGCAACTAATTACGCTTATCTTCCGTGTACGATAG
ACCGTAGTTAACATAAGGAATGGAATAGGAGAATTGCGGC

>RXN03055
ATGTATTCCGACAAGCTGATTCTCTTGTTCCTTTCTGAGCAGGATTCAAGCTATGAATGC
TGCGTAGGTTTATTAGATGGCTCAGATGGACGTGATTATATTGAAAAGCTTCTGAAGGGT
AGGAAGCTGAAGAACCATTTTCTTGAATGGGAAGATATTAACAAGGCTGATGTTGCTCGT
GAAGAAATATATAAAGGGCAATTGGTGCATCTGGTGTTTGTGACGGCTCTTTCCACGCCT
GGTGAAATTTCTTTTGTTTTTCCAGGTCAATCTCTTATGAGTGCAACACTCGAAGAAGAC
TTTGCTGCGCTTGTGCTCGAAGAGGAGCGCACATCATTTAGACCTGAACTGTCTCACCTG
TGGTCACTCCCCGTAGGGTGGGTAGCTCCGGGGCTTGAGGGTTTCGTGGAGCGTAATTCC
GAGGCAGCT

>RXN03055-downstream
TGAACCACCGCTTTCTGAGCCGG

RXN03059-upstream
GTGTCATTTTCTTGGCGGACGGTCGTATCGTGAACCAGTTGTTTGATCCCACCATCGAGG
AAATCTTGGCCACGATGAACGGAATTGAGGATATTGCCTA

>RXN03059
ATGAATTCCGGTTCCACAATGCGCAGAATCAGTCTGCGCAATATTGGCGCGCACAAGGTC
AGGCTGTTTTTGACAGTTCTGGCAGTGGTGCTCGGCACGTCTTTTGTTTCCGGCGCGATG
ATGTTTACCAACGCGCTGTCCTCCACTTTTGATGAGGCTATTGCCAGCAGCTTTGACGGC
GTGGATGTGGTGGTTTCACCAAACGGTGCATCAGAGGTGCAGGGTGTTCCTGTTGAGACG
GTTGAATCTTTGCGTGAGGATTCCCGCATCAACCATCTCAACATCAACGGTTCCCAGACT
GTCGTTCTGGCGGATGCTGATTCCAAGGCAATTCAAACGACTGGGGGATCGTCGTTAAGC
ATTTATTACAGCGCGGACGACGCGGTTGCCCAGGCACCTGAATTGGCTGAGGGAGAGGCA
CCGACTGGCACCGAAGAGGTGCTTGCCTCGAAGGCGGGCGCTGAGGCGAATGGCCTGGAG

>RXN03059-downstream
TAGGGGACCAGATCTTGGTCGTG

RXN03062-upstream
GATGAGTATTCTCTCCGAGGCAACGAAGTTAATATGTCCATGAGGGCGAAGTTGTAGACA
ATATTTGGCCCATATGGATAATTGACAGGAGTTTAACGCC

>RXN03062
ATGGAAACCCCAACCCAAGACATGGATGTCCGCTGGTTATACACCCAAAGCCAGCTCAAA
CTCCGCGAAATTCTCCCCACAAACAAAACCTTCGATGTCATCCAAATCAGCGAACTCGTT
GACCCCACCGACTTCATCAGGCCCAACAGCGTGGTCTTATCCGTTGGCATCGCCTTCGCA
GAAACGCCCGACGGGCTTCGCGATTGGGCACACCGACTCGCCGACGCAGGGGTCATCGCG
ATCGGGTTCGGCTCCGGCCTCACCTTCCCACAGGTTCCGCAGGCGCTTATCGACGCCTCC
CTCCACCTTGGCCTCGGCCTCTTTGAAGTCCCCCGTGAAATTCCATTTATCTCGATCACC
TCCAGCGTGCGTGATGAGCAAACCCGCCGTGCCGGCCGCCTGCAACAAGAACTCCTCCTG
GAACAGGAACGGCTTAACTCCATCGCCATCTCCGGTGGCATCGAAGCCCTGTGCCGTGCT
GCCGCCGACTATTTGGGTGGTGCAGTAACCATCGTGGACAGC

RXN03066-upstream
AACTGTTGGCATGGCGAAGTACAATGTTCGTGCAACTGGTCACGTGGAGCGCATCGTCCG
CGAAATCACCGCGGCGTAATAGCACCAGCTTAAAAACCTT

>RXN03066
ATGACATCAGACAAAGACACTGAACAATTGGAAGCGGCAGGCACTGAAATTTTAATGCCT
CGCCGCCGTCCGGCACAGCAGCGCAGTCGTGAACGATTCAATCGAATCCTCACCGCTGCG
CGTTCAGTGCTTGTCGATCTAGGTTTTGAATCGTTCACGTTTGATGAAGTCGCTAAGCGT
GCAGAGGTACCGATCGGCACGCTGTACCAATTCTTTGCCAATAAGTATGTATTGATCTGC
GAATTGGATCGTGTGGATACCGCAGAAGCTGTCGCGGAGTTGAAGAAATTCTCCGATCAG
GTTCCTGCGTTGCAGTGGCCGGATATCCTTGATGAATTCATTGAGCACTTGGCTAGGCTC
TGGCGCGATGATCCGTCTCGGCGGGCCGTGTGGCATGCCATCCAGTCCACGCCGGCAACT
CGTGCGACAGCTGCGGCGACGGAAAAAGAGATGCTGGAAATCATCGCGGAAGTTATGCGC
CCGCTTGCCCGCGGTGCCGGCTACGAGGAGCGCATGTCACTGGCGGGATTGCTGGTGCAC
ACGGTAAGTTCCCTGCTTAACTATGCCGTGCGTGATGTCAATAGTTCCGAAGAGGATTTC
GACAGCATCGTGGAAGAAATAAAACGAATGCTGATTTCTTACCTCTTCTCCGTGGCTACT
GGA

>RXN03066-downstream
TAGTCAACACGCACGTTCCACCG

>RXN03067-upstream
TTGCTGTTGTTGGCATTTCCCCGGATCCGGTGGACAAGCTGGTAAGTTCCGTGAGGACCA
TGAGCTGAACTTCCCTCTTCTTTCCGATGAGGACAAGTCT

>RXN03067
GTGATGACTGCGTGGGGTGCGTTTGGTGAGAAGAAGAATTACGGCAAGATTGTTCAGGGT
GTAATTCGTTCCACATTCCTCATCAATGCTGACGGAACTGTTGGCATGGCGAAGTACAAT
GTTCGTGCAACTGGTCACGTGGAGCGCATCGTCCGCGAAATCACCGCGGCG

>RXN03067-downstream
TAATAGCACCAGCTTAAAAACCT

>RXN03068
ACCAAGGAAGCATGCGATTTCCGTGATTCTTTGAGCAACCTCAACGATCTCGACATTGCT
GTTGTTGGCATTTCCCCGGATCCGGTGGACAAGCTGGTAAGTTCCGTGAGGACCATGAGC

>RXN03068-downstream
TGAACTTCCCTCTTCTTTCCGAT

RXN03073-upstream
CGAAACATCTAGGCAACCCGACTTTTATGTCCCTGCTTGAGTTGAAAACTGCTGTCGATC
AAAGGTGCCCCAATTGTTTCATGCCGTGAGTTTTGCATTA

>RXN03073

ATGGACTCCGTAAATGTCCTGCTCATTGGCATAATCGTCGCGATTGCTGCTTTGCTGCCT
CGCAAGGGTAAATATGGGCCAATCGCCACGCTACTGGTTGCCGGCGATTGGCTTGGCGTT
TTCCTCCTCAGTATTTTGGTGATGCTCGTTTTTGATGGACTAGAGGATTTAGTTCAGGGC
TTTTTGGATTCAATCTGGTTCGGAGTCATCCTTCTTGTAACTGGCATCGTTTCCTTCGTT
GCGACACTGGTTTCTAAAACCGACAGCACTAGAAAGCTTGATGGATTCCTAGCGCCAGTA
AAAACTCCTAGTTGGAAAACTGTTGGAGCCGGATTGATCCTTGGAATCGTTCAGTCAGCG
ACATCTGTACCTTTTTATGCAGGGCTTGGATATTTGAGCGTTGGCAATTTCAGTCCAGAA
ATTAGGTATGGCGGACTTGTGGTCTATGCGACCTTGGCTCTGAGTCTGCCGATTATCGTG
GCAATTCTCGTTGGAATGGTTCGCAAATACCCTGAAAGTCCTGTTGGTAGGTTGTTTGAA
CTGATTGGTCAAAATAAAGAGAGAGTCACCAAATGGTCGGGCTATCTCGTGTCACTGGTT
CTGTGCATAATGGGCATTACTTCGATCCTG

>RXN03073-downstream
TAACTAGCGCATGTACTCATGAG

RXN03085-upstream
TAAGCAGGATTACGACAAGCGCCAAGATATCAAGCGTCGCACCGAAGAACGCGAAGTCAC
CCGTGAGCTCGGCCGTCGCATTAAGGGAATCAACGCGTAA

>RXN03085
ATGAGTATTCACATCGCAAAAGTCCACGACGTCCTCAAAGGTGAAAAAACCTACGGAACC
ACCATTTTGGTGGATCGGCTCTGGCCACGCGGTGTGAAAAAAGACGACCTTGAGCCAGAC
CTCTGGCTCAAAAGCGTCGCCCCCACAACCGAACTCCGAAAATGGTTCGGCCACGACCCA
GCTAAATTCTCCGAATTCAGCACCCGTTACACCGAAGAGCTCAACGCCAGCAACGACAAA
GACCTAGAGACGCTTGTCGACGCCACCTCCCGCCACCCCGTAACCCTCCTCTACGGTGCT
GCCGACCGCGACCACAACCACGCCATTGTTCTAGCCAAGTGGCTAAAGAAA

>RXN03085-downstream
TAACTCCTTGCAAATAGTTGCAA

RXN03089
CACTCCCTCTACCCCATACCGAAGCCAAACTCTGGATCTGGCAACGGCGGTAATGGTGGC
AATCCCGATGGCGGTCCTGATGGTGGCGACTCGGGTGATGACGACTCCGGCGATGATGAC
CCCGACCCCGAACCGGACAAGCCTGAAGACGGCAAACCTGATAGTGATAAGCCCCGTAGG
CCACGGATCAGCGCGGAAAAACACGCCATCATCACCGACGAACTCGCCCGCCTCAACCCG
AATACCACACCCAGCGCCGAGGAACTACGCACCCAAGCCCTGAGTCAAGCGATCTGGCGC
ACCCCAGAAGACCTCCGCACGTGGCTACGCCACCAGGTCACCACCGCGAACAAAAACAAC
CCCAACCCCATCACCGCCATGAAAAGGCGCTACCTCTCAGTAGGTAAACCCGATGCCGAC
AACATGGTCCGCATCAGCGGCCTCGTGCCCGCAGCCACCGCAGCACTGATCACCGCGAAC
ACCGCACCGTTAACCAAACGTGGCAACCTCGTGGATCTACCAGCAGCAGAAGATATGCGC
ACCCGCGGGCAACGCCATGCGGATGCGTTGCATCACATCATGGAGATCTACAACCACGGT
ATTGTCACCCCAGCTCGTGGTGGAACAGCCAGCATCATCATCTCCATGACCACCGATGAT
CTTGACGAGATCAACCACGGTGATCATGGCGATGGCAGTCTACTTAACAACCTGTACCCC
ACGAACACGGGTTACTCATTGAACTTGGCGGAGATCATGAACCTCATCGCTGCGAAATAC
GACTTCGCTGTGCTCCTCGATGGTGAGACGGGGCAGCCGTTGAACGTCAATAGGATGCAG
CGCTCAGCGAACCTGACTCAACGCATCGCGTTGTTTGCTTCTGAGTTGGTGTGCTCGGCA
CCCAATTGTGACAGGCCGCAGTTAGAGTGCGAGGTTCATCATTTAGATCCCTGGATGAGA
GGTGGGCTGACCAACCTGGTCAATCTCACGCATCAGTGCTTTAATCACCACCCACGCAAC
GATGATTCCAGGAGTGGGGTCAATGGTAAAGGGTTTATGGACCGCGATCCCGTCACTGGC
AGAGTAGGTCACTACTCAGCAAGTGGTGAGGGGCCGGTGTTTAACCGGTCGGCTGCTGCT
GATCGTTCCGGTGGTGCA

>RXN03089-downstream
TAGTCCAGACGTAAGCATTATGG

RXN03098-upstream
GACCGTTTTGTCGATCGCACCGCTGCTGGCTCGCACCATCAACGAGATCTTCGAAAACGG
TTCCGTCACCACCCTCTTCGAGGGCGAGGCCTAAACACCC

>RXN03098
ATGCCCACCACGGACGTCTTCAACCGCGTCCGGTTGGCATTGGAACCTCTAGCTGATCCC
GCACGTGCCACCGGAATGGCAAGCTACATGCGGGATCAGTTTTCTTTTCTCGGCATCCCA
TCCACCCCCAGAAAAGAAGCCTGCAAACCCGTGCTGTCCGCGCTAAAAGAGTTGGACACT
GACTTTGTCTCAGACTGCTTTGGCGCAGCTGAACGGGAATACCAGTATGTCGCCTGCGAT
CACATCAATCGCGTCGGCATCACCGATTTAGGTTTTGCCAAAGCATTAGTGCAGACCAAA
TCCTGGTGGGACACCGTCGATTCCCTAGCAAAACCGATCGGCGCCAAACACGATGATGAT
CTGATGAAAACGTGGGCGCTTGATGAGGACTTCTGGGTGCGCCGCATCGCGATCATCCAC
CAACTGGGCCGCAAGAAAAACACCGACGCTGCCCTGCTGGCCTGGATCATCGAGCAGAAC
CTCGGCTCCAGCGAGTTCTTCATCAACAAAGCGATCGGCTGGGCACTGCGGGATTTCGCC
CGCCACGACCCCAGCTGGGTCCGGGCTTTTGTCGACGCCACGGACCTTTCCCCACTGAGC
CGGCGAGAAGCCCTGAAGAATATT

>RXN03098-downstream
TAGCCCTCAGGCATCATCTGAGC

RXN03099-upstream
CCACGCCGTAGCGATCATTGATCACCTTGAGCACTGGGGTAATGGCATTGGTGGTGCATG
ATGCTGCGGAAACGATCTGATCATCTGCGGTGATGTCGGT

>RXN03099
GTGGTTGATGCCGTACACGATGTTCTTCAGATCGCCCTTGCCCGGCGCGGTGAGTACAAC
CTTGGCAACGCCCTTGGACTTGAGGTGCTGGGACAGGCCTTCGCGGTCACGCCAGCGGCC
GGTGTTGTCTACCACGACGGCGTCATTGATGCCGTATTCGGTGTAATCAATGGTGGCTGG
GTCATTGGAGTAGATGACCTTGATTGGGGTGCCGTTGGCCCAGATGATGTTGTTGTCATA
ATCGGTGGTGATGGTGCCATCGAATCCACCGTGGACAGAATCACGACGCAGCAAGGATGC
GCGCTTGACCAGGTCTTCTTCACCATTTTTGCGGACCACGATGGCGCGCAGACGAGCACC
GTCATACAGTGCCTCGCGGGAAACCAGGATGCGGGCCAGCAGGCGACCGATGCGGCCGAA
ACCGTACAGCACGATATCAGTTGGGTTGATGTCGGTTTCCGCACCAATGACCGGCGCGAG
AGCGTCCTCCAGGAAGGCACGCAGGTCGGTGCTTTCGGATTCTTCGAAGCTGTAGGCCAG
CTGTCCCAGGTCGATCGATGCGGTACCAAGGTTCATATCTACCAGTTCGCGCAAAATATC
CAAGGAGCTTTCCAGTGGAAGTTCCTTGGATATGATGTGGCGGGCGTAGCGGTGAGACTT
GATGATATCGATGTC

>RXN03099-downstream
TGAGACATTCACAAGGAGACGAC

RXN03104-upstream
ACTGCTGGGAGTAGCCGAAGAGGATGGTGGCGTCAGTGGTCAGGGCGTCAACGTTGCCCT
GGGACAGTGCCTCAACACAGGAAGAGTAGGTGTCGTATTC

>RXN03104
TTGGAGCTGAACGCCTGGGAGGACATCCTTGACCTTCTGAGCTGGAGTGGATCCGGAAAC
GGAGCACAGGATCAAACCGTTATCCAAGTCCTCGAGGGTTTCAATGCGATCGTCATCTTG
GCGAACAAGCAGAGCCTGGTGGGTAAGCAGGTATGGGCCACCGAAGTTGACGGACTC

>RXN03104-downstream
TGAACGGCCAGCGTTGATGGAGT

RXN03106-upstream
AAATGCCCTCCTGAACTGGAAGAATCAAGCTTGCTTAGAGTCCTGATTCACCTGCCAGAA
AGGCACCTCACAGGTGCAATTATTACACAACCCCACAGCG

>RXN03106
ATGTCCGCATCCTTTGATGACCCCAACCTCATCTCGCTTGCTGGACTGGTTCCAACCATG
CACTTAGCCGATGCTGCCAGCCTGTCCACCTTGGCCCAGGACCGGTTGAGCATCACCGGT
GATAAAGGTGCCAATGCTGGTGCGAAGATCGCCTCCCTAGTCGCGGGCATGGTCGCCGGT

GCTGATTCCATC

RXN03107-upstream
GGATTTATATCAATTTCAGGGCGTGGCGAGCTTTTAGTGATTCACGCTCCTACGGTGGGT
ATCACAAATACCTCAACTAGAAGTAGGAGATGAGCACCAC

>RXN03107
ATGAGCGATTTTTCCAACAAGGCAGAGGACCTCACAGGTAAGGCTAAAGAAGGATTCGGC
GAGGCAACTGATAACGAGTCCCTCGCTGATGAGGGCCGTGCGGATCAGGCTAAGGCAGAC
ATCAAGGATGCTGTCGAAAACGCCGGTGAAAAGGTAAAGGACGCAGCTAACAAGGTTCTG
GGTGCGTTCAAGAAGGACGAC

>RXN03107-downstream
TAATCCCGTACTTGTTCAGGATT

RXN03113-upstream
GTTGGATCTTGCATTGAAAAAATGAAAACCTCGTCGGGAATGCAACTTGGGATCACGTCT
CGGGCAAGAAACGTCCTTAAAAAAAGGGGAGTGATTGTGA

>RXN03113
GTGCTTGATTTCTTAGCTGCGAACCCGCTGATTGCGCTGGTGGTTATTTTGGCCGTTGGT
TTAGCAATTGGTCAGATTAGGGTCTTTGGCCTTTCTTTAGGTGCCGCCGCGGTGCTGTTT
GTGGCCCTGGTGGTTTCAACTGCAAATACCGACATCGTCATCCCCATGATTGTTTATCAG
CTGGGCTTGGCGATGTTCGTTTATGTCATCGGTTTGTCCGCCGGACCAGCATTTTTCAGT
GAGTTCGCTAAAAAGGGCTGGAAGCTCACCATCTTTATGCTCCTGCTGCTGGCAACACTG
ATTGGTTTGGCGTGGGTGCTTATTAAGTCACTGGGGCTTGATGCAGCGATCGGTACCGGT
ATGTTCACCGGCGCGCTGACCTCGACTCCCGGTATGGCAGCGGTCGTGGAATTGATTGAA
GGAATCGATCCAAGCCTTGCCAGTGAACCTGTTATTGGTTATTCCTTGGCATATCCGGGA
GCCGTGCTGGGATCCATTGTGGTGGCCGCGGTTGGAGCGAAACTGCTCAAAGTAAATCAC
CGGGAAGATGCTCGAAAAGAAGGCATGATCACCGCACCGCTGGTGTGGAAGGGTGTGCAG
CTCAAACCTGGAATCACAGGCAGGGTGGGAGATCTTCCACGCCTTGCAGGTGAAAGTATC
ATCGCAACCCGCATTGTGGATGATCCACATACACACCGCCTCGCGGATCCAGATCTGCCG
ATTACTGAAGGCATGGAACTGTTGATCAACGGCACTGAAGAAGCCGTGGATCGGGCAATT
AAGGCGTTGGGTGAAGAACGCGAAACCAAAATTGAGGACACAGAGCTGATCTACACCCGC
CTGACGGTATCTAGCCCTGAGGTTGCAGGTAGAACCGTTGCTGAGCTTGATACTGTAGCT
CACGGATTCATGATTGCCCGTATCCGCCAGGGCGATTCTGAGGTAGTGCCTAAACCTGAC
ACCGTGATCAACTACTCTGACCGCATCCGCGTGGTGGTTGCTCCTGGTCGTGTGGCTGAA
GTGCGACGATTCTTAGGGGACTCTGAAAAGTCCCTTGCTGATGTTAATCTGCTGCCTTTA
GCCATCGGATTATCTCTTGGCCTGTTGTTGGGCGCGATCCCGATTCCTCTTCCAGGCGGC
ACCACGATGTCCCTTGGCTTTGGTGGCGGCCCGATTATTGCCGGCCTGATTTTGGGAGCA
CTCAAGCACACAGGACCGCTGACGTGGCAGATGCCGTTCCACGCCAACCGCACGATCTCC
ACCTTGGGCCTGGCGCTGTTTTTGGCTGGTGTGGGTACCTCTGCAGGTGCAGGATTTAGA
GCTGCGCTTACCGATTCCTCCTCCTTGATCTACATGGCCGGTGGCTTGGTGATCACCTTG
GCCTCTGCGCTGCTGTGTGCTGTGATCGGCATGTGGGTACTCAGGTTGAGGTGGGATGAA
GCCATGGGTGTTGCCGCTGGCACCACCACAAATCCTGCAATTATTTCCTATCTGAATGGG
CAAACCGGAACGGATCTTGCCAACAGGGGATATGCCACTGTGTACCCCACGGCGATGATC
GGTAAAATCCTCGGCGCGCAGATATTGTTCTTGCTGCTC

>RXN03113-downstream
TAAGGTGATTTTTGGGCAGTGGT

RXN03115-upstream
GGAACTGCTGGCAGGCAACGTCCGTGATGGCGATGGTGTGCTTGTCAACGTCGCCGACGG
CGGCCAGAAGCTCGACGTTTCCAGGGCGGTCTAACGGCTC

>RXN03115
GTGGGCAAGCAGGAAAAGCTGCGCATTCCTCTCGATGTTCCGGGAGTGGAATCAGAAGAG
GTAGGTGTAGAACTGCTTGCCGAAGGCTACTACCTGGTAGCCACTTTGCCGGCTGTCGCC

CAGGACTGTGCCCTGGGTGACGTCGTGCGGGCACATCATGTTGATGAGGTCTTGGAATTT
CAAGAAGTGGCAGTTGCTGGCGGAAACAAAACCCTCCGGGTGCTCGTTGATGCCATCGCT
GCTGACCACGTGCGAGCCCAACTAGAAACACTTGGGCTACACGTGGAAGCTCCCATGTCA
GAAATGCTAACTGTCAATATTGCCCCCGATTCACCGTCGCACGGTTTGGAGATCCTGCTC
GATGATCTGCATGCTCAGGGGGTAATTTTCAGGGCGTTA

>RXN03115-downstream
TAGAGCGCCTAATTGTAGAGAGC

RXN03122-upstream
ATGGACCATGGCGGGATGAGTGGAATGATGAGCGAGGAGGACATGACAGCCCTCGAGGAC
GCCCAGGGCACCCGAGGCTGCCCGGCTCTACCTTGAGCAG

>RXN03122
ATGACCGCCCACCATGAGGGCGCGGTCGATATGGCCCGCGATGAGGTCACTGATGGCCAG
AACCCGCAGGCCATCGCTCTGGCTGAGCAGGTCATTGAAGATCAGGAGGCCGAGATCGCC
GAGATGGAGCATATGCTCAACGAGCTC

>RXN03122-downstream
TGAACAAGGACATTCCCCGACCA

RXN03134-upstream
ATGCTGTTTCATCGCTGGCGTTGGCTTTTTCGAGCCATTCGAGCTCTTCTCCGGGGAGAT
CCAGTTTGCTGATCAGCGGGTTTGTTTCGCGTGGGGCGTG

>RXN03134
GTGGCTTGGCGCGTCGGCCCAGGTTCCCATGAGCATGACATAGTTGGGTCCTCCGGCTTT
GGATCCGAGGCCGACGGAGGATTTTTTCCAGCCTCCGAAGGATTGGCGTTGGACAATGGC
GCCGGTGATGCCGCGGTTGACGTAGGCGTTTCCGACATCGACGTGGTCAAGCCAGGTGCG
GACTTCGTCGGCGTCGAGGGATTGGAGTCCGCCGGTGAGTCCGAAGTCGTTGCCGTTTTG
GAATTCGATGGCTTCATTGAGGTCGGTGGCTTTCATCAGGCCGAGGACTGGTCCGAATAC
TTCTGTGAGGTGGAAGAAGGTTCCTGGTTTGACGCCTTCTTTGATGCCGGG

>RXN03134-downstream
TGACCAGAGTCGGCCGGTGTCGT

RXN03135-upstream
TTAGCTTGTCGACGTCCCCCTCTTCCAACACCTCCGGCTTTGTTTGTTTTTCCAACCAAC
CGGGCTCTGCTGCGGTGGCGACGGCTTTTGTGGCCCACTG

>RXN03135
TTGGTTTTGGATGAGCGCTGGGTTGGTGTCGGGCTCGTTGATAAATGGGACGAGGGGGGC
GTCGAGAAGCGTCTCTTTGCTGCGGTCTTGTGTGTGGTTGGGGCCGGGCGCGGGCACGTC
GATGAGCGTGGCGAGGTCAGATATGGAGGCGCGGAAGCGGCTCTCCTCTCGCTTGAAGGA
CGGGTTGTCGGCGTCGAGGTCGAAGATGGCGGACATGAAGTTTTCGCTCGCGGCGTTTTC
CTCGAGGCGGCGCACGAGGTAAGAAATGGCCACGTCGAATTCTTGTGGGCGCACGGCTGG
TACGTAAAGCAGCAGCTCACCGACGTCAACGCTGACGGCGCGCGCCTGATCGGACGCCAT
GCCCTGCAGCATTTCGAACTCCACACGGTCCGCTACCCCACGCTCCACAGAGAGCAAATG
TGCGAATGCTATGTCGAAAAGGTTGTGGCCGGCAACGCCCAGGCGCAGGCCCTCCATGTT
TTCTTTGCGCATCGTCCAATAGAGGACGCGCTTGTAATTGGCATCGGTGGCTTGTTTGGA
AGGTTCTGTGGCAACTGGCCAGCCGGTGATCTGCGCGTGGACGTGCTCCATAGGCAAATT
AGCACCCTTGACCAGGCGAACCTTAACGCCCGCCCCGCCTGTGTTGACGCGCTCGCGGCC
GAACTGCGCCAAGTCCTGGATTGCACCGAGGGCATCGGGAAGGTACGCCTGCAACACAAT
TCCGGCTTC

>RXN03135-downstream
TAGTTCATGCAGCTCTGGATTGG

RXN03138-upstream
AGAATGTTCCAGTCTTGGCATCCAACCAGCCGATTCCGCTGGCCCACACTGGGGCGTTGG
CGAGGTCTTTGGCGGTGTACAAGTTGAGGACTACCTTGAC

>RXN03138
TTGGATATTGTTCCGAAGGATGTCGCTGAAAGCTTCGCCGTAGGTGAGGTCGTTTTTCTT
CGCGTGTTGGGTGACGGCGTCGTTGATGATGTGCCCGTCCACAGCATCGACGGAGGCTCC
GATTTCGGCGGTTCCGTCTGGGGAGAAGGTCACTCCGAAAGAGCTGTCGTCTTGGGTACC
GCGCGAACCGGTGGCTCTTGCGTCGTCAAGCAAATCTCTTATTTCTTTTATCTTGCGTCC
TATGGACGCCGGGCTTGGCAGAATCTGGTTGGGGCTGGTGGCGGTGAGGTATTCGGTGAG
GATTGCGTCGGCGCCGGCGAGGTTGTCGGGGTTGATGCCGGCGAGTTCGTTGCTAATGGT
GATCAGTCGGGAGAGGTCGAGGTGGTACAGCTTTTGTTGCAGGGCTTTGAGTTCGGGCAA
GTCGGCGAGCGTGGCAAACGCGATGGATATGCGGGAGACCTGCGCTTTTGT

>RXN03138-downstream
TAGACCTGTGACGATGGCGAGGC

RXN03140-upstream
CTCAAGCGATCGGTGGAACATCCACTAACGGGGTTACCAAAAATCCTTCGCGGACACTCC
CGAAGGAACACTTCTTGCGAGAAGGAAAGGAAGAAGCACT

>RXN03140
GTGAAGGGCATTCATCAGGAAATTAGCCGTATCGAGCGTAGCCACGATTATCTGTGGAGC
GTCCGAGAAGACCTGCATGCACGATTCGACAACCAACTGAAGGCACACTTTGTAGACAGT
GTCCTGGATAGCATTGCAGAAGGATATGAAGGCCGAATCAACCGATTCCGCAAAATCTTC
ATTGAAATGAAAGCGGTTGAAGAGCTGCGCACCATCGCCGCCACCCGCCCAAGCCACCTC
TTGGCTGCA

>RXN03140-downstream
TAAGACACTTAAAAGTTAAATAA

RXN03141-upstream
GGCCCTGCTGCTTCATGCGGTGAGCTGCGCGACCGAAAGCGATCTGTGAGGAAGCGGTGA
AATCTGGGTTTCGGTCCAGCTTGAGGATGTATTCCACGGT

>RXN03141
GTGGTTGAAGCCACCGGTGTCGCCGGTGGTAATCACGTGGCCACCGTGTGGCATGCCGGT
GTGCTCGGAGTCGAAGGTTGCTTCGTCGATGAAGTTGACTTCGACTTCGTAGCCAACGAA
GTAATCAGGCATGGTGCGGATGTCGTTTTCGATGCGCTCGTGATCGGCCGCGTCGGCAAC
CACGAAGCATTGGCGCTTGTGGGTTTGCTTTCCGGTAAGGTCGCCGGCTTCGCCGCGGCG
GGCCTTTTCCAGGGCGTCTTCGGATGGGAGGGTGTACTGGACTGCCTTTTGAACGCCAGG
GATGCGTCGCAAAGCATCGGAGTGGCCCTG

>RXN03141-downstream
TGACAAACCTGGGCCCCAGAAGG

RXN03146-upstream
TAACGTGGGGGTTTTAAGCTTGCGTAGACATATCGTTTTTCGATAGATTTACATCTTGAA
ACGATACGCCCATCCACGGCGCATGTCTGAAAGGTTCCCC

>RXN03146
ATGAATCCCCGCATCCTCATGCTGCTTCGCATCATTTTCGGCGCGGCCTTCCTCGCACTG
TTGGTGCTGCAAGTCCTGCTCGCCATCAAAATCGTGCGCGATGGCCTCAACTCCGGCGAG
CTCTCCCCCATCCCGCTCACCATTCTCGCGAGCTTCGTGATCATCGGTTTCGGGCTCGTG
CAGTTCATCATCGTCTGTCTGTTCGCGCTACTGCGTCTCGTGGAAGACGATGAAATCTTC
GACGCCCACTCGCTCGCCTGGGTTGATCGAATTGCCATCACCATCGCAGCCGGCGCCGTT
TTACTCCTCCCAATGGCCTACATCGTCGCAGAAGTCGACGACGCCCCCGGAGCCATCGTC

TTCGGTCTCATCCTCGCGATGCTCATCACGGGCGTATCCCTGCTGGTAAAAATCATGCGC
GCACTCCTGGCCCGCGCCATCGGATTCTCCACGGAACTGGAATCGGTGATC

>RXN03146-downstream
TAAATGGCCATCATCGTCGACAT

RXN03147-upstream
CCCTGATCCCGAGGACGATGACCGCCAAAGCGATGGCGCCTCCAATCAGGATGTACTGCA
GTGGGATTGGGCGGGCGTCATCGATGGCATCGATGCAGTT

>RXN03147
TTGGAAATCCTCTTTAAGAGCGGTTTGGGATTCGTTGTAATCATCGGTGCGGTCGGCGAA
TACTTCGGCGCGGATTTCTGCGGTGCGGGTGCCGGTGGTGGCGGCTTGTTGAAGTTGGCT
GAGTACATCGCTGGCTGGATCGCTGGAGAATCCGCTGATGATGTCTTTGGCTTCGTCGTA
TGTGTACTCCGTTTTGAAACTTTCCTCGGCGTTGGGGTCTGCCAGCGTGGGATCGTCTGG
GAGGAGCATGGC

>RXN03147-downstream
TAGGCCTTCGCCGGATTCGATGG

RXN03149-upstream
GCTTTACTAGAACCAGTGATCGGTAAACTACCTTTTAGTTCGGCTATTAGCAGTACAATC
TCTGTGGCGCTGGGATTTATTTTAGTTACCGTATATCGAT

>RXN03149
GTGGTTATTGGCGAACTGCTTCCTAAGAGCTATAGTATCGTCAATACGGAGAAGGTCGTC
TTGTTCGTAGTTAAACCACTTCATTATTTTTATAAAGTAATGTTTCCTTTTATTTGGGTA
TTGAATCATTCAGCTGCAGGGCTAGGGAAGCTATTAGGTGTGCGTCTCGTATCTGAAGGA
GAAGAGACATTGTCTCAAGAAGAGCTGACATTAGTCGCATTGAATTCTTATGAAAAAGGA
GAGTTGCCAAAGAAGAATATCATTATT

>RXN03149-downstream
TGAAAACGTGTTTGAATTTGATG

RXN03152-upstream
GCAAAATATCAGCTTTGACCTGCACATATAGTTGCACAATGGTGAAAGTGCACATAAAGT
AACTTTCGTATTCGAATATTTAAACCTAAGGGGTTTAGCA

>RXN03152
ATGAAGCTATTTTCTCGTACTCCCCTCGTCGCACTCGGCACAGCTGCTGCAATGGCAGCA
ACCTCCATCTCCGTTCCTGCACAGGCTGAAGAAGTCGCACCAGCACAGGTTGTGTACGTG
GCTGACACCGTAGAAGAAGAAACGGGTAGCTCCAACGGATCTTCTGACATTGACTCTGAC
ACCATTTTGGATTACGTCGTCGTTATTACTGGCATCGTTGGCGTCCTCAGCGCTGGTTTG
ACCTTCGCTACTGCTTTCCAGCGTTCATTGCAG

>RXN03152-downstream
TAAATTTCAGCGTTAATCACCAA

RXN03153-upstream
TAATTTGAATTTTAGGGAACCTACCCCGAGCTTTTGCAGTCTAACGCTTATGAGTGCCTT
TTCACGGCCCTCGTTACGACTACAAAGATCGGGGTATTTT

>RXN03153
ATGCGACGAATCTGGCTGCTCGTATGCGGCATCGCATTGACTGTCGCCGGCTGCACGAGT
GGATCCACCACTCCCACAACCGTCACGGTAACCGCAACGCCAACGTCGGAGGAGGCTGCA
TCCACGGAGCCGACCAACGACATACTTGCCAGCCAATTTCATCCGTGTGAAGTACTCACG
CAGGAACAGTTCGAAGAAGTCGGATTGGGAGTCTTGATTGTTGAAGACGCTTACCTCGGC

TCGACAGGTTTAGGTTGCAGTTTCGGGAAAGCAGACAGAGAGGATTTTTCAGGTACGTGG
CTCATTTCAACTGACCAAGCAAACCGACAATTTGTTGAAAACCAAGATCTAGAGACATTG
GATTGGGGATCCAATGACAATCCAGATCTGTATGTGCATCAAATGTCCGAGACGGGTCGT
CAATGTGAGGCAGCAGTTGACTATGACTGGGGCCGGCTTACGGTTGACTATCTCGAATTA
GGTGAGGGCTGGGAGCCAGAAATTTTGTGCTCTGATGCTGTTGAAATTTTAGAAAATCTC
ATCAAGGAACTAAGGGGAATTCCA

>RXN03153-downstream
TGACATTGAAAATTGATCCCTCG

RXN03154-upstream
AAAGTGCCCTCTCCTAAATCGTTTCTAAGGGCTCGTCAGACCCCAGTTGATACAAACATA
CATTCTGAAAATTCAGTCGCTTAAATGGGCGCAGCGGGAA

>RXN03154
ATGCTGAAAACTACATTAATCACCGATACCCTAGGGCACGTGACCTCTACTGAACCCACC
ACCACAGCCCATGTTCCACTACCTGATGGATCTTCCACTCCAGTCCAAATTTGGGCGTCA
GATAACAAAGACTCCCAACTGGTGATGCTGTGGCCAGGTTTCGGCATGGGTGGCTATTAC
TATCGTCCGCTTGCGGCAGCGCTAAATAAAGCTGGATTCCATGTGGCGATTGGTGAACTT
CGTGGTCAGGGGCAAAGTTCCGCGAAGGCTTCTCGGAAAAGTCAGTGGGGATACCATGAT
CTCGCATCGGTAGATTTTCCGCTGCAGATTGCCGCTGCGAAAAAGGCGCTTGACCTGGAG
GAAGGCCATCCCATGAGGTTTTTGTCGCATTCGATGGGTGGGCAGATTTCTTGTCTTTTC
GCAGCGAGGCCGGAGGCTGAGAAATATAATCTTCGGGCGATTTTCGGGGTGGGTGCAGGG
TCGCCGTTTAGGCCTACGTTTAGTCCGAAAATGGGGAAGCGTTTGGGATTGGGTGCGGTG
CTGCTTGGTGGGATTGGTGGCCACATTGTGGGATTTTGGCCCGGCAAAGTTTTAGGAAAA
GACCTGGTGGGTTATGGCCGACAATCGGGAACTCACATGAGGGAATGGCGTCGATTCCAT
AAGCACAATTCTTTGGACGATCTCACCGCGCAGGACATCAACTATGTGGAGGTGATGAAG
AAGGTGAGCATTCCTATTACTTTTAGTCGTTGTCCTGATGATGAGGACTGCCCGCAGGCA
TCGATTGATGGGTTGGCGAGTTTTGTTCCCGCAGCGCAGATCAAAATGATAGAAATTCCA
GAAGCCCTGGGACATAACCGGTGGGCTCGGGAACCTGAATCAACAGTGAAACTCTTCCTG
GAACAAGCTCTT

>RXN03154-downstream
TAGTGACCGATGGAGCGGAGGTA

RXN03156-upstream
GTATCGACCTCGATGATCGCGTTGCTGCAGAGATGACCATTTTAGGTCGCCCTGTGCCTA
AAGAAGGATAACCACCACACCAGAAAAGAAGTACCTCATT

>RXN03156
ATGGCTCGAACCACACCTCCACCAGCTGATGTACTCGACATCATCATTTCCACCGTGAAG
CAGACCATCGGCATTGATCTTGCTGAACTGATTCAGGGCCGTGCACTCGGCCAGGCTCAA
GGTGAGGCACAAGGCAAAGCTAGTGCAGCAGCCCTTGAGCAGGCACCTCATAATGAGCAG

>RXN03156-downstream
TAAATAACACACACCACATGTGC

RXN03162-upstream
GGTCAATCAGTTCCTGCCACTGCTCTGGCTTGTCGTAGGTGTACTTCGCGCCGGAGAACA
GGGTTGCGGAGAAGTTGTCGCCGCCTTCTGCTGGCTTCTT

>RXN03162
GTGCACGACGAACACTGGGTGTGGTCCGACGAGAAGGATGCGGATTTCGCCTTCGACGAT
GCGTGGCATGAAACGCATATCAACGAGCATGCCGTTGTCGCCGATGATGTACTGGTCACA
GAAATCCATGAACTCGCCGAGCTTGCGGACTTCAGTGTGGTTGTCGACTGCTTCGGTGCA
CTTGATTTCAGTGTCCAATGGCAGTGCGGTGCCTGGCTCGATGGATGCAGCCAGTTCCTT
GTCTACCAACTGGACGCGCCAAATGCCGGAGCCGGTGGAGCCACGGTTTTGCTTGAGCAC
GCGCTCACCGAAGGACAGGGAGGTTGGGAAAACCTTGTGGAAGGTCTCCACGTCGTAGTA

CGCCTCGGTGTCGGATGGCACCAGGTCGGTTTGGGA

>RXN03162-downstream
TAGCTTGACCAGCGCATCTTTCG

RXN03167-upstream
GCCGCGACTGCGGGTGCTTTTGCGCTGTTGCGTAAAAAATAGTTTTTATTAAGGGCATTC
CCTGATTCCCAGGTGGTGCCACATTGTTTATGGTGGAGAT

>RXN03167
ATGAACACGAACTTGCCGAACCTATACACCGCATTTGACCTTGATCGAAGTGAATCCTCC
GAAGCTTTAGGTGTTTCCCTTTCTGCCCGCGATCTTCGCTTAGAACAAATGGGAATTGCC
CAGGACGATCCTCGACGTGCCCAAACCGTCCAAGCTTTCGCAGTGCTTGCAGACCCAGCA
AAACGCGCCACCTACGATGCTCAATTAGAAGCTGGAGTTCCACTCACCTGGGCGCAGATT
CAGCATTTAGGAAACTTCGGCACCTTGCCTTCCACCCCTACTGCGCAGCCGTTTGCGGCA
CCTCAGCCGGAGCCGTCGCCGGAACCGCAACAGCAGTGGAATAGCGGACAAAACTATGCG
TATGGCAATCCGACCATGGATTACCAAACTCAGCAGAGCTACAACCCGATGCAGGACCAA
ACCCAAGCGTCGATGTATGCGCAACCTTTCGCGAACACCCCTGCACCGATGTACAACAGC
AATCAGGTTTTTAACAGGCCTACTGCGGGTACGCGTTTGTGGATGGCGATCCTCGACAGT
ATTTTTGCCGGCATCGCTGGTGGAATTGTCTCCGGTATTTTCGGCTTTGGATCTGAATTC
CTCACCAGTGTCATCATGATTTTGGTGCTG

RXN03170-upstream
GTTAAATCATTGCCGCCCAGAAGAAGACCGCGCGGGCGAATTTGGGCTTGGAGGGAACCA
AACGGCCACTTTTCCAGTCCAACAAAGTATGAGGATTAAT

>RXN03170
TTGCCCCACGCCAAAGAGCTCGCCCACGAGCTGTGTTTGTTGCCCACCCCTGCTGTGCCC
GCGCTTCCCACTGATTCTGGCGCGCAGTTTGATATCCACCAGGCACTATCCGCCTCCCTT
GCCACCTATGCCCGCAACCTCACCTTGCTGTCCCACACCGCCGAGAATTTAGGAAACCGC
GCGCTGACGGGCCTCGCTGAAATCGAAGACACCGACGACCAACTCGCACACGCATTGGAG
CGCCTGACA

>RXN03170-downstream
TGATCGGTCTGATCAGCGCCCTT

RXN03172
CCAGAGTGGAAGAAATTCAACTCCGGCGACGCAGCCCGCGTTGTCCCAGACGCCAACGCA
GAGCTCGACATCATCGGCGCACCAGCACTTCTTGCCGATCGCCCCTCCTACGCAAACGTC
AAAACCCTCTCCCGCATCTTCGCTGTCATGCGCAGCCTCGGCCACGTCACCGCTGCCTCC
CCAGTCACCGTGTTCTTCTCCTCCCACTCCGTGCTCAGCAACGTTGACCGCGGATCCGAG
CACTACTCCGGACCCAACGGCCTGGGCGAATGGACCTCCGTTGGTCGCGCAGTAGCCACC
AACTGGAACGGCGTTGTCGACGCCCTCGACGAAGCCATCACCGTCAAGGAAGTAAACAGC
CTCTTTACCGAAGACGCCGCAACCCGCATTCAAGAAGCACAAGCAGCTGTTCAGGCAGCT
CGCGAGGCTGAAGAGCAAATCGCCAAGGAAGAAGCCGAAAAGGTCGACCCTTACGACAAC
TCCCCATGGGCTGCAGCAGGCATCGACCCCATCAAGGTCTCCATCGACGGACGCACCATC
TACACCCTGCGCACCTACCTCGGCGGACAGCCAGTATTCCTCGGAAAATTCGGCGAAATC
TCCACCTTCAACAGCCAAAAATCCCTCCTGCGCTGGCTCGTCGAACACGATGACCACGAC
CTCGCCCGCGCCTCCACCTGGAGCGACCTCATGCTCGGCATCAACGCCGGTGAAACCGAA
CTCCTCGTCCACAGCGACAACGTCTACTCCTTCAACGGCCTGGTCAAAGACATCAACACC
TCCGTCGACGCCGTAGACACCCAACAAATGGCCCGCGCCTACGAACTCATGGCAGACACC
GCCGACTGGGCCGACGACGACTCCATGAATTCCTACTTCCTGGCCAACCCACGCATGCAG
GACTACATCTCCTACATGCTCGGCGGCAGCGACACCTCCGGATATGTCCCTCACGCACCA
TTCAACGACCACTCTGAGAGCTGGCGCGAGCTGGAGGAGATGCTGATCAAGCGATTCAGC
AAGTTC

>RXN03172-downstream
TAGGTCGCCTATTTGGGGTTCGT

>RXN03173
CTCAACCGCGACACCCATCACCTGTGGGTCGTCTTAACCACCGACTCCGACGACTTCGAC
GCAGACTCCTTTACCACCGAAGTCATCCGGATCACCGGCTACTCCCGCCACGAAGTCAAC
AACGGCCTTAACGCCATGGCCGCGATGACCAACCTCCCACACCTGCGCGCCATCCAAGAA
CGCTACTACTTCCTGAGCATCCGCTACCTCGCCTCCATCATGATCGCCGTGGCCAAAGCA
GACCCCACCCTGTGGGAAGAACTCGACCTGCGCATCACCGACGCCTTAACACCAGTCACC
GCAGGGGAAGTCATGATCCAATCCTCCACCCTGTCCAAACGCATCGCCGCCTGGATCAAA
GAACTCGACCCCGAACCCACACCAGAGCCCACACCGAAAGAGGACTATGTTCACGTCCAC
ACCACTGATGAGGCGACCTATGTCCGCATCAAAATCAGCGGCCCCAACCGCCTGATCCTC
AATGACATCATCACCCAACTCAAAGACACAGACACCGAGGACAGCCTGCCTGAAGCGCTC
ATGGCGTTCCTGACAGAGAAAATCCAGTTAAAGATCACCAAATACCTCTTCACCCCACAT
AAGCACCCTGAGCAGGTGTGGTCACCGGACTACGGTGACATTGATCCCGAAGCCTATGCC
AACGCCACCCTCGTGTGCGCCAAGGACTTAGATGAGCTCGCTGGAGCCACGGAGAAGAGC
TACACCCCGAGTGAGAAGATGAAAGCCCTGATCAGAGCTCGGGATGGGCATTGCCGCTTC
CCAGGGTGTTGCGTTCCGGCGAGTAAGTGCCAGGTCGATCACATTATCCCGTGGGCGGAG
GGCGGCCCGACAGCGGCGTGGAACCTGCAGTTGTTGTGCCAGCGGCATCACAATATGAAA
ACCGATGGTCGCTTTACTGCTGATGCTAATGGATTGGCGGAGATTAGATGGATTGGGCCG
ATGGATGTACCAGCGGTGACCAGGCCGACGGGTCCGTTGGTGAAAGCGATGCCGCGGGGG
ATTTGGGGTCAGGTGTTGAGGGATCGGATCCAGGCTAGGTTTGAGCGGATCCGCGACCGC
GCCCTCAACAAAGAAGAC

>RXN03173-downstream
TAGAAGCGCACAGGTTTTTGCAT

>RXN03174-upstream
GCGATGCTCGAACGCGCAGAACGCTCCTGGGTAGACAAAGCCGCTGCATACGATTTGCGC
TGGTCAGATCACTCACCACTGAACGTGATCTACTCCTAAA

>RXN03174
ATGCTGCTGACAATTCTATGGGCCATCGGCATCACCGCCGAAGGCATGACAGGCGCGCTG
GCCGCAGGCCGACAAAAAATGGATCTCTTCGGAGTATCCGTCATCGCATGCGTTACCGCG
ATCGGCGGCGGATCCATCCGCGACATGCTGCTGGGACATTACCCGCTGGTGTGGGTGGAA
AAGCCACTGTATCTACTGCTGATCATTGGCGCAGCCATTTTGACAGTGTCCATTTCCTTC
CTGATGGAGCACTTCCGTGTGTTGTTCCTCGTGCTCGACGCCGTGGGTCTTTCTGCATTC
GCTGTGATCGGCACACAAATCGCACTGGAAATGGGCTACGGATTCATCATCGCAGTAGTG
GCATCAGTGCTCACAGGTGTATTCGGCGGCGTCATGCGTGACCTTTTGTGTGACCGCATC
CCACTGGTATTTCAAAAAGAGCTCTACGCATCAATC

>RXN03177-upstream
CTGCCCGATTTATGTTTTCCGACGGCACCATCTGCAAAGAACGAGTGTGACCGGTAGCTT
TATGGGCTGAACAATTCTAAGGAGAATTATCC

>RXN03177
GTGAAAAAGAAGCTTATGTTGCCTTTGATTGTTGCAGCTTTGGGGTTAAGTGCCTGCAGC
TCCGAACCTGCAGCAGCCCCACTCGAAGCAGAGCCATTACATAACCTGCTCATTGATGGT
TCAGAGTCCGGCTTGGACAATGCCACTGAAGGAAACGACACCTCATTAAGTGGCCAACCC
ATCAATCTTACAGTGGTCAACGGTGCCTTAGATATCGATGGCTCCTGCGGAAAAGCCCTC
CAAGCTGTAGAGGACGTCAATCTGGACAGCGTAGCTAGCGCATCCAGGGCACTGGCATCC
GGCGACAAACAAGTAGGCATCGCCATGTACTCAACCGCCGAAGACAACGACATCTCACCA
ATGGACCTCTACGCAGACATCGCGAATGCTTGCGAAGACCCCGTCGTCGATTCTTCCGAC
ACCACCTACACCTTCGGCAAACTCGATGATGCTCCCGACGGCGCCGTTGGATTCACCCTC
GACATTGAAGTCACCCCTGACAATCAAGGCTCCACCGTGATGATGATCCAAGAATTAGGA
AACCACCACATCATCGTCGCAGGACTTGAAACCACCCCAGAAGAAACCGCCACTGTCTTC
GAAGCACAACGCACCAAACTCGAAGAAGGCTTGCAGCTTAAACAGAATTGGCAGCTTGGG
TGGGTT

>RXN03177-downstream

TAAATGCGCCCAACCTAAGAAAA

RXN03182-upstream
ACTCGACACCACCGTCACCAACTTCATGATGGTCATCGCACTCTTAGGATTCATCAGCTC
TGTATCCGTAGCCCGCTTCCGCAAGAGGGATGGTGCCTAA

>RXN03182
ATGACCCTGCAACTATTCACCGACATCGTGTCTCTGGTGTTCATTCTCAGCGGCGCATTC
TTGTCATTCTCCGCATCCATCGGCCTCATACGATTCAAAGACACCATGTCCAGAGTCCAC
GCCATGACCAAACCCCAAACAACCGGCCTTATCCTCACCGTTGTAGGCGCAATCATCCGC
ATCTTAGGCCACGAACACTTCGATCAATCACAACGCAGTGACCTCGGAGTCCTTGTTCTC
CTCGTACTGTTTGCACTGCTCACCAGCCCAGTG

RXN03184-upstream
GCACAACGTCGCTGGTCAGTGCCATTAGTCACGCAAGAAATGGGCGGGTCCGGTGGAAGA
CTGGCCTGCTGTTTGGTGCCGCGGGC

>RXN03184
ATGGTTGGCGCGTTTGGCGGTGGCGTTCTCGGGGGCTACATTCCTGGCACGATTTTGATG
ATCGCGTTTGCGCTCATGATGATCGCCACGTCGACTGCGATGTTGCGGGGGCGTAAGCAG
AAGAAGGGGGCGTCGAAAAGCTCTCTTTGGCGCGTCCTTGTTGATGGCCTGGTGGTCGGC
GCGGTGACCGGGCTTGTTGGTGCGGGCGGCGGCTTTTTGGTGGTGCCGGCGCTGGCGCTG
CTCGGCGGGCTGTCGATGCCGGTGGCTGTGGGCACGTCGTTGGTGGTGATCACGATGAAG
TCGTTTGCGGGGCTTGCCGGGTATCTGACCAGCGTGCAGCTGGATTGGGGGCTGGTGCTG
ATGGTGACTGCGGCCGCCATCGTCGGTTCGCTTGCCGGTTCGCGCCTTGCGGGGCGCGTG
CCTGAGACTTTGCTCCGCAAAGGGTTCGGGGTGTTCGTGCTGGTCATGGGCGTGTTCGTG
CTCGGCTTGGAGCTTTTA

>RXN03184-downstream
TAAGCTTTTCGACGTCTCC

>RXN03185-upstream
AGCGCCCAACCGTTCAGACCAGCGGTTTCTCTGAGGATGCAAAGTCCATGATGGGTNAGG
TCACTGAGCTGTCCGAAACCACC

>RXN03185
ATGAATGATCTTGCAGCTGAAGGTGAAAACGATCCTTACCGCATGGTTCAGCAGCTGCGC
CGCAAGCTCTCTCGCTTCGTCGAGCAGAAGTGGAAGCGCCAGCCGGTCATCATGCCAACC
GTCATTCCGATGACTGCGGAAACCACGCACATCGGTGACGATGAGGTTCGCGCTTCACGC
GAGTCCCTG

>RXN03185-downstream
TAAAAGCATTTCGCTTTTCGACG

APPENDIX B: AMINO ACID SEQUENCES

> RXA00003 (1-741, translated) 247 residues
VQVRILSSEL VCSLSGAIRG VNLDIAAPKP KKSGRRTLTK PEWDAVIKHL LTRDTEPLLT
PTKHKNIRQS TKNIHARIVR LTLLQAVSGL RIAEANQLQW KHIIDGDDGM LINASADIVK
GRKGKERGRY IPILRADVAE YLRTHREDDE HFIVGSPTTT ARPWDATNAD DKVPELYRQI
AEATGVKTLQ DLRSHSWRAT LHGVYADVMD PATRAAIFGH TEQVAEEYYN DRQNIESLMR
QVKRAYA

> RXA00008 (1-492, translated) 164 residues
MAKKKKKVDE NNSVLATNRK ARHDYHIIDT WEAGVVLLGT EIKSLREGKV SLVDSFATID
NGEIWLQHLH IPQYSMGSWT NHTPKRTRKL LLHRNEIDSL MGKVRDGNRT LVPLKLYLKN
GRVKLELGLA QGKQDYDKRQ DIKRRTEERE VTRELGRRIK GINA

> RXA00015 (1-309, translated) 103 residues
MIDMCTTPRQ EIMIREQFKE INNGRVVPHY DQLEQLAEIF STKDSIDMVN EILNRDTDFL
SNEGTIFMEY IFNGGFHTDN GYQPLSYAYV ERGLAIRPPR IVL

> RXA00018 (1-1299, translated) 433 residues
MSALSRPHKI ATGVAVATLT LTLCTSAAGV VHAAQQSISG PESSCAFNQQ RWDDSKVKLD
DTIATAKNSL VQTGELHRNE QDLLTGYLFQ QPHSSNYLAL NNAYADAVAI KDSFVRPTCD
GSKESKIASE HAVSEVVGAV NVLARAQKAL QINSDTYEQQ RRCDALRLAS RDESDVLMRI
DRTMLQLRRT LADIDQASTD IRDIRAQTTS FERDLAREQK EADAAARAQA VDTSTTPTSS
TEDRVNDILK ESRTDHSGDS YTRSTTTSAQ STEPDSATNT SYLSRRLDSL ERSAQHIDLN
TQCDNLDDLR ELTNNDTRDH TGSVISIADQ LTDITNEINE LRDSTFATRD SAQQAQDQVI
AQREELQRAK EARLEEQRLA KEAEEGARNA AIQERDAAEA ALREAQDLLS RLDDTGNATS
DDTAALVDGL LNN

> RXA00020 (1-780, translated) 260 residues
MTVTTAQRIA DEFQRGISIG PWDLCEVPAG DDYLEHTTKV RRRHSTAVEI HTDSLIICAP
EGSTYSHNRT KAGLASTGTV TVPVKGLSEP VKLSLNLLAD YGNSFDTVHD DLWQRELREQ
TRGQLLTLNA VSGLGDDSVA IMGTPWGDGL TGEANTIKGR EHFVMWAAGC RFEDGYGRHA
LREDRHVRHQ ARAGEDSTAH HGWLLKGTVF GKELTGDAVT AAMTVFSDVV VTVDEGRIPG
MKSGQPFSMA TRLRASSAPV

> RXA00021 (1-1773, translated) 591 residues
MSDTTDSHDP ATSPTVDSAA SGTSDPNQQP KKKFTIIKQV NMIARTAIDD CINRLGPDVV
TMSSEDIADQ VVNSINVAIA RENTRAQDAN AAVRYTPIFK LDFSHVAVLM RRLHVIINIA
PSHNSDPDSD MLAIYDPNPR SEHYGIYRTS EAEIRRVARE YCPDLTSAQF RELQMALSDA
APRKVRHKQR DLIPVKNGIF NYSTKQLEPF SQEFVFLAKS AVNYNPNAQN PVITHPQDGS
VWDVESWMND LSDDPEVVNL LWEIIGAIVR PYVSWNKSAW FYSEAGNNGK GTLVELMRNI
LGAEAYTSIQ LSDFSKEFHL ESLTRAQAIL VDENDVGAFL EKSANLKAIV TNDVISINRK
HKTMLSYQFY GFMVQCINGF PKVKDQSESF FRRQLFVPFE KSFTGAERKY IKDDYMSRTD
VLEYVLHRVL HMNYDNLSTP AAALAVLDEY KEFVDPVRAF WNEFSDQFVW DLLPLQFLYE
FYRKWFDRDS PSGSVLGKRS FIQKITTIAV DSGQWEYPLT AQRPGGDMAV PEPLVIDYDL
TEWQNATVPK GHVNKGLPLP LKANYRGLLR KPLTTPATPP AAPVNPTPPT P

> RXA00022 (1-735, translated) 245 residues
MSAPTIYPGT KTSIDPITMD DARIIFFDIE SLHNIFTVAT YDSLSHHVDV FYLLDHTTSP
QITVLPHSMD YFDQTRSDAV MAAIIEQNPA FAEIKGSPIT TADVALHNLG DTNANRRWQS
NVLLARLLGG ISVRGEVPEH QSHNHLAKQF AEATLVTRDF DVNYDPTSAH PFTAGFNSIN
YDTTLLSLYF AMLTSNIGST PTYFPVITAQ ELRAHNDKLF SPEFIKNMPK YFWDRDSGAG
LRAAS

> RXA00025 (1-1437, translated) 479 residues
MAWMNVSVIV PGSDEELFVK GLFTGEGLTW LTTNLGANYI GFPPLLTVLP ILLAVGVAER
SGMLAALIRK LFGSAKKIVL PYAVGVIGVT ASIMADAAFV VVPPLAAMVF KAAGRHPVAG
LLGSFAAVGA GYSTAIVPTS LDALFAGITN AVMETLPGIA TTEVNPVSNY YFNIASSIVL
GLLCGFLIDK VLEPRMWRQK IATEYAESIE PTSAADDEEI SATLTAQENR ALTISMWTTL
ATAIIVLVVV LIPGSPWRNE DGGFLPTSPL LSSVVFIVFL FFMVMGLAYG MVVGTIKNMD
DVVNMMGEAI KDMIGFLVLA FILGQFVALF NWTGIGTWTA VQGAAGLEAI GLTGFPAIIA

FIILASCLNL LIISGSAMWT LMAAVFVPMF ALLGYEPSFI QAAFRVGDSA TQVITPLNPY
MIVILGLLRR YEPDAGLGTL MSRLIPFVIP FWLAWATLLA IWFYADLPLG PGSAIFLEG

> RXA00027 (1-366, translated) 122 residues
VDERSRFARS VFPDGEEPDP RFTLANERTF LAWTRTSLAF LAGGIAFEAF QISGLSDTVR
TTIAVFIIAV GMIIAAGAAV RWMNVERAMR KQKPLPVPAI IPFLSIAALV ASAAVLVLII
VQ

> RXA00028 (1-1947, translated) 649 residues
MTLTASSLEA GKMSFSGGYI VGETMIFLVD PDEVEIRRSP NSLHVLRNGS DILRRNEHHC
WVFENFNKPI DPPVRLGPRD IICPSALAWV LQQHSISRSL SHHLHADKIT AGEIAGRPTW
ILREEPTSGG QDPSRLVSLE IDQEHGVILA VETGQERLEA TEISFPDTLP NPSWDGAWEP
FHYPDSTPHT APDVAEIPGY IQSLPPQSED PRRLRVFVNE IALEGDFPDY RQGQSVRLTL
GISSSPVPLE GMTTRRRGRV RNLGEEASPG DDGMPQWPIL LTGDGWTALA YTPIPKRGDA
EIQGWFYYSA YGIVDVPTDL RVERIFAGIG TSGTNERLWQ EIDNTSSAYH SEDWWIRDVV
LDVTLDGAVP PPLRRDVFTA VDPIVAGDKL WLCDVHFPVA RCWETTTGRY LGQTLXPAPL
RDRSYVLELH SDQQLGAVAA SGKSGWILTP GQAVATKAPD WTPPTRATDL PQVPSPWEIV
AVRGQGLFEL QVETSRRTAL GRVNATGGVD IGELPPNGYT ISSVVQIGDE YIVGRWVEEY
RLNSKLEVIS TKELDISASG WKSKGTVAYL SEDTHICFFD QVSGAELPSL GIAEGHQGEV
MSATSSESIV LIYRRNPNNS MSIVPTSVAT YDNGTWTTMP LQEAPAELS

> RXA00031 (1-402, translated) 134 residues
VAAGQWLAGN IGEIDHVLCS DATRTQLTWE RVQLGGATAK GSSFHNDIYE NQVSEFKHLI
TGLPDVVGTA LLIGHWPGVE ELAHYFGIRD EHPGWDQMEE KFPTSAIAVL EFNTPWSKLE
RNSARLTDFV IPRG

> RXA00036 (1-1416, translated) 472 residues
MLERTQVFVD TSYLLASFYN SWETGARAQL EIDLPEVVGV LGRMIEQQLK QPVQRQMWYD
GIPDSGPHRY QRALRTCDGV QLRAGQLIEW GERRTQKAVD TRLVADLVLA GVRGQCSDIV
LVSGDADMIP GVQEAANAGL RVHLYGFGWD SMSSQLRHCC DTTTILDPRE DFAECMQLQV
LEGPLPPVVR VKPINDAEPI EDLDFTPVPG VASPFEEVSA KDEKFSPRPS EPAEALSEQV
CEAQYEISKH EGQTADSGEI TESFEAAEIK VTEFFGEPAA PVAESGVEAP TPEAPTVPEA
AKPTPAKPKT PKAEPQKQES PKPGTPKPKA PSPADIPPKA PADTEEHSEV EAEIEDSRPK
IPSPSMMAPR RKLRSRYVPL PNEVWATAGF QTPYDVGQQY ASWWFENAAT STQRDQAHLL
SGGGLPPEID RPLLQFACET LHEYTLTEAQ RVALRDGFHS GIRGVLLNQR DS

> RXA00037 (1-873, translated) 291 residues
MANPLSKGWK YLMASFDNKI DENADPKIQI QQATEAAQKQ HQQIMQHASQ IIGQQKQLEM
KLNRLVTDRD KLQEQARQAI QLADKSANEG DSVKAQEFNN TAEVFASQLV AVEQQLEQTT
ALHQQAEVAA KDAVAKSKES EMRLKEQMSQ IDALRAQADQ AKMQESVTKS MDSLNQFGTQ
DSSVPTLDAV REKIERRYAD ALGAQELTQN TVSDRMAEIA QSGTDMRASA RLAELRAEAL
GTSATPKGQL EAGVEDAEEL IDETSTPSAT PETASPEADA PEASADESEK K

> RXA00049 (1-687, translated) 229 residues
MPTPSQHKDA STAQTDNQVP TGRRAQKREQ TRARLITSAR TLMAERGVDN VGIAEITEGA
NIGTGTFYNY FPDREQLLQA VAEDAFESVG IALDQVLTKL DDPAEVFAGS LRHLVRHSLE
DRIWGGFFIQ MGAAHPVLMR ILGPRARRDL LHGLETGRFT IEDLDLATTC TFGSLIAAIQ
MALSADQDSN DDKDQIFAAA MLRMVGVQAA EAREIASRPL PEISPVKPQ

> RXA00052 (1-711, translated) 237 residues
VAFILFNFVK TNDETSNVSQ SESTAETVSE TNGVLSDGAE NIASQSDESK SGVEIIDSGF
GQSSNSAMAI VIAKTSGGSL AGEFVTATVN FLDESGAVVA TEDQVETLSW EDQELVLPVS
HYKEDSSRPE ITSIEAFLSV TDYGSGQPDE TALPVLETTD ISNPYAGSYN ASFALKNDSS
DDFKNLRVGI VCYNEQTDII GGGFKFPNLV PAGGSIRMDA SVTVSEMPAS CKAYLNH

> RXA00054 (1-2913, translated) 971 residues
MSPFDSKLGR DTHFGFLDKT TASQQLLNPS LISNEDPHTM LQAIKLELRT AQSFTFSVAF
ISSRGIALLK QALLDFKGKG RIITSRYLDF NDPTMFRELL TLENVEVLIH QGDGFHSKGY
VFHHDVGITA VVGSSNLTDN ALLVNREWNL KFSASKNGDI AFQLDDAINR QIERSTPLTP
EWISEYEATR RVPERLVSQN IPLEDQSNAG TIVPNVMQEE ALDALLSLTE KGEKRGVIIS
ATGTGKTILA ALATRMLKPE RVLFVVHREQ ILDKARSEFI KVLERPAVDF GKMSGSTKEL

DKPFVFGTIQ TLTKEATLSQ ISPTDFDLVI VDEVHRAGAE SYLALLNHLQ PQFLLGLTAT
PERTDGFNIY ELFDFNVPYE IRLQAALESN MLVPFHYYGV TDFTLDSETT VTDTSKLSAL
VSEERVHHIL EALKTYGHPE NVRGLIFCSK TEEAEELSKL LDQSLFNGSL LKTKALSAKD
SIPYREEVVA ELESGDLDYI LTVDIFNEGI DIPSVNQIVM IRSTQSSIVF TQQLGRGLRK
AAGKDHLRVI DFIGNYANNY LIPIALFGDN SRNKNSIRRR LIESDIDGTI SGVSSVNFDP
IAQERIFAAL KAAKLDSKAQ FKQDIVQLQD RLNHVPALLD FARFNTVDPF ILATHSGNYW
SLLSSVKFVD HAPSESEKYF LDFLTGELLN GKRPHELLLI QELMKQPETS TEEFRKLLQA
QSTSSDEQTI NSVERILSQE FYTGPNRKKF GEHPILSVQN RTYSFTPEFR RALDESLEVT
DRDEAAQNFK FHVQDIIDTG LFIARNNGFW QGNLVVGERY SRRDVCRILN WERNNESTIY
GYKVDSYTST CPIFVTYHKA DDVSESTRYQ DELVDPNTLH WYSRGNRKIT SNEIKPIAAN
AVDLHVFVKK DDAEGLDFFY LGQAHSENSK QSSMPGNKGV VQPVVTMDLQ FDTPVEQSLF
EYLSTNLAVT E

> RXA00056 (1-750, translated) 250 residues
LLNRVSRIAG ASAITLCIGL TTILSPTSTA QSLEQITPLP ESAIDLNAEI HVNTSDISAE
QILGAQDEIT TMYDSHDPYE YFDTLTDIEQ RSIIAALKRD PSSLQQRQET RLAAQSDPYK
IYISGLEMLS CINLVDVVSC GIANQAATKA NNEAVARYPG DSLRNGKGDA FRHCSWNALM
TIRIGSNGAE RIATNHETIG DGPADENAMD LFNNAQGRQI GAGFINSKDE TSALAICALW
TNLGRLKTLK

> RXA00058 (1-564, translated) 188 residues
MKFFGFYRPI ALIAGITVSA SILTSVATAA ESPTSFQAIT PAFSSSSAPE ADAEANTSEA
TADLLYVAEN QLLIKLSNAV VEDVNGEILM KDNKGTLLEN LTAELQAQPG FSIEKVDSHT
ALLTMNPDEV PDLQDWRCGV GALSGGVAGV VATGLALAAL GVATGGTGFA VLAAGGLAGY
GTGAVANC

> RXA00059 (1-282, translated) 94 residues
VLTGILLAMV STALRIRFGS GVAIAATVLW TVISITLGGD VLAETMLWLV AVPSWPETAD
TTTRFLIAML LQAVLITGST IWAIREIRDS ERRG

> RXA00063 (1-285, translated) 95 residues
MTDGDLDADI SPRQIGLMTT RTVVEIVRLR HMIAQQLERA TIMENEYLKE IAALKKELAH
YKQKDHQNQM VIDILGKAIG TRPNPGEGLD EEDAT

> RXA00065 (1-273, translated) 91 residues
MANLPQEGFS VVHGILADPR IWGPEIPYVR EEAGQVNVEA PDEAGDLARL TLPLQLILLT
EEEFAIALNE GSDVMFERMA EQEVDLLDLK R

> RXA00067 (1-486, translated) 162 residues
MVDAQRPKAG IFGSHTEETW VWLGNELFDE SGEVIADVRS DVLYVDRERL LIESTPGTMR
FRCRATLSGG EVYTMTQNSF TVGDLTAVCG RRTYSLKRVS PWRKERLITN NGVEVARLRP
MTSGKVEFIV GTAGSEALPF VDAVFLSWAC VLVDSAVRRP KI

> RXA00068 (1-582, translated) 194 residues
MTSKDLIVTS YTSWGKRFKN DGKLFINLLR STTDSADEKV LATFGEVPSK SFETTATVDE
QQWELSFSID GTATAKLPDG RVFSANAGEK TFTKSKRIEI DMDGTAMAAV NEDKNNWIID
DSEENKVAQF TGMNNGVRRA IVEFEPDVEV TQEQEIFLSW VARKTLESRM LGSSWGLTLF
LIILTPIIIF LTFS

> RXA00071 (1-1452, translated) 484 residues
MSITTHVQAL TTALNAIDNH LASMXDHGVT PDQYKAIEPD LIALEHTINH HATIAAQTXA
LAERTXXXXX IGSTHLIDYL TTTFGLSKAR AHHRINLAHS LYPIPKPNSG SGNGGNGGNP
DGGPDGGDSG DDDSGDDDPD PEPDKPEDGK PDSDKPRRPR ISAEKHAIIT DELARLNPNT
TPSAEEXRXQ ALSXAIWRTP EDLRTWLRHQ VTTANKNNPN PITAMKRRYL SVGKPDADNM
VRISGLVPAA TAALITANTA PLTKRGNLVD LPAAEDMRTR GQRHADALHH IMEIYNHGIV
TPARGGTASI IISMTTDDLD EINHGDHGDG SLLNNLYPTN TGYSLNLAEI MNLIAAKYDF
AVLLDGETGQ PLNVNRMQRS ANLTQRIALF ASELVCSAPN CDRPQLECEV HHLDPWMRGG
LTNLVNLTHQ CFNHHPRNDD SRSGVNGKGF MDRDPVTGRV GHYSASGEGP VFNRSAAADR
SGGA

> RXA00077 (1-1362, translated) 454 residues

MNDENIQSSN YQPFPSFDDW KQIEVSLLDV IESSRHFSDL KDSTDRSALD AALERAKRAA
AVDTNAIEGI FQTDRGFTHT VATQVGAWEQ QMAMKGKHVK PAFDDTLEGF EYVLDAVTGR
TPISQQWIRN LHAVILRSQE SHEVFTAVGV QNQALQKGEY KTQPNSPQRS DGSVHAYAPV
EDTPAEMARF ISELESKEFL AAEKVIQAAY AHYAFVCIHP FADGNGRVAR ALASVFLYKD
PGVPLVIYQD QRRDYIHALE AADKNNPLLL IRFFAERVTD TINSIIVDLT TPIAGKSGSA
KLSDALRPTR VLPELHDAAH RLQESLFTEI RSRLDEEGKR NGLEFLLQRI FIGSPFNLPE
GYNAFPDSYC LTLAFNSNSP KQIFHPLSIV IAARDGKRAS SDLVAATSIG YNFHAYGREV
EPVVTESFRE RVKIYADGIV DHFLTELAKK FQQN

> RXA00079 (1-222, translated) 74 residues
MGLVHTEFTP INTYGILDHV VTLPDGTKVL NPFRVIPHDT GSELIFTVRP NENFEEDCQA
VAADLERLVA LAEK

> RXA00080 (1-420, translated) 140 residues
MIVLLFINLP FAQLWAKLLL IPNHYLYSGI ALFCGLGIYA TSGAVFDLLM LLGIGVVALI
MRRYGYPLAP LMIGMVLGPL AETSLRDALL SSVGDFSILV SSPITWSLYA VLAIFIAVSV
ITAIRGRRKH LTSQLETIDA

> RXA00082 (1-564, translated) 188 residues
VNVTEQSGES HIDIPESHQL PGPRPVGEGT FWEGRSGLIM PAILTAFSLY LLIGVLNMDV
GNAAFPGPRF FPTILGIAGL LVAVALTIQT IKYPMHPENE SGRSWKFHSD YVSLAWAIGG
FFAFAVLLPY LGWVLAGSLL FWTMTRAFGS KRPGFDVLVS LMMSSVVYLA FDVGLGLNLP
SGLLGGGF

> RXA00083 (1-300, translated) 100 residues
VLALPSSIID PLWCQFAALI PPVTDTHPLR CHRPRIPDRI IFDKLIQVLV LGASYAKIAD
TTCSATTLRT RRDEWITAGI FEQLEQICLE FYDRIVGLDL

> RXA00087 (1-528, translated) 176 residues
MIGGIIGLIL SVIIMAEKLA ILEDPGHITS CDFNAVLACG DVMRSGQANA FGIPNPLIGI
AGFAAVAIIG AGILAGGGFR GWFWFGAQAG LTFAMMFCHW LAYQSMSVIR ALCPYCMGVW
TVSIIMFVLV TAWNVKTFSG SDSTFVNALY KYKWVIAIVW LLLIAAAAVW SFRYMF

> RXA00093 (1-2223, translated) 741 residues
VTTLLAATRP TLRDAFKHPW RSLAAILLVA VPMFLVSFFL TYDQSINNAA SYPGSQVQAH
YDGEGAYQLL QENLPEDFHL ELFANGYPEV SFGDEEVNFF VVQSTNVQQA SFPADALDVL
GATIGDTVTI HGTPVEVQSI SPTNILLPEG TLFSLENFSE SETFSGTWYF PGSNFTEENR
QALEAVGFEV NEYRRGPISV DPNLIPSYIM GFLSTTILAV VALMLISPVF TISASRQTRT
FALLASQGAT PRHIRWAVLT YGLFAGLVGA SIGLVLGQIG IYGWWKYTYP EFSLTTPWLV
LVGFWALAII ASTIAAFLPA VFVSRSSIIN GIYGGISDKI IRWSPRMLIG PIVLIAAAVI
ALFIGDGEWG GVVKQLCFLA AVIALPASVP AVLWALGRLP GLTFKLATRD MLRRSMHSIP
AIGALAAVIM LGTFMQTTGL ATQASDREAT ASVYPEAVFL RGDTQIPGLM GQKIDVYGDN
HGFGIYELDV DFYSANYVPA LTSFFGGPVI ATPKILDMFG VHEQADIYAP STYNSGLQEY
AIYPGDETYM LDTAAVLPPL YSHVLLSPET FEEIGGQTEF LGTIVLPQEL DDQTVQAINR
SRDAHFSHDG HNSSLASSAA LTAVAIVVVS LVIVLANRKL QQHALIAIGA TPGTIYKVNA
LNAALLALVG GIMGLVSGWI AALLTGTTDE IVDGAILNYG TLEHMMLPWP LLVSLLVVAP
LVCAVIGAIA SPSGRHQEAS I

> RXA00096 (1-303, translated) 101 residues
MTNAGDNFEI RMPSGTDDPL SDAEIQKYRE EINRLDREIL DAVKRRTKIS QTIGKTRMSS
GGTRLVHTRE VAIINQFREE IGEEGPALAG ILLRMGRGKL G

> RXA00097 (1-1161, translated) 387 residues
LFTNFFAVNN PDSPPARQKT KLRELEHRFW QEHLPGDDDD HSTAISSLAI VTGLTKAQVS
RISIAFATLA DLPELKALQQ KLYHLDLSRL ITISNELAGI NPDNLAGADA ILTEYLTATS
PNQILPSPAS IGRKIKEIRD LLDDARATGS RGTQDDSSFG VTFSPDGTAE IGASVDAVDG
HIINDAVTQH AKKNDLTYGE AFSDILRNNI QVKVVLNLYT AKDLANAPVW ASGIGWLDAK
TGTFWSEKAN KEQDMDAAAK ISTDKHDPPP ALRDALIGRD GTCRFPGCSV PALKTQADHR
IPYEEGGETC LGGIGCLCQH HHNMKTDGRV TYLLDPFSGI IVWLMGDGTW AVSEPNGPLN
PKNARWAQTV AQHRARHHKR WVKEDAK

> RXA00101 (1-408, translated) 136 residues
MRLILNLIWL FFGGIWLALG YVFFGIIACI FIVTIPAGIA SFRMANYALW PFGRTVVRNP
KAGGFSALSN GLWFIIAGLW LAIGHLTTAA AQAITIIGIP LAIANIRMIP VTCFPFGKEI
YDSNRIPFGY EPMVKF

> RXA00108 (1-543, translated) 181 residues
MKKFFVAGAV LSSALVMAAC SPANQSDSTS TSVETTSSSS TQVSDAVITT ENAVVRASVE
DSDMTAVFAT LVNNSDDEIN VSGFTADVDA ASFEVHEVVD GVMQEKPGGF VIPAGESIEL
APGGDHLMIM GLANPIEAGD EVTVTLELAD GSEVKLDPIP ARTIAAGDED YGDLGTEGHE
G

> RXA00110 (1-549, translated) 183 residues
VSNKDGLFTD GNSTFAPKVD SIPLSDVDTS VSGEASIGTL ISNATSQMSS LFRAEVELAK
TELAGEAKKA AIGGGAFSVA GVIALYSSFF FFFFVAALLS EWIKPWAAFL IVFLFMLVIA
AALALFGWRK VKKMGAPKNT IQSVNQLKNL VPGQASEKLE KANKRGLYTS ASFHSPGAIT
GDH

> RXA00114 (1-489, translated) 163 residues
MKLLKFAAAG TFALALAGCT QTESLVATIE SATSAAQASG NDVEGDQTSA FELSVGECFN
DTYEEEISEV PIVDCAEPHD NEIYYLYDIE GDDFPTDITT TGYEGCLPTF EGFVGAPYET
SIYEVYPMTP TFGSWTNGDR EVVCSVYLAT GEQMTGTAAG TAQ

> RXA00117 (1-591, translated) 197 residues
MTSAQPITSV DAQTLKSWID KHEGLTVIDV RTAHEFSNLH IKGSYNVPLT TLAEHSEEIS
SRVGEHVVLV CQSGIRAGQA QQKLAPLGIS TVAVLEGGIN SFAKADGDVV RGTQVWDIER
QVRFAAGSLV LAGLAGGKFL SPKVRTLSGI IGAGLTFSGV SNTCAMGKAL SALPWNKTKP
VPTETETLSK LPSPKEN

> RXA00118 (1-255, translated) 85 residues
MQLNPDEITP VLNRLKRAQG QLTGVIRMLD EGEDCKAVVT QLAAVTKALD RAGFAIIATG
LEQCLTNPDG DMDKKELEKL FLSLA

> RXA00119 (1-759, translated) 253 residues
MLEFPADVIP ENIKHIAQTK FQTEATSVED IRRAINLLSD QAERAGASFN PGFILAQVGS
TIVEVYGGAP VAWLDAVELL ISPDVEWVGV HGSRKLDINV SGELSGVISA GDKLGELLGD
DWTINIVHGE YKIQIEDARP STAFLADATE LINQANSEIV PFHVRMLSNS KIVMSGFSDY
SLAGDAITSA GKLAELARPF AHWKENVIPT IEIAMDYEPS PVADLWQGDS SETPEPFDDF
ERLLREEMLI PEI

> RXA00120 (1-654, translated) 218 residues
VESLYFDSAD LRCYTEKIEG LKFRRKLRIR TYGDGVLTPE STVSVEIKQR VNKVTQKRRL
DLPFIYALAL GDSTGAAVGE QVDVEKLLEI SPENQHALIH EMASFAKNYR LRPIATTKYH
REAFVGADAE ESSRVTIDHG VSGRDRDFLL GQDLEDRPTV AQGLAVVEIK CDERVPFWLT
DMTAQLEMSV IRMSKYCETI EAFHNRPASA FGAVDPIF

> RXA00121 (1-711, translated) 237 residues
MLSDLSSIFD FQDLSGTFSV VDVLITLVLS FVLTSIVGVV YQKTHRHISY SQSFVQTLVL
VGMVIAIIML VVGSNIARAF ALVGALSVIR FRNAVKETRD VGFLFLAMAI GMTCGTRFYV
LAIAATIVVC GVLFIMYRFD WFKADIQRQV IKVQVPADGQ ADSGRSYAEE VELILAQYCT
SFEMMSAESV RGGALTEFSY TAQMRKNVKP HELVAKMRDV NYGQKATVLT GHDQTDV

> RXA00122 (1-1623, translated) 541 residues
MNRRLFLGTS AAIIAVGGVL GGVQVVPYIS SGEIQTSASS TATIDVGAGN VDIFDTSVSH
EISLQVSQES LDEMLADYQE DGSKTWVKAT ITIDGVTIEN VGIRLKGNST LSGLGRTSEE
GGPQAPEGVE EFTDLSEEEI AQFEEQFAAQ QETTDASETG ETAENEETRG PGGGMGGGGM
GGMTSVDADD VSTWPLLISF DKYEDGRVYQ GMTQLALRPG TTVVNEAMAL ALTAETGQVS
QQSSFTTFSL NDEPSTTRLL LKHPDENYAD ALGNGVLFKA DSNSSFTYQG EDQTEYDGQF
KQINGDGNGD IQPIINLLKW LDTASDEEFA EHLSDYVDVE SFARYVATQN LLVNSDDMAG
PGSNYYLWYD YDTGLISVIS WDLNLAMSGS TDAGPDDEIS MGGGGGGGMR PGGTTDTEIE
GTATEDMPDM GNMQQRERPE GMPDMGEMPD MGDREGGGSM GGNQLKERFL ASDAFTEIYE
QVYWELYEEM YGSGTAIELL DEIAASIPET DAVTADEIAT EVASMREWIT ARTEALAALQ

E

> RXA00127 (1-456, translated) 152 residues
LSPYDGPHRN VLIALKEHGR ADLVAFVGAV VGASISYLAA QGEIEHDITL VPAPTRATSR
RRRGGDPVER VCNASRLSTF PCLQISSRTP DSVGQTAQQR RLNMRVELVR QPRGSVLIID
DVVTTGATIS ASANVLRAAG VQVRGALTYC QA

> RXA00128 (1-1704, translated) 568 residues
VSKISTKLKA LTAVLSVTTL VAGCSTLPQN TDPQVLRSFS GSQSTQEIAG PTPNQDPDLL
IRGFFSAGAY PTQQYEAAKA YLTEGTRSTW NPAASTRILD RIDLNTLPGS TNAERTIAIR
GTQVGTLLSG GVYQPENAEF EAEITMRRED GEWRIDALPD GILLERNDLR NHYTPHDVYF
FDPSGQVLVG DRRWLFNESQ SMSTVLMALL VNGPSPAISP GVVNQLSTDA SFVGFNDGEY
QFTGLGNLDD DARLRFAAQA VWTLAHADVA GPYTLVADGA PLLSEFPTLT TDDLAEYNPE
AYTNTVSTLF ALQDGSLSRV SSGNVSPLQG IWSGGDIDSA AISSSANVVA AVRHENNEAV
LTVGSMEGVT SDALRSETIT RPTFEYASSG LWAVVDGETP VRVARSATTG ELVQTEAEIV
LPRDVTGPIS EFQLSRTGVR AAMIIEGKVY VGVVTRPGPG ERRVTNITEV APSLGEAALS
INWRPDGILL VGTSIPETPL WRVEQDGSAI SSMPSGNLSA PVVAVASSAT TVYVTDSHAM
LQLPTADNDI WREVPGLLGT RAAPVVAY

> RXA00134 (1-570, translated) 190 residues
MAVHLTKIYT RTGDDGTTGL SNFERVPKDD PRLIAYADSD EANCAIGQVL ALSSPTEDMA
TLLRTIQNEL FDVGADLATP IEENPKYPPL RVLPEYIERL EKECDKWNED VPALDSFILP
GGTPAAALLH TARVITRRAE RAAWIAVREF PSTTSTLPAQ YLNRLSDLLF ILSRVANNGN
DVKWVPGGKR

> RXA00140 (1-186, translated) 62 residues
MSDESIEEQE KELAALKAQI DELEKKDKQN KLIIEILSKA VEKNVAEAEA KRARKYPPNP
LW

> RXA00141 (1-462, translated) 154 residues
MTTDSNSATI PTPKPIPVTI DRISLIMKEF GIDLSIADEQ GTGSQVASAN LNGHHVMFAV
IGSVLIVRAD RATEMPVSDG NPAWHLACNQ VNCFNFAAKA VVVDRTDNIV IRAEKDVPIA
AGLNDIQLSA MLKNAIDHVL AIQDAVANAG KEIG

> RXA00142 (1-477, translated) 159 residues
VPQSPTAHDP NDIQEFNLDA VAGILQDEKL DYRIDEHDGE KVIRTGFINA AISFILLDGS
LTMEAMWRGA PSTDAAAQVL AATNEWNLTQ FAPTIRFFEL NEGTLAINAL RHVVVSAGMS
HNQVGSYVMS SIESAVQCFE WLEQQFPDLV TWKDEHHDH

> RXA00150 (1-774, translated) 258 residues
MVFSMHDKGE TQENPADMSG RLNTPISTVF HFFSSLFHDA LRSVAQWSAW KKIAVSVVIV
AIISVTFLVD VPPISVYRDW ANNAGDAFVL VFCAFYILIT QFPIPRTVLT LASGVLFGPV
LGSVVALGST TVSAVISLLI VRGLLGDWMA PRLTHPAVSR INTRLEQRGW LAITSLRMIA
AIPFSILNYV AALTSVPVFS FAIATLIGSA PGTIVTVVLG DAVTGSGNWT AVAFTVFLAI
LGVLGIFLDQ KMPVKPGK

> RXA00151 (1-597, translated) 199 residues
MWALHARYRG RDTRRAELVK RFAEALSTLE GAGQFEVIGV EDIRAHITSP LTTCDVVMAL
LAAGDWAIGI GVIPTVDGTV DESDEAIIEQ VKKISSDALR PTAKAGTVKV RIAGTKRDNT
QAFNISAAFT LIGQVLSKRT IEGREATALV RSGLNQNEAA QELGISKQAM SQRLQAAGWQ
AESAGWQLAV NLIEQAGKR

> RXA00153 (1-426, translated) 142 residues
VGAIIWFIGA LVLAGLELAV GEFTLLMLGG AALATAGVAL IGVPVWAEFV TFAVASAALL
MFIRPAIRKR LLKPKVLDSS PRALVGHRAE VLEDVGATSG QVRLDGSIWS ARSMDPTHTF
AEGEIVSVID IQGTTAIVWK EA

> RXA00154 (1-843, translated) 281 residues
MSFSDPYAGN IFGGHSRNKQ PEYPDVPAKP GLVVEVRGDG FVGAVTGFER TYDGDFVRLE
DRRGRDALYK LRKGAFMIDG QIVNLTRFVE KQAPRKSNSG SRRVENAQAK VAAPSRIWVE
GIHDAAIVEK VWGHDLRVEG VVVEYLEGLD NLEERLAEFQ PGPGRRIGVL ADHLVEGSKE

TRMTKSLPAD VAVTGHPYID IWAAVKPERL GLKAWPEVPY GEDWKTGICK RVGWSDPKEG
WHRVYNAVNS FRDLDYTLIG AVERLVDFVT NLDLSKEDVL A

> RXA00155 (1-783, translated) 261 residues
MEIRANVYSP LQNTAVWLGA WLYELVPTED VIDAFVDLGG PHTFGDGGLL DMLRTLKELT
STLIDAPFHG PILTLALSGP GQVPALPAGS RAAVLASASK EGALVLGGVD KQHSWALIPT
RGKDATEWNL VEVEGFLPAI ATVSPGEADQ LLRQATDQAA NIIELSGYAS LAPKSLKNPR
LTVGMLSDFY DTPGLPYAVP ERSAKLFARA DRVAAIAETV QETIGDHSLD PQLIFLWSHI
RTARMAGVSY ALAEFARDYH S

> RXA00159 (1-1182, translated) 394 residues
MENVSSVTSD GSVADVHAER WQELLARLDA DAPDIAEGTA AKLLATIPGY ELVDAGPIRE
SSIRNTALII RVINAGTEPK AEDLPEALRL ADERIAQNVP LGSVLHGFRM SLGEILEHLV
QLGPEYNIDP GRMLRWSTLM WAVNDAFSTR ATRVYRDHEV ATAIADSVRR SEWIGKAVSE
GSELSELLWG AAMYDVPADT PLRALAATSP DHAKAETQIQ KWTQRAGVRV LASVQPSVIV
GIVIGEPKRN VDGPGFAVGL GRAEVLSKLA DSYKDASLVL KAADNLKLNE VQRAQDLSWK
LAIHASPRVT EILAQKYVKP LRESGEFAHE IVESLRAYVD NQMNIPAAAR SIPVHVNTLR
YRLRRFEELT GCYLEDTSTV IEVSWVLEVF GREL

> RXA00161 (1-462, translated) 154 residues
MSEPGPSGVK EKKKVKASHI VFLLICFIAA CALAWWQWSR FQSGSGTFQN LGYAFQWPLI
GAFFVYAYRK YLQYENESIE LENMEAKMMA EQGKTPVAQS EQEDSFVQLS HRPSLVEDDS
VKEIDESFLP SRPTMDVEEF NRLNDPHARR RRKA

> RXA00162 (1-354, translated) 118 residues
VSTTTPIHPE RKKRVRQALT MFSIAAWVTG VFLLALVAEM IMKYIIGMDL PEWARFVPIA
HGWVYIVFLM TTLNLGLKAR WNPTRWVTTA IAGVVPLLSF FVEHNRRKEV TQTFQLNS

> RXA00167 (1-261, translated) 87 residues
MYLLNPPVTE PEILTVNEIP TVVAVFDNHP MNDMPAAFDQ TYQVLFPTLG AKGIAPIGPG
FALYTSEPTD TVSFEVGMPV SQPLEGE

> RXA00169 (1-2073, translated) 691 residues
MSLGNPAAML AAYNTSTQVA PQPQLGPRAG EVQLSSEQQA MIDYVLAGKD VIVDATVGSG
KTTAIQRLCS IMGADHDVLY LTYSKLLKVD AQQRVRGAKV QNYHGIVYPH LLKAGIKCGI
SESIREFNKN FKHISRTFPS YDLLVIDEYQ DINEDYAELL RNIKSVNPLM QIVMVGDLEQ
KVRSDTTLDP QEFAAQLCED PVFAPFTQSF RIGEAMAAGL ADAWNKPIVG ANTAQQIEYR
SFAEAVVLIQ STEPSKLLCL GSRNGQMSDA LNVVERKSPA KFNKKTVFAS IRDGDSQIAH
PNDAAVFTTF DSSKGLERDT CVVFDYDEEF WDMRLGYPNV DPVVMRNVFL VAASRGKNKV
VFVRSDSLQA AYEAGADWAA GLAVGVVDNN TEVAPEVDAH TPAEESKGDV GEVQSQIERM
MGFIPVSVFK ELPELAPSEY ARPISVTEAF DFKYAENVEA CFDLLDVKRL DNGKGAAIEV
NRSDGLIDLS PTVGNFQEAV FFKDYNVHTA LSAYPSQFAK NLKRLVKKNN SVWRNCLIVT
AASTEQMRYV DQVRSSIPVA AEKALVSRLS TRLNADSRNQ IPLILDGEAV QSKVVRTPMS
FAGVADAVHK GVLYELKFVS ELTHPMFLQL AMYLVMSGMK DGILWNTRTD EAWQVRVPDP
KRFLNAVVLC VSKQDYRVGN FDLPSTGGGA R

> RXA00170 (1-1854, translated) 618 residues
MLLAIGVASP VAQAQVEDQF ELVKEISDEQ FADDGVDYVP NRNAPTVKEQ LEDFESAHPE
VVIEYHEHVN DSKDNVEELP LPKRDIVAGE MRSDVIELPE GVSKDEADQV EVAEARLNEG
ARLMAATGCE AMWPTGFSVC GRILDAYRQV GGQLSWLGPP KSNELTNPDG VGKRSEFVGG
AIYWHPDTGA YAVTLDGLRQ WGTLNWESGP LGYPTSGPMD TNYPLTQRQT FQGGDNYYNP
LTGGAVWGDI KQRYEELGGS NHAIGIPITN ELPSGTEYFY NNFFNGTISW RNDRQTRFMY
LATQRVWDAL GRETGRLGFP EADETPEVSG LFHVVNFAER GVIAWNGILG ARELYGDVYS
LWLQYQNTDT PLGWPIPSLT SLNESLEQEF TRGVVLGSGD ALTWIPDDEE RSLEDFLPIG
SSGSSSSSQE MTLFSQRAQY VDCKNLPDLD EQRKTENNIE KNGGPIKKEY SSRGFPTEFR
FVVRKGHYDR YRNEGWGYLK NYCKHNFANH AMAEAVVDKA VIDYGSSPGT SYYKFEKTVY
FLDCRTYTFN KNSGCKEMHA PQWVTIIYNP HTFTGANSNR PKGVISAWCN STPPGGIEHE
PEISQCPDHV NLYNKLRI

> RXA00171 (1-231, translated) 77 residues
LAAEVKRLRE RDDARDQQLG VLNEAMFSLL GDGLDRFRES GDEASFNAAL NYQAVVAPEM

FKTVYGVDPS TGEPIPT

> RXA00173 (1-333, translated) 111 residues
MSTTIKAAAP YSLHAHDLEQ LAVDLTLVTT FDSNAAVDVT PTHTEAPGFT LHEGTDTAPM
APTLVVPISS DISTAVSEIS TLVQQARTDA ASAIHEAEAE FYNQLAAVLA Q

> RXA00174 (1-285, translated) 95 residues
MPNHPPISTF DDRRSAMREG ITDYLANTNA NGLGGYSISD THLDNLAEKF TRTHGEAQYD
AGFDPNDLEP ETFVRDIEMS WDERAIDRAL IHTQL

> RXA00175 (1-630, translated) 210 residues
MAVCQLPQPE KTTLIKKDLL LMTSTTNSTA MFNDHLIPMA ELDEQALRDS VGSWAQYKHP
LDQRKEPELV LIRRVNSSER VWVLSFTDLR ADAGLVPRST PNADPSNIRN TIFSVAVRDL
VLDRSLPRLL NLNGQPPAGE WEEGFVYVDY DQSDTVDGYL IEHSEPVSIE SQTTGEMHYF
DKVPGGVAVT NNPDGTEQGD ARRWVSHWES

> RXA00176 (1-159, translated) 53 residues
QLMYSTSSFT TVKQTIGIDL AELIQGRALG QAQGEAQGKA SAAALEQAPH NEQ

> RXA00179 (1-459, translated) 153 residues
MIAIHAIAAI LFLGPATVAN SQFHVRAYDA HNGNTQAAGS AKTLFKISQS YGMLSLLVPL
LGIAIMLLDW SFYKSEGQFH AAIALSVITW ALLLFVIFPR QKKMMGALDL LEDDEQAAKT
YEIENWDKAK SQLSMFGGIW ALLWVIIAVL MFI

> RXA00180 (1-540, translated) 180 residues
MKNFIRVLIA FSVFLCIYTV APHIGRGPGD LAPVTAIPQR ATVLGYDRAS MFGGWLGGVR
EGIVDEAGDT DPYSGNRLDL SSAEVDHILP LSAAWDLGAH RWSAGERISF ANDPLNLVLV
SKAENQEKSD QLPSEWLPSD RSARCWYVER LFAVANAYEL PLPENDIRVG RKQCGFAKPW

> RXA00183 (1-852, translated) 284 residues
MTESRRVKMD NVIYANFGSK QRVSTPDDRT QVINKSRHKQ FSPAGTRTVM LTEKNADSGR
RSRGEQYYRN GNVTGMTVLE GRVECTVAGS QNEPFVTTVT FPYRSSEKLR EAYAAIADTP
NGLRLVRDGH LTSSMLDHLV GSPDESIYFD CTCPDRSLVC KHAVASAYHV AEKMTANPGL
ILDIRGQGMA GLEALIRTYH TKVETEPEDN DSFWNGRELP ALPDPKIAPA IDDSDINYLH
KALRMVSYTS LEQLRAVSDI EDMYEILVAN HPDNQQVYEE EDTD

> RXA00185 (1-2628, translated) 876 residues
MRIHEIIIDN FRAIEHLELR DIPDQGVIVI HGDNEQGKSS ILEAIKTVLN SKHRTTSKTI
KAIQPVDRDV PISITLEATV GTVRFRIHKR FLKSTAAELQ VIEPRPSNHR GLEAEAALAE
ILESHLDTSL LDALFMKQGE VEAGISAVGI PTLTSALNAQ NGNTEDATED TALMEAVEKE
YLKFYTNSGK ANTRFLQFSK QVETLRTDLD EANAEVAKLS SHVDRVKRLE IDRDQATAQL
PKAEEELAGR KAELEEAQKV KAQATEILAQ FSRAEEQLEQ ATGAQKRRKE LRNKLELAQT
EVEKAEAGQE NLAQEASREA EEFLALSEKF EAARAAETLA VEKVKAARQS VAGIKNRDRK
EHLTVMLGEL DRIGQRLYEL RSVQHSSVRV SQRDIDALQK AITEVDIQRT LVEAQQGSIT
LSASTPTDIQ LGDDTVSATD AGTTVALDRE LTVVVGDVTL VINPGKTAAE SRTDFESAEA
ALAELLDQLD VSDLDQLRER FTAQEQRDAD IAELVREQQR MSGGTETTVL RAELEGLHVP
EDLDPSISVD DAQTQLNEAE ESRELAAEAH KHANAALDGL RSRPVDKALT VFNAQLAALQ
RNLSSAQVEL DRAVAETSDD EVDAAVQRCA EALAGVRVQK QEIEQVLAKT NPDMAQRLCD
AAEANVRSYK TAVSDATTEL VRLEGLIGVA AGAKERLDKV KSALTAAENR FESEQRRAHA
ARRLYALMVF YRDESRKRYA APFADKLSRL AASVFGESAD FDLDDELKIS SRSIGPRTVD
LANLSGGAKE QLAILTRFAI AELVAESSAQ GAVPVFIDDA LGSTDPERLT RISTLFSDAG
KDSQVFVLTC VPDRYNYVEV TQKHSIESLK TANALL

> RXA00194 (1-285, translated) 95 residues
VAGSSHTIEP EIYRGVSTLD EPSAAWGWHG LKRNTIQLAG WISVLFMLGY NFGNHKGHVE
TIWLLVITAL LVIGLLIHLF EPKALPGSHH HFSQQ

> RXA00197 (1-1011, translated) 337 residues
VAAYLLGVVL FFLGIAVTIA LHEWGHFITA RIFGMKVRRF FIGFGPTVFA KRRGETVYGL
KAIPVGGFCD IAGMTAQDEL DPEDLPRAMY LKPWWQRIIV LSGGVIMNLI VGFLVLYGVA
VSSGIPNPDV DTTATVDTVQ CVPETQISAT ELSSCVGSGP AGDAGIEHGD KILAVNGQEM

ASFTAIRDAI LELPGETATL TIEREGTLFD VDLQVASVTR LASDGSEITV GAVGMSSLPP
TDVYKKYGPI EGVGATARFT GDMISATWDG LKAFPAKIPG VVASIFGAER DVESPMSVVG
ASRIGGEFVE RSMWDMFMMM LASLNFFLAL FNLVPLP

> RXA00199 (1-1419, translated) 473 residues
MEDLEIFDRH LQHSDFEDQG SIGLELELNL VDKHMQPALA GHAVLSHLDD EYQSEIGNFN
VEMNHPPLSV KGDALRRLEQ GITSRLGRVR AAATSENVNV AMIGTLPTIT PEFLEDPAWM
TQENRYRALS NAVMESRGEL VHINIADREQ IIHDFTDLAP ESTCTSIQLH LQLAPNKFAA
AWNASQAIAG VQAALSANSP LFLGRRVWHE SRIPVFQQAI DTRTPELVNQ GVRPRVWFGE
RWITSVFDLF EENVRYFSPL IAESRALSGT PMMKGKSPAL HYLNLHNGTV WRWNRPIYAP
GEERSHLRLE NRLLPAGPTP IDITADAAFY YGLVKYLAEE NRPVWSRLLF PDAEKNFQSG
ARSGLFARMT WPTLGQVNVA NLVQEHLIPQ ARIGLERLEV NKDLIDQYLG IITERAKSRQ
NGATWQLRSL NKLEAHGSMP GSDARKAGLA AMLQQYLQNQ ESGQPVHTWA IGS

> RXA00200 (1-303, translated) 101 residues
HYAGVTEIPE YRISPDHGGK STLSPFQDWA GGGSMGTAEA VNNAYEIPSY LRNDWGRDWG
SIERYSLRTN SNGDAPKVAD INLETIQRSG LWNPGHMKVD E

> RXA00207 (1-318, translated) 106 residues
MEMKLKKASQ VSTATVVAAG LIGGWLTARE SGIRPLGTIP LAASGALAAR SWNEKKGPAV
ATGLLATYVG AFGLSHPLAK KIGAWPAVLT VTAGAAAIAY AVSDSQ

> RXA00211 (1-663, translated) 221 residues
MSFLIRVLLS DTPGSLALLA EALGIVEANI QSVDVVERFP NGTVMDDLVI SIPRDVMADT
IITAAEEVDG VEIDSIRPFS GTVDRRGQIQ MLAAVAHQRR DITAAMEEMV DVIPRTMTSG
WALVIDLKGP ITRIAGSLAA PEDDGTVPEN IVLKEARMLN PENDPWIPES WTLLDSSLAI
APIGKHGLAL IIGRPGGPDF LASEVEHLGQ VGDIIGAMLQ K

> RXA00218 (1-1140, translated) 380 residues
MSARNPFRPT FGVSPTVLAG RDSLLQSFKL GLAEGPGSPF RALLISGSRG MGKTVLLNEF
EDAAASQGWI TLRAYPDNSM VDGLVNSAIP EALQNLDGPQ SKRMLSGVAI PGIATVTAIA
DPTKKDPTPT LISRLRELAT RLQKHGSGIL ITLDELQSAN VDLLHVLATA VQDLLRDDFD
IALVAAGLPE GIDRLLQHEG TTFIRRAERI LLNPVNHEDS VEMFLDTAAE GQRHMTSEAA
ELAAQISKGY PYSMQLTGSL AWARSTLDNS DTIQAEQVDA VRDEVVRRMG MQVHEPSLHQ
VPDGELTILY AIAQLSKNGE MVSTGDIAHL MGVKPNALSM QRKQLLSRGL VEVPKYGFLN
FTLPYMREHL LNSPHHRPIT

> RXA00220 (1-504, translated) 168 residues
MSAFHIRAEQ SHDISAIHDV TEAAFTGIEH SDGTEQDLVD KLRAAKALSL SLVAEADGEV
IGHIAASEVL IGGGVQGWFG IGPVSVRPDK QQQGVGIALM GSALDQLRAE GAGGIVLLGD
PGYYRRFGFE VVPGLVYPDA PAEFFMAVCL NAPAFPQGVV EYHSAFGG

> RXA00222 (1-1146, translated) 382 residues
MTPTADIWFK DTLAAHFTRD GDQTTFSYTA DYAGPPIATS LPINSEPVIT RSGAIPPFFA
GLLPEGRRLS SLRRNIKASA DDELSLLLAV GADPVGAVAI FPHGENTQPA PPTVDFDDEL
DFSAALTESG IADPVALAGV QDKASARTIA VPVASDAILK LSPPEYPYLV ENEAACYQLL
TKNKLRIELS KVEVLHDKHG RSGLLVHRFD RTPKGKIPVE DAGQVLGIWP ADKYLVSYED
IAQALTKVCA SPILAMRNLA FQIAVAWLSG NGDLHAKNIS IINKGRGFEI SPIYDIPATA
VYGDTTMALE IQGSKKDLSQ KKFLKFCTSI GLPEKTAMSV ANAALLATEN AAETILASGN
FDTRMNRDLA RVLKHRRSAW GA

> RXA00230 (1-720, translated) 240 residues
LIHEQDVQKL LNYITSHFGV DPERWFHPEG YQSIALAILD SIYSTGNRYT GVLNLVNRYC
GLRANEGSHP EADTATDLIE TFYRWGGVDE FVLKTNNRWR TSSKIHAPYK AYAALEAAKV
LAGHSIESIS DVVGRFDSRE SREHSDIARE WLMITGQSSA LTWSYFLMLV GVPGVKADRM
IVRFVTHVLE RPKEISRHEA SRLIEEVADI MCVNYIYLDH TIWRFQSGRP YLQEDSSPFE

> RXA00232 (1-510, translated) 170 residues
MNDRAHQRIG DIERSQALDR LGSYFADGYL DIDEFDTRTG AAAIARTAGE IDVLFTDLPE
QQASTAVTPV QDDTEKELDL VLQRGKKLKQ IDSAIWAVVM VSFFLGLFVF NVPYFWVVFI
LGGAASAGAR FLLKVDDADE KLFEELHSKE QSEREARLRI AAQRRRELEQ

> RXA00233 (1-417, translated) 139 residues
MSVNEADLNA VEEQLGRAPR GVLDISYRSP DGVPGVVMTA PKLDDGTPFP TLYYLTDPRL
TTEASRLEVA LVMKWMTDRL STDEELRADY QRAHEHFLAK RNAIEDLGTD FSGGGMPDRV
KCLHVLIDYA LAEGPHHFL

> RXA00234 (1-540, translated) 180 residues
MAKQKKTHKG LVPVSSRERA SESVSATRAP FRLGAVGIGA IALVVLLILF VIAIPVRNYF
QLRSDIAQTE ASIEAKEQQI KQLESDLNRY QSEAYIREQA RLRLGVIEPG ETAFRIVDPA
LDTDTSVTSD GNEEKPLGAW YENLWDSVTK PEALGEEEIA PPAVEGEVPT LAPTEEATVQ

> RXA00236 (1-726, translated) 242 residues
MVISFVGWAL SFMDGTAPIR QLQQIPEDVP PARGVEVPQI DTEADGRTSN HLRFWAEPIA
QDTGVSAQAI AAYGNAELIA STAWPGCNLG WNTLAGIGQV ETRHGTYNGK MFGGSSLDEN
GVATPPIIGV PLDGSPGFAE IPDTDGGELD GDTEYDRAVG PMQFIPETWR LMGLDANGDG
VADPNQIDDA ALSAANLLCS NDRDLSTPEG WTAAVHSYNM SNQYLMDVRD AAASYALRQP
AI

> RXA00237 (1-378, translated) 126 residues
MKLSHRIAAM AATAGITVAA FAAPASASDF ANLSSTNKEL SPQYNWVACG ILEGGLKAAG
VLEEGQYNRE LAEAIAAKGE GFWTTQFPQI GDWNEDQAAA LADRAQTCGL VKADTYLSEL
SSNFSS

> RXA00238 (1-369, translated) 123 residues
MKKLRFATIA AATVALTASL TPSASAQDFN QIIDNFDCGI LQTAIYTTGL AHENSTRSEL
AANLRNSAAV GQLDFPLNIA ATGYSERIAN RALTCGIVKE DPQDFLSQLQ LLSSNLSSSF
FTA

> RXA00239 (1-585, translated) 195 residues
MRVVVVDPKH PVLPVSFLEA VLGRGEPVSI DPDFPFDIEK WGIKTSTSAS WFIIAKPQST
LLIDAPLNPL HEAVGVMRAA VGRGEWERTQ THESLIPYLE EESQEFIEAI HGGDDEHMKS
ELGDVLLQVL FHAEIAARQG RFDIFDVAAS FVAKMQSRSP YLFDGSTGIV DTDEQQRLWA
QGKAQEKLSS EEGRR

> RXA00240 (1-210, translated) 70 residues
MGIFDEAKKK ATEFLDSDSG EQKSDGLLDK AADKAKGLLG EDKADQINKV RDAVDERIGK
NNGGEENPAN

> RXA00242 (1-1203, translated) 401 residues
VNEWRTVSLV DSTALTVIIS VAVFTSAVAL LGVVKKRSRW RVLGALISSA VLTSGAWVVI
EKLWKPFPDP NPWTIYLSAG LAVFPLLSIL FRTGRTRILM ATLTVIALVN TAAVINVIYQ
PYPTLGSFNP VPTAVSMSYA DFESQTTAPT MDDREVGALV QVPLAGTTDD STSGFDARDA
YAYIPPAYWD NPSLQLPVLV LMPGNPGQPD QWFSSGNADQ TADNFQATHD GISPIVISVD
GTGSFSGNPA CVDSDAQSVM TYLSHDVPML IKQKFRVNQD QRTWTIGGLS YGGTCALQIM
TNHPEAYGSF LDFSGQEEPT LGTRQQTVDQ LFGGDEDAFK AVNPEDLLNQ AISSGAHTYS
GISGRFIAGS NDKSAVSALS HLDNLSNQAG MSTTFDTVAG G

> RXA00244 (1-636, translated) 212 residues
MNDQLWEGDT GTLTFGSRKA LVQLLKGPMV NALQHVEVWR AITTDQDALN AVLNNLFLEL
VLDEDAGVAF TRPANGRQEV LVGNNKTEAM PKVLRTETLS HFDTLIILIL RQELTMAPPG
ERVIVDREEI REQVLLYRVD EERDEAKLAK RFDAAFRRIV DYSLAKKTET PERFEVSPAL
RQIFDADTVA GVRAEYEKFN KAAHDGNEEE QK

> RXA00245 (1-1485, translated) 495 residues
MTVVSHALGF KRFRQESLEL SLLRSDNFPV VLAVVAQYFP QGAIAKPASE LYQLLSDDFR
VLREEGFELP KSPSDYVSDW VKSRWFVRRP GSSQTGETVE PSEELLAVLD SVQRWDNPHR
SISASRIESL TQALQTLALE SDPSTAKRLA ELERERDRIE RQIEAVHAGE FEVLTTVQIG
DRVADILDLA ASIPADFARV RHELSDLNRK LRRQLLDPED SRGDVLEEIF RGVDLIGDSD
AGRSFNSFFD VLLDRERSSL IDRWIREVLG RDEAIDLDSK LRTGLYRIFR DMEDASFEVN
GEMTGLARSL RHYVTTEEFA ESRRMIQLLR DTRSAAAKAA EAGEVTSLNH MDTPLVRIGM
DVRSIAGLKL KNPGEERVED LPEPVEEQEL DTEVLMEQIR ASEIDFEELE EAVSLVLAEQ

SHATITEVLE HFPATQGLAS IVGLLYLAMR DGVPTGRAQI VEWESDDATH RRRITGWQFI
RGLNSEDLAE SEMDK

> RXA00247 (1-927, translated) 309 residues
MQTLIFIAIA GVAAQLVDGG LGMGFGVTST TILIMLAGLG PAQASAVVHT AEVGTTLVSG
LSHWKFGNVD WKVVVRLGIP GAIGAFAGAT FLSNISTEAA APITSLILAL IGMNLVWRFS
KGRIRRDYSD RPHSRGFLGG LGIVGGFVDA SGGGGWGPVT TSTLLSLGRT EPRKVVGTVN
TAEFLVSLAA TLGFVVGLWD DLVANLSAVL ALLIGGAIAA PIGAWMISRV NATVLGGFVG
TLIVTLNLPK VLNVVGLDFI PTGLIQVTVL LIGLPLTYLG FRRYRKNLLN ETISSEVVSE
PKGQKIKST

> RXA00248 (1-723, translated) 241 residues
MIPLITLSHG SRKKSAAAGI TALTHEAGRM LETPAVEAHL ELAEPSLDQV VATLSAEGVT
RAALVPLLFS NAYHAKIDVP EAVKDASEKY GVELLVGPHL GTGSDVASVL AQRLSADAPT
DAHVILYSVG SSHVSANESV IDLAHTIALL TGFSVEVVPA TGGPGAGGAG VIEVASKHKA
VHILPLFVTE GLLLDRAIDQ SANIAAATGT NFTYSEPLTT DLAPLVAARY HAALSALLAH
I

> RXA00250 (1-216, translated) 72 residues
ALGAALGQFD FVRNNIDLIF LLIVFISVVP GLVGMARKLA DGHKQANTEP QENPAVQTAP
VKTQEAQEAP QN

> RXA00252 (1-243, translated) 81 residues
VFAGGVDGVA GVWSVAGAGV DVDDAAGCRA EGGQELATQL GRDNDVEIKV CVPFGHTAGF
DGRVTRHRRG VHQRIHVVEV F

> RXA00256 (1-771, translated) 257 residues
MFMSLKTRRI FGALAVSLSI SFSAIATPAA SAQELVVSTS AVNEFGVVTS DITAEQILQA
QDLIAEMKQS EDIYEYFGAL SDVEQRSIIA AVKENPYLIE NESPRMRVQS ETPDEETPDK
KKPSKTYKLY MSILEMMSCI NLVDVPSCAQ ALKAANIAER EAKARYPDSV TNGKGDALRH
CAWSALMTIR IGKDAAERIG NAHETVVRGE PEEREMDLIN NALGRDIGER FIINGDETGA
LSTCVSMANI GLLHTLL

> RXA00257 (1-456, translated) 152 residues
MKIKKFSITA LASVLMLTGC ATNHSSPLYS YLNASTSTTV EQVRLSDLYG EQWTEFALVC
PYTTKDEVKE ELGIKINTYL TDSTDDSSND IVLRDKDGSY DWIYFNRFDI VYLCNGSAEN
LKIYPIDSVL EFEHRDDYGT WKLSAITEPG NQ

> RXA00258 (1-672, translated) 224 residues
MRHTTSATST TSIIKRAMTI SAAVLIASAV GLTTSASSLN TLSATSPESP DQAATVSQAE
SDSELDDGMK KLATKILNRA DNAENNDDTG KNLNNDDKKL NTKQPQRPAE KVAQAIELSL
DTTTNAEKPD KSFHHEKPVN AYVTSVSYNK SNDTWTIKPS DSAVNTPTND AERISNIIQE
ARDLGLSDDE SLTQQIAFHA HAANYLVTEW VLRGYQLANP KVLP

> RXA00260 (1-1176, translated) 392 residues
MHSDAVLAGA SIRAKIGALA TIYGAQNLEN VIHSVSFTDR RISPDGQLSK ELFREAWSAN
LLIPDPSSDV EAFAWSEKNS TELAGGIFVE KMLFTVPDTG RSNNRVQSFS EELRNHISLK
DMYSTQREEL LDLAYELMVG EAVRFANFRL YDQNLPPLTE ANIDKLRAHL REAAASASLG
VLYLMVWRSV KDAAAAHTKH TRMSKENATT HSVTKVSIFV DQLLSGTFPC SKPFHESSQV
PLSEATKIVF NLIMESPPME TEPSVLRNSL QEHSDWELLQ QCDEKIPDRE FLMEWLYQEQ
TWTAEQFFDA LAMVSSSEFR ICAPGCAHQV SADIATQVLE FHDRVSFHDD RKSAMLAAEA
TIIGNKIGSQ ARAGDFVLGE VITKLQNIPG EV

> RXA00261 (1-429, translated) 143 residues
MYSDKLILLF LSEQDSSYEC CVGLLDGSDG RDYIEKLLKG RKLKNHFLEW EDINKADVAR
EEIYKGQLVH LVFVTALSTP GEISFVFPGQ SLMSATLEED FAALVLEEER TSFRPDLSHL
WSLPVGWVAP GLEGFVERNS EAA

> RXA00264 (1-378, translated) 126 residues
LLVDSGDVQL EGVTVEPTQL AYTGINETQL RIRNIGTTPA RTVLLGGEPF TEDIVMWWNF
IGRSHEEIAE YRKQWQAEAD RFGITHGYIS HHKDGLTRLP APELPNAAIK ARKNPAPTAR

PETRID

> RXA00267 (1-270, translated) 90 residues
VSVAVITRIA SSPSFIAIVA IIVAAIALFV GLNSRVGTKL VDQPVVFTQE QIDQLKELKS
RDQEAAAIRQ AQLWSRGSSS EAVAEAVRKL

> RXA00271 (1-990, translated) 330 residues
MFSSRSKVLA SIFTVGALAL ASCSSDSSDS STSTDAAGGD SYRVGINQLV QHPALDAATT
GFKEAFEEAG VDVTFDEQNA NGEQGTALTI SQQFASDNLD LVLAVATPAA QATAQNITDI
PVLFTAVTDA VSAELVDSNE APGGNVTGTS DIAPIEQQLE LLQQLVPDAK SIGIVYASGE
VNSQVQVDEV TKAAEPLGLS VNTQTVTTVN EIQQAVEALG DVDVIYVPTD NMVVSGISSL
VQVAEQKQIP VIGAESGTVE GGALATLGID YTELGRQTGE MALRILQDGE DPATMPVETA
TEFTYVINED AAERQGVEIP QEILDKAERV

> RXA00272 (1-372, translated) 124 residues
MPEPETSTMG SIQKSGEWLV PAYSAYKLNG ADLFLDIRHA TAAAPVITFD VNMTMGSMTL
IVPPGVYVEV QMASKNWSDF KVQTTNPLPG APRVFITGVA RASGLKVFTK HPHEPFGFWQ
KMFE

> RXA00273 (1-1113, translated) 371 residues
MSLKLNSRRL ASIAVAVAVG VSGVAAVGAA PATAQQVGAG TPIHVVNLDR TVVDPVTGDI
TFHFTDGTFV TLKAGVDGKD GTDGQDGVIG KDATIVDVAT ESNGDVKLTF SDGTVVTIPA
AKDGVDGEDG KDGEDATVVS TATDANGNIV ITFSDGSVLV VANGKDGNDG SDGQDGADGE
NGKDGENGAN ATIVDQIAND DGSITIVFSD GSEVTIPAPA KGATDELAQC LLNPKMLLLA
AIPAAGAIAN AVAPAIPRVV EDVRAQFNLP SLNPQFDQWL YNATKDIDAG LLISGATGLA
VLSVLADDFC GDIDADDNAD GDVAAEKPTG SSGLGSSEQS EKVDGDDDSV IDTETDADLE
VEEDPELVNA G

> RXA00274 (1-2610, translated) 870 residues
LSLNLKKNSA RSITALTVAG LGLSIVPAAS AQDVADDTTN SDSTRDAICA AAPLVAGAAV
GVGLLSQQPE FQHMVSQIQS DAQRIGQDLS NQFNNSLESL NIGLGNGVHG PQQNAVQGID
LTEAARTMAG WNDLAAQVGQ TAGPAIGAVA GTAGLIALVD YCWLEGFDFA GGSSGTDGEN
GVDGQDGTSI TITEIKTDDD GNTIVVFSDG SEITITNGKD GAAITIVNTY RDDEGNTVVE
FSDGSTIVID KGEDGKDGED GKDGEDGKDL TVTDTYINDD GDTVVELSDG STIIVKKGTD
GKDGADGSDG ADGVSITVEN SYVDADGNTV VEFSDGSNVT INKGEKGDKG DAGADGEDGA
DGESITVVNT SNDAEGNTLV ELSDGTVITI NKGDKGDAGA DGEDGSNGAD GESITVIETR
FDADGNTVVV FSNGTEITIN KGEKGDKGDT GEDGKDGLTP YIGPDGNWWI GENNTCTAAR
GNDGKDGDTP RIGDNGNWWI GIVDTGVPAR GQDGANGADG ANTVEIINGY WYINGENTGV
KAVGENGTNG ADGQDGENGT NGANTVEIIN GYWYINGENT GVKAQGPKGD KGDTGDTGAP
GEGSGNVDIE IRESSYPGGG QATIIILDQF EYEIPHTVIG DNGNWYIGEK DTGIPAQGGT
GTPGEDGLTP HIGDNGNWWI GDTDTGVSAS PTPVGEAVAG VTDVVFNTSD EPKTITATIN
GEEYDYTLPP HSAVVFYATG SPMAYSLPNA SGLTVIGTEE TPGFTTIRFS DHSTVTIPHG
RDGTNGTNEL TVRMVSPRTS VRTETGGSAK RTLVFRQPLA VAATLVPAMT ASRSQVMILD
SQMMLRPVQR PVQMPKVLLT KGHRATTMTD

> RXA00275 (1-459, translated) 153 residues
LDKRRPELSD DFIKAFDDFL HSFACLDKTT ITLLAQSPVR TSTGYTGTFI GIPNNEPLSE
EPTPTIYIVH DNHTGIIHSY PARMINLKSE LGSAEMIHEA IWGSPHQQQL ISWYETYYTN
IYYGFNPPTE PHKSLEIFAQ DFCLTPPEKP PFF

> RXA00276 (1-342, translated) 114 residues
MDDLSSRQDH EAYGTYNPDN GVMPDHVIVP SPYEPYDDAA PIDPFDYDED LLDEIKEERA
AHAVDAQVTE TTKADADVAQ LATAIDEQNR PTKSCSLRQI ARNYSPGWIS VAQN

> RXA00279 (1-1386, translated) 462 residues
LDTDDSPDHW LDPLTEKDTS KRTLVNSIVQ ETFGQPIFVA RKIWAFVNTS PGRMTLMTII
ISIAIFAAGY AMSVSSDTRQ SNLDDLITNA EPVSYNAHVL YTSLSVADTT ATTGFVQAGV
EGPVNRVKYH TAIDRAAVAA THTAASADSS NEHLMELVLE IQRQLPVYTG LVETARTNNR
AGNPVGVAYM SEASAMMRNE ILPMASELYN LTSRAVSDQQ RSVTGPQWFP LSGLLAALAM
LIVAQWWLMR ITRRRINKGF ALATVMMMTA TLWVSAANWA TWQAGTKGFE EASGPLNSMT
TARIYAQQTR TTETLSLVRR QSIQGSGTGF TATINQIKRA LDEYETTAQS QTPEHQQLIT

AIRNAIAAWT ADHDEFTVLL ASGDYNGAVN AVLNKDEEGQ TSFDELDTAL AELIADSRSS
MRSYIQSGLQ ATELVSVMVM ILSVVSVLAL WVGIRPRLQE YL

> RXA00282 (1-789, translated) 263 residues
MSRDDQTNNN GEGDDTSREQ SWDQSWQNLN KDSQYGPTSH PEDAPGGFQG NGQGNSRGNA
QGNGQGNGQG FGPGNASGYG GYGQPYPQTP YQNSYQGYGA TSPQNDVALE ASNGKVDIMR
AIRFGFKATF ANPAVWILGT VGLGLAFMIV SGLLGYLSFL IDPNAGTTTS GFSVSETLLN
VAIGIITFAI TICVMRGALL SVDGHKVRFG DFFKPINVGQ TVILMVGLGI FGIILGTFTT
FLTQNLVSFN DAAGTVEVNN SGL

> RXA00283 (1-1128, translated) 376 residues
LALAFLARYD ALIMAFVAMW TVGFMTWRAR YRRGFRDRIG FALVDMLLLV WPIGFAFVAW
TGASWLTTGE LFAQFTSTDG NAAIIAASGG GAIGPQALFD ASVRTFLISP ALLLVAVVAV
FFAYRRRDPE PIIPLALIGS VVFFQIITYS LGSTFGLLRF FLTALPLTII LLFQIIPPRH
RFPSLRPGAC YRDRVTGKYV PKTITGVLVL AIFGGTGITL YGMSSANWAP QEYAIQELVF
NMGSPSQDAV HTLNTFSTEM DVADFVDSLN LGDGEVLLST TYGFAVLTAS NNQKQFIIPS
DEDFITTLNE PAEHGVKYIL ALPREGRGAT DPINLRYPDM YETGSHIATM EIEFINQGQG
QPNWRLYRVL TTPEQS

> RXA00285 (1-513, translated) 171 residues
GTELGALLLR VLNREEMMDR FARELGFFVD KQLEEVERIN CHHNYTVQEE HYGETIWLTR
KGAVLADEGT PALIPGSMGT ASYVGSGKGN AEALRSAPHG AGRRMYRNQA KKRFSTADLD
SRMAGIVYRP GKEWIDEIPD AYKDIDQVMA DAADLVTIRH KLRQIVNVKG T

> RXA00286 (1-564, translated) 188 residues
VLKIPRLLLR RVLPVLITLA LLCGLVLAWF IYPAKAEPKK DDVVLVLAGS SDGRHEYGAE
LVEEGYASNY VVSNPSGSKD KVGYAHCAGK SRPKNAESFC MDPYPVITSG EARTFNELAK
KEGWESVLVV TSRTHTQRVR TMFDQCYTGD STVLNVNSLG RTGLHNAVLH EIGGFIKFWI
TAPCADTN

> RXA00294 (1-429, translated) 143 residues
MSISNAILRG VSGAYILQSG YGKLGLPNEA AAGIQGLAAT GIPAVADMDS DTFGKFVAYS
ELGIGGALLA PFIPSRLAGL GLGAFSTGLL AIYFRNPAMT QDDGIRPSQD GTGLSKDLFL
AAIAGALVFA PAKKRKKAKN KSK

> RXA00297 (1-912, translated) 304 residues
MGFTVVFIVI GIGWILGRRD TLGTHAQKPL SLFVYYVATP ALLFDRVTKS DTSTIFSLNF
VVIALSALIV GFLFFLLMRF VIKRTAAVSV IGMLAASYAN AGNLGIPLAA YILDDFTVVI
PVILFQVAFY APITMTIMEM LTNKKSTNLV RNLLVTPLTN TMVLAAIAGI AVSLTSMSVP
VVIAQPVEML ANASVPLALV VFGLSLSKSK ILEKGQVSRR DVFTAALFKN VLHPIVAGLL
ALAFGMEGTA LLSAVILGAL PTAQNVYTYA LRFRTAESMA RDTGVVTTLI SFPVLVAVSI
IFGS

> RXA00318 (1-210, translated) 70 residues
VSDVTVGDIL RILDEAYPPA LAESWDKVVL ICVDPTESVK RVGLALDCTQ ALADKAVDMG
LDMLIIHHPL

> RXA00320 (1-180, translated) 60 residues
MAKEDLKWFY DLATGKVFQG KVSGFETRMG PYDTEEEAHH AISIAAARTK AAEIWDDKED

> RXA00321 (1-1815, translated) 605 residues
MGQHLEVETK FSVSESTQIP QLEAIAEVDH IDRTEIHQLS AVYFDTVDLR LTRAKITLRR
RTGGNDAGWH IKFPGTIGRR EVQAPLDGEG ATETLPPREL LGHIRALIQG RELTPIAQVD
NERHMSYLAD EDGAVIAEFC DDHVSTVSHL PGGVRKQWRE WEFELADGTL AEEAISVLLQ
SAQSVLTAAG AFVSNSPSKL VSALDESVNH APKPPQMAQL DKNDPARGVL AAIAANASKI
AEYDPRVRAD EYDSVHQMRV ATRELRSHLQ TFEGILGGED YLNLEKELKV LANILGRARD
AEVVEERLSN LINTEVGDSI EEETKKELLE DLGAEYRREH ERVVRALDND RYTDLLQALE
NLLVDPPLIT EVEEPEATEA PESAETTEST DVSEATEEAD AEAESVEEAT EQEESADAPE
SADLDALDEE YSPGSQAPVE EPKEPKKVDA ALVLLEHLDK AHVKLVKLEK KARSQWDDLS
IPMLEREENF HNLRKAAKKL RYSAEAVGKA TTVETKKLYK ACSGLQSVLG DYQDAITSRN
ELLRRAQVAR RQGRDTFAYG ILYQHEQTLS REYLTGYSDA FKSVEKAYAK LAEDTAKRSK

KNKRK

> RXA00322 (1-1104, translated) 368 residues
MTLSHFSDNV TDAQDSYRQI LEESIISHLG FCALRGWTPA DLRHEFSADI DPLLFHALPE
IAYSCSDEMY TLWVNGTRAA ETSHLPVMTL EKILTELPKL STLPDWAMLA ELHALDNQDT
SPMTPAQAKA HHRITALLKK AESTNFEEEA EALILKAETL RQQYRIESLL INSYDQDVQA
RSSTIRASRV YLEAPWIRHQ YKLLNAIARV HSSEALLITK SGICTLFGEQ DDVAHIIDLF
NSLNRQRAHF MKTSAGARIA QLNGETSSYR RSFMISYASQ ISRLLISAKE DAFNELAGQA
PLAHSAIVPV LENRSVRSKE ALKETFPNMR TMTFKSTNRR GIIDGFNAAN ESHLGGESAS
LEDSTFMF

> RXA00325 (1-645, translated) 215 residues
MTSIIASNSD LSEALRTHTA QAHEEAEHST FMNDLLTGKL DAQAFIKLQE QSWLFYTALE
AAARACAEDS RAAGLLDPRL ERKETLEADL DKLHENTTWR DNVTATAATA SYVERLESIE
AAKDFPRLVA HHYVRYLGDL SGGQVIARLV NREYGVSEEA LSFYCFEDLG KLKPYKDNYR
AELDALELTA EERAALLDEA SDAFRFNQQV FQALA

> RXA00326 (1-480, translated) 160 residues
MAIKLSIDLS DATFAELSAV IGYAHQLGVD ADEKLTFEGT VLNIEFDGDL QFDDVFDAFD
EAEIELDNPR EDGPIYADDL IDEDEDYRAQ TKSQINDEVI NEIRDGISSF VDGIVNGLGQ
GRRGGRYGDF GGPRGPRGPR NDGPFGPFGP FGPGYRGPRF

> RXA00334 (1-336, translated) 112 residues
MAKLDDNVQI ETVNVSFEAG GRTNWHTHPV GQNIIVLSGL GIYEAEGEPA RLLEPGDVVF
AAAGVRHWHG AVSGAPMFHV VVNLKGIDGE TVDWEEPVDE EHYRSVSAEL QR

> RXA00336 (1-471, translated) 157 residues
MAKPKRSWLD GPEIPADFDD PDAPGRWPGE KLGLPQEGAG SLSSVARRIG GVCVDWGVSW
VIAIVLSNFT DVLGDVATST LIIFVILGWL TGWIFARTPG HAVFGMGLAR VDAEERVGWW
RALVRPLLTI LILPAVMVDA DGRGLHDKAT GTAVIRG

> RXA00337 (1-525, translated) 175 residues
DVEGGVEKHS LSTADIAARA HAHMKSHDVL GRQTTPPQPE GGVAARLGGI AWTMIHKQML
SRDTKGLDIT VLSTIPEGVG LGENSAMDVA LALALYRENI EEAPTKARIA DICSQSAFMF
SETSVLRARH TEALRGETGH ISVVDYADGS VTQAPHPVSR SAGLSAFVAA AQTET

> RXA00338 (1-783, translated) 261 residues
VGITAGRPIA TRLLGGMDKW GVHVLPKDAA YLKKMLFDAG AGAIGDYREC AFEIEGTGQF
RPVEGANPAE GDVDKLFKSL ELRIEFVAPR NLRARLTSVL REAHPYEEPA FDIVEMHSAE
SLENATGLGR VGELPEPMRL ADFVQQVANN LPVTEWGVRA TGDPEQMVSR VAVSSGSGDS
FLNDVIKLGV DVYVTSDLRH HPVDEYLREG GPAVIDTAHW ASEFPWTSQA QEILQDKAPQ
VEVDVISIRT DPWTMSARAV N

> RXA00339 (1-717, translated) 239 residues
MKLDPSLHKT LLQLATTLRT QNANSAPKTT PEQEAVDKAV AELSRNRDAA SAGQMAVDDM
ENEILRIQSD ERKLRRRKKD GQDALGAETD EERRRDLNHD VYTAKSRIAD LMSELQEAHN
EIHALRNNRD LAQSRVKDTE RKVADARAAA EAAAAATPEG EDPAVVIAHL EEKLPSEALA
EFHAQRLENG VGAALFNGRS CSGCAMVLPA TGISDIRNTP KDEVPQCPEC GSYLITDIS

> RXA00342 (1-429, translated) 143 residues
VADAPGAVKQ GAQDYAQLLG IQSGHIVQEI GWDEDSDTLI SESIEDAIGE ELLDEETDEL
CDVVLLWWRE DDGDLVDGLV DSIRSLAENG RIWVLTPGIG KEGALAPGVI SESAQLAGLV
QTKAERLGNW QGSCLVQRGN KKP

> RXA00344 (1-579, translated) 193 residues
MSFGLGLSVL FIHLYPGRSS TAFSLLTGQI VGVSSSSLWI LVAVTVIVVS AVVIFWRPLL
FASADPIMAQ ASGVNVRFIA VAFAVLVGLT TSQSVQIVGA LLVMALLITP GAAAVAVTAN
PVKAVVLAVI FAEVSAVGGL LLSLAPGLPV SVFVTTISFV IYLVCRLIGW LRGRGAQRDE
DAYRRRQHDH HPH

> RXA00349 (1-1059, translated) 353 residues

EKILDELEQS PASYGFPVAL LGWPMMGGAV AVLLGGGCQV SLIAFITAFT IIATTSFLGK
KGLPTFFQNV VGGFIATLPA SIAYSLALQF GLEIKPSQII ASGIVVLLAG LTLVQSLQDG
ITGAPVTASA RFFETLLFTG GIVAGVGLGI QLSEILHVML PAMESAAAPN YSSTFARIIA
GGVTAAAFAV GCYAEWSSVI IAGLTALMGS AFYYLFVVYL GPVSAAAIAA TAVGFTGGLL
ARRFLIPPLI VAIAGITPML PGLAIYRGMY ATLNDQTLMG FTNIAVALAT ASSLAAGVVL
GEWIARRLRR PPRFNPYRAF TKANEFSFQE EAEQNQRRQR KRPKTNQRFG NKR

> RXA00353 (1-693, translated) 231 residues
VGRSFTNRTF DPLPFMVVYP DGVDQHWNDA RLGLDENTRH LGIDDVGFFV KLATHLGNTY
GIKRIFIVGY SNGGQMVLRL MHEVPKMLSG AATIASNMPV AENTLPQVKT FKTHPVPYLA
MAGTADTFSP YEGGDAGIGR EHRRGVGMSA FDSAAYIAAR NGLTEHRHDV IDDVVSIDTW
DGENPVEFWT LNGIGHLVPS GKTYPEFLGP STTSVIAAEE IGKFFDGVRR R

> RXA00355 (1-126, translated) 42 residues
IAFGRAAHRM KQQGQSGAFT VLEVAPYLLS PENLDDLIAR DV

> RXA00362 (1-960, translated) 320 residues
DEKTGWTAER SATLVAGNSG LGVALPPNST MFIILALPAA AASSASQVYI ALACGGAYAV
LYRLAVVFYW TRKDKIPATP DDQRVSFGEA MKTGWRSPLI FLGILIPVIL TIGPLSEWLK
THGVGESGVK SMSIIVWVPI LITAIALIEG RKRIANNMAH FRVQISKDLP QFATVGISLF
SALAAANIME ELGVGPQLSN WLDSMDLPKS VMVIIVCIMC IVVATPLSST ATAAAIGAPA
VAALAAVGID PTVAIVVILL CTSTEGASPP VGAPIYLSAA IADANPTKMF VPLITYFVVP
MILLAWLVGM GFLPVIVPTG

> RXA00373 (1-339, translated) 113 residues
MDIQQLDAET TAWKDSLLRA AQEAGFHFEP PKLFEDFETM VEQYKQAAAS DPDIDVTDIQ
QMWGIVVGEY LREKMGMEWV VITDDYGTDL AILATAPNGD HVYSCPIIVV GKR

> RXA00375 (1-501, translated) 167 residues
MFPSPATGGD DINRRPLNEP NADATTIPTA LKVVFWMLFA TAAFMIFTGL VMYTAGYTGP
DDVDESYKAV VVNNQEFIGG INAFAGVVIA ALTSQLPKGG KNPRRLLLAI MLLVLLTDLL
SFATRAGGFA LAIIAVLLAL EALLMFRPAV NDHIDRNHMA RVMNREK

> RXA00380 (1-621, translated) 207 residues
VRLTKLAATI GCVTLSGLAL VACSSDSTAG TDAVAVGGTF QFHSPDGKME IFYDEADRQQ
LPDIGGDSLM EEGTQINLSD FENQVVILNA WGQWCAPCRS ESDDLQIIHE ELQAAGNGDT
PGGTVLGINV RDYSRDIAQD FVTDNGLDYP SIYDPPFMTA ASLGGVPASV IPTTIVLDKQ
HRPAAVFLRE VTSKDVLDVA LPLVDEA

> RXA00387 (1-813, translated) 271 residues
QNDPETWEDY ELRVNHPLRI EGDRVYLQGH GFAPTFTVTW PNGETRTQTV QWRPDDPTFF
LSSGVVRFDP PAGMYPDLYE RRQNQLAIQG LFAPTAEWEG DNNELLTSSY PAMRDPAVAI
DIYRGDNGLD TGIGQSLFSL DSSLMHSGVL QKIERVNLQI GDTVTLDDGT TVSFDGASEF
ANYQISRDPT QNWVLVTTVI SLVSLVGSLM IRRRRIWVRF YPQENGTTRV ETGGLARTDR
AGWGGEYEKF HRELLGLKEE DEDEEYFDHD D

> RXA00390 (1-405, translated) 135 residues
MSTTREIAFL IARILLGVIL IAHGWDKFAI TGLEGVTGFF DSLGIPAAGI AAIAAAVVEL
LGGILIILGV FTRIVAAFVA IDMLFAALFA HVSSGIFVTN NGWELTGAIG AGALLLIAVG
ASAWSIDGVL AKRKA

> RXA00392 (1-864, translated) 288 residues
MWVGYAVRQI ASVFLTLLRM LPLAARNRVA RGRIPETGDV VISLTTHGKR INYVHFTIES
IARGHVKAPI VLWLDKPDFD APWPATIKRL VARGLQVRCS DGFYGPHTKY WNQFREIHGT
GVRVATVDDD MIYPEWFLQR LLFIGDLRMD AVVAYRAHRI ELRDDRMLPY VKWSAADTSK
ASFLHFATGV SGVLYPVTFI DYVVSQGDVF LENCKRADDV WLHACALRSD HPIRQVYAQP
RHFAVVPTTQ VGALVVGNTL MGGNDEQIAK VYTDEDVAKL VAASKNED

> RXA00394 (1-333, translated) 111 residues
VSESNTPNLQ THQAPELNPE LQKAARKNVL IYGLARLLLF VVLTLIIHSL ALLISAPVPL
VMSAMLALIV AFPLSMLVFS KLRMNATQAV SQWDAQRKAH KEWVRSELAD R

> RXA00395 (1-300, translated) 100 residues
VGRLLLIILV IVAIVLLWKA FKPSTWKRNA EINQGQAPRA VKGPDDDEEF LWNIEKNRFK
QRRADEAAQL EEEERLKRAR ERYAKPESSE EGPEKPTEDS

> RXA00396 (1-471, translated) 157 residues
VTEIAENLQR LGIELPDLPA PQYSYVPFNR QGNTLYVSGQ ISRTAAGDIL AGRVGEDATL
EEGIHAAEVA TINLLARIHQ SIGLDNVAQI LKLNVWVNSS DDFIQQPQVA DGASQLLEAV
LGEAGKHART ALPTNTLPQG ALVELDAVVA VTEAAEV

> RXA00397 (1-540, translated) 180 residues
NLHSSNRMLF PGPPVDFPIN AETRCIQLDA GVAVKKDGVV LGTSDMARSL PRTAAGQEAY
EYFFKVVREG IIGQLRPGVI CADVHEATLD YLSPQLPRMI DIGMLGADTD FNTIYRKRNV
GHLMGKQESF ANELRPGYKH ILHHGSYGAA EIPWRYNGVA IGTEDLWYIG ADKTYILSQR

> RXA00398 (1-681, translated) 227 residues
YLPEPFTVED YTARVEGLEV AGGAIVSGSF QAFDQGYLKD ALAVLGPGYV GVTQIPADTS
DQEILDLDKA GVKAVRLNLK RGGSAGLDDL ETLARRVHDL AGWHTELYVD ARELDELEST
LASLPAVSID HLGLHRDGLP ALLRLVENGI KVKATGFGRV ELDPTEVIQA IMAVDPTALM
IGTDLPSTRT KRPFEDADLD LIAETVGEDH VDNVFWNNAA AFYLGDQ

> RXA00399 (1-315, translated) 105 residues
MSHNDSPNFA RRALNWLRQG YPTGVPRHDT FALFYVLERE LTEEDLNELA ELLIAEGENN
GLHDNPITRE KIGKLITHVH SQPPEDEDID RIQKKLQAEG FPTRN

> RXA00408 (1-447, translated) 149 residues
MNPVSPKLTT ARYLTRIPWL LISAIVFGVL GVFVSSWFYA GVIVVAVILI WQLWLIPQQV
KRLGWLETSD ELLITKGKLW HTFTVVPYGR IQFVDVTAGP LERAFGMKQV QLHTASASSD
STIQGLPVAE ADALRERLAI KARERMSGL

> RXA00409 (1-1413, translated) 471 residues
MSSLEGFRKV HRATPFLRIW TIIVAVLAAF AFNSGASVLS FIWGVVTGEY GFAVLPILLT
VGGAVIVVAL AWIITGIWWK AVGFRITNEE VQLQRGVISK DLRTARFDRI QAVDLVESFI
ARIFRLAEVR IETAGGSDSA ISIGFLRKSE AEALKRELLD ASQHSVATTP AGVPAEPGVG
ETVVVESAGD VLVPQIPVQR TLASTALSLA TIITAIGIVI LLFVPFGVSI AVPFFVGMVP
AVWNLIDKSW QFTATQRNDV LHVSYGLANR RKQSIPLGRI HAVKLKQPLL WRLVGWWTVT
VPVVGYGDTT QGGTSKILPV GSKELALKVL EAVGPLNSAD IAESADPSHM SRPQYTPPVA
ARLLTPVDRT RQGVTLIGVA GAPGAVVVHE GRFMPRMSVI DTSHIQELTL KHGPIQRILG
LSTVVFNLVQ GPVGMAASDL SAADGKELLN ILRNRKLPAL ESAPLGQNSL D

> RXA00411 (1-675, translated) 225 residues
MNEMILAADW NRLGPTFQTA IIDTLLMVII TMVVAGLLGL VVGLLLYTTR AGGILKNKVI
YTILNVLVNF VRPIPFIILI AAIKPLTVAV MGTSIGRDAG IFVMVVAAIF SVARIVEQNL
VSIDPGVIEA ARSMGASPMR IIATVIIPEA LGPLVLGYTF LFIAIVDMSA MVGYIGGGGL
GDFAIVYGYR AFDNEVMYVA VLVIVIIVQA AQLLGNWLSK KIMRR

> RXA00416 (1-327, translated) 109 residues
TSHYANPLGE FGNRNAFIED LAIRSWNELA DPQQFSDALN TSPWTIPEVF IFRGSIDDPD
AGWKYDVAED LYPNNPNVRF RGVYFNPESF DQMWQTKQVG PFVVVTHNE

> RXA00418 (1-1065, translated) 355 residues
LASYLSPTAL VVAVLAIPLS ATRLYLDGIS VDQGFRTQFL TRMADDIGLS DMNYIDMPTF
YPAGWFWLGG RLANLLGLPG WEAFQPWAIV SMAVAASVLV PVWQRITGSL PVATGIALVT
TCIILAMNSE EPYAAIVAMG IPAMLVLASR IAKGDKFALA GGIIYLGVSA TFYTLFTGAI
ALSAVAVCIV VAAIVQRSIK PLLWLAVLGG GSIVIALISW GPYLLASING AERSGDSATH
YLPLEGTQFP VPFLASSVVG LLCLVGLIYL VVRFHNNEVR AMWVGIAVFY AWMGMSMAIT
LLGNTLLGFR LDTVLVLIFA TAGVLGIADF RLASVYQLYP TQITERTATH LTNLI

> RXA00422 (1-423, translated) 141 residues
MPTNYARDNV ISLASAREQR SGKPEPKPEL TLIVRATNVQ ADGEVHRQIG LNSAMSLDEL
HNVLNIVFGV GGEQSPWRFE DQFHQPSAPD TNLGELLPEP GDFLFYFWGL WQFNLQCVEM

YPRDNGTPRA LCIGGSGGLG D

> RXA00423 (1-453, translated) 151 residues
MTYPVLSVLD NSGDHNIIWH VQTYPAALPT GAWIADEQQL TDLLKDTVVF LTPGSTAPEN
APVATIEGVR VDVDKQVAEY NKHGIRLPSL GARTVEAQYR GEPEAEAAWR TAMELVEIAG
GWLEIEAKRR ARKALAEAFG AEVQPLPLDT E

> RXA00424 (1-471, translated) 157 residues
LQVAAGSALI GAGVAVNDYV QSPVRRAISY GALALSGATV IAMGQDPTGE RSIIAKDSAT
MVDQIRQEIG DLGVTPGPES DVDAITERGP LVTWLLLAVF VVAFFTLAYF SMRMDVAVMR
RIAKFFEKRG ASRPFTCTGM VYAAFIYAIC ELEARTK

> RXA00425 (1-225, translated) 75 residues
MFERFKKAKA PEVHIAAERT NLPLNDFMTR LFAQELPLLD STSRSEVYRL LREYDGPTIS
SQEEIPAEIR ELMDL

> RXA00428 (1-633, translated) 211 residues
MPGLVLSTNV AHIQQDPGGD DRISGINKLP VATGIDVFIP GPNYGDGSGV VGDAIGDSLH
HGGAHKAIYA YSREELDFFD PTYRNGYFGE NLTTSGIVLE DLLINQQVRI GTTLLEVSIP
RRPCRTFAHW LDIKGWLKTF TQRGLPGSYF RVIEEGHINP GDPIEVLQAP DHDITMSMAF
RAKMGNKDLA RRVVAANCLP ARYHEELLKL I

> RXA00429 (1-402, translated) 134 residues
MKTFNPTMIA GLIGVLYFVL LTLIFSIQDM ELAAEIAFGI VTIVGLIAVW DNFRDRNNST
WKTWTGLVGG LLIAVPGICL LVGNLVLLAV DGNPSTMVNT LLSVAGIGAI FLLPIGIIMC
LIAGFNRYYA ALKV

> RXA00430 (1-411, translated) 137 residues
MSLKTQAFRF ILTGGLSAIV DLGLLSLLQL VFGLPVPVAR TISFIAGTTT AYMINRRWTF
QAESSTSRFL AVVALYGVTF LINIGLQTLC SALFENWGWN EAVAMVVAFV IAQGTRNGHQ
LHRPKNHHFP SEVRYPS

> RXA00433 (1-525, translated) 175 residues
MDVLKIAIIA AAMIGVPVLV VFLIVFAVHK LAKEVPRSGR RPGIGLGLLL GFVAGLIVWF
VWLSWGGYYE NEFGQMQGPY RPWQVVACGV TMVAVTVILG LWTRWTASGP FYSALGGASG
FSFAWAMDAI PQDETGLSAF GLVMVIVGVG AGLNVVATLT SIGATIWNNR LPSNA

> RXA00447 (1-300, translated) 100 residues
MLGSLWRFAV RTAAGAVALW VVIKLIDGIS LSFPTTPLYQ DGQHDNLLTF LAVAAIIVVL
NATVKPVLKL LGLPLTIITL GLFSLVINAV IMLLAEYVSD

> RXA00451 (1-492, translated) 164 residues
MNTEEDGLSF AVTATLVEGK WQVREFEDHF SKLSTSINAV RSLRSEGPAF ALLCVDDEYF
VMVRPTPSRV FLFLSDAPMA VDDDFAAAVM DELDADLPDI NPDDLDDIDP WPEGDFDILA
DLGLSEEVLS VICDDMDLDP SEQLLRIAEE LGFDNDLARV VGFD

> RXA00455 (1-618, translated) 206 residues
ILLALFVAVF LISNITATKG VEIGPLVTDG AFFLFPISYV LGDVLAECYG FKSTRRAILT
GFGITMLAAL SFYISIWLPG ASFWEGQEAF EATLGLVPQI IVASLAGYIV GQLLNAKVLV
AIKKRTGEKS LWARLIGSTV VGEFVDTLLF CAIAAPVIGI ATAPDFINYV VVGFVWKTLL
EVILMPITYA VIRWVKRREG YETFDA

> RXA00457 (1-1080, translated) 360 residues
MTIALEHPVL HSTAIALPAR FQASYTTRLV AVGVDKRPSD FWLETAGTPQ AGDVVIARVT
AINNHKRVET PESRKAILFE GVLVMLAYGH RYAADQFLAH VPEDLGPCHL VAAGGIAGTV
TALHDRVDEP TEIEPLGLLT NARGTVNVRD FAAFDNPLKV EAPNKRAQVI AVLGTSMNSG
KSTTLACLVN GLAAAGQKVA AGKITGTGAG NDRMIYHDAG AHSVIDFTDF GYPTTFKLNF
AEIRALSVNM INVLADSGAD TVIVEIADGI YQGETSRLLR DQVFQEAVDH VVFSAVDALG
AKAGVQELQA AGLHVAAASG VMTASPLATA EAAAVLEVPV VPTFDLTNPE IVTAVLTDHA

> RXA00462 (1-1380, translated) 460 residues

MEAIAILFVI GAILVVAVIV LGIFFLTSRT WIKVAAADEA LIVSAKKKGE SQVIVHGKAV
VMPITQTHQK ISLRSRQVNM QVTAQSDDNV TLNVEAVALV KIGSEAEFIR RAAQRFASSD
KEIVRFTQDQ LEGVLRGVVA QQTVTSLMRE RKKFSEQIAE TVIPELEKQG LILDSFQIRG
ITDDVGYIKS LGAPEIQAKK QAAEIAETEA ARAIAKSRIA NQEADLVEQT QLDANKAAAD
AQVGEARAQA MQAERLADEK ARLEVLRQQA ENKQIELEAE VNKVADAERY RRKQEVEADT
FEQTRRAQAQ VEIAEAEATA AKVRAMAEAE AVRLKGQAEA DAIKAKAEAY RENQEALLAQ
QAMEILPELM SNFASGYANI GSMTVLSGGE GSENSVGSRF AGEQALGLKS IIESVKQTTG
IDLAEIIQGR AAGHAQGSAQ GAAIAEALSR DETVEDRSEK

> RXA00463 (1-822, translated) 274 residues
MQTTTGETSI SNETSFNASR ETSLTALGFL DYLDEEQRAA LLGEGLDIST LTWANQVTAL
RVLESLFNEH AYELVSAVIQ HVAQEPGDNP HHFLKFSPEP STENSWELTL DGPTVGLKVT
FDPDGQITFK DAHLGLSPAE VVSVTEALDT SYSESQIKKA AEQLVGSLNP TQQAALQGSG
LRGAQLTEEQ KTLFLKMTSN WIDLANGDSG SEQQEEIADT FSDTYIIWNE QKDGSAFFQM
KGPELDFSYK ESVPENAELS ARGVPNIQTS FQSP

> RXA00468 (1-819, translated) 273 residues
VKVVDAQVVM GPTHAMSGAA VGLAVAQILP AEWGGVTTAT EAFIYAGLAA GAALLPDLDS
PQATVSRSFG PITQVISRFT ENICQTFVNV TRGRKDKHCN NGHRTLTHTV WSAAATGAGA
TALIGAYGKP AVIGLLFFFL GLAIRGLMPE WSKNADWLLV TGASAALAVG VWNYAPESSF
GIVLGSAITV GSLTHLAGDM ATKAGIPAFA PVIPLKGKRW WNLKLPKFLS IRANGPADKF
LLFVFSVAVI IQIGLVSSGN MSTIMMNLLS PAL

> RXA00469 (1-1176, translated) 392 residues
MSTFQEPHHN QGFIPFAQPG YEAPTPHLAT GTFQQMWQTR PARIPAKQGG HAKVAGVCEG
IGVRYQIDPV LIRLFFVVTG VFGAGVAAYL IAWLCMPRYS VPVSPIEALW TPGHTKDRNH
GWWLVIAFFM FSGVLSSGAG GISGPAAAIT YLCLLAMWWA LHKKQPLPPR GLLTTEFTVS
EDATMKNEDL YPRPQPDLST ITPVEGYYAP FAQQTPEAPH WDPLAQNQYN TWDVQVPPQK
PQKKRHVWPW IVGGVVGTGV VMSALAGLFI SNIDPIYFED DPGIGDVNLI PTNDELLSSY
TSGVGEMNLD FSNLTQLDQE QNVQITSGIG EVMVTLPDDV PVSLSCSAGV GTARCDVGDL
AAHNADLEGP MLNLVVNSGI GDVKVEFADQ ND

> RXA00472 (1-861, translated) 287 residues
VSSVATKTTS TLPEMNSAVS ADGVTITIDS AFTTDSVEME SLDRPSGDIQ PEMSREDGIF
VVVETTIKNE SGADMDITCA STGSTVYAEI STNQEAVYQP IRDLFLIPGN PECNHNLGSG
FDAPMTWVFQ IPKDATAERF GFTHSELGDG KLTWIALNDL SNSEPATEST MRDEAAIDPS
TPQQTPVQET VISQNTIETP VAPAPAVPAY GASCPVSMLQ QPSQAADGSA LVCIYAGTPN
PIWVYGPEPL GVGTATPGGA CEGYEAGGQD ASGNIMMCSG GQWVYGP

> RXA00473 (1-765, translated) 255 residues
LWGDGTPVSL PDLSGLSRAE RIDALRSRMS TMGAAVPKFE PSVEESAEQK QDSLAEKQDI
VAVPSAFSDL FPGDGLPRRA VTQLVEQPLV VVDFLAHITA QGGHAAVIGW KDLAYAGVID
SGGVCENIIA IPNPGTEPLN VAAVLCEGLD VVVYKGPEIS LSPTRARPLL GKLRQGTAAL
VMVGTKVSSP ALSVDAEITD YVGIGAGSGR IRGVEMQVRA VSKTHGVRSG KVLISRPQDA
ALLEPEQPTT LRAVP

> RXA00474 (1-1578, translated) 526 residues
MALWFPDWPV QAVHLDEDAP AHNKPVAIAA HYRIQVCGVA ARKRGVRRGM KVRQAQAVCP
ELEVVDADAD RDARMFEGIV ASLGEVASSV EVLRPGLVAV DAGAAARYYG SEDIAAQMLI
DAALRQGIDV FAGVADEITT AVIAARANGG TVVKREASRS FLQQQPLGVL AAEEALGCEA
EVVRALADLG MRTLGELAEL PVEAVATRFG NAGLRCHNIA RARHDRKVAP PITHADWEVS
HVPEEPILRV DAASFVARNL ASRLHQLLSK GGVVCQLLKV TADFSTGDTV SRIWRTGEPL
TEQATADRVR WQLDGWLTAR GVHSDDPNEH DGITALWLIP LECVPPDMAS GGLWDTGRSQ
QHVARQVIER VQSSLGVDAV LQPVPAGGRG VEERIHFVPY GEKRDAIRNP AGSWPGKIPG
PLPARLGGGI NHPASQVTMI DTEGQRIYVT AEALLSSSPY ALSWGPARYL ITGWAGPWPV
DDRWWEKNGT KYARLQVVGR AVSEERQLNA WLLMWKDNKW RIEATY

> RXA00475 (1-660, translated) 220 residues
VTQGYGVCMI VQPTSHSKHR ARLKTLAIVG ASALTLAGCG TSNSTTNDAS SVTQTMSATA
DGAQLSNEAS TGPTALGEAD VAMKTLRPDA PAQLMVTDVR IGSHSGFDRV VFDLTGTGTP
GWFIDYTSNP TQQGSGNTIN FTGDTALNVN IDGTVYPFDL GLEDPEIGTV DGSGSIVTQV

VSAGTFEGRS QFVIGLNGKH RYSVTELQDP HRLVVDVLAQ

> RXA00476 (1-861, translated) 287 residues
MTLRCSDVNV EPLPGTAKTG SGFVLLEHAG SWSRDVLDGG TFDPELTDQL KRHLKASGMG
LQLIRKPGRE GRNVEKHNLF LVFAEASIIE HLVVDAPADV LDLDLSGPGK NNAQRMDDPM
LLICTHSKRD VCCAIKGRPL AAAVEPQFGP LHVWEASHTK GHRFAPSMLL MPWNYSYGLL
DEAETVQLFQ GALDNKLFLP GNRGRGTLDA RGQVAEIAVA EAFGEAVAPA SLQVEFEDDS
VLVTHPDGRT WVVELERIEV DGVVSSCGDQ PKTGKAWVAR QVTELIG

> RXA00481 (1-585, translated) 195 residues
MLNMQEPDKI HPAEPTLRNI YDVKTSDPKS ELVDRSGMSE EDIAQIGRLM KSLASLRDVE
RSIGEASARY MELSAPDMRA LHYLIVAGNA GEVVTPGMLG AHLKLSPASV TKTLNRLEKG
GHIVRNVHPV DRRAFALMVT DATRGEAMRT LGKHQARRFD AAKRLTPQER EVVIRFLQDM
AQELSLNNAP WLNTE

> RXA00485 (1-2043, translated) 681 residues
LPQGPGEIAV TTAPGAPEVG EHVSIRLSQN TEDTEVLVVG VVEPAAQETL GGAPFVVASP
DALMEWNSSG VRGEFRVATS DPASLEAASF SDATVVVASA EGHVDKLADS YLGQRDRYFL
LLAAFVAVAA AVAFLVVFSA YSVLTGERVR EFGLIRSVGA STPQILGSVI FEAGILGVVA
AGFGAPAGLM AARLLADNAA RFGIRVPIDV IDLPSSTMWL IAGVGVVMSV IAALPAVFSV
CRKSAVESLS TPAISRTSPW FGALWLLLAG IVGAGGMWAY EATSDYRGMR SVALSIAGSG
ALVCALLIAT AVLVPWLLHV FSRIVGGTVP TLQLGLAFAA KQKSRSAALI AVILAGSALS
SAVLHGQAHI GTHLVAVAKG MGGTDMMVTA LDGEIPAGML EEISSIDGVK TAIAPATTAV
ELEDSGNFSV LMLAEEDGAS VMRAGDTGAP AGGLVLGRNS PDQDAYPAGQ AANIIVADTP
TQAEIFHSDN YFSMIDPALA TGPSTTRNVL ILLDGDSNQA PDNATAQAVR KTISLFDGRY
SITEGFSARQ NTFELVSRIT TMSTLLAIVA LAIAAVGLIN TVALTISERA RDRYLLRTIG
LTSTGQILVM AIEMIALSLP AAIVGAVSGG FLGRFVASSA TNTAATAPLQ VDILGGTVLA
MVAGSVLCAL IVLANKRRRV V

> RXA00486 (1-702, translated) 234 residues
HAIMAAVDHA RAAVLDSLSE VSGTLKVTSF QSLLFTLAPK AIARLTEKYP HLQVEISQLE
VTAALEELRA RRVDVALGEE YPVEVPLVEA SIHREVLFED PMLLVTPASG PYSGLTLPEL
RDIPIAIDPP DLPAGEWVHR LCRRAGFEPR VTFETSDPML QAHLVRSGLA VTFSPTLLTP
MLESVHIQPL PGNPTRTLYT AVREGRQGHP AIKAFRRALA HVAKESYLEA RLVE

> RXA00490 (1-903, translated) 301 residues
MNKQSAAVLM VMGSALSLQF GAAIGTQLFP LNGPWAVTSL RLFIAGLIMC LVIRPRLRSW
TKKQWIAVLL LGLSLGGMNS LFYASIELIP LGTAVTIEFL GPLIFSAVLA RTLKNGLCVA
LAFLGMALLG IDSLSGETLD PLGVIFAAVA GIFWVCYILA SKKIGQLIPG TSGLAVALII
GAVAVFPLGA THMGPIFQTP TLLILALGTA LLGSLIPYSL ELSALRRLPA PIFSILLSLE
PAFAAAVGWI LLDQTPTALK WAAIILVIAA SIGVTWEPKK MLVDAPLHSK CNAKRRVHTP
S

> RXA00491 (1-420, translated) 140 residues
VYWVLATSAN RVEDVNFDAM MPRDPFADDP NDPASFITDD DPYDHPEPLS EEERIHVSQD
LRLVMEFKKV LGPRGIEGVF FMCEDCEEFH YYDWDIMAAN MRATLAGELS PVHEPSAQPN
IDAYVPWDYC IGYLDGLEAK

> RXA00493 (1-324, translated) 108 residues
FEGDQKVGVR ALATALGKPA YWIASNAGLD GSVVVARTAA LPNGEGFNAA TLEYGNLIND
GVIDPVKVTH SAVVNATSVA RMVLTTEASV VEKPAEEAAD AHAGHHHH

> RXA00496 (1-402, translated) 134 residues
MTRRLHGGEQ DGQEHVKGQL KQLFDDDAFL TDLSRGVDPS EGDDALAGLL LDLTKEAQEP
PATMPDWSTL LPGILDQDQD LPVESTSDTT VMQASNPATQ EFAPVSISDT PNTATNSADA
DESATVVPLA ARRE

> RXA00504 (1-246, translated) 82 residues
MTYGFLVNTD LTHRAIDFDL ENAAKFLGGA DDGRVAVAFQ EDGTLYAALY SASAKDEGAA
ANPVASLGRN AAATGDGSFF SD

> RXA00505 (1-252, translated) 84 residues
DLIHMDAYRL LGEDSEDADP IGALDSLDLD TDLDLAVVVA EWGGGLVEQI ADSYLLITID
RETAVQEDPE SEARIFHWEW REGR

> RXA00506 (1-1341, translated) 447 residues
VLDFLAANPL IALVVILAVG LAIGQIRVFG LSLGAAAVLF VALVVSTANT DIVIPMIVYQ
LGLAMFVYVI GLSAGPAFFS EFAKKGWKLT IFMLLLLATL IGLAWVLIKS LGLDAAIGTG
MFTGALTSTP GMAAVVELIE GIDPSLASEP VIGYSLAYPG AVLGSIVVAA VGAKLLKVNH
REDARKEGMI TAPLVWKGVQ LKPGITGRVG DLPRLAGESI IATRIVDDPH THRLADPDLP
ITEGMELLIN GTEEAVDRAI KALGEERETK IEDTELIYTR LTVSSPEVAG RTVAELDTVA
HGFMIARIRQ GDSEVVPKPD TVINYSDRIR VVVAPGRVAE VRRFLGDSEK SLADVNLLPL
AIGLSLGLLL GAIPIPLPGG TTMSLGFGGG PIIAGLILGA LKHTGPLTWQ MPFHANRTIS
TLGLALFLAG VGTSAGAGFR AALTDSS

> RXA00507 (1-855, translated) 285 residues
VAENLNKHLS KLSKRGPHRV LVGDMNYAGI PGKIYTPAEG DGIPGVAFGH DWMKSIKYYH
QTLRHLASWG IAVAAPDTEN GFMPDHKGFA SDLESSIQIL GGVKLGSGNV TVNPACLGVV
GHGMGAGAAV LSAANRDLVR AVGAIYPAKT SPSAIDAAFA VKAPGLVIGS SSLGLFESGE
PAKLAANWAG DVCYRESEKG NQQGFSEDTM FKLVAGIGSP QTGAQETVRG LLTGFLLHQL
AGEKKYKAFS EPDAEAKKVV SYFGQELQEH AFPKDTSPFA FLNEK

> RXA00509 (1-177, translated) 59 residues
LVDVELSAAL LDPPELPELA VLELEPPEEA AAEEVAPPDE PPEAALHNGF GSVSQTCFP

> RXA00510 (1-531, translated) 177 residues
VEKPVEKTPE KPVEKPVEKQ ECEEKPDPDP EXMQXXEPVE CEPTPKPETE PEPKXDTHAX
XPGTPTPIPX ARXLRIXXXX XQGXXGTDSX XXXXXESEEC APELNDVPEE SDLIGQLIKG
AIGIGIVVVG VGLLVNFLEQ CVPVIEEVPV PEPEPIPEPA PQPEPTSVKP PESELDK

> RXA00515 (1-480, translated) 160 residues
IESYIAQDDN APTAAELQVR LDAIESGEGL AMLLPDDPTL ADPNAEESFK TEYTYDEAKD
IISGFSSDPA SDVLSQLQQA ATTGTRTAEI RAEVFADRTD DYNESQTALK EDFQNCIDAI
DDARPIPLQY ILIGGAIALA VIVLGIRAWT NSRKQSKHSQ

> RXA00519 (1-513, translated) 171 residues
MAGGGLFETG AGGSAPKHVQ QVQEENHLRW DSLGEFLALA ESFRHELNNN GNTKAGVLAD
ALDKATEKLL NEEKSPSRKV GEIDNRGSHF WLTKFWADEL AAQTEDADLA ATFAPVAEAL
NTGAADIDAA LLAVQGGATD LGGYYSPNEE KLTNIMRPVA QFNEIVDALK K

> RXA00520 (1-198, translated) 66 residues
MRFSRVLPAL LITTAVSIPT ASAATLTGDT DKELCIASNT DDSAVVTFWN SIEDSVREQR
LDELDA

> RXA00527 (1-1764, translated) 588 residues
VIATSDVREI SSEGIVARVS VNGNIEAART TTIYTSLTVP VANLPVAVGD RVAADQVLAE
LDASALQRQL DETDANNARA AMANRNSIAQ SQQAYEQSRE LLDSGLSPEI NSARSSLRAS
SQAYQDAIRS FEAKQRDVDG GLDSTMVAQS DALKAAREQA DAAEIERLRA DFGLLNNDRS
NLNDVIGLLD ERESLASAES ELAQARAAGD LEAVAAAEAK VAGLEQSIAS KTSTWPSQDQ
TYLQSYTALE EAERRVASTT EALEIAERIY IDSLGKVDSE LAAAQRAVAE AHSAQQDAAL
GLETAQLSTQ HQLEAQSSAI DAALGLASVD NEAATRSTSQ LRMDINNTTV RSPYSGIVSS
VQAAQGQPAA GALLSVADDS ELKITANVKE AEISNVTIGS RVTFTTPSTG TKEFAGRVSK
VSPIAAAASA PATGEGAAAG ATTTNTDVTF PIEISVTGDR EGLNLGGSAR VRIVHEIAPH
VLTVPLEAVY KNDDGKDAVL IISDDNKVEE VEVKTAESDD FDIAVSGAGI SEDARVLTQP
GNYRGLIGET VKLHADTVEQ AAAPFSPAAP FDPAAPAVSA KQTVGQVI

> RXA00528 (1-1089, translated) 363 residues
MSTSTIRVAI AGVGNCATSL IQGVEYYRNA DPSETVPGLM HVKFGDYHVG DIEFVAAFDV
DAEKVGIDLA DATEASQNCT IKIADVPQTG INVLRGPTLD GLGDHYRATI DESTAEPVDV
VQALIDAKAD VLVSYLPVGS EEADKFYAQA AIDAGCAFVN ALPVFIASDP EWAKKFTDAG
IPIVGDDIKS QIGATITHRV LARLFEERGV RVDRTMQLNV GGNMDFKNML DRNRLESKKV
SKTQAVTSNI PDGPLSGKVE DRNVHIGPSD HVQWLDDRKW AYVRLEGTAF GGVPLNLEYK

LEVWDSPNSA GIIIDAVRAA KIALDRGIGG PIMPASSYLM KSPPEQLPDD VACERLEAFI
IEA

> RXA00529 (1-543, translated) 181 residues
MKLKWIAPIL PVLALAGCGN YVNVESQGKS GISHDEDGNI SVHMYICGDN AVDELILSGG
FYDGPPGTNN PALGMLKTSN PESGYVVVNI ADPAPWEVVE PINLPTEQGK YIIANPRLVD
KGWPIPFAKE KYMPSVSTSV GMLEGIDPGL VMRDMYTEST HVFGTAEDFV EAGQQWCEDY
F

> RXA00530 (1-1281, translated) 427 residues
MSIGFDRDLY IKMQSQHINE RREQIGGKLY LEMGGKLFDD MHASRVLPGF TPDNKIAMLT
ELKDELEILV AINAKDLERK KTRADLDISY EEDVLRLIDV FRELGFLAEH VVLTQLEDDN
YQALAFKQRL ERLGLKVAVH RVIPGYPTDA RRIVSEEGFG INEYVETTRN LVVVTAPGPG
SGKLATCLSQ IYGDHQRGIK SGYAKFETFP IWNLPLEHPV NLAYEAATAD LDDINIIDPF
HLAAYDTKAT SYNRDVEVFP LLKTMLEMLS GSSPYKSPTD MGVNMVGSAI IDDAACQEAA
RQEIVRRYFK ALVDERREEQ DDTISARIAI VMSKAGCTVE DRRVVARALD VEESTGAPGC
AIELNDGRLV TGKTSELLGC SAAMVLNALK ELAGIDRSVD LLSPESIEPI QSLKTQHLGS
RNPSPAH

> RXA00535 (1-717, translated) 239 residues
MWWAGMSTAM LAYFLQTVAL GFGTLLVVQP VLVLSLMFTL PLSARFNGYR LRRTEIFWAT
LLTVAVGIMI VLGRPLPGNP HPPLDRWIPV LLVGVAVMGG MWLLAEYVLK KDKALILGLV
TGALFGYVAV MSKAAVDLFV HQGITGLILN WEGYGLILTA LLGTIVQQYS FNAGELQKSL
PAMTIAEPIV AFSLGYLVLG EKFQVVDWEW IAMGIALLVM IVSTIALSRT STMPAGSKR

> RXA00540 (1-243, translated) 81 residues
VARVVVNVMP KAEILDPQGQ AVHRALGRIG VSGVSDVRQG KRFELEVDDS VTEADLKKIA
ETLLANTVIE DFDVVGVEVA K

> RXA00546 (1-690, translated) 230 residues
PVLGGIFQWI CGIITRFLYP VVDVIPFHTL PESGLYFIVT ALALAFFWVL VIRMMVELTG
NRVWDTVLVA ASPLVAVHAF TNWDTPAIAA VIGAMLAVKR GNPLVAGVLI GAGTAFKLWP
LYLLGAYLVL AVKNKNLKPF ITMAAAAAVT WLVVNVPVMI AYPKAWNEFL RLNRERGAEW
TTIYQVIDRN LPINLNDPVL LNVLSFGLFG ASVCGHFDPW AQGAAHSPSR

> RXA00547 (1-414, translated) 138 residues
VAILILGLKV QRTPRVAELA FLIVAAFLLF NKVWSPQYSL WLVPLAVLAF PQWKVLFPWM
VTDAMVWPIL MWHMLGTDNK GLPHEMLDLI VISRDAFIVV MISRCNPADA RTTCKSGDGC
ARRARIVGRA LRRKRSVE

> RXA00549 (1-396, translated) 132 residues
LTENGETPYE GIILGQYESR PLDMASAMAT IANEGVWHRP HFVSKVETVS GEVLYEFEDG
DGERRVSEKV ALNLLKAMGP IAAYSNGNAL ADGQVSASKT GTTQLGDTGA NKDAWMLGAA
PQLATAVWVG TA

> RXA00550 (1-321, translated) 107 residues
MYGSNSPATI WKQTMDNALE NSPLETWDIA PALGYGNPPV PEYVWTPSPN IATNDPEGAT
EEAPVEDPNA VIDTPAVDPT APAEETGNGQ VEILPGLTIP GDLLGIG

> RXA00552 (1-717, translated) 239 residues
FKWSEGGAED FPKLSVKVRD EIVAFGAPDE LKVDENGVVG GGVHLKPQQV NELVEARGDE
VVFFDGRNAM EAQIGKFKDA VVPDVETTHD FIAEIESGKY DDLKDKPVVT YCTGGIRCEI
LSSLMINRGF KEVYQIDGGI VRYGEQFGNK GLWEGSLYVF DKRMHMEFGE DYKEVGHCIH
CDTPTNKFEH CLNEDDCREL VLMCPDCFAN VETRHCKRER CAAIAADFAE QGIDPLVTS

> RXA00553 (1-321, translated) 107 residues
MSIVKINAIS VPEGAGEELE KRFAARQNAV DSAPGFEGFQ LLRPVSGEDR YFVVTQWADE
DSYNAWRDAE KAKGGHGQGA HGSDKKPVAS GASLLEFEVV LGSTGAK

> RXA00554 (1-471, translated) 157 residues
MNTQPEHPEN DLVDEADFSN RPRIYSDDPD SLADAPDPAL EHEKNKKSSR QALIYLLQVP

LVTFVSAYVL AWVSRLQGGP ICDAGEAVWI CSRAAELWWP ITTSVIAFGG MLGSAWILYD
KYRNYLRWRP WMGVLWILIP FSMLWGTSVL TLSILGH

> RXA00555 (1-891, translated) 297 residues
SGGKRSEQND AVFEFAAWLA RTSDINVRGI TTFIRPWPSS SISKLGGKYH KWYKNLDSYY
RSRTIKGLKE AGVEKSQWDD DVSVFVDGPS ESTLLTHAAE EFEADLILLG SDATAPKGRF
LASSTADALL HSSPVPLGLV PRGVKLSKKG VTRVNYAFTN ESDDFEQGLR SSAELATNWN
VPLRILAFSP TGITSAPTSR SLDISTELSS EWRELTLAML DRARDGVLTD HPNLSVSSET
GSGWGWSGAI DALRWKKGDL LCMGSHRTDT LSRVFVGSET MEIIRNSPVP TIIYPGL

> RXA00560 (1-237, translated) 79 residues
MRIDPLETRQ AVLAVKDWIE GEGDVKKPGR AALAAATRLS VRLLAQHAPG NSVEVRVPPF
VAVQCIEGPK HTRGTPPNV

> RXA00563 (1-2739, translated) 913 residues
FYKDLYARSA RGTAALWIVA ANLSSYSDID AIINWVGSEQ TTTVNGASKL VKPALVPTLL
FPFAAPRVSG SMADAGPQAE SQMRLLLWSV ERLIAGLAPL GSSINVGHRL HVVIPGSPNR
GRFGGDGAYG ESKAALDAVV TRWNAEQAAW GAHTSLVHAH IGWVRGTGLM GGNDPLVKAA
EEAGVETYST QEIAEKLLSQ ATSTVREQAA SAPITVDFTG GLGESDLNLA EMARAEAAKA
ANAPVVEAPR TVAALPTPYR PVVQTTPDFA GQVTQNLDEM VVIVGAGELG PLGSARTRFD
AELNGSLSAA GVIELAWTMG LIHWDEDPKP GWYDDSDDAV AEEDIFDRYH DEVMARVGVR
KYNDMPEYGM IDNFAPELTT VYLDQDLTFN VGSREEALTY VDSEPELTFA SFDEAAGEWK
VTRKAGSAIR VPRRMAMTRF VGGQVPKDFD PAVWGIPADM VDNLDTVALW NIVCTVDAFL
SAGFTPAELL ASVHPARVSS TQGTGMGGME SLRGIYVDRI LAEPRANDVL QEALPNVVAA
HVMQSYVGGY GQMIHPVAAC ATAAVSVEEA LDKIRIGKSD FVVAGGFDAL SVEGITGFGD
MAATADSAEM EGKGIEHRFF SRANDRRRGG FIESEGGGTV LLARGSLAAD LGLPVLGVIG
FAESFADGAH TSIPAPGLGA LGAARDGVES RLAVALRSVG VSADEISIIS KHDTSTNAND
PNESDLHERI ASAIGRADGN PMYVISQKSL TGHAKGGAAA FQMIGLTQVL RSGLVPANRA
LDCVDPVLSK HSHLVWLRKP LDLRAKAPKA GLVTSLGFGH VSALVAIVHP DAFYEAVRVA
RGAEAADVWR ASAIAREEAG LRTIVAGMHG GVLYERPVER NLGVHGDAAK EVEAAVLLDS
RARLVDGVLR AEG

> RXA00564 (1-405, translated) 135 residues
MKYNVDVSRE SEDWLATVTN LEGVSTWATT FANLDRNGRE AIALAEDLPE GAESSLTISW
SVPTDSHPEL DTAIQIAQQR RYLVQAQQDL EPKVRSAISA LTQAALLGMT AGRVSPTHNP
GSRAISLDQV SGVLN

> RXA00573 (1-651, translated) 217 residues
MLVRPCGEQA VIIDLLAEDA EAVQGSILDA VLALNRSLVG MQVPGIIDTI PAAQTLLVTF
DTKQITPNRF AEIVDSIALT PAAKGAAELT DTIEIPVVYD GPDLETVAQH TGLSVEEVIA
THSGTVWTAA FGGFAPGFYY LIPQTPLWDI PRLESPRTKI PAGSVAVAGE FSAVYPQQSP
GGWQLLGTTE IPMWDVDRWQ PSLLKPGDSV RFVQVKK

> RXA00574 (1-879, translated) 293 residues
MSFKVISTGP QAIFQDRGRF GFASAGVGTS GSFDRLSAAR ANHALGNDPN ATVVEILLGG
FEVEALHTTS IVFTGTEAEV MVRTAGGQSK NATTNTIIDV AAGERIRVEP ATYGMRAYFA
ARGGFAVKKT LGSASTDLIS HMGPCPIEPG DVIDVATDIA DSQWWPKLRQ LPTLWKRMPT
ETLTVIRGPR DKWFTQESLN NFFTQVFTVS NDSNRIGLRM HSSEPIQHRV EGELKSEGMV
RGSIQIPPGG NPVVFGPDHP VTGGYPVIAV LTSRSCDRSA QLLPGDKVRF KLL

> RXA00576 (1-672, translated) 224 residues
MLTLSFITGT EPGKWFTRFR DRTHHGGLET LDSDDALGLM LAGQAQLALT RLPDARIDAS
LHVVTLYQEQ PGVAFPKDFF LSAEEGAVDL ADLDGEIINW SMPDSGEVDA AAVRDALQIV
AANVGVVIAP RPLLKVLSKK LVEHRDIKGG TETSIALVWK KDEDSEEIQD FVGIARGRTR
NSSRQQTVKL SAREKTLAKQ ARRQGEKPKT PKRPQARKRP GKRR

> RXA00577 (1-348, translated) 116 residues
MKPQTAAKKL GLFLPATPEE FQTGALTHQE FKNLQENPPE WLQTLRREGP HPRPVVAQKL
GITIAALKKN DMDKPLTTAE IKALLENQPE WLRTARTQLA EGRETAKKET EETTED

> RXA00578 (1-723, translated) 241 residues

MTYLVWDGAT LVEGALESTP TVVDSYLAKD HRVVRWDLHE QRFATSVDVD PWDFLHAVRE
AIPRQGSWFP KVEWHGDDLF AVNIRPAPTL RKATSLWLSE DPDPRTQPTI KGPDLDVLAH
LRSRANDNGC DDALLISADG FILEAANATV VFWADPQTVI VPRGDVLPSV TLAATIPLWE
KAGITLRYQN IRHIGFPAWC GSSLHGWTPV VSWGRGLGKI AAAKAPSVKP WNEKLRPTIF
L

> RXA00582 (1-519, translated) 173 residues
MSDYIVAFES AYGSTKQYAE SLAQRLGVDA LNFEQACAEL AANPTAAIVV LSFVHGPSHP
GAKFITDTDL SGHRVALCTV GMTLDDVVQK KDGAARSLGN KADDVTRFYL PGRLNYSELS
TAHRTTMWTI VNMLKAKPLK NDNDKMMINT FDTDVDRVDE SRLDAVEEWA RGL

> RXA00585 (1-318, translated) 106 residues
VIDLSPVFNT AAGVYNDTNA IILAQQQQGG PLGPEFGKAS PVGLLLIVAM LVAILVLGWA
FHRRWSRMNR RRIFAERNGL DPFDIEGVRK AMAEAGLNEK SKKGFL

> RXA00586 (1-882, translated) 294 residues
MKHVSGLRLM AIHAHPDDES SKGAATMARY AAEGNQVMVV TCTGGERGDI LNPAMDKPGI
LDNIFAVRQE EMAKAMEILG TEHRWLGYED SGLPQGDPLP PLPEGCFALE DSDKVTQDLV
KILREFRPHV IITYDENGGY PHPDHLKVHE VSMLAWEKSG DAAYAPELGA PWEPLKLYYT
HGFIRQRMEM FHDLLIEQGK PSPYTPMLER WKANEADVMA RVTTQVPCER FFDQRDDALR
AHATQIDPAG AFFGTPVEVQ RRLWPTEEFE LAKTRVKTSI PEDDLFAGIT PDAE

> RXA00587 (1-483, translated) 161 residues
MSTNSNSPSN ASGASNIPNT QRPASRYNSP RPEAAAGRNI SGKIIAVIGV LLVIAIVIVG
ANFLKNRDAQ TVSGQMGSFE RIDDDTFRFE VDVTRDDPSQ VAYCIVTAKD YSHAEVGRRE
VLVEPSDHST VRISTLIPTR EPAVSGGVYG CSTVIPSHMN L

> RXA00589 (1-363, translated) 121 residues
MTTLSRKFFV SATTALAAVA LVACSPNEID SELKVPTATG VSLPSKNVSA TSTATTDEDA
PGYIDCVAAP TQQPAEISLN CAMDIDRLTD ISWSEWDTDS ATGTGTRIVT AANGQETETE
D

> RXA00595 (1-330, translated) 110 residues
RNIAAWIAIA AIIIASLGAL LSMIRVWREV FWGGAMHQRG VSPQLRISPA KIAPALSLII
LSVGMFIFAG PLIDATLTAT DGLLNTDAYQ QAVLGENAIG VPSPSYQGGN

> RXA00597 (1-270, translated) 90 residues
MTAFGIVTTV GICMFAFSLL SALVLILRTK DFLTRVVLSD MVFYSMIAIY LIWVLNNPTS
IAFEIALLAA VLGGVLPTLS MARIISKGRR

> RXA00598 (1-318, translated) 106 residues
MTIPEIIVSI LVILAGLFSL GTAIALWRAP DPLTRANLLG TTVGVSIPLL IIALLIHTWS
VDGFNPNNFI RAIIAIIGVW VIGSVGSYYM GRAIYGVTVV DNRRSK

> RXA00601 (1-291, translated) 97 residues
MRFKSVAAIA LSTAMIRGGT ASVANAQQVS PSSTIEIPQE FVHTVQNFVP GMTYGDAGSA
IQSTAGSVAL NSTAGIILPI VLPFLGLGAV GSAALSA

> RXA00602 (1-753, translated) 251 residues
VQKTQEIHSS LEVSPSKAAL EPDDKGYRRY EIAQGLKTSL AAGLGMYPIG IAFGLLVIQY
GYEWWAAPLF SGLIFAGSTE MLVIALVVGA APLGAIALTT LLVNFRHVFY AFSFPLHVVK
NPIARFYSVF ALIDEAYAVT AARPAGWSAW RLISMQIAFH SYWVFGGLTG VAIAELIPFE
IKGLEFALCS LFVTLTLDSC RTKKQIPSLL LAGLSFTIAL VVIPGQALFA ALLIFLGLLT
IRYFFLGKAA K

> RXA00604 (1-291, translated) 97 residues
MRMKSIAAIA IATAALAGGT GVASAQEAGS TAGSSNLSSG IQLPQEATDL LSFLPAAQAA
QVEGAIQSTA GFFAVGLGST AIGSTAVTLG IADLLSS

> RXA00610 (1-864, translated) 288 residues
MEPKKPVTYK ELAHEYSRRT FNKLFTKITG FVYLKNDLIN DPNLVTQALL KRCPEGVLRG

YAALKQRGYQ LLDDQWMPII SVSGDLNRRD CSRGEILRRI EPENTLLSGN IRFVNDVQAI
QDVFDLHSLN DFEDQVALID HLIRQRPELF QELIQEPKLK KHTQYANPFA ESPQESRLRV
RLHSLGYHGF IPQIHVEYDG QSYFLDLADP LWQVALEYNG GWHYTSEQRE KDSHRKNALK
SAGWDVLEVT SKTLQNPNSW NNLIQQINSS LRRKQAQRRR RLPMQTVG

> RXA00611 (1-1476, translated) 492 residues
MSAAASRSRN ILTALLLLVP LIAGTIYASA MGLDVSRAWS SADEVTGAPA ASVATNNQEL
IEARRAAGEA GAQAGFLTSG TEELTSGTQE LIDGAAPLEE GVSAAADGAA QLHDGLIQLQ
AGTGQMGTGA TEIADGVQNA VEQLGGLVVV QQQLLGALNE ADKQLASSKI PEAEDLRKQI
TEVRGHLENF GISVEMTDQL DQLRSGTRDL ANQLAVPGYG FHDGIYSATN GAAELSAGLQ
ELEAGVGTAV EGFTALDEGA NRLDSMATLN EEKTSAVQRA LPVPQVPAGT IEGTADEERT
SALAPMYAFL ISALVMLAGA ALGWATLKNK WLMAFAVIGV TAIGGIILFT VALGISIGAL
FGALGILLLA TVVAGILSRI LLDVLGTTGA IVVSVLGWVA QAAVIGHVWS VTAVSDIALV
WRVVAGMMPL HYPTFAVTSI GNGGSAAAIW MSVAVLLAMG AIGAVALRKP KAVAVEVEEA
VDADADQAAS ES

> RXA00613 (1-453, translated) 151 residues
MSELKDKIRA DLTTAMKARD KDTTGTLRML LSALTQEETS GTKHELNDEE VLKVIAREIK
KRRESAEVYT ENGRQELADV ELKEAAILEG YQPEQLDDDQ LNALIDEAIA EVGGEADMKK
MGQIMKAATA KAAGRADGKR LSTAVKSRLS N

> RXA00614 (1-915, translated) 305 residues
VNKVSTIAKT LTFSSAALLG AGIATAAWGY SELKKFELKT VELPILKPGT LRGKKEFRLL
HISDLHMIPG QETKKAWVSA LDSLSPDLVI NTGDNLSDEK AVPDVLRALG PLMNRPGAFV
FGTNDYWAPR PVNPFGYLFG KKREVSHIDL PWRAMRAAFI EHGWQDANQK RLEFQVGSVR
LAISGVDDPH HDLDDYTEIA GAPNVDADLS IALLHAPEPR VLAQFEADGY QLSLSGHTHG
GQLCLPGSKP IVTNCGIDRK RATGLNKFGD MWMHVSNGLG TSKFVPFRIF CRPSATLIKI
TEQAL

> RXA00616 (1-345, translated) 115 residues
MKSLPRFAPL ITILALLVLV AIGGSALANN RATPNVESEP ATVNQRSTPT TSAYEPPATE
SPEEPTTQIQ ESPVQPPVPA PAQIPQAPQV PLNYQYYDDD WDDDDDDFDD DWDDD

> RXA00617 (1-1083, translated) 361 residues
MTAVVFLTLA SVVIITRSVL LSEVTNTANS AVEQEIEEFR RFAAEGIDPT TAQPFESGHR
LMEVYLSRQI PDENEAIVGI FPGELIQVDY SQLSGAHPLP LEHSDPLISE IRQTTLNSGV
FSDLERGTTH WGKVNFQTAS GEADGEFVVA FFADNLKDQV NGQIQILILI GTGGLIASIL
IAWLIAGQII APIRKLSSVS AKISNSDLTW RVPVEGRDEI AQLARTFNAM LDRIEIAYND
QRQFVDDAGH ELRTPITVVR GQLELLATTP PEEQARSIEL ATTELDRMSR MVNDLLTLAV
ADSGTFIHAH PTDVTDLTID IEDKARTISD RILLVDAAEG LVSLDEQRVT EAVLELFGNA
L

> RXA00628 (1-408, translated) 136 residues
MASVFTKIIN GELPGRFVYR SENVVAFLSI EPLTYGHTLV VPVAEVDRWT DLPQNIWSEV
NEASQLIGNA IRTAFDAPRC GYIIAGFDVP HTHIHLFPTD KMADYDFRNA MAADATDPAK
MDEAAEKIRE ALDGLV

> RXA00631 (1-1455, translated) 485 residues
MENPYVAALD DENQEVGVKK EAEKEPEIGP IRAAGRAIPL RTRIILIVVG IAGLGLLVNA
IAVSSLMREV SYTRMDQELE TSMGTWAHNV ELFNFDGVRQ GPPSDYYVAK VFPDGSSIIF
NDAQSAPDLA ETTIGTGPHT VDAASGSASN TPWRVMAEKN GDIITVVGKS MGRETNLLYR
LVMVQMIIGA LILVAILITS LFLVRRSLRP LREVEETATR IAGGDLDRRV PQWPMTTEVG
QLSNALNIML EQLQASILTA QQKEAQMRRF VGDASHELRT PLTSVKGFTE LYSSGATDDA
NWVMSKIGGE AQRMSVLVED LLSLTRAEGQ QMEKHRVDVL ELALAVRGSM RAAWPDRTVN
VSNKAESIPV VKGDPTRLHQ VLTNLVANGL NHGGPDAEVS IEINTDGQNV RILVADNGVG
MSEEDAQHIF ERFYRADSSR SRASGGSGLG LAITKSLVEG HGGTVTVDSV QGEGTVFTIT
LPAVS

> RXA00637 (1-753, translated) 251 residues
MTDRTIGEAA ELLGVTTRTL RHWDSIGLLQ PSWRTTTDYR LYTEDDVERA LQILIYRAAG
IGLKDIAEVL DQPDSANQHL RRQRELLVEQ IGQLHRMVRA VDEILGKDAI SVKEKIEIFG

EDLPKYQEEA FQRWGDTPEW KESQKIQEKM TKEDFQRAKD EHEGFVEKLI DASLRGIAPG
SAEGNELALA HRASIGQWYT VSANKQVILA RMYVEDERFN ETYKGHASYL LTLIEALAQV
EGVDLENVEW E

> RXA00646 (1-441, translated) 147 residues
MQRRARREVG LTEVLDRLPE QPKKRGRIPF TRADLDNDAE LAEFETLEAI AAGDTLITGA
VFTGTLEGVA WEVQVDVLVR NPDGSYMPVM VSNHRVARPD PHKTMQGIAV TRLGLGQPLE
LKATLRHHTI DGYRLTLALM GLEEAGA

> RXA00647 (1-633, translated) 211 residues
MGIFEAIRAA RAKTKAEIKA AEAKVKTEAK NKAKLDLKRE KLLVQQEKNL LKVEEKGLKK
RNKHELKMAK NILEQKRQGR LNKDKVKRWA GTARVLTPLL LPIIYRLSTE ARDQVVKGRA
RRAGVTAEQL SQFAGHAAAL KARIQGVRET AKNSSLPAGF VRDVEERLNE LEAAANNSEF
MSPQQRNRAH QSISRDLNQV SDQIQDRLLD K

> RXA00649 (1-456, translated) 152 residues
MSTDPIAALE YESTIFARHR NQYTGQAGTN AGVLDSSGYN LLTLLQLRGP STIGELSAIT
GLDASTLNRQ TKALLTKGFV ERIPDPDGGI ARKFHPTDLG NELLNEERTS SQEKYAELLS
DWPEEDLRTF VKLLEKLNKA VETRVGKHWP RP

> RXA00652 (1-549, translated) 183 residues
MRRTLPTILA ASIMLTACTP AEPEATPETT TEAAPEVITD GLPIDAMPAV ERTAQTACPY
LGTDWVADTN GQRVTGYGTD ERFSTPSCVF YSYPEEPQLT VIVRDMATTD DAIAVVDWAA
PIDSTEPAEE PAGWSGGRRG GNDTSGALYA VQNGPTAVIV FTNQDQSLKA QLIAEEVIQN
LGL

> RXA00653 (1-765, translated) 255 residues
VSVSQVVGEI LLTVGILALL FAYYEAYWTN VESGKLQESA GQKLDEDWNE ARVNPRQKLT
PELGEAFARM YVPAFGSDFN FAVIEGTDEE DLLAGPGRYV DSQMPGEAGN FAVAGHRVGK
GAPFNDLGNL EVCDAIVVET YNSWDVYRVM PMSTNGADRA AEAADCFNEN QVSRMAEGDY
VNVSGRSITT PDRIDATYPT PGVFDTAVRE GSEALLTLTT CHPQFSNAER MIVHAMLVEE
IDKSSGERPA ALEEN

> RXA00654 (1-1266, translated) 422 residues
VLDILIYPVS GVMKLWHLLL HNVAGLDDSL AWFFSLFGLV ITIRAIIAPF TWQMYKSGRT
AAHIRPHRAA LREEYKGKYD EASIRELQKR QNDLNKEYGI NPLAGCVPGL IQIPIVLGLY
WALLRMARPE GGLENPVFQS IGFLTPEEVE SFLAGRVSNV PLPAYVSMPT EQLKYLSTTQ
AEVLSFVLPL FITAAILTAI NMAMSMYRSF QTNDYASGFS NGMLKFMIVM SILAPIFPLS
LGLTGPFPTA IALYWVSNNL WTLLQTIIMM VILERKYPLT DDFKVHHLEQ RDIYRAKQKE
KRIFLWTRRK NRALMILTPW NASTLHATNV ELTKTRTAEI NEAKQARKEI ANKRRETQRE
MNRAAMQRLK QRRAEVKAKK KGLIDASPNE DTPSENEETK LSSPQVEPTT TAEPNREPSQ
ED

> RXA00656 (1-261, translated) 87 residues
MLALGWITWI IIGGLAGWIA SKIKGTDAQQ GILLNIVVGI IGGLLGGWLL GIFGVDVAGG
GLIFSFITCL IGAVILLTIV QFFTRKK

> RXA00657 (1-903, translated) 301 residues
MSTEDIVVVA VDGSDASKQA VRWAANTANK RGIPLRLASS YTMPQFLYAE GMVPPQELFD
DLQAEALEKI NEARDIAHEV APEIKIGHTI AEGSPIDMLL EMSPDATMIV MGSRGLGGLS
GMVMGSVSGA VVSHAKCPVV VVREDSAVNE DSKYGPVVVG VDGSEVSQQA TEYAFAEAEA
RGAELVAVHT WMDMQVQASL AGLAAAQQQW DEVERQQTDM LIERLAPLVE KYPSVTVKKI
ITRDRPVRAL AEASENAQLL VVGSHGRGGF KGMLLGSTSR ALLQSAPCPM MVVRPPEKIK
K

> RXA00661 (1-690, translated) 230 residues
MNPITELLDA TLWIGGVPIL WREIIGNVFG LFSAWAGMRR IVWAWPIGII GNALLFTVFM
GGLFHTPQNL DLYGQAGRQI MFIIVSGYGW YQWSAAKRRA LTPENAVAVV PRWASTKERA
GIVIAAVVGT LSFAWIFQAL GSWGPWADAW IFVGSILATY GMARGWTEFW LIWIAVDIVG
VPLLLTAGYY PSAVLYLVYG AFVSWGFVVW LRVQKADKAR ALEAQESVTV

> RXA00662 (1-1269, translated) 423 residues
VSTIPLNRLA VIAAIIGVGT GLFVAALNWS AIGVERLVYG ADHLHNYNPV ANVSPLRLSI
TVIVLSVVAS WAWFFVHRTG PKEVSIVGAI RGEKMPILET IASAFLQVTT VAAGAPVGAE
NAPRIAGALV GERFSRWLQL DIDAKRILVA SAAGAGLGAS FHLPLAGVLF ALEVLLVEAS
TRTVVIAIIT TTAAVATTGF FVQTPDVFST VPLTESPWML LAAMVTGVVA GMCGHWFSAA
AHKMAQASPK GVKILWQMPL GFVVIAAVIY FFPETLANPR WLADSMLGDG LILSTILLVL
VLRTAMFLLA FRVGMVGGNL IPAFALGSMV GGVVGAVLEP ITNVPIAAFA LLGAAAFLST
TMAAPLFGLI AAVEFTDMEA QGYLPIFLAV ASAVLAVRVW SVIAKHELRA IPITYASWTG
ELK

> RXA00666 (1-387, translated) 129 residues
MTAGEAIAHS VRAAQIAEEH NYARFWVAEH HNSEGLASSA TTLLMGHIAG HTSRIRVGSG
GIMMPNHSAL HVAEELGTLE AIYPGRIEAG LGRAPGTDPM TARELGRASS LVDDVLSTIV
SLQNYLDTP

> RXA00667 (1-585, translated) 195 residues
MIALKSMSNR VVQKPKMKAP LPIRDGLNPS RVRLPLDAAP IRAIDFVEYL ISTQRHRNPA
DNAEALQARF DADLVVNHYG EPYAPDTMVQ PDDDIWFYRM PAAERPIPYK IHVIHEDDDI
LVIDKPPYLA TMPRGRHITE TALVKMRVLT GNNDLTPAHR LDRLTSGVLV MVKKPELRGA
YQTLFARREA SKTYE

> RXA00668 (1-792, translated) 264 residues
MLTTLWIAVL VFTVPGLVVS WVSGLKVPWA IAASIPATFG IYGLSAWLLG LWEMRFDLHS
VVISTLVFAA VALVWRLFFV GGWLVRRRKA RIRRQTLADE ERAENAEVSA GEPAESSTNE
AAESESETSE RRGIWRVIFD YMRDGGILDH RWLLPAAGAI TGAWLIIDRA VDLLLSTEHG
LGDIVQGWDV HWHASTVRFI DETGIASSTM MGQLRNIETQ QDLFYPSAWH AGAWVLSDVG
NLTIVEATNL TGIVLSGLLL PLAV

> RXA00674 (1-750, translated) 250 residues
IFAAALAFMG MFQLHPAPST IVIMVLLLWW LLKLVVVPSQ KVKGWKAGIG IRLKDVGILA
ITGIIGVLFM LPQVISGSEQ TEDVLSYSAE EQVTRSESWL VSIFMETRHV DFFGNIDIVP
VLVFAAIGGV VALVWRGNLW APVFYFASVA LTANSLKPFE EPWGDWLNIV GGLHYSTGHR
LIMPVAMFTF AAAGIGAAAV IRLICLGPIK KFTTVSGVVS VVMALVVAVP LQTWAKDFVE
EGSETTILAP

> RXA00676 (1-747, translated) 249 residues
MAKNSRIRYS ASIKRAAAAI LTAAATSVAL IAVPATASAQ DLATGSSQIQ TDAREGAWAT
RNTIQDQLAS IGPAALPVRA AVDNAINGMF PGLVDEKVAA EQEAARAEAE REAAAAREAE
AARVAAEEAA RFDRGSCPAI ADVCVDIDGG RTWLQENGQV TYGAVPVSSG GVGQETPRGT
FYINRKVKDE ISYEFGNAPM PYAMYFTYNG HAFHQGNVAT TSAGCVRLNT QDAIYYFNNV
GIGDMVYIY

> RXA00678 (1-735, translated) 245 residues
MTRSNLPAWE QADPSVHASD PRAITFAEDF GIRPIPAVGP IDTTAICATP SNGFEQLWKA
IEPETRTRAN DIHLPIVVAY AERLCDAYPL ADRELVLVAA ILHDTGWAHV DESRIISEGF
SGNWRKAAIR FEHETEGCTV ARRVLPSLGY TVDFVEHVCD IIDGHDTRQV AYSLEDALVR
DCDRLWRFDR AGITASSSWF GMPVSDYVDR LHREILPELI TEAAHQMATA DLNRAKALLR
TDAIR

> RXA00691 (1-930, translated) 310 residues
MVEGNTIGCA DAGGNGYQTL LDAGFDVETT VQFPEFLCRI NDFPGPDVDD CMTASPAEAY
WSYWHAPLGG DEWEYSNLGA FLYYPKPGTV EAWYWGDTDR PGAIPVSKSQ AELGLDSADP
DYKIDFDPND FITTTPTSES PIADLGGDEE PTETTEAPIA GAGAGSARGQ AAEPTVEVNP
ENPNEVLVYQ DSEGNSITKG QYENLVAAAA AKTTAAVQAP AGAGEANSQP QATAVAEAPE
VDPMTTQVLM APAGQDGDVM AEGSTQQTYA TGTVDSSAQG WIIGLTLAVI SLVSASAVAA
WAIRRSEVQG

> RXA00692 (1-1134, translated) 378 residues
VALATGVSLL APQVVAAQDA SSDIQLATQF IEKEFATNGL IPGPVGTPDI GLNQDLLLSL
NALAPDSPEI DAAYAAIAPE LEGYVSVSDY IFSDRLAKTV AFQDALGVRD ADFIAQLVSA
VQENGQIKNL DNGEATTAIN NFSQAWGVLA LHRVGETEAA ERATEFLKTQ VCSDGGVQLA

SAIEPTCKTT DSDVTAMAAQ ALTLANGAQD PTTQATLDYL VTTMDETGGV KNTWTGVNSN
STGIVGSAFA LAGDEENYLK AREYLASVQF GEDADPSIQG GFAFTVKAKE TNTAISDQIR
RATGQAALGF AGGNYANDKL ITIANPVDPT PDPEIPTPPA DSEGSTGGIG GAGIIIAILA
ILAAIAGVMG PMMANLQF

> RXA00693 (1-483, translated) 161 residues
MWKEALEEFG SGPIHGSGYF ENYLPIDYSE AGFHHYLKER TDAADPSVPP PEGFVHCSYF
WIVDDDDVLV GFLALRHELN QHLLEVAGHI GYGVRPSARR KGAATAALKL GVHEAQALGI
DKVLLCVAGD NEASRNVIEK CGGVYESTIR GMRRYWIATD S

> RXA00701 (1-375, translated) 125 residues
LVGEPRSDSC GEQRGCEQSG VAEDESEAGS EGSSAEDEDK EDCFKACCAG TEWSDYGNHG
GEDAEHGYGF NVESVFTDFG DDSGQHEGND DRDVEGRLGF VGQEGFRVDD QRPEENHDAQ
NRKEA

> RXA00704 (1-513, translated) 171 residues
LTITFSRVAL TTLAVTATTL SLSTAANAQS SLLDKTLDAR QCIDADNVWV SVDYGADSEK
EPEGACATEF TDGVVALESA GFKLTFDESE MGKYMTGING VVPDWVETGT YWSYYSGEVA
DDYSVDYTYY EVGASNSEPE GGTVEAWVVG TGEETPALET LSETSAATGS S

> RXA00707 (1-972, translated) 324 residues
MNVQRKLLAI VGAFMAGSLA LGTPTAQAQS IGSSASQRTE VLRGLTSSAG IPDATAPEGG
AKVVVFGDSH ASGTNAPFDV DERGCLKGNQ SWPDQLQAQQ GLQQGELIDL SCNGASINST
GFHFSDEVRH AEALGAIGPN TENIFIQFGK NDQWGHSPIN LRYSVINCLF DAANGCGEKA
VAAGTMQDPS SVTGENYAQR MKPVIDYLKY YAPNAQITLL GYQEYTPRSG SEICVRVGGT
ELRKPDATNL VSYMNNLESA IFEASEILDV QHANLREATA GHSSCSAEPW VNGVLDMRVN
AVGGTWHPSP KGDEVTAGLL GTLM

> RXA00712 (1-549, translated) 183 residues
AAEPTTRTTV QSATEASTTA PVQCNLDPRT SDFGPYLAQS RTPVGELAGS ADSVVQVPDW
FYHFQMGDNG YDSCSKLSYV VLNGSNGDAE RSTGTGAAIA DVVVLFIDGH MVARPAPFEM
KTVESVTRVS DSEIQVVYGH AGRSTAEGVT DYFTFNFFVD NGVLSGRGDL PEHIDTHMRL
YLL

> RXA00713 (1-963, translated) 321 residues
MTKVAELDQE WSEVDDAELD AQSAGTSDSS STDDFADAEN TSENLGPIGP EPLPEPDGDV
PASGFQVQLD NFEGPFDLLL QLITKKKLDV TEVALAQVTD EFIAYTRKLG ETSDLDETTE
FLVVAATLLD LKTARLLPRG EVDDEDDLEL LEIKDLLFAR LLQYRAYKQV AEMFAQWQRD
ARRRYPRAVS LETQFANLLP PVSLGHSLKS FSELAAVVFR PKPPETVKTD HVHQVAVSVP
EQAGRILNTL KLAGIDHYLS FQLLTRDCTA SMEVIGRFLA LLELYKARAI ETLQEEPLGE
LKVSWTGIDV DPAVVAASDW E

> RXA00714 (1-561, translated) 187 residues
MATITRTDRL ILVPLTVELE DEAHQIYSDS RIWEHRPQAR HTNVRVTRDI IKRTNESWGK
KDLGPWGVYL RDRPSEFVGV GGVELIDGKV WDLKYRLRPD LWGNGYATEI SNAATLATKR
IDDSLPLTAR VTTNHPASFR ILEKLGLTPV WEGRRVGTED DPNEPDVRIY SDRPLSDEIL
EMLKQRP

> RXA00716 (1-513, translated) 171 residues
MESILLVVDT PVSARTLAGV LGIDVPATEA ILKEMAFELS ERGSGIDLRE TAEGWRYYTR
PENADIVEQF LLDGNQTRLS RAALETLAVV AYRQPVTRSQ ISAVRGVNVD GVMRTLQLRG
LVKEVDVDES TGAHRYGTTE LLLELLGIDS LDKLPDLAPL LPDVDSIDED F

> RXA00719 (1-1629, translated) 543 residues
VTDKHTMPGE EDDTVFVYHT HKGEMDVEGA FADEEELAPH GGWASADFDP AEFGYEDSDD
DFDAEDFDET EFSNPDFGED YSDEDWEEIE TAFGFDPSHL EEALCTVAIV GRPNVGKSTL
VNRFIGRREA VVEDFPGVTR DRISYISDWG GHRFWVQDTG GWDPNVKGIH ASIAQQAEVA
MSTADVIVFV VDTKVGITET DSVMAAKLLR SEVPVILVAN KFDSDSQWAD MAEFYSLGLG
DPYPVSAQHG RGGADVLDKV LELFPEEPRS KSIVEGPRRV ALVGKPNVGK SSLLNKFAGE
TRSVVDNVAG TTVDPVDSLI QLDQKLWKFV DTAGLRKKVK TASGHEYYAS LRTHGAIDAA
ELCVLLIDSS EPITEQDQRV LAMITDAGKA LVIAFNKWDL MDEDRRIDLD RELDLQLAHV

PWAKRINISA KTGRALQRLE PAMLEALDNW DRRISTGQLN TWLREAIAAN PPPMRGGRLP
RVLFATQAST QPPVIVLFTT GFLEAGYRRY LERKFRERFG FEGTPVRIAV RVRERRGKGG
NKQ

> RXA00720 (1-666, translated) 222 residues
MASPRRPQVA APRIKELRLT GLDNADPQDI ESNEQIESCR FNEAELSERD LSGAGFIECE
FLGLEAHETE LRRAQFVETR IERANAPSFK AARSIWRNAT ISDSRFGAVE MYEATVQALK
ISDSKLSFVN LRGASLRDVL FENCVIDELD LGQARAERIA FKDCTVHSLT FDHAVLSNVD
LRGLDIERIS GVESMSGTVI SSLQAADLSG AFARHLGITV ND

> RXA00722 (1-504, translated) 168 residues
LLPNGLLTKR ELVSIERSSH AFEQSVVILP TATLVAGLAA VSVHEPAQPL AVDSYAMAEA
AGSMRTATIR AATSAALTQA GACSKGDLLS FIGPEIALVS EELNDALSRT ALRLLDGSSE
QITLLIAQDR QSAFDEDVFR RGLGTHTDVE ITVYPATGME NLVEIGVE

> RXA00724 (1-648, translated) 216 residues
IGEEVLAGRQ AYVVCPRIEG EGGVLEIHAY LSEQVYPGLN VGMLHGRMDT DLKDSVMQEF
AQGEIDILVA TTVIEVGIDV ANATVMLIRE AERFGVSQIH QLRGRVGRGQ HDSLCLLHTT
FDEDSPQGQR LAAISTTTDG FQLSELDLQV RQEGDVLGTR QSGSDTKLRH LSFISDQKII
ERALIDATEL VAASRSRALE LVSDIAMINQ EYLEKS

> RXA00726 (1-141, translated) 47 residues
HEMGFAHEVA DQVVFMADGV VVEAGTPEQV LDNPKEQRTK DFLSSLL

> RXA00729 (1-642, translated) 214 residues
TVVEDYQEFT RGLFLGMVAV SILVPLGMMD MRDAKKRLAI VIPLFIICAM LGFFGTSFTS
APRTDPSLIF VFICAAIAVC ALVLPGVSGS FFLLAVGMYA PIMESLSNRD LSVIGVFLLG
ALTGVILFVK VLSYVLEHHR TITLTIMAGL MLGSLRALWP WQDGDANLLA PGDNAVMIFS
IIILGGAIVA ALMFAERVSS KNIDSETVAE EHPR

> RXA00730 (1-333, translated) 111 residues
HFVVFQKQLQ QADPNAEYDL DVLAFDIARV ANLLRWAAYT DLLLPAEARW FQDQLGIAAA
VSFGSWEEYG ERYVRGLQKN FKGGNKPYIE GERWLNTEAE SPWKTQKWIS A

> RXA00731 (1-2472, translated) 824 residues
LLFGLRWLGR SLRFAPLSLL MIVVMRGLRE VFGAEDPANS SLVDNLGLTL PWSLNDPHFL
TAGFSASTTT AALMSTLWII VFAVPSERIL GSLKFAITAA LIHITSIPLG IGIAHLIEEA
DLNRWGNNML ADVLLTPDFW VFGVAAFASA SMPLLWRRRT RLFLFTITLT LLLYTGTLAD
VTMLTATIIG TVAGELNRHR KTPGGRWLPG SLTVREARIM TAILVTAVAA GPVLAALNPL
THGPFSSATK LIWQPLVTEE HMHHLCHTDS TSDACQGALD QLQQHGVGPS VANLIPLILT
VVLAMGLSRG RRLAWILAVL AQLISIAVLM FQLTKLSADS TDLLWSVNAF SVIVPWLVAL
AVLVFSRRAF QVKIDTTRIS KSLGALMVTW LATAALWILA TLFLPHAFHP HPTLGLAFKE
LPFRYLPPTI ETVLSHQLFP RSPAGWAVFE WTGTLFWLVV AATLYHLLMG VPSNKAHEDQ
ENAATLLRSG SGDHLSWMTI WGGNTYWWAP ENAGYVAYRV KRGIAITLGE PILGPDSSVS
KAELAAQFEE FASNQGWIVA WYSVCEEFSK ERINAGHHTL RVAEEAVLSS ANADFKGKHF
QNVRTARNRA AKEGVSSIWT TWADLSAEMQ HKIITLSEEW VSDKALPEMG FTLGTVNELS
DPDTYLLLAI DEEEHLHGVT SWLPVYEKGR IVGYTLDVMR RDPQGFKSVI EFLISEAVVI
ARDHDLEWMS MSGAPLSTPP GVADDGTIGQ ILELLGRAME PFYGFRSLAA SKNKFHPEHH
GWYLCYRDEL SLPSIGLAVA ACYLNEFPLP NWLKKTATSA PSHS

> RXA00738 (1-288, translated) 96 residues
LLNDATTQVS HILGNAFTRS GLNAEYANLY GQALVGMVSM TAQWWLDERT PPKEEVAAHI
VNLCWNGLTG MEADPKLTPI SSAEGAIFGQ EKESEA

> RXA00739 (1-816, translated) 272 residues
VTATVLEPQP VQLSEQDVDA EIARMELKHN RHKTWRRRTM AVVMTLLISV GLSFGAFGNK
EREANAFASA IIAQVVGAMG EVAFEAICPS DGDTEMLLKC ITENLGEMHI IEKCLEAEDV
LKCFYDAKNE EQRKEQNLDK APDYSMYRMA SAMASFYGNG RAATAGVEEG GPNEFLDSED
AGLKVWEGIL SKAANGGNVL GYADAKHNED SGWFFGNGVA NNEKTYSYDS LADHAFQGPY
HFALFGATLS GLGFDSSKAE DSQTDFAQRK GM

> RXA00740 (1-579, translated) 193 residues
MLKNKTLALL AVSTLMFGLS ACSSDADGPD SSGASSSSTG SSSASADTTD SAAVDKDAQL
DTFMRSAVAD GSSAAVAVDN AVGKGFDKAD AQAAAERLGD GFQFAADYQA VGYLESWYFG
GARSEKLDEV RSDVIAHLSE LGFTDLEAES SASRITLGDY CDGVPEYCEL FFDGESPDLY
DMGTELDSYK PTE

> RXA00741 (1-933, translated) 311 residues
MTDSLLVSIR KGLIEERPLT ELLRACIFLG SDTNSDSLQE WAKNELNGYG SIDGIPEYRK
LKGPPVFAKI QAGNSIMSNM VLGPHNVPER ARKYFPEELH FDQPIQTLIE WSTRQDGINL
SPPNLLRVRD LHNDQYAPLN QILNLNVYLD NSYFSGIVDR IRTLMTSMIA DLTHATPLDE
LPSSEKVNAT VMKHIENNYE TTITQANGAV AIGNSAKAVQ KGLSVDDLLK IMQTINPEKF
DLGEARAEAE ESIQSIADEL KKESPNKGFI QNAFEKLKEL SIKAGDKAFT TMLNLVGKQI
IENIPQLVSG G

> RXA00742 (1-1650, translated) 550 residues
VNVQIKGRKV NAKAADLNSY PVSVVDLRGF VTLAGLLFFV VDIDKKSNKK YPKYVLLKPF
YIHDLLSKAK PGQKTISVRL KRLPSDEDRM EAIIALALAS RQEKIVENPS NYLYENMESI
TVKSAEPLNR DKLAVYDGSS PDHSIIIRTG DGIEQFVNAT VEIIPPNMQF HQANYNVSCN
GVVYDNVLHR NIDDEHIELK IGKGITLRLQ KLAIDAPGSV TVEFQDSLPE RLKDIEFFLG
VLQANTFFIN EEPVVLKINS NRTVADLKDE AGVLRQLVEI ANHFNIDPSL IRIGEITEKQ
FWQLDIVYRT AVKGEYVKNL EVKDETRLIL QPFGRWNLAL IAHPGDVAGE WTYHEVISKR
HHFAMTPSTD RSDSSIERVT PYELIDNRWL PSVLNLHLDK LVDFYSALEE TVDVDNLATW
MVLRLIKAAD SEQSRKTAFL IAAQALNDWL VERDREESPI YRLNGWQILY RQTGLLDSQR
TEIRSFRHNL DQTMHPDNYS EIMIGCALLL DDREEANFLL TQLSVDRRAV FNEWPIAQLM
TGALKEEIEK

> RXA00743 (1-423, translated) 141 residues
VQHLVLADVK YRELSALSVK IEEPSDRPEF KLGVTVNDKS KDEEGVPRII EVSLRVSIEV
PDGKITVEPE AIYLIPENKV YLTESDAMVD YFNNHAIFTL VPYARQAVSD LGQRAFHTQI
LMPALGPGDL VFSKSTASRE W

> RXA00745 (1-534, translated) 178 residues
VAYLYGSADG MLNTDGFNMF PRASYTILGP MDADAVGVYQ QLLNSTIPMD LARLVTTHNS
GASYLRRGAT NVVFETNLAL GVNPYMKKRR ATEAQRGKKR FKRDSHYGGG TVTTGTADLD
VVAMQARAEH REERLGEKST RKKEELAAVE AKELAAKKGP QTVEEGLAAV EKKHLAKR

> RXA00746 (1-1191, translated) 397 residues
LVHTDRVSIH RAKNGVRRTR KHIKTICIKH PIGRSVQISH SPTALSDAEN NAELTTAQIL
HIDPVTGVAI PRQNILLGED FQTMASSFSQ IRHGWGITQL IGQDPNRNQP IRSADTWTVT
GSTGLTGFNT ATHNTDDTDA TAAYTMPASD PAVGLCALES NKDAPVDEFR DLSLSALRTA
TVMSSSGSAV ITMHDPMVMS TTGALEARAY VDGEVINQHD LDSLRDQLGI TTDSADTTPA
LPADPLAALG LSTPTTSALV PGLAELDCLN TDQARTWHDR DNSIGTGKPA ILAVINAELA
DDYTLQILKN STATPTDSTD SSDTAERFVA QLPAETAFVL IDPDIGAVTD LFFINSINQD
LPAPTTQINS VAVDQRDPNI IYATFANDDR VYQLMLG

> RXA00747 (1-588, translated) 196 residues
MTFLHRSASF HPRTHDHLSE LGLDPYKLSQ DIPTVIYEVQ PHSVFILKFN TADVRVYQEH
SDLFVRHAVL VDPEQRKHEH DQLLKEILDL DAPRVNDDIS GRTTVFLHDK TVVTHSGGPI
AIIPHNPDVA SAAASANKHK QSVMTTSRHP YAQMSLSDML KQGFTLTPLE FPYCAVDDPD
SSRHTMHVIN VRDHTV

> RXA00748 (1-444, translated) 148 residues
MTYFALVARN YAETGVSVEF HEVDDDADNS NGPNNTSNLP LKLLRDHSFD ATVVYGDLVL
HTSAHLRDTA IANSDNRPRV VTTAQKFFDY IRLATRHGAI HDMINNAPDT GTDIVVITAT
NDALISDESE YYDELFHILE SAQGVILK

> RXA00749 (1-699, translated) 233 residues
MLRKTVTGGI VALIATATLM NSVSSAEEVS GDVSAVDLAF AEFERTTAED VANGVPEAIA
NAEKISNFTP SELEGFKSLL ASDAVLRSVS GEEILPDNVE VVQTDNVGDE DPNVISPAAW
QGSDYIEGCL TNTLYGIEVL KVCTGGTYYS NVGIATSVSN PRSYVKYNSA PGLAVTTSNP
RGGIEGGLAA FYGDVNLVAF PNIPWVGPIS SSAGTHRVVA RSFPNSVVLN VYY

> RXA00750 (1-438, translated) 146 residues
MDWSIIINVL AVATVVILTL IIAAALYRGF TRNKIKKLEA IREAQQHERD NPTIRIADLR
GIMDTHHYIY TDVMVTRAHE LMITAPAFFD VTLPEAVLYE DTKRAAHDAL NGYKDTTVAS
AEKIMLVDAV TAAWTLYSTK ANTGST

> RXA00751 (1-828, translated) 276 residues
MLVRSRTLVT AALSCSLLFG ATVNGTGVAI AYENVSMAAQ YEPRYESLET RLGSSGVFPK
SVEQSVENLA ELPEETRFLL EGDSFSIIID DGLLASRLDP NTGEIRHTLG ASGISYTPGE
MKRSYTDRVT VKVVYPDGSF DRVTPHSVVY VADSIYYGIE STGYPKVRNG QTVKIPLRVT
DGGTGAVGGV PQGSKVVRDR YGSIENAELM GAIILIDEKT GDLTFTAPDD RTGQLWFRTE
VTFPDGSDSE VQYVIEVTDQ PEPVDVIRPA GSSLSS

> RXA00752 (1-429, translated) 143 residues
MYSDKLILLF LSEQDSSYEC CVGLLDGSDG LDYIEKLLKG RKLKNHFLEW EDINKADVAR
EEIYKGQLVH LVFVTALSTP GEISFVFPGQ SLMSATLEED FAALVLEEER TSFRPELSHL
WSLPVGWVAP GLEGFVERNS EAA

> RXA00757 (1-1254, translated) 418 residues
VSFGVVKRPD ACYALFAILI KRNQATAVSA PMARQRQWVV HARRGHFERV TRSEVELSAL
LGGVEKLSDF LAEYFQLVEI GAGIRIYLDG DGGFWTCFGH FQALEVEFVG CGERLDERRQ
NFSGWKSHKD KDNLPAKIIG LLHCEAMRRR IPSVLGVSLL AAFLVACTPS PNPNAALAQM
YQDALFDSQA MSEAEPELAT LRSQHADELL AEIRRICGFD EGQVPESCQV TVPAIAILPT
DDPEKYVNDS QALILDNLDD IPEDSVALVV EQYIAQAEFA EGSEVSVPVD LELTEAELAA
AKDLADREFS AAWSLGVALA QLPETDREEV ETAISNHHDR ASQLQIITSG TTPAPGYVSE
LPDPTDETSA RSNIETVENN VTQAWHAAAS AATTDAWRVF CAHIAGDTAR ELTLIDVS

> RXA00763 (1-783, translated) 261 residues
VEKSRKRLVT IAASTIGAVA VAGGAFWIVD ASIAAHAERN LSKAVAESAD LENDPRVFLG
SSIYSTAFFT GKLDSVSIDM LDVEIPGVGM VNARTEVESV EVSRDQILSG DLDGTTAETF
TRTLRMDGVA IGAQLGITDL DISHPIDISP SGGITSEALL TGTPPDMEDP VSVLVTLRLV
GSEFQMLPYE LIDAPSGLTL DDVAPDFTWK IDTLQLPLAD RAMAVYLSGG SVHFQSEARN
VQLTTRELSP LAAPEENSDE S

> RXA00765 (1-687, translated) 229 residues
MSENSTPNNP VVPGAGADGP SLSDSASISG SDAVNLAAEQ SKSTAHRNIP GLGDLPIPDD
TANLREGPNL HDGLLALLPL VGVWRGEGQA DTAEDGQYAF GQQITFAHDG ENYLSFESRM
WKLDEEGNPT GVDQRESGFW RINLKDEIEF VCTHAGGVVE IYYGQPLNER AWQLESASTM
VTATGPSTLG PGKRLYGLLP TNELGWVDER LVGDALKPRM SAQLTRVIG

> RXA00767 (1-714, translated) 238 residues
VGTIEDVANE QIEVANNTDQ IPAGYKSPLL SRSGAAEAQG AAAQAGTEGV AWHYGSPLVE
QRIFETGTGL VDRSNRKVIK VEGPDAPTFL NNILSQKVDS VENGFTAGAL DLDAQGRIQH
TMQVTVVDGV FYLDTSAAEF DTLIGFLTKM IFWSEVTVQE ADLAIITLLG QEIALPDAVF
ARRVDWNGPS RIDVAIRREN LEEGVDKLLE AGAKLTGLMA YTARAREGVG ARCGRGFG

> RXA00768 (1-444, translated) 148 residues
VKALEPAAGV DLDDKTIPHE IPHWIGRGEH LGAVHLTKGC YRGQETVARV DNLGRSPRVL
VLLHLDGSAP LDPVTGAEIK AGARTVGRLG TVVHDADYGP IALGLVKRSA LDKELHIDDV
SVNVDRDLLP AEESEQRGRA AINKLKGL

> RXA00769 (1-213, translated) 71 residues
MGRGRAKAKQ TKVARQLKYS SPDMDLDSLQ RELANQSPRR SYSDTPDDED QYAEYADWDE
DDTDNRAYGT N

> RXA00771 (1-678, translated) 226 residues
MTNPYEAFIP LKHRTGIEPE HTFWEWENKR VHIARRRREA PVRVIVVHGL GTHSGALWPL
VAAIEGADLA AIDLPKTPLY DDWLRLLESF ISSEDDGRPL ILIGAGTGGL LCAEAAHRTG
LVAHVIATCL LNPSDQPTRR ALFRFSPLTR LIQGRLRNRE IPVTRVLNFS KISRSPALSK
LCAADEFNGA FKITWGFLAS YVQHKAKLGA VPLTLMHPDH DLFDSR

> RXA00781 (1-288, translated) 96 residues
MSENKNIEIV HNEGQKRFVI SVDGTPAGFA SYLDGPDIRN FNHTVIKPEF RGQGLSAPLI
KFALDDARES GIRIHDACSA VAGFIQKNPE YKDLKN

> RXA00785 (1-621, translated) 207 residues
IIATLGVTLL VEARGLFLTV ASIPILFGIF TPLTSWFVSQ QGVAANVSPG VSVTEILTAV
YPLAQLFPTL IMVTLVAALI AVVRIILLRR NQESRQVSGE LTRRAQREAE EANQNAARRA
RAQSTRVQSS KTRNRRAQPT GDTGSQVTVD ELIRRSQERR QTVAQRQTER GVPFTPTPGP
VVAPKPRPSA PEAPAPTDVG ERRQAAP

> RXA00788 (1-225, translated) 75 residues
MASSINIGVF NLGNAVAAWL AGATITTSLG LTSAGLVGGL MTSLGLVLAI VAVVLRRKAQ
GTQATISVVE HQPAQ

> RXA00795 (1-528, translated) 176 residues
MIISLVVSAI IMLVAVGFTG MCSFNTGSPE NGQVPEVDAS TFMSMEARAM TDHATRLPET
PEGWTTNSAR RTMVDDTPAS VVGYVTADEG YIQLTQTGET VEDAVAGYDT RWRDLSESYD
LDGHDVGIYT SQESDVRDLR VMDLGDARVM VSGAATDEEF NDLLRAVANS EPLPTN

> RXA00804 (1-444, translated) 148 residues
MKIRSAREIA EWFVAWGDEL DAEVSPLKLQ KLLYYSQGEH IAATGRKLFS DKILAWQHGP
VTPGVYSDTK SYGRNPIDPD EFVSDEFNWD DYSDVSDELV TVWRKYGIYS AWALREKTHS
ESPWLDAWAQ GQNIEITDAA LKDFFLVH

> RXA00805 (1-882, translated) 294 residues
MAESFIEVSA GHADRRIDKF LRAQLKGVPA SLIFRQMRKG DIRVNGRKVD PNYRLQEGDR
IRMWQMDLLA DLPPPVVDKH IFKAVADSVL FEDAELLVIN KPAGIPVHGG TGHGGGVIEA
LRQKFPQERD LELVHRLDRD TSGLLLVSKT TSVLRELQEI LRDREEEIFR GYLLKVEGAW
PGDLRQIDVP LKRTETTVVP HSDGLRARTY FEVVKRLPGA TLVKAQLATG RKHQIRVHAQ
YAGHPIVGDP RYGSRGGRAA TMHLHAAELV APRGAGKRQK FTAPLPKEWG MGRV

> RXA00808 (1-678, translated) 226 residues
AGFNEMMRGL RERQRVRDLF GRYVGAEVAK RALEERPTLG GEDRKVAVLF VDVIGSTTFA
VNHTPEEVVE ALNEFFEHVV EVVHRNKGVI NKFQGDAALA IFGAPLPLSD ATGHALAAAR
ELRAELKDLQ LKAGIGVAAG HVVAGHIGGH ARFEYTVIGD AVNQAARLTE IAKTTPGRTV
TNASTLREAN EAEQARWTLM KSVELRGRSQ MTQIARPIRP TLADRS

> RXA00812 (1-1059, translated) 353 residues
MNTITHQAIL IAVEDPVLHP EAMHVAAATG RPVIETTNLM DISRHFHRTS AVLIDASMAS
QLSPGKRRDR VFLLDSDPGP SDWKTAMKIH AEQAMLLPAQ AGELLSALGR DDKQLPVASG
HVIGVAGVVG GTGASTFAAA LAKRRAESVT TVLIDADPSS GGIDLLLGIE DVPGARWPDV
GLRRGTVQAA DVLKALPSTP DEVVVLSTAR SNILDPFALS ESDVSAAIDC FLSADRSVDV
VVDLPHARVH PDIAERLSHL VLVIPAEVRA VAAARARCLE LQQLHVSITC VLRHRGWSGL
DVAEVEEILG ADITAEVGSI QRLAKSVEMH GLTGSLPRVL SSACDAVLGE VAA

> RXA00814 (1-774, translated) 258 residues
MVYALGLLSV AVLISGSRGP GARTRPPTPG NGVHLFALIA LFCLATVLFI VVDAYTMIAG
IIIATTLFWY LRQTHAAAQR TKQSLQLASF LSLCAGNLRA GVTMVDAMDY ALDNTTPDKF
LSPTLQTAAR QARSGGSGPR VLIDASLPDL QRLGHLWETS ERHGIPLVAL IDQMRSRISS
KQRHGESTRA ALQGPQATAV ILTVLPLAGM LMGTAMGANP LGLLTGGGIG GFLLVIGVGL
DAAGFVLTHK ILQSASPS

> RXA00815 (1-573, translated) 191 residues
MITALVLAAV AMFLGSPNPG VRGGLISPKS GKSLRIRAGP KKLGNADPVD VSADIELFSA
CLDAGLNTRD AAQVVAHVAA ITHRELWTHV VALLSIGVSA PQAFALMAGV DGLDELANLA
TVSHRSGSAL SDGCRNISTS LLASAGDKRT AAAERAGVFI ALPLALCFLP AFMIVGLAPV
VLSLGTQLIN F

> RXA00816 (1-297, translated) 99 residues
MTIASAGVAS ILISLLVVLA WQAGNLVARE QAQVAADVSA VAGAYAFARG ELPDAACATA
KHTAEANNAQ LENCATEGED LTLTVTVRGQ EAHAKAGPL

> RXA00826 (1-531, translated) 177 residues
MITVLIDGQS GAGKTTLAGE LAARTGFQLV HLDDFYPGWT GLEAASEIVA RHVLDADNPG
FFTWDWHNNC QGDWIKLEPG RSLIIEGSGS ITAATKRKAS LLGELVTVRI TGPEALRKQR
ALNRDPDYAP FWKVWAQQEQ RHFSLGVEVD HEIVLGSDEA SGRPEEIYDS LGTAQSS

> RXA00830 (1-723, translated) 241 residues
MENPGDLGAM PQYGFEHISM LITAVVLAIL VVPIARRFNF APAFGWVLLI ATLLSNLWNF
MPGYYTLDQS WPFHFSDALR IIAAIALINR ARWAVSVTIL WGTTINLMSL LTPDVQYLQV
PWLEFLMYWF MHISVFLAAI ILIFAFGEKP GLSGVVMSVA VAISWGIMCL MVNAFLGTNY
GYLSTEPESA SILDLLGGWP FYIVAEVLLL CAVWALWSYL IDKLPITYRP AYRPKTRKAA
A

> RXA00831 (1-702, translated) 234 residues
MSALETLQWQ DWSSVLIVVA HPDDPEYGLS AAVKEWTDAG VEVSYLLLTH GEAGIQGLDP
KETGSLRAAE QRAACDVVGV RNLTILNHPD SMLVYNLVLR KDIAREIRIR KPNAVVVSNF
DVEAYGGLNQ ADHRVAGLAA IDATRDAANP WAQPELLQED LQPWGAEVII IAGHPEPTHT
MDLAKDSVDA GVASLQAHKE YLAALPDPPK PEEFIPAFLE VEGGYAAAFR VFGR

> RXA00835 (1-690, translated) 230 residues
FAPWALTPIL MLGGSYLCFE GAEKIWHSLH RRIKGEQHST EPKSQESPKS EDQLVKSAIT
TDLILSAEIM VISLNQIADQ TIWMQAAVLF VVGIGITALV YGVVGVLVKM DDVGLTLSKR
DSAGIQKFGR GLVKAMPIVL QVISVVGVFA MLWVGGHIMV VGTEELGWEL PYHLVHGLES
WANGIGGSAL GWVGNTFGSL VFGLIWGAII TVVVSVIKKF IPQRAQNSSH

> RXA00836 (1-1671, translated) 557 residues
MYTHSTGTPQ LDFDGDIYPL HLFFSAQTAQ HFALERVNWH VLRAIVKPEQ GELIVEALLA
PIESATKIGV WVQDEFLGVI AESQFLLNSQ LSRIFASGHL ISSQLLLTPS KGSLASVLLP
NLKFGLISND PPRADSHLLP LGRMWRVEPT VHALFEDFSL GSTILFGLRL DLEALIVSYN
GIECGILNFD DASALSSAVK FSNANGLTPT VLGHVVRENG ETSFEIDVLP LELWSKKQHR
LEVLKIPRLI PKEADSQNYV KATALLSDEI LRPQTLSKKA LSLSDTAVKY SPHVACGVGM
FSLFAVIPFD KLSDHSAMLL AVISLMLFVL ALVILFKRIQ STNTQRWNLA SSVGLLATLP
IIIFLVADTL IPQGSLENHA QPDVQVTTLA NRRPSSPTSL DSLGALNSPS SPNSPSSSML
QNSEMFASPP IASGQSPVST FRSWLDRSIL PLTRENSASE SAVTALGPSI VQPASESITT
PAQTSQSRHA IDDGDDSKTS TGRPAPTTNS PIIALPPTWI IGPEDPESTD PTAPTEPTEP
SEPVATDEPS ETSEQTS

> RXA00840 (1-714, translated) 238 residues
VTKTLPRLLT VAAALAIALP ATPVASAVTP VEQAFNASSN LSSGLPVDQW GRPNEQFRQQ
IEQAVNQPWV PQEIKNIVSQ AMGFITGDGS EGGDIEIPDN APRIAQFFWP TRSENCINGN
SAAVGSAFAV PGPADLPLPG AGVGQTSFVF TALGTGPLAE QQSTAMTVQW ANLSNFTHGT
TTLSNTGINP DGPSTISGVA DTGRGIIVAS MSGGLTTSTE NGSANCNFIP TAVVFDVR

> RXA00841 (1-537, translated) 179 residues
MTDLHPVKQE IFNTAESINT DPKGFLREVD TFKVTDFGLY MARGANHPKF GYLESWLLPE
LGLRANIFHF RKGVDERQDY YIDVAEIRVE DNIWTTRDLY VDLISVCGEP VTVMDIDELA
AATSAGLITA DDAERAIDAT LNAVEGITRH GDDPMQWLRS KGIELTWADA SQVELVPAE

> RXA00846 (1-387, translated) 129 residues
MLKNDLSGAR VVAVHAHPDD EAITTGGVLA DLAARGADVT VITCTLGEQG EVIGETFAQL
VNGDADQLGG FRIHELYASL EILGVRGIHL GGAGCWRDSG MVGDPANEHP RAFIHSGDRA
VEQLKELLA

> RXA00853 (1-603, translated) 201 residues
MPTSSSPATV TPLKKQSSRK QLQDIALIAV FAALIIVLAF VSIPVGTAGV PIVLQNASIV
LAGLILGGRR GFLTALLFLA LGLIGLPVLA GGRTTLAALA GPTAGYIVGY LISPLVAGII
AYLAPKKRGA GMFIVLGLAG LAGLITQYAC GIVGLVLRAG LSLSEATIAQ GAFVLPDLAK
ITVMVIIAAG VHAAFPDIRK K

> RXA00854 (1-213, translated) 71 residues
MRLSEFRQLI EDEFGEAKGE WIAHSHVIGA LGVTADVAVD TGVDLRDVWE QLCIDFSVPE

ERRLGKDEPG F

> RXA00855 (1-285, translated) 95 residues
MTYFAVLYTY NPDSEKVAEV RTVHREFIAN LHAEGKIVGS GPFVDGDGGA LIVIKLEEGS
NLVDAETLMN NDPFHVENVL DNRVIRSWNP VTKDF

> RXA00861 (1-426, translated) 142 residues
MAPHKVMLIT TGTQGEPMAA LSRMARREHR QITVRDGDLI ILSSSLVPGN EEAVFGVINM
LAQIGATVVT GRDAKVHTSG HGYSGELLFL YNAARPKNAM PVHGEWRHLR ANKELAISTG
VNRDNVVLAQ NGVVVDMVNG RA

> RXA00862 (1-564, translated) 188 residues
VTETETANPV TTTRTPSDAA PSPTTSEPTG SESTNSPSPT ALPPLGSPSM DQKQQAQVGD
SDMSIAGIRV AEHETFTRVV FDIAGNGQPG WWVDWATDPI QQASGLPVEM AGDSFLNVNI
QGTGYPDQVV VPGIDTGSYP GAGIVEDINF TSIFEARSQV LIGVSGQPRN YSVSLLQEPT
RLVVDIVH

> RXA00869 (1-792, translated) 264 residues
LFIVAADHPA RGALAVGDNE PAMANRYELL ERMAIALSRP GVDGVLGTPD IIDDLAALGL
LDDKIVVGSM NRGGLRGASF EMDDRYTGYN VSSMVDRGVD FAKTLVRINL SDAGTAPTLE
ATAHAVNEAA AAQLPIMLEP FMSNWVNGKV VNDLSTDAVI QSVAIAAGLG NDSSYTWMKL
PVVEEMERVM ESTTMPTLLL GGEGGNDPDA TFASWEHALT LPGVRGLTVG RTLLYPQDGD
VAAAVDTAAR LVHTDIQQFT SQSI

> RXA00874 (1-1089, translated) 363 residues
MSIGQHIITE RFYGAKSHTI DNVDIVLSRE CGENTLAVVR INNALYQLLV NDDGKDVLND
HVEEVGASFG AWTGSSAFPI GPFTPLGTEQ SNSSFITADN KAIVKYFRKL ESGQNPDVEL
ISKISSCPNI APILGFSSAE ISGANYTLVM AQQYVPGLDG WSHALTTTSG SFAEDAEKIG
EATRNVHTAL ASAFPTRVVP VEALADALTT RLNELISQAP EIARFKEAAI DLYQSLEGEA
HIQRIHGDLH LGQLIKTPER YILIDFEGEP ARPLNQRRLP DSPLKDLAGI IRSIDYAAYF
DGEHTQWANE ATALFLDGYG SIEDQELLNA YILDKALYEV AYEINNRPDW VKIPLEAVER
LLD

> RXA00876 (1-1755, translated) 585 residues
MTLKIDPSSI SSAVSRLNEL QHQAITASQV GMKSTILSAF SPVSGLDQLG SGHGNVINGG
AGAANSVLNS YAEQIEWLSA ALQASGAALT GQDELFARGM DVADTGGRVV EESVMFPARP
APRFESFVFN PPAVSPSLSL DALCSQFSGT NSGAVLEAQG SWGSMASAIS NVSASLSSIA
GEILAENSGE TFEQAAARIN EVAAAGATFA ANAKMMGASV GTLNRIYMGH RMQVFMAATS
IKAILDPVQR LAAERAFLAS FQATFQADVL TGMPPVSNLM QMKGANGSAG EIALGMDEIA
GSGQAWSAAG LTPSGAAQGG VANAGSIAPD AAVQGAAGQS GVGSFGTVTD QLDGINIGDM
LTSAASAGQS LANGLAMPTS TPNSASGAIP SSMSAASPLG AFGSGAGLGA QGGSIGSSAP
GAISSRAAGS AGGSVPGMTG GPGAPGITSD SLMGARTHGA SSAGAVAPMM GGAGGMSGGV
VGAGGTGSQS KYARQTGSSV GSSSQSGSGL GMVGSGSGKP SISNFGRGMM PMMPMMPMGG
AGGGQKNTGK VKTVTSAVEE DRNLAALLGD RGPVVPGVIG DWVRG

> RXA00881 (1-378, translated) 126 residues
MSNTETQFDW DGSTWTRTEV GEAPTRFAVG VMEDFAYIAA TGTDGDEEFF TLGSNPGLTF
GDPEWLFAQD NPQYVVECIG QQGTEPAALK VVDKYLSRLS DEESRGEPTR ILNELVSAME
LPALPW

> RXA00882 (1-678, translated) 226 residues
MSSTTAQLRH RELTQEIYNI GDEVAEYIEH IMEAVSDWDL ELVEDCLAEF DEIITEARDD
SRTVVAELSG LRHALTTGIR QGTVSARATV EVDVDKPERL TASELERDFD IDAGLVDVRD
LSTALNARTD AVVKRLEATV EWVLAETDKV ANDLDSLSLP LLYGRVAAVI ESATSAWINA
VGTANPAYVR TMRGSNPPRF LLERARIDAV VARVADKLAQ KRNAVS

> RXA00883 (1-519, translated) 173 residues
VQGMKRKMVA AALATALLFG AAPAHASELV EPTTVAESVA LDPNKAINIL TPDLWEDIEA
KPGDIVHIPY QGTRNYEDLT VEVAKPFEDF QILVGLDNSI VIAVPKNLSG AASVAPVFTV
SDKNGEIDSF TIKVSVEPRR QSDEEKRSAL FDVISELAYR MPHLPFVSEL LKY

> RXA00887 (1-723, translated) 241 residues
MSLPVFISDS AAGPGETIEL AGPEGRHAVT VKRIQVGEKI SLIDGRGTAR TCTVTALQGK
DRLNAVVDLV EEIPAPNPQV TIVQAIPKSE RSELTIDLLT QAGADRIVAW QASRCVAKWG
GKEAKSLAKW QVAAEAAAKQ SRRATIPEIL GVVGEEGVEK LIDESDLAII LHEEATAAIR
ELEFSGNVVV IIGPEGGVAP SEISRFVDAG AHTVKLGPEV LRTASAGMVA LAAIGVLSDR
W

> RXA00889 (1-588, translated) 196 residues
MSIEVFNESG YDGVNEEMLI DVLSFALGEM DIHPDAEASI HIVDVDTIAD LHVKWLDLEG
PTDVMSFPMD ELTPGYSRPD GATPGPAMLG DIVLCPEFAA KQATKAGHDL AHELALLTVH
GSLHLLGYDH VDPAEEREMF ALQNELLADW YDNVEARGVT YQPKPSGAGA FPTAADRLEL
DEKMEADDSG FGGVES

> RXA00893 (1-597, translated) 199 residues
MVESQHIIFI PESQQTPDEF TEVVNEIPAG IKPRIVPWSG SVSAGVQAVE SILDREEIRR
VILVGAGTGA GVALEIAKNQ PRRVERLVLD SPLVTFDEKQ LKGMSTALKM MPGFFFRKKN
KKDLLQQVEE ARTAVPMGFS EITMPTLIIR GSAAKAGIDS DLEKQIPSAR ATTIIGANWL
TYTTHGRQTG AAIAEFLAQ

> RXA00895 (1-591, translated) 197 residues
MRGLAMILIA VAVLLAAWAL WSMQGKDDTS TTSAGQTQST ETNAGTIAES SGSSDSEQAS
AEPGTSEETS AEQPAADGEA ANAAGAAAAG GASSANGNST PVNTLYVLNN STVPQLAARV
ADSLSGDYQK VESGNLPDTI IPQNTVYFTA GNTEAEKAAR ELADRVSGVA MERSDALPTE
TEGKDALVLV LVQDVAL

> RXA00903 (1-633, translated) 211 residues
MGNPLAVIAD ADDLSAEQMA RIARWTNLSE TTFLLKPTQE GADYRVRIFT PTGELPFAGH
PTLGTAHVFR ELHGEQGTQL VQECVAGLVA VRAIDGPASG LAFQAPPTLK DGPLDASDLD
AACEALGISP DFIRAHQWVD NGPGWAVVEL PSAQHVLDLE PDFSAHPTLK LGVIGAYPEG
APHAFEVRAF AQGIGEDPVT GSLNAFIAQW L

> RXA00908 (1-558, translated) 186 residues
MSLYTRTQNT RHSTIIEFRR EQTRNHTMEP IQSEPRIYAD DPFRARFGHQ LPRGLREEAR
GMEWRTFTNT YAPTGNLRIS NLESEARRGG MFHFNATLIN NCQGERTTTD AHIMATGPVS
ACTNLLADAG RRVEILEFHQ FDIFEATVTF IYTCNNVSRT WAMGFGGTPE QSAASAMSSA
AHLLYG

> RXA00915 (1-510, translated) 170 residues
MSAAYSQDTI LTVFLGRGLT AEGIRQTLED FAETGLVRNL VWIDADSFHE SSSEVTHLAT
NQDGLPELQR RPFNELVSRS RTTKLHIGVI NVIDGSEGML HAEELNPLVG IIDSVCSHHQ
IHRSNVMIGA VAATLDEELP ILRGYVNLML APEDSHSPGT ATVTYRHGFS

> RXA00916 (1-3591, translated) 1197 residues
MKKVLVVGCG GSGAKTLAYM MDQLKTTLAD SLPERYPNPK EAKLPGAWQF VSVDVPTSPE
SPGPNLPNVP EAGGRYISCG SSDRYATVDT AVSNQLSSRG ALGGVSSWAL RNPDSETTPI
SKGAGQYRSI GRMLILSRLQ EIQAELRKSW DVLFSGETER ELADLRSALY GTSVSSGETS
KEQPIIFGVS SMAGGAGASM ALDICRLLTG LEGNAVGLSS LFMVTPDIFS QLSPDQVAGT
NPNALAMFAE LAAAQMGAAS EEDARLFNAL GVSVGDDSIP VGRIFPVGIR SGENGALLGD
GKPDTVYRAL GRGLAALMAD EVSMDNFEQF TLGNRGGGSA DQSKYAWGAQ EAKNIPWGSY
GYSQLSMGRD RYAEYAAQRL ARSAVDRLLK GHFDPSNDAA SDQQLQKRLE NNRPSLMGNL
SDVLPVNAPA GDWIFHSFNQ MIENWTQRMK AIIKSQIPAA NGQRGSEWLG DVQRAFQSSS
QMIDNDSRHE LYMGVADWAS ADVLQRRVVE LLRDEIAKLG VPYGVSVIES LSATIQNQLI
GQLSDLANNR APEAVQLDDV SRSELDNSKG RIDDSDSYIQ EIVSRSTGQL HTRAVQYIAD
HMASVLDDFL KNFIYPLQRT IQREHHSLEK DYQLTNDVNL GISQLKTNVP ALWPDESQTT
VPSRFSQAAN EVFLTDVASF PEQFQAHVRS STDDINEQND YSSALQEAST RVVSGVWESK
SGSEKAPRDL IRLIDVWVAR DLTRDPSGSG SLRDPKQARF ELKIDTGEVL ERSRQYIRRP
GFSFQQFIAS SLREFITAPG LADHERRARR QQVLSKFSEA MTYALPLAQI NPQLVRALYG
DEVRYNFNFS RIPFAGDELG SSLEQAVRDY PNHRPADISK PLGKALVSQG EERSIDIFGS
YPNYAPIVFD SLLPPIEKQW RQITGDRTEF WHGRRTRPLT AALPMTDLER NAMVKGWYIG
RLVGRVFFPA TLDTADTTPV QIYDEKSDSW INFSTPMLTP VSRFRGSLDW LPNLLESASL
AWARAGERPV FESVEPYIQL RQLWDDAASP SLPGRTTRGE KLLHDWLFDG NRMAGNVLQI

PGTEAGVTPA ARFEAAKNFL QRQNEISQNY VPSDKLRQGR LFTTADRPFG DVKDRELAAQ
IPVFADLAAD VFDGTQEIID ILEKCLAAGP PSAQVFDMNV ARRDVSSGPS LPGEGEF

> RXA00917 (1-1383, translated) 461 residues
QLNMQLVGRD GQPRILEGSA LVDLGFTRAD TGEFAPLAQG IDISGGELSF PLDTISQLPA
IGTVEARTTI TTAGVDDLPG TTLSPILNTT RITITQRDMP QLPASVRFTA DEDVVTVDIP
ITGPGKVWIA PGTQLSGVLP DGVDGIAASS TFDSPDNALV LGLDEQGTIP VELTVSDLRD
GLVNGSIPLQ ISNAEGANET SVDLPTEGTL SVPINASTFA LAFILALVLS LLIPLLILYI
VRFLSAKVPS SAMSGVRIPV EFSGEALRYA GSTMPDLASQ TTATKQVVVH GDTFNVEGHK
LKVQRFQLNP IASPAVIVQT DPSISFDGKQ KGTQAKLPLA VQGSWFLTAS GADPSKMELI
ALTNLPLEQG QIDRMIAGIT SKAPDRAREL QKLLDDAATS QPAKVPPRAP AAQGHVEKQA
PSFGTGSGGG FGSSNGGGFG SGSGSNDTNG GFGSSGGFGA R

> RXA00921 (1-1899, translated) 633 residues
VEGGTWSAQA TKEDLQFIAE VAPTHIETVT PFDDFISSED IDALPRRFEY RPLAGRSLIM
QSVPAGKDAT GRPGNVFTHA VFDGDLESPL ESVYPISLYR SPDLLTPFRA AAVNAAELPL
DAGEPRIGPI TDLSLSWMMI DSMFGDRRQQ FYQLQDALQA GDKATVLVLN STNEAAYWLQ
ALSSTLTPNE ARRLLHFSTF ERAATLPAPD KSMEARSLFV VPGIDRELLA EHSGIVIIDP
EIPQSQPFGP QGSWSRMTEG LFSDGFDADE LVAGLIRANE NLDNSQKELA QFGDGLARFI
RNGRFSGTHP LRVLADQHMF GKVPDKPAPK VEPVAPAPNP NAIWARASEV VHNPRRASES
QDWPSLRRLP DSRRRIINMS EQAINSIEKL HDSPAQDLVA YLDFLLKTEL ATSINASDPF
FRSSFSDFPA MDNWRHIKFT EDAHPRLREL LVDAERDARN RAPAAIVLDH IVPNFSRDRS
LPDIEDWTRS DEAQQIFAGI IAGASVQTGR SHFMWDLLRA YFGVALIGDE DTYRAFTTLT
VDSVLSFVQL TLQEGRTEDI RRFEKYGEQI AREDLPSILT NARAVQQYLG YIDQDIINKK
VSRSRDVNQI FTEMARAIIR AISRNNIGKD MRS

> RXA00926 (1-363, translated) 121 residues
MDIVFLIILL AIFIVPTFLM SRRQRARMTE IQKLQDSVVP GDRIVTTAGQ HATVISTTAE
TVDLEIAPGM ISTFEKLAIV RVLSKANEPQ MLDEPTLFDQ PEDDQPNDGF DGRTDGHPEN
R

> RXA00930 (1-753, translated) 251 residues
MSGHSKWATT KHKKAANDAK RGKEFAKLIK NIEVAARTGG GDPSANPTLD DMIKKAKKAS
VPNDNIERAR KRGSGEEAGG ADWMNIMYEG YGPNGVAMLI ECLTDNRNRA ATEVRTAMTK
NGGNLGESGS VSYMFTRTGV VTVQKGDLSE DDVLMAVLEA GAEEVNDNGD LFEVTCAPTD
IQAVRDALVE AGIEVEDSES DFRASVQVPL DADGARKIFK LVDALEDSDD VQNVYTNIDL
SDEVLTELEN D

> RXA00932 (1-474, translated) 158 residues
MTPQKLHRFA ALLEMGTWTL LIIGMILKYS GVTDAVTPIA GGIHGFGFLC FAAITITVWI
NNKWTFPQGI AGLIVSVIPW AALPFALWAD KKGLVAGGWR FSDPSEKPHT FFDKILAQLV
RHPIRSILIL LVIIAVVFSI LLAMGPPYDP DAIANTVD

> RXA00933 (1-462, translated) 154 residues
MTLVYLLIAV VVTATVLWAY FTAQRLNRLH IRTDSARQAL QAALDRRAAL VGALLPDAAE
ASKRAEAIPL EYSRFSQRAR AEREISELIL KQGKTLPDSI VDAATRVELA HRFYNEAVSD
TRDLRTRLMV RSFRLGGTAP LPEYFELLDT DLLT

> RXA00940 (1-396, translated) 132 residues
VILVLLEAES MRGYQIITTI SEQTEGNWTP SPGTIYPTLS MLEDEGLISI SHEMGRKMAR
LTEEGAQEVA KNKDAWGSIL EAYRNPESRE VRVFNIRSEF HKVREAAKAA PDDKAEQIIE
ILRRAADDIK RL

> RXA00943 (1-507, translated) 169 residues
KPGVKWRATN ATKRGKKQLQ QALSTKSETE KFGEKASDWF NDTSDKVTEY AYTAQDFVGE
NKDDWIKSAT ETAHKVADTV SDYAHKATSY LEENSGDWLE AAQANAKTAR KSAVKAAGKA
HEKANFALQV AEETSGRANK KATKSYDKLQ KQADKAIDRA QKKLKGIEL

> RXA00946 (1-774, translated) 258 residues
MTHTLQATNP LDQTAWHAWH FSRNKEAISR TGATSLSATE WISATTLKDA HTFPSLPGRW
YKRGGGVVGA HLPPAFATTG TVQLRPGELL IAEDFTLTVI ERLGQFALQV FDARNPKRFE

FHSIAAFPPS EEWRIEARFF PEPDTVNTAA ADGVIVATPT AGWVHFLKGR LDYRLRVTVQ
KNNLRALFSD NSSTLGVYQH RFVDIPRPDA EGNTIIDFNR AYLPPKALNR KFLCPSPSLN
NHLNLTVEAG EKWVVAGG

> RXA00949 (1-648, translated) 216 residues
MKVFIIGAAG GIGNRLSSLL HARGDAVSGM HRNLEQASKI TDTGATAVLG DLIHNSTEEL
AELFRGHDAI VFSAGAHGTG QENTTLIDGA GLRKAADAAS AANVSRFILV SAFPESSRGE
NTTENFEHYM KVKKSADVYL SHTDLDWVIV RPGVLQDEAG DGLVTAGLAI NYGNVARDNV
AAFIDEALHQ PQLSKIIVEL TDGSTPVAEA VERLIK

> RXA00959 (1-327, translated) 109 residues
MTVIGIILGS LFGVLAVLLI VVGALGWAAK LPGNPVVGIR VPEVRKSQEL WDMAHRVAGP
LWVLSGVSFV IASLVAFVAS GWMWLVVALG VEAAIAFIGM GAGMAAHTG

> RXA00963 (1-438, translated) 146 residues
MRLATIRTNG TTIAARVESE NTATTIEGFA NVGELLQESN WRELAENAAG EAVTFENKEL
DAVVPAPKKI VCVGLNYANH IKEMGRDLPD TPTLFVKFPD ALIGPFDDVV VPEWANKALD
WEGEMAVIIG KRARRVKQAD AAEYIA

> RXA00969 (1-147, translated) 49 residues
IRQEERDDDA RLIVVTHSAL ESDLSRTVEL LKAKPVVKAI NSVIRLERD

> RXA00971 (1-273, translated) 91 residues
NHAEAEELDE ALSPLINRLR EMGFDPTETE EANSLALHSC PFVVNDKRPS AFVCAIHAGF
IQESLGENNR IQLELKPLNA PGTCKVHVFS E

> RXA00973 (1-603, translated) 201 residues
MNHSDDDRMQ KWFQIRRELG KEIVKQLQKD LPAVASDIGS MVYSSDQVPL GNATLTAYGD
IGNRVASAAT SARYNVEELL DAIENARFAI WVPNYDNSYY LSGEEGADEF QTYLIKDASR
FLESSGNTPP ENPQYSDSKL TFASELLPFY TAFNNSTYPL LHACVQGEPT EVDLYFYELE
QAELKEKETA QLSSGSSFGS S

> RXA00978 (1-615, translated) 205 residues
MSRSPLTKGL NQLEHLELDK SLTAWSWAED DPLYLAGENL NGSYLIVAGR VRVSRDTIDG
KELTVDIATP GDVIGAIDTE PQPAVDSAWA IETTCALFLP ATALATVIEQ HPSFALAMIR
MQQQRLATAR DHEINLTTTT VEQRVAIAVR TLGRKIGQRR PDGILLIQVR IRREDVAGLA
GTTVESTSRV LARLRKEGVI DSGRE

> RXA00986 (1-342, translated) 114 residues
MTLKDKYDTE VAVSNNQDKH QFEVSYPEDA VTAGFAAYLD KGDSRIFYHT VVGDEFGGKG
LASILVSEAL KATKEAGLTV VPVCPFVKGF VEKNAFEGYR KPNHEDMELV KSQM

> RXA00987 (1-465, translated) 155 residues
MPKSLTFEDS INIAAPINQV YALVSDITRT GEWSPVCEKC WWDEDEGPVV GAHFTGRNVT
PERTWETRSE VIVAEPNRCF GWSVTDGNVK WIYSMEPLEE GTVLTESWEF TPKGQRFFHD
KFGDKSIEEI EKRRLAAITG IPETLVAIQR ILEVE

> RXA00988 (1-423, translated) 141 residues
MSKREESIEY GPLGKGHDPL KDPMKGIRGV MAGTLVMEAI TLGLVLTVIL RVDDGIYWTT
FNWVYVSAVA IAHFVAAFLQ RFSWSIPMNI VLQVLALAGF FVHPAMGFAA IIFIIAWAYL
FYLRSNLIDR MKRGLLTTQH S

> RXA01005 (1-846, translated) 282 residues
MELARAHHAR ADSFTKDHLK RRQAHIKHPV FDFLFEYYPV RVAHLKTWHP GIGVFLEGTP
PHATMRDFLL VDASLHHAAG VQLDLASYMQ RRGSSVRYIH ELLSATRDNH AQFDCFGLHE
WAMVYKSNDL RHDLPLRLTP SETDRVVESH NIKCTHFDAY RFFTTPAIPL NLTVLTREDQ
PRNDQCGCLH ATMDLYKWSA KLGPLVPGDL FLDAFELARD TRILDMEASP YDVRGYGFGY
VPIETAEGKA EYVSRQRELS ERAKPIRDRL VSITKQALQA SI

> RXA01007 (1-1707, translated) 569 residues
VFKKHRHGLG SPETKPRSIT RRFFTAAAAT LAGLAVLSGC TAQPSQAEDN TLTYLEPQFF

RTLYPPSAGF YPNGSVVNNI ADRLLYQDPE TLELKPWIAT ELPEVNEDAT EFTFNIRTDV
TYSDGTPLTA ENVVKNFDLY GLGDQDRRLT ISEQITNYDH GEVVDEDTVR FHFSEPAPGF
AQATSSFNAG LYADSTLEFA NEDFAPGNAQ NVIGSGPFVI TDETLGTNLT LTAREDYDWA
PPSREHQGRA KLDAVNYVLA GEESVRIGAI VAGQGDIARQ IEAPVEAHLK DAGIPIISAA
TNGVNNSFNF RFKNELLSDI RVRQALIHAI DREKIMRVLF SDSYPLATSV LAQNALGYKE
QVDAYVYDLD KATALLDEAG WTLDSDGMRR KDGELLELTF NEALPQPRSR EVVTMVQEQL
GDLGIKVNLN PGDQAAQDAD SKDLNKIQVR HTMVGRADYD VLKSQLYSTN RNELLNMTVE
GETADIGDPH LEELLMAIAS SPREEDRAAA SAAAQDYITE QAYVLPLFEE PVVYGVQPYV
KGFSPEVIGR PSFYETYIDH SSDHSSEED

> RXA01008 (1-1941, translated) 647 residues
VSTTDKQVAI VGVGPRGISI LERIAAALNT VSRPKQGLTI HLIEDAQMGA GNVWRTDQTR
TLCMNTLAGA VTLFTEPGST VSAPVVEGPL QFDWIRLLRG DEDLSGIPTK AIELFRTYPP
AASVAEDFKE ELAATVIQSN PSRALYGAYL RWAFDVALQL LPQWVKVEQH HARAIGIRED
GDRDVITLDN SEMISADSTV LAVGWQTPAP NAEELSIAAA LEENPDLVWV KPGNPVEQDA
SLIPAGEQVL VRGLGMGFFD IMALTTIDRG GIFHEDPSTR SGLRYEASGE EPHFVISSGR
GYPYLPKSDY KSLPPGAKLA RLKAVIAAIN AQNRGVASIN YDAEVWPAVA RDAYEAYYET
LDRVSPESIR TGLDKIVEII DEVDVDKLPK ALAAHTDDVF DLHAWEFPLA GINESVEALT
ARIADGMARD IRHAVTAWDS PLKSALWSIS AARKPSSILG AEGRLTFESR RNRFAAVMAI
GQMVGSGPPL FRTRELLALV DAGLAHFAGA RPRLSVSDGQ WQISSPTTGD TPLRSKVLVD
AWMHNPDVRR NADPLALSLE DADRVRPFND YSVDGTAAPT GSPEVDPATR LLVHPNGNLD
PRVHLIGIPT YGQLADTTIS PMPGTNPLML QETDKTAVHV LKQLGLI

> RXA01011 (1-1233, translated) 411 residues
MSDLIDMLVG EDLPQLRDNR PQARDNAQKS FEALLEPVNP GTFSFGERYA VATYVAGLHQ
FAPAVDLYQD LLLDDAPTTL ANAVSDAIDE GLSAGPYGTY REPGLESESE PGGSVRNDAA
KLGERLAAAF DYAHLLVFHP RDSRPEVLGR LSGAGWSADD TVTLAQLVSF LAFQLRVAYG
LRTLKGEDIQ VKAPRLSIPE AKWELSNNGF EISTYEELNR PEAFVNHSLG WKPWVPPVAK
ADLTEEQLDS LIQPERADMP YFRLLARDPA ALKARTLTDL DIFFNTDGEG LGRAERELGA
TVTSRYNGCV YCASVHAGRA QEESGRADDV NALLASIDSD LGSDQWNVIR DAARALSSTP
AAFNQGCITK LRGVGFSDLQ IVDLINSVAF FNWANRLMLS LGEPEVPKRF L

> RXA01016 (1-648, translated) 216 residues
LLPYAIVGLV ILLPSSWLPR WAVAVLGEVS LVPAVVFGGG FLLIPSMFLI GSALVRYGVV
DRAENAPRAM GVFFAVSAAI AIPTLIIQAR DITSSGFSIV STVAGLALGG VYISLVLLAL
HTPIRGALAA VFAPLGRMAL TNYIGATILM LIGGLIVDLP HSTSWTATVL LAAGILIIQE
LLSALWLRHY TQGPLGYLWR WVTWGSRSPF LTRSAS

> RXA01017 (1-609, translated) 203 residues
MAQKVTFWFD TTCPFCWVTS RWIKEVEQVR DIEIQWVPMS LAVLNEGRDL PEDYKERMKA
AWGPARVFAA VATDHADKLG DLYTAMGTRI HNDGRGPIEG SFNDVIAEAL EEVGLDAALG
EVADTTEWDD ALRAFHQTAM DEVGNDVGTP VVKLGDTAFF GPVLTRIPRG EEAGEIFDAS
FKLASYPHFF EIKRSRTENP QFD

> RXA01021 (1-522, translated) 174 residues
MSSSESSRSE GSQPAPSVQP ERRADSTGAP AAASKEASQQ MDAAGVLEWA RTAVEQLSER
RAEINALNVF PVPDADTGSN MTYTMTAALD EALKLGELGD VARITEALAV GSVRGARGNS
GVVLSQVLRA IAQAAADGVI DGHTIQEALS IARSLVDRAI TDPVEGTVVT VLRS

> RXA01023 (1-951, translated) 317 residues
PANGGINKTP MIIALVLSIV LVLAVLFGAR VLLGPAGQQQ IAMSGLPAPD AESAECAALL
EDLPGEAFGH TRAEIMDPVP PGAAAWSTSD LERVTLRCGV DMPFQYTALA NTVDVDGTTW
LPVSDMTPGS SLETWYSVNR FPVVAITADD ISTDSADNPV DPFSSAVDKL EKRDGQPFDA
PLTGLSSAGT TCTSLFDALP RQLEVGGDDG TTYERIEEDR MQAAGYSDDA VAWDTPGLEP
IVIRCGVEPS ENYAAGAMLQ QIDDIPWFED TILASGTTSS TWYALGREID IAVSLPQAAS
SSLITISGFI EDTVPAE

> RXA01028 (1-624, translated) 208 residues
FYQNILASSR GSNTFLFSVP YIPATEGEET HPATDTSTIA TPTLSFDAYG NKAEVMPTQS
TVDKRVPSLL QYYTRTFHVR QDTQQAVFDV IGANPVLIAA AKAASISPAS ADSRRKKGLA
STNADPVAKH VLEIAGADVE SLRHEKDLKV TKHTGQDPAL PVVVFNQTIW HNPNDDVINA

LLGAIDQDAY IDMAISSYNK SWHNIIPA

> RXA01029 (1-489, translated) 163 residues
MLQTISFKKL NLLTTLKRKG ELVIMITRHD VPYIIAPPVY AIFASLMTTP PWFYRTTYTI
DGFDFKISWV YTITIYISLM ILIIGFYQAN MRKACPYEED PLVDIWHKVW STALFILPIV
LSIAVYSLIT QRGFDWYVMV FILPVGLMIA YGFFKPCDCD KHR

> RXA01031 (1-666, translated) 222 residues
MKLLQYAGGA VYVDPEDSAQ SQDLDASTAR DVIDATNTAM TTITSRPTMI VHLHKVRKVI
EILCNPALGG EPVNIDQDET GKQVYTPTPT LVAYRFISDK EILLHYLAQA GVQGVEVFDG
SPDMLSRWNA GRIPVLLLQP ASAGHGLNFQ HGGHRLVWYN LPDNNEHYMQ ANARLHRIGQ
KNPVTIHRII TADTYDANMP AILAGKANRQ QRLIDAVRRD PV

> RXA01032 (1-375, translated) 125 residues
MSDHDAPQTP IPKGFWQQID HQLDRLGTQR PETFAALRDI LLDPAYTAIV HDRNRYGVVT
FDTNSAFFSG SGGDNGLADV LINCDWRMTD YRAEYYYVMT HKYTKESFTY IEGDVKRGDL
IPPNN

> RXA01033 (1-336, translated) 112 residues
MTQIAMYLAG PMTGIPEYNY PTFHAAANKF RAAGYTVLSP AEDEYESQLT APLPENAEHK
YDHYLRLGIE KLLKADAVHM LQGWQSSAGA TLEHDIAQKL RLAITYEEPP AS

> RXA01034 (1-354, translated) 118 residues
MDMAIIQSVE YTSDVSHERI TNVVSVGVVY EGKQYVVDLN GDDIDTELDM ITLKEVIKIG
REESARQIRR GSVDAELHRK ARLWAIDNDM AVGQRGIVPQ EIIDAYKEYC EKEGIPFE

> RXA01035 (1-606, translated) 202 residues
VLIRIAEHQG RLHVHSPYSK AFAARARKLN GLWSPETKTW HFSPDKEQPV RRALKDVYGW
DEFTTPELCT VQLTVTPEAV LNKHTLTIAG VTLLSRLRRN YSVWLGDNVR IISGNFPEAA
GSPQYPLIMG VKAQPVVIHV QEFPVDAVST IPPRFNPIVI TAPPSIDIAA LRAEREQLTR
RISEIDKKIA RAVHPTIQTE AA

> RXA01036 (1-453, translated) 151 residues
MHTVGYKLDT DLRKLTNTDV LDLINALFGT TVTSADDEAA DFIDSDPQFA VLVELAYHDC
ARRAAMGLSR VQQLIYDNAA KSTYYRSVAA RHRKHIRELH EQTQRDGIHF DNPLSRAVIN
DLSMSMNRAR LNRIASWKSA GVQRYLNPTI S

> RXA01037 (1-528, translated) 176 residues
MTTSSPLKSK NSLNGAQTTF VRNCVADGPT EVKATIDARG GIEQLRDNEI SQLPDKLWFN
SATSASNDEF TTDNIRLGLL YNMALNKASA HRYELAARWY AIVSPQPSQE ASHKRIASWH
LTQLHALVTL SRTLGVIIPG DEIDALAQSM ENARQVGTEN WSTVTMRTYV TNRKAS

> RXA01038 (1-747, translated) 249 residues
MTRDIFHEAA KLIAHLGWRD AFPALQRTDP APTHAVPIRA FDLKAGAVIT DENRSNAYIY
DTLVITQPYK HELPHQNTHP FEWALEQIAT LDPAFSIKLD RSVTVPEIGL YARTLHDLNT
RHQDFLAQRN AMLLVVARRG VDPKNIADVL GLTTNQIHRI LSATPADSPT DLGVNPATTM
GDVVRFIKKR RTTMQLRGTA VRALLYHGLT PAVISRLSGM SRAGVINAAK AFPTTINHKV
KKRKQHFHV

> RXA01039 (1-576, translated) 192 residues
MAIKGAMPKN RVPGVAAGAF IAAAVIAGGS GVTFLAQGGG DVNTVAVVEP QDEVKNQVVT
ETEIVTKVHD PSSSDASDAD SNTGTAEGAD SDHKEPREHD SAQEPTAPTD PTLTITGNGD
TPVSALDAVA GPARPGTVHV IENGETLSSI SQDSGVPVGL IIDRNKLVDP DLIYAGTPLA
IPTEQELAAA IQ

> RXA01040 (1-903, translated) 301 residues
MTYPVTPQPV QPAPVAEKIK ASSLKEGTQV FIKGRVNYSR IASFITGTER ENRNRDRLHP
IEFDYTSLTL SHPEIIYGNP QQKTNEELFL EQRIFVGKKR PEEGPKFSID NKSNRLPQVW
VPSTNADGTY EQLEGLEGEL DAGLNVIILI EFYKPRTQVN RGSRLNAVFL QEPIRYYTPG
YNADKLAALG IVLNAPPKDT IQLVPNEVAA GQDQSTTDAS GLPLPGQGYS APDQPYQAQP
QYQQATPAAA PQQYQAPQPQ YQQSAPQAQP APAPVAQFQQ ASASGTCSAS TAAVSGTTSC

R

> RXA01041 (1-153, translated) 51 residues
VPQAPAVQAA PAVAQAPVAP VVDMTEPASP WDLPAAPSQP AQPAQGITYP A

> RXA01042 (1-1278, translated) 426 residues
MVNPFHTLDN SPFDPVAQFP AFYHNPLINH LGRRRAWTIS DINKRPINVQ QMLTTATYGS
PVIHGARIED AATSLLTLDE LRTQIPTAAN NAFYLDAVQD GCLILDIEKT CPPEVAATLL
TLSPTAFYTE VSMSGRGYHL VMPIPENFAA FPAVHNKPSI KHPKRWFEIL TSQWITFTRQ
PIPEHVLHHS ESANTSAVPW LNDQPLTWEN VFADLAKTVA PNLKTGAGLT ITPNALMPPD
LSDAERIRDD EVIDSTCRLF AEHYSKTLAD FYDDASRFEF SQIGVIINLL LPTMRMHPTT
ISLDKPINSD HIIRLLFAVA TRVITHRSKH DEERSGVPYL MYQVISCLDM REHPDNGDYR
VVPSRHNRDQ HSNNPSAHVV HQQPQPQPSA ADSPHHYRAL PQENTVSEHS FKIYNPPATP
PLGGEN

> RXA01043 (1-573, translated) 191 residues
MLKFRIISTV TTGSQPTPRK SWSHPDTTLL VTMVTAPSLC SAINVWNATE RIPAQKILNV
EEVHVLGECS DAIISTSLTK KDNPHALVPD DFDQIGDVFG YAQDNVAVFD VIVAALGGAG
YGLLPGLVMH HIDEHTVALV FDTDSPTGTH ILGERCVYSD IIHMTDDKSA RGWGAVIAIA
RAIILKVEQI M

> RXA01044 (1-1257, translated) 419 residues
MSLYLDDTLS RIVELDLKDT RIVPFLAGEP GIGKTSFIYG IGERAGYKVF SISVNTLADK
GDLTGARTLQ DPADGKWKQM FFPHATFVEA NDYALANPNE TVVILLDEIN RTDSDVTSAS
MTISTERRVG TTDLAPNVRL AVTGNLTGNV THLDSASLTR FSLYEVKPSA ETFMNIMGGR
LNKYIRTVLT KYPEYIFMKP TTATALITTG DDDDDHTTNA KQMMDFNAVL GSDQDMVQFT
APRTIEGLSV WLNNADDDFL RLLLQEKVDG LARSMSLLQA TLESHTGDTA FTAEVLSEMT
NDLLSSASQA PSGPIKPFVY DRLAAAPSNT VLEQEVHTLS LNDRADVLLF ALHDTVNNAA
PSIIAHLASE GVLDELPKDR ISKIVSLGPV PTANYHALTR QDTTLTRNLG PAVLGFLES

> RXA01045 (1-1824, translated) 608 residues
MVTFSVANHA PHTFSPFDIE PPLTGNATTD EHGYEHTSVL EKLASNHLFN PINPQHPVTI
TATENGSTVD LDAAALAQHL ALAITPDSML ANHQGYNRDM MGLLSQLTNH VGFDRRFIVD
QLFISQVLKA NRLPAPANNV IYTVPNDVIP SAKDILSTTA KMNNPLTVTA SAPITVDDIH
TAYEVFFASL ASVFFPYTYG AVFLNNAEFV EFVDYLINEA TTLHSASLIS NNTFNRFQSM
RNISIDNLTA EFLLRKNEAE TTDDYSFPRV LVSLLHSWVK LNHDDARANN DAPTCALAPF
SVAQWIMPET IVFINAEAHA HASSQDIEKK WKEINAALTG SIRIMSPNAI SKLQSAQHLG
MQAQMQAMRA RKDHHNMQKR SSQENDFSKA LPSPQTIVLS VAEVLRKLTH VRQSHNPQKY
QKKSLTRASR RHPDNPNVPG TIKSKLFYPD LHVYVDTSGS ISEESYRNSV VLLMQLATKL
DINLYFSTFS HVLSEEVLLP TKGKTPQQLA ALISAIPKVS GGTDYHQIWD YIQINPQRQE
RMNLVLTDFG FMPNRGLNID HPSSIFYVPI LPDYGSWSMV RRDMSHFANE MVDFDPYIHS
RLLGVHGK

> RXA01046 (1-1779, translated) 593 residues
MIPFPGQPQQ QSAPNDETRF IDLNERHKDD EPALFRDDVI DQTLAILISK NKPNALLVGP
AGTGKSRIAE DIARRLANDD VSIPDQLVGH RILDVSIAEL VAGAGVVGQL KKRILDLIKY
ATDPSNKVII FIDEIHQIAG DQSSHSGSQA KVAQILKPYL ARGDLRVIGA TTTQEARDFD
HDPALKRRFS RVNVDEFDRD QTLTILHAAR DGYLKHFNNA VTVSDDVLGY VYTYSQQFNP
GNTAQPDAAL TLFDKALASL TMEKQRLINN HVIAPSLKFP VSERHIHNTA RKLAFGSQVP
ASINTDDARD KLETLFGQDH IIEPVLTAIK REQLGIFPRT KPLSWVFAGS SGVGKTEMAR
ILSRAINGGD PIIINGPEYI SPESITGLIG SSDGYIGSNS KRAKPLDPLI SNPRQVIVLD
EFEKSHPHFQ QLFMAALDTG TMAMANGTTL NFSQAIIIAT TNAARDKIGR DSFGFDSDNS
GVLGSAQAAT DPRAQERLKS LMSKDFLLNC STVSRISLPS TALMQAPTVR FWTISTSVAV
TPCCLATPHY AAQIPADIDS DTLDQLVETT FISDFGARPA ARTIEDHIAS LLM

> RXA01047 (1-474, translated) 158 residues
MIDTTANSTS GTLPTLTADQ AAFITGFCEA AIFTATVTID NEPIFLDEAF FLGQETYTDI
LMNQLRTNEA IVKDCLDFFL DNYTTMNKLI VDGLCPDWEH HGHDFLLTRD HHGAGFWDRG
YDEYGAQLTD NAEKYSENCL NFWIEPDSDP LIINFEYH

> RXA01058 (1-321, translated) 107 residues

MRKLRTASVA LLTAGALALT ATPAMAQSTT GSSASSQVGD ALGASDYERD IWGSSKDFDD
VTPFGSAWYG YTLAATAVAI SGLVYANLPA IEQAAAQAGI KLEIPRY

> RXA01062 (1-486, translated) 162 residues
MNEQEREALE DAALEEAALA DELAALEAEA GVQGSVEPYD YAADLDDEDE FDEDPFAQDE
PRDAGPLGEL SSDNHVSEAV AEDTGTSTEE SAQEGSHEES VDNPRDFTGT ATAVRSFRPR
LPVPNALRPG PPIRTQPAVN TDIYDGGQEN TAGATAADVG AG

> RXA01063 (1-330, translated) 110 residues
MADEKKVHVR ATLRFDSDTH QRAIYWADRK GISLSAYAEE AIREKIDRDN GVHVIPNSLL
DNRMNQIIDQ LSSFGRELAN NTTVVTSGFN TIIGMTRGDS YLSDDLDDLG

> RXA01066 (1-726, translated) 242 residues
MRRDSFRDRA LVVKTYDFGE ADRIIVLLTR DHGIVRGVAK GVRRSKSRFG SRLQLFVELD
VQLYPGRKLS TISGADTVGY YASGIIEDFT RYSCASAILE IATHIAGLEN DPHLFEETTR
ALKNIQDSPE PILNLDEFML RAMNHAGWAP SLFDCAACGR PGPHNAFHPG VGGAVCLYCR
PPGSAEVPPE ALHMMWLVAN GQAARIPREH PEQQTTIHQL TTAHLQWHIE RKLPTLAVLD
QA

> RXA01068 (1-1071, translated) 357 residues
MPTNQPTPAQ IKRWRGYLAN EQAEAAAYRD LAKRREGEER DILLALADAE HRHAAYWVEK
LGPDAENPPK ADVKTRLLGF LARRFGSVFT LALMQSAETR SPYDDDADAS RQISADERIH
AEVVRGLASR GRERMSGNFR AAVFGINDGL VSNVALVMGV MATGVPAQIV LITGISGLLS
GALSMAAGEY ISVRSQTELL DASLPDPKAR EALHALDVES NELELVYRAR GMSEDEARAK
ASQVFQRISD QKRISDNVLG STEIQSAGSA RSAATFSFLS FAIGAFLPIV PYVFGMEGLA
GAVVSLVLVG LSLMATGATT GLLSGKPPGI RAVRQLSIGY GAALVTYVLG LLFGMIL

> RXA01069 (1-603, translated) 201 residues
VNDLPNLPKL PFNWTWVLAT VATTVVLAGI GLYVYYPSLP DPMPVHWNGS GEADNWTPKS
VGSFLSLILI GPGIILLTLS GMQALLTMQS GVITQRGGAK SANEAHRQWE TYKATSMHMG
WYMFVLNALI LVMILNEFRP NPLPGGFIIG LIGIIAATIV LLVLIGKTTT SLAKKYPMPD
QDGKTWGIFY NDPDDNRILV D

> RXA01071 (1-387, translated) 129 residues
NILYALLALS VIVAIIGIIN TLALNVIERR QEIGMLRAVG VKRGQVRTMI TLESVQIAIY
GAVIGIAIGL GLGWAFVTVM SGEGLDAAVS IPWGQVGLML VGSAVVGVIA ALWPAVKASR
TPPLDAITD

> RXA01074 (1-705, translated) 235 residues
LAEAAGLRWL AEASSAVAQV VSADAEQITT VGVETQLPTP DAAFKAGEEL ARIHLAGAPA
FGCPPAGWAG LNYIGTQGQA CLSTPTWGVF YSQQRVLPFA RRARRRNHLT EHALWVVEAA
CDLISELPDD VPPARIHGDL WFGNLLFGTD GPVFIDPAAH GGHPETDLAM LDVFGAPYLD
EIREGYLSIN PLPDGWRERT PMHQLHPLAV HAASHGPSYG VELLHAAKAT LKLLD

> RXA01075 (1-411, translated) 137 residues
MDNPVNILNE QEALERLQSV SLGRVVVRRS DEMDIFPVNF IVDKGAIYIR TAEGNKLFSM
NLNHDVLFEA DEVKDGKAWS VVVRATAEIV RKLDEIATAD TLELKPWIPT LKSNFARIVP
NEITGREFTL GEEPERY

> RXA01076 (1-1020, translated) 340 residues
MTPAHIFSEG PINSVVLSQD EDGNFTTSYQ DTFSDPSFLG EGDVLIEVGW SSLNYKDAMA
LKGDKGVVRT VPLIPGIDVV GTVIESADPR FGRGDEVVLN GAGLGENRHG GFTQRLKVPS
EPLLHIPFNF SAQQVGALGT AGFTAALSVN ALVDQGIKPE DGEILVTGST GGVGSIALHL
LNKLGYTTVA VTGRREAHAE YLTSLGASDI IDRAELSEKG RPLQKGRWAG VVDSVGSHTL
VNAIAQTKWG GIVTACGMAQ GPDLPGTVLP FILRGVHLVG INSVDAPREL RRRAWALLSE
HLDTAVLDDM TTVIDVKDVA QAGEDLMAGK LHGRTAVRVH

> RXA01078 (1-834, translated) 278 residues
MSNAVPHNVS FNFVPRAYRP EKPRTFGMTE IRAPYYSTFG TRHLQDVFDV AGQWVDGIKW
AGGSFSLVPT EQVRAFSDIA HENNAYVSSG GWIETVLRYG DDAVDHYLKE AKEVGFDVIE
ISTGFIMLNT SGLQRLVEKV VKAGLKAKPE LGLQIGSGGD SGEAELAAEG KKDIGDLVDR

GKKALDAGAS IIMIESEGIT ENVTEWDTGA AASIINGLGL ENVMFEAADG PVFEWYVKNY
GNECNLFVDH SQILQLEGLR QNIWGNKSTW GRVINPAP

> RXA01083 (1-276, translated) 92 residues
MFPRIPLAMC AVAAIPAVVL RFSELSASPV ATMLIFGTAV VAASFVLAWA AEAVRKDISG
ALAVALLALV AVLPEYASET VVEHTYQTSA AN

> RXA01085 (1-957, translated) 319 residues
VTDKARNRDV HNEQQLARGE IGEMRSPMWV EVGAAILGVF VLVVMWLAWG GIGLLIQTMM
NTGSPNDKEL FDELGVRPYY VAVEQQIGTS SAHTTCYQPL DEFGNNFGDC TRSVPKEPVW
YADYVASVFA EHGFDAPEPI DNSVGSWLLF GHVGIIRVTF VIAVAAGVYA MSRAAMMRQL
ETQNVAVDTT DINQHTNDAR LAIPQEIVRD LSLFPDVGAH SPVQPSSMIS HVMLSNKGLK
KVDVTQFAQE TIIDNDTGEI VSEKGEVLYD GAGQPITKSL PMIDNEFSHA IFDKSDVPNL
PELRRFFNPA KIEWNPGGS

> RXA01088 (1-1182, translated) 394 residues
MGLWIDATAG VAGDMLLGAL IDAGAELEKI QQVVEAVIPG DVLLRTEEVV RQGQRGIKLH
VDAQHEHHHH RHLSTIKELL VNADIPEQTK QDALGVFELI AIAEGKVHGI EPEKIHFHEV
GAWDSIADIV GVCEAIRQLN PGLIAASPIA LGFGRIKAAH GDIPVPVPAV AELVKGWPTQ
TGALMESTEP VGELATPTGV ALIRHFATQD GPFPGGIINE VGIGAGTKDT EGRPNIVRAI
LFNTSRSNPD TRTLVQLEAN VDDQDPRLWP GVIEILFAAG AVDAWLTPIL MKKGRPAHRV
SALVDSSEVE AVKTALFAAT TTFGIRSWEV EREGLDRRFE QVEVDGHTIN IKIGSRDDQV
ISAQSEFEDI RSAAVALGIS EREVVARIPQ GTTE

> RXA01091 (1-471, translated) 157 residues
MVPNTVLIHD ETADLATQIQ RLEHIMACLR DPVSGCPWDI EQTFASIAPH TIEEGYEVAD
AIAQEDWPEL RGELGDLLFQ TVFHAQMARE AGHFALVDVV KAISDKMVLR HPHVFGAQSN
AKSADQQVKI GKSSRRPSAR AKRKRAFWMA SRWDCLP

> RXA01092 (1-180, translated) 60 residues
VETAAFVAEQ LRSFGVDEIH TGIAKTGIIA LIHGREAGPV VGLRADMDAL PLTEITGVYY

> RXA01096 (1-699, translated) 233 residues
MKPRVLSALG IGAGALVVWI SSRMNWVTIE AFDDKSGSVT QSIVGATWST EIMALALALL
AAFAAALVLK RMGRRIIGGI SALIAVGASL SPLALLTQDP DAERARTLLT SGVASQKANS
GTLLSDWAEI INTTTHPLAA VVAMIGCALA LVGGVVLAMR PAEDTAKSNQ YERKQARAEK
IHTDLAQDPD SGRVMWTHSM KTLTSPRRLR NPKKPQVKAR VWHPDFFRHV CSG

> RXA01102 (1-1245, translated) 415 residues
VAVLVAVAAA FGSWSLLLPV VPLAVLNNGG SSAVAGATTG IFMAATVITQ IFTPAALRKI
GYTPVMAFAA FMLGVPAIGY IFSVEPIPVL VVSALRGIGF GALTVAESAL VAELVPVRFL
GKASGMLGVF IGLSQMLFLP AGLALGDQFG YNVVYVLGAV IALVAAVMCL RIPQVKAAAK
QQPQVSEQER SVSTWKLVLV PSLAVTSLSM TFGAVSSFLP AAVIELDPGL GAALAGIILS
ITGGSSMVFR YLSGVIADRR GVPGTTMIPA QIIGFLGVVL ITVTIFQGWS VWLLIIGAVM
FGGAFGMVQN EALLSMFFRL PRTRVSEASA IWNIAFDSGT GIGSFLLGIV AASLAYSGAF
GSGAVVILFG IVLTTADRII GRHRITEYNN TRARLRQVPV ARRAVQGLRN RRKDR

> RXA01103 (1-225, translated) 75 residues
MNSSPISDMV TAAVQNEPDA GDRWFIYGLF LIAGLFFGGA WSAYKSENKI LMVAAGLIAV
LAVAGGILWL LGEMT

> RXA01107 (1-1200, translated) 400 residues
MDFTSVNDRN VPAPNTSIPF PVDLNRVTEA VDSLGYHYLS SEDRIIVPWQ DHRISMYFSH
ESGQMLTILG RTRLNLDMFA INDAARAVTE WNAERIGPTA LVHLGNDGEV ELKFRTTICI
DEGLSTQQLR QFINLSLDTT AMAVTYILER FSELNFSDTG SPDDTNNADE LSDEQDQADL
VEKIRGLYVP TPVEELIESL EDAEWEESDM ADEDAEDDYL DDDSEIEWET DDDYFEPEEV
DMDELLNGFL EDSDIPQEVT LERIRAQLHA IGVVKTSGED DFIIAWINEV FLGFFVDNGP
TFLVKGHWDP SMDPTRDFMK LFMMCNQWNE NSLTTKAFCH TDDKGLQVRV EFAVSVAEGL
NDDQLQHNIA LSIHHILQAI DSISTEATGS STVEWPEKNR

> RXA01108 (1-651, translated) 217 residues

MTYPGITSDH NPYDGYTGDD GAGNKRNLPN RKKINKSVGV YAGVFALTLA LYAIGGAAWG
LLRPTYTAYV EDAETASIAV ETNTSFAGYA WFAIATGVLA AAIALFVFLR TPQHRGPVML
LWLGIVSIAG SVAFLVFGNV ASTMLHGSPS DYASAIGASF QVAPTITPGV AFGVAPFLSV
CMYWCAAFVT PEEEIDQDDA GQGTSKASGS EMTGASG

> RXA01109 (1-642, translated) 214 residues
LSISLSSKKV AFAALMVTPL LLTACGSDSS DTEAASSSAA TTTNSSSSSA ATSAEAAETT
SSESESSEAT TINEEQQAQL DVLSQELSEN PITFAEAAPV ENGETASPED TAAIEALVRG
YTDTNTLRSS LAYTINNTCT RVLEASGADA TQLDLNTIPD IPLGGEGTGT VDSITDVVVN
GQEASAWVVA TAGGTTDSAT QRFFNEGGQW KFCD

> RXA01119 (1-930, translated) 310 residues
LAGVITGFAI ILSVIGVGFL LAKLGVINDD KQRLVLNRIA FYAATPALLF NVVARSDPSA
LISPVIVVTF VATIVTAAVY CVISAIFFKK DIATTATGAA ASAYVNSNNI GLPVSIYVLG
TGAYVAPILV MQMVIFAPMI LAALTSGDVK GSRGQKIWAA VKGSLLSPIV LASIAGLIVC
LLEIQLPAAV MEPTIILGGA SIPLILMSFG ASLPSTNVLA SKADRPSVLT ATAIKIVGMP
AITWLIAKAF GLEGDYLYAA VILAALPAAQ NVYNYAATYR KGEIVARDTV FLTTFLALLG
MLGIAALFGR

> RXA01121 (1-678, translated) 226 residues
MNPEFIHGAT EIETTNRGLR PHRLSKEIVE RYCDPQFSAM ERQPSGVRVV CRTTATSVTL
TTYSTRVVYL DSGRPGGKID VLIDGAPTSS TPTSGGETTE VNFITGATER RLKDPQVLTV
DGLSEQEKVV EFWLPHNEEI EVISLKANAA LNTVEDTRPV WINYGSSISH GSVATAPTKI
WPAIVAQSKN YNLRNFGFGG SAMLDPFMAR LIRDTPADLI TLEIGI

> RXA01122 (1-522, translated) 174 residues
MPFPALLLPL IFWTGIAALS SWAVSRALPL RADNSIEIDA PVEKVWDFIE ETNRVPEWNE
HILYVQAPGE IEQGMKLKMK TRHPETNRLT LKFRPTIDVL RPHRELTWST KIVARWLLTV
TDTIELKPLE DGRTEVDQSM SFSGVLSPGV PFLASISRIK ENSNRQLKAL IEAE

> RXA01123 (1-447, translated) 149 residues
MRTLAAELNI KAPSLYKHVK TREDIAAHIA TKAFIQLGQS LHEHCESVED LLAEYRSMAR
ENPNIYRLLT SSEFPRELLP EGLETWAGTP FYLVTGHDPI KGQALWAFAH GMAILEIDAR
FAGPNNGSPA DGVWEIGARA FDTQVFDQG

> RXA01127 (1-279, translated) 93 residues
GIGLAASGNI DATGTNPSMF EPVHGSAPDI AGQGIADPTA AILSAAMLLR HLGDEDNAVR
IETAIAADVA GRDNSQPIST TEVGDRIVKA LQS

> RXA01128 (1-1014, translated) 338 residues
MSFTFIRTFF VLFGITLLVS CVPEPPDSYT KESTVLRYQV SDFNLNFVEL AVALGYLNNI
ELQVVGSVQG GVESIESLKK DDIDFAAVPF IGLVAGEIAT GAPIKAVAAS YGISHDSSSA
LLVLKDSEIH EVHDLIGKTV GINTLGALGS AMVERHLFDA GLTEPEIVSV TQRALPGEYL
EQRLYQGQVD AIWVTDSAKH QALETGDFRI LAEDSDLVQE LNTGCMVVSQ KLIDEHPAVV
GELVDGVAQA IEFERSHSPE EVREVYFNYL EAHGQSDRIS SFRYWEHSGI ATRGGVLSDR
EFSMWSHWID RQYDVPDINP ASIYTNQFNP YRKVNPSP

> RXA01129 (1-1866, translated) 622 residues
MVNLMSVELE EIRDFLAGFE PFAQLPAEEL DQLPGKMSLR YFRRGEEIIP IGVPNHYMGV
IRSGAIDVLD QEGVLLDRRD AGRSFGYSTM GPERNSRYRM VAVEDSLVLR LGRDDFDELA
KRNPDLNRYY SSWSKRIRAA ADQLRQESSS KVLRTKLGEF KIANPISCSP DTTIMDAAIK
MHEFGVSSLL VQIDGELKGI ITDHYMRSRV VAKHLDIQLP VSEVMTVDPR CATSQGLAFE
AMLLMSELRI HHLPIVDDGQ ISGIVTAADI MRLLRHDPIY LTADLSRKNT VEELANTFQS
AAEVASRFID RGASAEEVSS LLTVAADSLA RRLLVLAERK FGAPPVPYCF VVVGSQGRKE
MGLASDQDNA LVLDNSYNDR EHGQYFAALS EFVCQGLDRA GQVLCPGDMM ASNPEWRKTA
DQWISTFHSW ITAPEPDALL HAQTFFDFRG IYGDTEMAKD VHQNAVNMAR GARRMHAHLA
SLAARRDPPL GFFRGLVVER SGEYGATMDI KKGGTAGIVQ MARLYALATG SDAIGTRERL
IAASGHGQVS RKGAQDLLDA FDFLAAMAFQ HQARLIKVGE KPNYHIDPKT LGKMDREHLR
DAFSIIKDMQ SALATKYPVR NI

> RXA01131 (1-867, translated) 289 residues

MPPATLFNVL TSAGLDPHQS GDAIVVESAH FTLTFTWDEW LRAQATWVGE LSASDYVRSI
VAINSAHDAR ATPKMMLDAP TGLTTVLKAD KGQLQAFAVE ALPIGDGLSE AQLAGFVAAA
FDGAIDLTRE FHALYPERSP QERGAMLNIK LVDASPSQTV TPVRVANWFM DQGVEEVPYD
AASGRISFEL GDTPVDVILD DPELLKIQAV VVADRDVEAT EVLHLCNRAN LDSDHSTIFM
RSDGDDVDFV ATVAVPIRAG LNDFQLSQAL HDGVVGVVGQ VRAVINQLH

> RXA01134 (1-459, translated) 153 residues
SATQDTGVWK GIFALLMGRG ARDWRTGQQF DRWTFDELGC NFHQIFPTKW CKERGIDPVL
TESVLNRTPM GRRTEVVIGD TPPSRYLSRV QSKSLMGDEE FDQMLDTHLL SAEDLHSSNT
THFFASRRTN FIDMVEDAIG KAVIRDVNES DLT

> RXA01137 (1-360, translated) 120 residues
VRPTFVILRI SEYFGVAEAA INAATGRLTS LSEVFIDNAA EIQDNLSSLV ALQKDLAERV
NVEGVNPVTP VDLLELRLGS AQLAVAATAI EVRVAGGAGY VKSSSTSRRF RVEMGACTGP

> RXA01140 (1-786, translated) 262 residues
MALDTRGEEM RFRPRALSGA PDTGKDPGLL LLDGQQRLTT LYHCFSGDGY VNTVDFRSKK
VTRKFYIDVA KAVESPVMSD EAIFSVDETG KIISHFGPVI DGGITDLETA LAHGCLPVSV
LLDDNGTDFL FDLADMAGEG AREHAKRFQS QIVKTLVSYD IPMIRLDRET AKGGIGSIFA
QANSSGLQMD VFDLLTAVFA ADESVETEFS LRDDWVRVER NLRQHSALDG IGSTEFLTAV
ALLVSARKGH ASGYREDILN LT

> RXA01148 (1-600, translated) 200 residues
MTSPVENVKK KPRPLALSPS RAGDYQQCPL LYRFRAIDRL PEPKTVAQVK GTLVHAVLEY
MHKLPREERE YPAMVKQLKP TWAQMCEEDA ELKELVPEDE LYDFLVDSRT LLRGYFEMEN
PQGFDATECE MYVDTVLPNG VPVRGFIDRV DTAPPAKSEL STTRLARNQS RSGASKRSSR
CCSMHWSTGA CSMKSQLSFV

> RXA01153 (1-543, translated) 181 residues
PFLSPIVTST HAVVAYSTAR GFGEHRVRWD YAQESPLRDT RGFDLRRYHQ APVVDPHAIG
VANVFVPNGA RFYVDHAHPE YSSPEVTNAW DAMVYDAAGD HILMQAVSDV ASFTSQNRSV
LDGHDPCPAL KIYKNNVDGK GASYGFHENY LYSRETDFDV LAQALIPFFV CRQVIIGAGR
V

> RXA01154 (1-603, translated) 201 residues
EGIINTRDEP HTDADHWGRL HVIIGDANMS QTANFLKFGM TSLVLDAIEA GVDFSELKLK
NAVSEVAKVS HDLSLTHQLR LADGSELTAI DILRRYLDKV QPFAETPVEQ RVTALWGEVL
GLLENDLLST SHLLDWTAKL ALIKSFEARG LSINDPKMYL IDLQYSDIDP QKSLYHALVS
KGRMKTLCSA QDIADAAATS P

> RXA01155 (1-1365, translated) 455 residues
VESALTRRIM GIETEYGLTF VDGDSKKLRP DEIARRMFRP IVEKYSSSNI FIPNGSRLYL
DVGSHPEYAT AECDNLTQLI NFEKAGDVIA DRMAVDAEES LAKEDIAGQV YLFKNNVDSV
GNSYGCHENY LVGRSMPLKA LGKRLMPFLI TRQLICGAGR IHHPNPLDKG ESFPLGYCIS
QRSDHVWEGV SSATTRSRPI INTRDEPHAD SHSYRRLHVI VGDANMAEPS IALKVGSTLL
VLEMIEADFG LPSLELANDI ASIREISRDA TGSTLLSLKD GTTMTALQIQ QVVFEHASKW
LEQRPEPEFS GTSNTEMARV LDLWGRMLKA IESGDFSEVD TEIDWVIKKK LIDRFIQRGN
LGLDDPKLAQ VDLTYHDIRP GRGLFSVLQS RGMIKRWTTD EAILAAVDTA PDTTRAHLRG
RILKAADTLG VPVTVDWMRH KVNRPEPQSV ELGDP

> RXA01156 (1-201, translated) 67 residues
VSVVNAKQTQ IMGGGGRDED NAEDSAQASG QVQINTEGVD SLLDEIDGLL ENNAEEFVRS
YVQKGGE

> RXA01158 (1-942, translated) 314 residues
MSIVEHIKEF RRRLLIALAG ILVGTIIGFI WYDFSFWQIP TLGELLRDPY CSLPAESRWA
MSDSEECRLL ATGPFDPFML RLKVAALVGM VLGSPVWLSQ LWGFITPGLM KNERRYTAIF
VTIAVVLFVG GAVLAYFVVA YGLEFLLTIG GDTQAAALTG DKYFGFLLAL LAIFGVSFEV
PLVIGMLNIV GILPYDAIKD KRRMIIMILF VFAAFMTPGQ DPFTMLVLAL SLTVLVELAL
QFCRFNDKRR DKKRPEWLDG DDLSASPLDT SAGGEDAPSP VETPEAVEPS RMLNPSGEAS
ISYKPGRADF GDVL

> RXA01159 (1-315, translated) 105 residues
MSLGPWEIGI IVLLIIVLFG AKKLPDAARS IGRSMRIFKS EVKEMNKDGD TPEQQQQPQQ
QIAPNQIEAP QPNFEQHYQG QQVQQPQNPQ TPDYRQNYED PNRTS

> RXA01160 (1-975, translated) 325 residues
KSSNKISDLA RQLNLLPYFT RYKGRTVMEA ARDLGQPSSQ IMEDLNRLWM CGLPGLLPGD
LVELDHSFKE VKIHNAQGMD KPLRLTPTEA GVLLLTLESL ESLPGIAKQE AVVSAANKLR
AIMGEYSSTV FDSTGEDLDA EVLEIIRDAM DLHQQVSFEY HSHRSDNTSL RQVSPAHIFT
HEGETYIKAW EEAVNQWRTF RLDRIRSIVL LDSKAVHPAR GVSVSTDDPF EFAKSSDIAT
LLLREDAMWL GNYMAMEVDE TVEPIRDSDG FSWHTVHFPL LSRDWFVRFA IGHAEHLKVT
SPEDLRKCIK QKAFSGLSAY DHHVE

> RXA01163 (1-705, translated) 235 residues
MGYTNLNDTR VLRAGSCDAW WRTMSPLVQQ GSEAVFRRIM GLSRRPDRKP GFDDVPHFGA
AVRVPGLKHG TLVNAAPLKV LGARGEPNPA SSYRFEYITG DSAGRAITAT GAVLFSTRPW
TTGPRPAIAM APSTQGVAQH CDPSHTCAIG LNAFYDKPFD AIIAYELPVI LWFLAHGLDV
VFIDYPRDPA TGVQYYCDSI AAAKSLLDAV LASRQLGLSP EAPLGLWGFS QGGGA

> RXA01165 (1-573, translated) 191 residues
MVGHVPAAIA IPYFIIEILA FIGVVMWLGF GWALGLLVLF FVGGLLLAGV ELRRISKSAA
IHQASGQGSA GAIAGNIGLT AAGAILVAMP GFVSSIIGLL FIFAPTRALF RKVLAKRMRS
AIENLGVRGF EAVNGYRTQA SYGNFGAAFN GGAQQPSNEP IVIDEDEIQA WTSDLKPEDF
TKGKDESDGE K

> RXA01166 (1-483, translated) 161 residues
LTGVIAYAIA GLAVNSSEMF EEIMSVLNER GVSDVLKNIT SCAGGSLLAS GYSSSRGWTH
QGTPLADILD DLPLVVAEFG KQKLGRVAPE IPVLLWGSKN DDVIPIDPIR ELRDSWADKG
TPLTWHESQA PRVPGRTGLN HFGPYFRNLE KYSGWLIDHL V

> RXA01167 (1-321, translated) 107 residues
PRQLVKYKTA DGEIYEVPFA DDAEIPEEWM CKNGKLGILM EGEGVESKPV KPPRTHWDML
RERRSIEELD VLLEERIEAL RKRRRNAAKL LKAQQEAEEA EKAAEEV

> RXA01169 (1-567, translated) 189 residues
IPVFLAVFVG SDALGSISFG PFVEAFFLLI LIPLVAAAGT QQVARKWQVG RTIMAAAEAI
MVPLMMLTLF AVIASQVEAV SGQFTDIATV VPLYVAFLMV MIPIGGGISK LGGLGFKEQR
AIVFSGATRN SLVVLPLALA LPAGLEIAAV VVVTQTLVEL IGMVVYVRII PLIFHEKQTY
RKLSGIGES

> RXA01170 (1-483, translated) 161 residues
VSLSNKAKGI VAVIIVAWIV AMAGMVAYAS SNNADKTFPT AGALEQTVAA FDRQGLQVSA
VALADIYGDE YVSAAILCEG TPTATLEQSL GVDLSELNLD ESGVPSGVSY LALSNQDGEV
VYDKIDRANV DLCATPLNGA FSAYSLMPVA KVGENSWAIA A

> RXA01171 (1-693, translated) 231 residues
MSQAAGKFKP MTSTLAESTL TSLKELEDPK ILSVNERHGD DHAVNLTKLR AVAKELKKNQ
PLARELWATD DTAARLVALL ICRPKEFDQS ELDSMIHEAR TPKVLDWLIN YVVKKNPHWN
DLRVLWLEDP AENVAAAGWA LNTHAVITKP DALDDSEILD TIEAQMKTAE PRVQWSMNEC
LAQIGIHRPE LRDRAIAIGE RLEVLKDYPT PPNCTSPFAP IWIEEMVRRK K

> RXA01173 (1-615, translated) 205 residues
MHVSTLPNKK LRTRIFAGTA AVALSLGVAS CSNAEDAVDS ATDAANSATS AAGSAINDAT
GTSSASTTEP SGTSGSDSGS DSAGGDTTEV ESADGSTISI PTAVVTAANA AGFSTPESVE
EGPNGESLVT FPEGYIVNSA EGGAQALVGM IGETWIGEGG LSAAVGLPTG PEEATTNGWT
QQFTSGVISW LDDGSGQFAA SVEPA

> RXA01174 (1-750, translated) 250 residues
MSNMQGNDSK KSSGASRAES PLIKFRTLII VIFVILIVGL ASIAVGPVVY QLIMGPGVKT
EGIQADGAAP ASTDMNGTWD VAPGSIPNTT SAGFTFAEIL PGEEKITSGS TTGVTGEVVI
EDNSLISGLI TVNMTHITTD QEKRDINVRT KLFHTDQYPE ATFEVTDSVD LSALPDTGSI

AQVVIPGELT IHGETKAVEP TFDVLRTGDQ VIVASDIEIN RLDFGVETPE FIAAKINETG
EINVRIVLEK

> RXA01176 (1-504, translated) 168 residues
VRYFYDTEFI EDGRTIELVS IGIVAEDGRE YYAVSTQFDS SKANAWVRAN VLDKLPNPSS
KVWKSADTIK REVYEFLTST GPTPELWAWV GAYDHVLLAQ MWGDMAGLPR EIPRFTRELR
QYWDMAGRPT LPELPNGNHD ALIDARHNLA KFKVCMAALP LGKRDRVS

> RXA01177 (1-1986, translated) 662 residues
MHGEKLVDGT EGNLSQFQWR DMATNQTLRK ALLVLSTIAL LLTLWPSIFN VRAIESFVFF
FHIDTDVYRA GANAFLHGEN LYTQDYQVGS IQLPFTYPPI SAALFVPLAI LASSVAGIAL
TLISTVLLWW SVAIVLRRVL KGLTDADSRF VSYLILPMAL STEPVFQTLQ FGQVNIILMA
LVLMDTFTKK PWLPRGFWIG LAASIKLTPA VFGLYFLVKK DWKGAGVAIA SGVGFSALAF
ILSPSSSKIY WTETLNDPSR IGNLSYIANQ SVRGTLSRMM HEQQDLVEKL WLVAVVLCLA
AVAVAMWRVV RAGNPYGAVM LNSLIALLCS PVSWSHHWVW LIPIAIGLGA SAWNQRRTAP
GIAATAGVLA LLTTIPMFIT TFWNMPYDSE SYPFWPLILQ PSGNAYVVVV IAILIVAIVN
PTVLGSGNKA VSGQAEKKSS PALLVVLAIA IFYLFANIWF KGNNQNKALI QYPLQTMEGR
GLTDFGELIF EFAASSNQLV SLWIIGALNA IALAITLWFL LQRFAGKKSS WLIYLSTVAV
ALMMFSVQDA LQFGSLTLVA LALITVDVLS VREIGRRGLL TGLAAALFGW PILIVIGFLI
HRRYAATITT TVTAAVLWIL GILLNPDAFN LNLLRQWFNG RDGRDNLSFY AFLARWVSES
PA

> RXA01178 (1-450, translated) 150 residues
MMFVWFIVAL GLGAWAIHRT WSHGFKDLSV ALSIALPTLV LPIVELHHLV LLLPLIAVLL
RQGRVAISYL IGFIYLVSWT PQHLSYSTVF PLNDPAPEGY VAHFGWYLLV EPMAVAPAAI
ILGAFIACAA TTPKTSQLVQ VDKSSAENTK

> RXA01184 (1-1473, translated) 491 residues
MGLFGFGIFL ALGLGQDHMG ILAGVVSVGM VAYCIAAFMW PSGEGQLDPT AFSTMPLSAK
QLLPGFAIGT LLQSRGIIAV ICTVATSIIA AVFLPVGSWP MIVFMMAVSL VTTLLLGELL
GALTSGSSSR VSNDRRTVLT SVVFMVFVVG YNMLIGADGM SRIDAIGAYT KWTPFGAGAG
AIEAFAVGLW GEAGLLTLLA FVYVAAGFWL WSQLINRALT APLDQGGQGQ SAKDSAGEGK
KVLFLPGIPW SVGGAIFSRS LRYMFRDSRL LGSMIVFPLL GVLFIFQSFT VEFFMIYVGL
IMMAVFAGSV ATNDFGYDGP SLWLNIVAGV KARTLLMPRH WASMLPGSVS IVVFMIITIV
LAENKTTAVL ICFIGLGIFI SSAAVALLVT TFNPYPTSKP GTSPWGDRSG YSGAAFVGAF
AALLLGWIPT IPTIALGIFG LVTDQMWMII LAEVLAIILP VAVYIGVAKV CIRKVEKDLP
EIFDKVKTHV K

> RXA01186 (1-1098, translated) 366 residues
MATPVPLVFN APKRGMPPTH FADLNDEARI EALKELGLPK FRLNQIARHY YGRLEADPLT
MTDLPEGARQ EVKDALFPTL MSPLRVVETD DDTTQKTLWK LHDGTLLESV LMRYSDRSTL
CISSQAGCGM ACPFCATGQG GLDRNLSIGE IVDQVRNAAA TMQSEGGRLS NIVFMGMGEP
LANYKRVVSA VRQITQPSPA GFGISQRSVT VSTVGLAPAI RKLADEEMSV TLAVSLHTPD
DELRDTLVPV NNRWPVAEVL DAARYYADKS GRRVSIEYAL IRDVNDQDWR ADMLGEKLHK
ALGSRVHVNL IPLNPTPGSK WDAAPKARQD EFVRRVIAKG VPCTVRDTKG QEIAAACGQL
AAEESA

> RXA01187 (1-459, translated) 153 residues
VDPFETNPND LPTGLDPAYE GNSELNPLGG KNIPDEPEVT ANTPAVQEEP AYSEPETAVE
SKRQAKQNTK KSEPVVAPKQ TLAGGTWVAL IVGALLLILL LVFIMQNQTT VELNLFAWTF
QFPAGIGFLL AAITGALIMA LGGGVRMFEY RRS

> RXA01195 (1-447, translated) 149 residues
VIVAVSAVLL AAWRFFTLRS RGTTVILREL PQSGVHGWRH GSFRYNGNDL EYFKLRSLSP
MADLILNRLS VTLLDRRDPA ADEAVFMSQG LKILHIKSKN DQIELALDAH GEMAFTAWLE
AAPDARAEHS LNPRDFNRFR ASKDTRKNR

> RXA01196 (1-690, translated) 230 residues
MRLVIARCSV DYVGRLEAHL PSADRLLMVK ADGSVSIHAD DRAYKPLNWM TPPCSLVETP
ITDEDGEATG ESLWVVENKK GEQLRITVEE IHSEQNFDLG QDPGLVKDGV EDHLQELLAE
HITTLGDGYT LIRREYPTAI GPVDILCRNS DGETVAVEIK RRGGIDGVEQ LTRYLELLNR

DELLKPVHGV FAAQEIKPQA KTLAEDRGIK CVTLDYQALR GIESNELTLF

> RXA01197 (1-453, translated) 151 residues
MSTEQSLNIP HEYVICLDHV GIAVPDLEEA IEFYRSAFGW VNHHQEINEE QGISEAMIGP
KDIKSTEGMI QLIAPLNEDS TIAKFLEKKG PGIQQMCLRT NNIDALSEHL RRQGVRLLYP
EPKNGTGGAR INFLHPKDAG GVLLEITQPQ S

> RXA01198 (1-303, translated) 101 residues
MIVAFSVAPT VTDNPDAEMA DAVTEAIRIV RASGLPNETN AMFTLIEGEW DEVMAVIKEA
TEAISRVSPR TSLVIKADIR PGHTGQLTRK VEAVEERLAR D

> RXA01206 (1-261, translated) 87 residues
VSAENTENTD SPFEISEFDD HRRPLQRALK FGSIALIVFT LISLAIWGAT RGVPGVSAVV
IGAAVGAGFV LLTALSVLFT TNSNVTT

> RXA01207 (1-648, translated) 216 residues
VSRIYDCADQ DSRAAGLKAA VDAVKAGQLV VLPTDTLYGL GCDAFNNEAV ANLLATKHRG
PDMPVPVLVG SWDTIQGLVH SYSAQAKALV EAFWPGGLSI IVPQAPSLPW NLGDTRGTVM
LRMPLHPVAI ELLRQTGPMA VSSANISGHT PPTTVLEARQ QLNQNVAVYL DGGECALATP
STIVDISGPA PKILREGAIS AERVGEVLGV SAESLR

> RXA01210 (1-693, translated) 231 residues
VFPVGIPLLL FLIGNGGAAE SANSFDYFVM YTLLFVQFYT VLSMATTRRD ERVLKRLRTG
EARDIDIIGA ICFPGALLTL IFTVVIIPLL MVLGAPAPIN LVPIVFAVLI GLLLCSALAL
MTSGFTRNAE AAQMTSMPVF MLAMGGLGSI RFVFGDSIVA DILAYTPFAA ISDLVQIGWA
GATFADSVGG VEAANFAGIF QDMLIPLGIL AAWTAAAVWA ANRYMRWDSY R

> RXA01213 (1-1227, translated) 409 residues
MTNPTEERNA RRLIWANGLQ NIGDQIVAAK TVLPWLLQAA GAPGFLLALL VPIREAGSML
PQAAITGWVL RQTSRSKVWV IGSNGQFVSA LGIGVAALFL RGWALGITVI VLLAALSLFR
SMCSIASKDV QGKVISKGKR GLVTGRATVI GGVMGLVAGL AIAIFLGSHS PTRVLAAVVI
ASSFSWLFAS IVFARIEYAK PATPKNAPSA NPWVRRCIAA LKDDKAFRRF VLVRSMMLVT
ALSTAFIVAL AAESGNSIDS LGFFLIASGL ASMVGGRISG IWSDHSSKNV MAGGALFGSI
VLILVVLSSA FAPAQINTLV FPLSFFLITL AHTAIRVARK TYVMDMAEGD QRTRYVADAN
TLMGVVLLIV GALSGFIAIF GNEAALLFLA AIGLLGTISA RGLKEVSAG

> RXA01218 (1-429, translated) 143 residues
MARLQHDMIF INLPVSDLAA SKRFYAGLGF KENTVFSDEH TASFEVSDAI VVMLLETARF
SDFTKRPIVE KNGSREVLNC LSVCSTEDAD EFVRRAQEFG GTITRELAAE GPMYGGAFDD
PDGHGWELMY FDPEALAQMM PEG

> RXA01229 (1-693, translated) 231 residues
MIISTNTAHP LHEPHVPSHH NRMNTLRAGV LGANDGIVSI AALLLGVIAT GASDTVVFGA
GLASTIAGAV SMALGEYVSV SSQRDTERVL IAKEAKELAE DPTAEHVELS EILHSYGISP
ETANQAATEI GQGDALGAHL QLELGIDNEQ LTSPLAAAFS SAVAFLLGAL LPMVSVFIAP
AGWDAGVVFV VTLLVLAVTG FISAQISGTS PMRACGRLVI GGALGLALTY G

> RXA01231 (1-504, translated) 168 residues
MLGYTFVIFI LAPFLILTGI AMAPAIRSRF PWYVKLFGGH QGARSLHFIA MVLMTGFVIM
HXRPGFLVHG DYNMVHMVFG DMNTDRAAQA YIIVITTIVX GGVXLXXAQY IXXWXTXXAX
XGXPPXSXEX XRKIFXXPAA SPDEQAXXHL HGQGHLAVPL DQWPAADR

> RXA01234 (1-384, translated) 128 residues
MWKFMKTQYV CTTYFIAAPE DEDEAYQTYR SRMNSLAALN GADVVSVADG LRMEVDQDIW
GSLAEQYQIE QEGLYPTGHN LYFVVTVVNL DDSDEVYDRT MEHLIMDDPY VRVDRFPSTV
HASTQIML

> RXA01237 (1-441, translated) 147 residues
MNVQFESDMA VQPGNTMEAT VTDIRDAKRK TTQLDSVTPF KKNCPSRTLL DTISDKWAVL
ILLSMENGPQ RNGEIKDQVQ GITPKMLTQR LGVLVEDGLV TRTSHAVVPP RVDYQLTDLG
ASVIEPCRAM YSWAVENIKQ VEAYRSA

> RXA01246 (1-639, translated) 213 residues
MKRTITIAAL ALTSTLVLSA CADNTEGENT DTTTIATTSA PDTTETTGAT TDPETETGAA
GEVSAEHNDA DIMFAQMMIP HHQQAVEMSE ILLAKDDIPA EVIEFTQGVI DAQGPEIDRM
NTMLETWEED PVTGDMGEMD HGGMSGMMSE EDMTALEDAQ GTEAARLYLE QMTAHHEGAV
DMARDEVTDG QNPQAIALAE QVIEDQEAEI AEI

> RXA01249 (1-300, translated) 100 residues
VSQDTFLTTH GLAAMDAVEI IDHLDRQKVT ERPTDLIASV RADELLLSSD DQEVVVDLPD
NQTYVSIAPY LNSTHDCFYH SLTTCLGDLD NEDIHVMITD

> RXA01251 (1-309, translated) 103 residues
MTQPDMSQIL AQAQQMQAQL QAAQQEILAT TVVGNAGNGL VTVTMAGNGE VFAVTVDPKV
VDPEDVETLQ DLLLGAFKDA HNKVANVAEE KMGPLSQGMG GLF

> RXA01263 (1-912, translated) 304 residues
LTPYDPTAVN KESEKEAAKN LFGAEALTVD PDAGEVVDRV DNFYPTTAKA KRDYPSNYAA
GCHQEVNETS PESCVYGDKN SDFSVALVGD SHAGHWLPAL EPIAEAQGWR LEVYTKSQCP
LISTAIKLGE TFYAECYEWN EKLLAKLTGP SAPNHVIVSS QRYASANPLI DSVATGTVSE
GYEMAWNSLK DAGVSISVLL DTPRPQIDIP ECVASNRDNL SECSVHRSVA LGTEAHPQQK
TAAQNIDVPV LDLSNWICPE EYCSAVIGNV LVYRDSHHLT ATYARSLSSA LWNELVASNG
EPFK

> RXA01266 (1-1035, translated) 345 residues
MPKVSVVTGF YNRCEHLERT IESILNQTYS DFELIVFDDA STDGTASRLL ELKEKYDDPR
FRFIIHEENK GFVKGLSEAI SGAKGQYIAV QGSGDVSLPR RLELQVEFLD ANPSVGAVGG
AIYNIQEDTG TRNPQRFEKP IATFDDLLTS NPFTHGEVMY RLDLYKSIGG YRSGFTFAQD
RDLWLRMAKK ADLGIIPDFL YHRYTLLDGV SFVPDKTIRQ RCFSEAAVRL ALMPEEEGAL
AYSRLEAEGP TAVVPIADRA VQKFVPKAAI RLCLYGAPET GLHMARDYIQ NPLRRTIVVV
LISIYSSRLI KPLQDILYKS IFKGVSISKP IKSSLVKFTR RIQGK

> RXA01267 (1-1314, translated) 438 residues
MYAEINGGFI PEGTVRVSGA KNSATRLLAA ALLTDEVVHL GNFPTKLVDV EHKIRFIEEL
GGKVHVDHDE QILVVDAKDL AAREMTTDEL NIPIRTTYLL AAAQIGRGEI ARVPFPGGCA
IGGGPAGGRG YDLHLMVWEQ LGCKILEKDD HIEVTAPQGF IGGVIDFPIS TVGGTENALL
CASIASGDTK IANAYITPEI TDLIELLRRM GAEITVYGTS RIHVKGRAGL LQGAYMDVMP
DRIEALTWIV YGIISGGRIT VEGVPFSSME VPFIHLEKAG VDLFRNSSSV YITPECLPSG
SVQPFELACG THPGVISDMQ ALFVLLGLKG AGTSRVYDYR YPERIAFVEE LTNLVSGDKL
SAEAGKITIQ GDATFRPGYA NSTDLRGSMA VVLAALCADG KSTINNVHMA LRGYNELDKK
LRLLGADLTI REGEVPSP

> RXA01268 (1-840, translated) 280 residues
VAARIARVPR IVYVAHGLRS ETVLGLKKKI LVFLEYLTQL FAHQTLAVSH SLKKAIEDAH
PRFKGRVQVL GYGSMNGVEL DRFRVPSLEE KLSARNALNL PSKSVIVGFV GRINKDKGGD
LLAALTKHEA FTRLRLHLLI IGELEDDDLR EAFIKLVNEG QVTITGWIDF PEEPLAAVDV
LLHPTQREGL GMSLLEAQAM GVPVLTNAVT GTVDAVTSGE GGFFADDDSV ESWVSKIDLL
VSDPKLRDRM GRAGRQFVSA RFNRDDVAAR FSHFVEQFKK

> RXA01271 (1-1812, translated) 604 residues
MAISIGKAGQ NLKGSVPIGK VLFLIDALAW ISALFIGVVL RYEFNLSSIN WSAFAWFGLA
AVILQFVLGL SLHLYRKGLR HLFGSFEDTL NVSISVIVVG VVLWIASLFV GQRWKISRGV
MLLVIPLALV FVLAVRYLAR MRVERFRRPA ADSTPALILG GGYIGTNLIQ WMMSDPKSPF
RPVGVIDDNP ELACQRVRGV PVLGKFDDIA QVASDTGAEL LIVAIGDADS ALLRRVQDTA
NKNGLSVKVM PAIDRVVSKG VRGNDLRDLS IEDLLGRQPV ETNVSEITGY LTGKRVLVTG
AGGSIGSQLC TEIAKYGPAE LMMLDRDETG LQQVLINVAG NGLLDTDAVV LADIREADAM
KEIFLKRKPE VVFHAAALKH LPMLEQYPDE GWKTNVLGTL NVLAAAEAVG VETFVNISTD
KAANPTSVLG HSKRVAEKLT AWYGQNSTSK YLSVRFGNVI GSRGSMLPTF TRLIMEDKPL
TVTHPDVTRF FMTIPEACQL VLQAGGIGRS GEVLILDMGE PVSILEIAQR MIAMSGKDID
IVFTGLREGE KMHEELVGDG ETEDRPFHSK ISHAHAESLA PNNLDRDRFM QRAGKLASTD
SEII

> RXA01273 (1-1434, translated) 478 residues
MELREYATIL MKNWVLIVIA SILGIAAGAG FSLLATPEYQ SRTQLYVSVR SGAGTTSDMV
QGANFSRQIV NSYVDVIKTG VVLEPVVDEL GLELTANQLS SHISAASPAD TALINITASS
PSPQQAAEIA NAVGESFKNV IQTELEPDSG DGMSPINLTT TQVALEPSSP VSPNVMMNIL
LGLLVGLAIG VGIAVLRAAL DTRIHSLRDI EEVTDKPLLG GIIADSEVEK HPLIIKHKPH
SPIAESFRAL RTNLQFLNVG GSSSVFVISS ANPGEGKSTT SVNLALALAE AGSRVALIEA
DLRLPRVSKY LGVEGNAGLT DILIGKAEVN DVLQRWGRTQ LYYLPAGRIP PNPSELLGSA
EMDKVIAELE ESFDYVIIDA PPALAVTDAA VIGHGKAGIL IAVSAGSTKK PELEATLSTL
ENADANVVGV VATMLPPKSV AGYGYGNYGY GDTSKINAPK PDNTELTTTD ASKANNEQ

> RXA01275 (1-918, translated) 306 residues
MEKIRSPAVQ SDALQVFKSA LAATVTWWIS VNLLNSQLPF LAPWVALMTM QFTVYHTFIS
GIQTAIASVI GVGLSFVIGT YLDVSVWTFG LAMVIGLIGA RVPKLRAEGI GIATTSIFLL
ASGFDDQQPL LYDRILEILL GVAVAIAINL IIFPPLRDQE ANMVVGNLDR RMGEVLQKMA
DELAEKWNID NADEWLEEIN SINNDLEKAW HSVRFVRESR RVNPRKIRIQ EGRPQPTETS
YESNLTSIDE GIAHLRHLAR TLRDTPIIDS DWGSSIPATV GIPYARCRSF ARRSESGNRS
YPRPAL

> RXA01276 (1-546, translated) 182 residues
MRKTLITMLA TTAIAFSAIS PVQAQTVDTD TDASVSSELS SGTSSGSSED SEDSDISNRD
IIFGIAAIAA VGGLIAGGVH WAVQQRMIPN PLPGIIPNPP ALAPQAPAPA PAPAPAPQAV
APQVVAPQVV APAPAPVQTN RTYKNCTEVW NVLGRSIRQS DPGYGTHLDR DRDGIGCESR
PR

> RXA01281 (1-762, translated) 254 residues
VGLSRSHYQL AAENTKSLVR MVPMTVPQGN EPAKKLATDL NRNQVVDELS AAVSRGQLTL
EEFEDRSSKA WNARHLDTLV ELISDVNDNP YTLLGQQFPG ASYAPAAYET TPPAMPNVSD
PVNIVRNRIT GNPNGSKMSV SFMGGTVRKG GWHVPNVHTS FAMMGGNQID LRDAFLESDR
IQINAYTFMG GIEIIVPEGV FVICDGMGIF GGFEQSVDKA GALNPARLPS NAPTVHIKGL
AFMGGVSVVT KKNI

> RXA01282 (1-780, translated) 260 residues
MDELLKQEVK DFLTTRRARI TPAAAGLETQ PWSDRRVPGL RREEVADLAG ISLEYYIRFE
RGNLKGASPE ILQSLAKALQ LSPIEREHLH NLAYRADHPR NLPSAETPTA PLQDIVDAVT
DKPAWIRNEQ MDILATNRLC AELYAPIFKD LPDRPNTARH CFIGATASEF WVDRDQFSAE
FAAKLRLEYA RRPSVPGLKE LIDELHQKSS VFRDNWASAD VLSFGSGIKR FRHPTLGERV
YEYETFNLNS APGYVLSIYF

> RXA01294 (1-666, translated) 222 residues
MSTIPDVFTS EVFPEISGTK EFRGLTYMFF DQFTLPTAEQ LEQAKAAGWS LITWGWWNSD
TDLEDVELED ITNEGDSLPK LTDEFAVSSL STFDLNSQGL PNDDREPQPI EEADSLDDIF
SEEEGWGLMA INCPNWQVPA ACEWLGCMNV GEPFEMSHVL RVWQNSWGVE ALAFGGEEDD
ADLLLRVPEE SEELLKALAV ASDQVTTYKH EDLGFLASLW FD

> RXA01295 (1-975, translated) 325 residues
MTENLDNALL SMRMKPVQMA LMTLGYNHDM AVTDSGMELI VRRPGLTVNF NLDSVTLCIV
ADFMWHGCVP AKKQAEYLRA ANEFNRPTRD LQVVLDEADS KNMTVRGREF FFSSVGATWE
QSAEFVHYCM NDVATTFVSW CEQIWPKFSP ERVEFNATPP DVDFEFSEDQ LKEGNPFGLI
DEPTPLVSLD RIYQQYELMG ADQLKMGEDF VEYLHMGQRV SAWLTDGNNG SDRKTLAVSS
GTGVKIKNKK QLQELLGLCN LYSKEHVLVT VFAEEIENGA RWGIFAEARI DLPAGLNDHQ
LWVFLANSSK WTAEVCLTVA HRLQN

> RXA01296 (1-1083, translated) 361 residues
MSIEQAITSL SARVRELKPI IETEEATKTA LIIPFISNVL GYDVTDPREV IPEYTADVGV
KKGEKVDFAI KTGDDFHFLI ECKKVGSPLS LDHANQLVRY FNVTDTEFAI LTNGEIYQFY
GQLDAANRMD AKPFMTLDLN NIDARQFPHL EMCTRKHFNP QALAANAEEL KYIAELKKVI
ANQFQEPDVE IVKMLAATVT TKRMTAQNLE FFTRLVNTAS SQFLKDEVNR RLRSAQVFED
PVQTQGADAE TPAEDEAVIE EVVSEIVTTE EEIHGHSIVR AICCSEVSAQ EITMRDAKSY
CAILFQDNNR KPIARFYFDR KIPRIGIFNA EGEQEHFDLE SIEDIYNHAD LLHSRVVALN
A

> RXA01301 (1-405, translated) 135 residues
FLRLEGIEPK GPARAYYFGD VSDTVDILIG FPVSPAQAES LRRGALSQSG GDIDDVVLHH
FRDMKTMHSR HSGPFDGVER VWDEILDEVE DLGCTLPSSS IGWEEYIEGP ATADTCDQLA
SEVYVQVCQA PVKSA

> RXA01304 (1-486, translated) 162 residues
MPAQNKNLPG SVIVVSDRIK SGERIDKAGP VAVDLLQESG VEISTFTVVE EGFEPVHQEL
VKALARRDRV IITIGGTGVG PRNRTPEATE PHIDTLLPGL MTQILFSGLS NTAQAGLSRG
LVGLSARDST AALIVNAPSS SGGVRDALGV VCPLFGSIFE RL

> RXA01306 (1-1008, translated) 336 residues
MTEWYVVLPA TILLIALSAF FVIIEFALLA ARRNRLEETV ETSRSSRAAL RSLNELTLML
AGAQLGITMV TFALGAITKP WVHYALMPLF EWARIPLVMA DVIAFILSLF IVTFLHLVIG
EMAPKSWAIA HPETALRTIA IPARGFINLF RPLLQWINKM ANDLVRKVGE TPVDRAAAGG
YDTDTLHALI EHSRETGALD QQSAAQISGI IKLDKITVGQ TLTASPFTHS ASATVAEVQA
AAQRSGSLRV LIDAPSHLFP HVIHVRDTLG ASPDEKASKW SRPILTVAET DTLHQALEYM
REHNEQISAV LSADGKTVLG VITWDHILKY LWPASV

> RXA01310 (1-327, translated) 109 residues
MSSAKKKPAP ERMHYIKGYV PVAYSSPHSS LERSATWLGM GFLLTALAGV GAVLFAVGAN
SVGQQQEHWV LYSIIGVVFA VVCTVLGTVL IIKGRAPYNR YVKETGRTQ

> RXA01313 (1-945, translated) 315 residues
ALRLISQLLA PSAALNFKSE RNAVDVAKHM LASQAQQRGS ALVALDTRSE NADAATALRK
SLLIRSWTQR GTHQILAAED VRWMTLLCSP RILAASAKRR SSLSLDSAAV QRARDALTTA
AEKSPVSRTQ AYEIFRSVDV DPGEHRGQHL LRHFGGEGDI VQGPPIGTED SFVLLDSICP
LSLALNGDEA LTEMTRRYFH SRGAATVKDL VWWTGLTVRD VKKGIAAVSS DGLIHSVEGP
NGEEMWIPTW ADDVTDAEVS DALALELTLP AFDEYLLSYT DRSHVMDPEH LFSIGPGKNG
VFKPFKVVQG EALPV

> RXA01315 (1-651, translated) 217 residues
VDIEEQPSLR EIKRQMTLEA IEDNATRLIL ERGFDNVTIE DICAEAGISK RTFFNYVESK
ESVAIGHTAK LPTDEEREAF LATRHENIID TVFDLVINLF GNHDNSKSGV AGDIMRRRKE
IRVKHPELAV QHFARFHQAR EGLEHLIVEY FEKWPGSQHL DEPADREAIA IVGLLISVML
QGSREWHDMP QGTQADFQAC CRKAIKNTFL LRGGFSE

> RXA01316 (1-303, translated) 101 residues
MDISMLNVIT SYTIWAIFAI IGICGFVGAF LAATTREDAF EVADRQKKMV WVAILIASGF
VLTALGPSIP ILPWVAIIMI GLYWFDVRPQ IKSILEGAGG W

> RXA01317 (1-420, translated) 140 residues
MSDAKDDSIL SKWSNAASEL SGAVSGVAKK LREELSEKET FSKLKTEASE AVDQAKSGSY
LDAGKEFARD AGSIIKDAAK TVKGAVSDSD KNDVKSAFGN AVEASRDKFD DTLEKRKAKK
DSPEPGDDDI IDGEVIPPQN

> RXA01318 (1-1302, translated) 434 residues
MGKHEVAQQT VPGPSPEMEA QRRKELRKHK AIATGLLIFA AAVYFLCRFV ETRPGETAAW
VGFVRAAAEA GMIGGLADWF AVTALFRHPL WLPIPHTAII PRKKDQLGEA LSGFVGDNFL
NAQLITEKVS QARIPERAGE WLAQPENGEK VSREVGKLTA NIVRAIDPSD AEAVIKSAVI
DKLAEPTWGP PAGRLLEQLL AEGKAEPVVQ ELAQWLHKKA LGSEPLIDRL LNERRPIWAP
KFTAQLVSGK VYDEVIKFTE AVAADPNHEA RKSLRRFLNK LAQDLQHDPG MIIKVEEIKR
DIMGSGAIAQ AAPTIWASAS ESLIESAEDE SSILRRKIAE AATSWGQRLL VDDSLRHSLD
TRITGAAAFL ADNYAPEVTG IISETIERWD AEEASEKIEL MVGKDLQYIR LNGTIVGALA
GLAIYAISHI LFGA

> RXA01322 (1-438, translated) 146 residues
MKLAPRMRMR SPKTFAALAS LALVIGLGQV PIAQAQTEYR TASDGSLNWG FRQSFRNYIQ
TGVAKGSITL GDGASDNGGN FAFTPRTNGT TVTSDSQGTV EFNGSVHFLG HQAEDKWILD
TTMSDIKMVF NGSSAQLVVD LVAREF

> RXA01326 (1-294, translated) 98 residues

LRERLLQNNG GEVIDNENND WILHPVRDDS DRKRLVRTAN DIIRETESAR EWDNFPENAI
AIANDGTGDL IILLPDDDAF YIWSHEDEPL IETELEDA

> RXA01330 (1-456, translated) 152 residues
MWKDLTEPLP EACAEGLEIR VVKSPEELAD YAAVLSANWN PPAETVQRFY TEAAEYALRK
NSPALYLVGY AGNRAVCSAE AFIHASVVGI YNISTLEHKR RRGYGGAITL ATLHTARNAG
CDTAVLQASE DGEPVYRKLG FTDCGRFTEY SL

> RXA01331 (1-576, translated) 192 residues
MNIMGDPADG NGWMYAYNGL HSVARHYAWP AAGEGSATAM LFWWPQLLGV GTDENPDQVN
DVDQAARDLN VGYFMISPWT FWDFQIPNFR QIDLLWQTPG VTPVCKKGDS VIFAVNDMFT
DAELDQMRAP GNSPEPLPEL PTLGELGLAE TEDEVDQTYY HRPTVPAGVN SEMPSAETLY
APDPTKPHTV PN

> RXA01333 (1-1005, translated) 335 residues
MPGGCSGNIV RMLPKSRNFS AILLGIGVAL VVWGLVAPRF VHADGRLPLD LEATTYVLHD
SDAQTTINSD PLAGVVTTPV TRQLHFEVMD PASADDATIR IGDSMLRGNP DTQGFEQERL
LSATVSSFRI DRTSGEVLSD IALTNQLASP TVQYSVDGIW LKFPTDAQET TYNVVDPVLR
SALPADFVES TEIDGREVLH YRQVIDNVNV AEYFADANNT TTLTKEDGGT TTGYFYHNVT
RDFWVDQRTG LVVDLAENID DFYGDRSGQK YEQKLLFDAS LDDAAVSKLV AQAESIPDGD
VSKIANTVGI VIGAVLALVG LAGCFGAFGK KRREA

> RXA01336 (1-603, translated) 201 residues
MEPTVKASAR HTIHVTADTW RIRLSASAHS HPNDAYARRA TAISAIGSVL IDVPLQGERI
SESTAYDGQI NADWNAEVTG TDVNIARDII SRLAAVPDVQ VDGPLWSLSD SLAAEAAVEA
LQGAADTARN TATAIAESLG GQLGALLYAT TDTHSSTPIP ARAEMMAAKA SIPPRTLDLE
LAPSDIEVTK EIAVTEEFLA G

> RXA01337 (1-1413, translated) 471 residues
VTFRGGNTGA KHAVVVGSGP NGLTTAAVLA KAGWQVDVYE AAPTPGGAAR SESVLGEGTI
SDLGAAGHPF GVASPAFHYL GLEDHGLEWA YSPFAMAHPL DYGRAGLLET SLPETAKKLG
PDARRWKNLH QGLTKNIDKH LANLLGPVLK WPAHPIRMAK FGPFALLPAK RLASAAFETE
EARSLFIGSA MHSVTPPHKP MTASLGLLFG ALGMSRGWPV AVGGSGRIVD ALVNVINHHG
GTIHCDSQID SLSQFRDTDA IILNQTPSQV LKLKGTDLNA GLPQRMSTWK HGPSSYKVDY
LLDEPIPWSN PQVGQATTVH VGGSSEEIAF AEAEVAAGRM PERPFIILCQ QQVADPSRAR
EGRHVVWAYA HVPRGFVDKR AALLITAQIE RFAPGFRDRI VHSVDTNAED LEAWNPNLVG
GDITAGSALL RRMPTKIGEK TYMASASNAP GGGVHGMPGW WAAQAVLADH R

> RXA01342 (1-1512, translated) 504 residues
METPTQDMDV RWLYTQSQLK LREILPTNKT FDVIQISELV DPTDFIRPNS VVLSVGIAFA
ETPDGLRDWA HRLADAGVIA IGFGSGLTFP QVPQALIDAS LHLGLGLFEV PREIPFISIT
SSVRDEQTRR AGRLQQELLL EQERLNSIAI SGGIEALCRA AADYLGGAVT IVDSDGRVAC
SITTDDLDAL PQAVSRLNGS SQALTDATNF GFIHRMTRYG DRHHVLSVLM PTRPTDQHRA
LIRHCAGLAD ILLQRPEAMR DREIEVRSLA MSLLLGRSDD LATIHRVFAD ITDASGNIRP
ILITGNTPQS VRKALSSVAT ALYKQERALA HLRLAESTEL LFLRGSRSVH NIVQLFGTAA
SGVRLCIGLP TRAENIDKKL IRELTATAKT LQLGTHAEPR DGTLLWLQNP ELRKILKIRS
RDTYDRLLDH DRTNNTELAP TLVSFTQHSG HIGDTAKELG IHRHTVRTRM IRIEEICEID
LNDPLTRAEL LLVIATKEGD VEKQ

> RXA01348 (1-492, translated) 164 residues
VGFVWSGSDS QIYPELRKME AEELLVGSDV PWGSKGATKT EYALSEKGWE ALRKAWYEPV
TYGPTRDPAR LKAAYFEVGT NGDARRHLRA HIAHFEQQKI QSESMIDELK AKTHPTLARR
LERSPKKEHE RIVAFKVLAY EGQIARAQAE IEWAEKGLKL LDTL

> RXA01349 (1-777, translated) 259 residues
MATSRRDAEN IDQAGSEFIE SDSGHTATPE EVVATALTFF AEDGFSETKL EKIAKASGMS
KRMIHYHFGD KKGLYIKAVS YALRLLRPEA EAMQLDSAVP VDGVRKIVEA LYTCITKHPE
AVRLLLMENL HSQDSVDSTA AYSDESNVLL NLDKLLMLGQ DAGAFRPGIS AEDVLVLISS
LAYFRVSNKV TLKNLYSLDL ESEANIEGMK RIVVDTVLAF LTSNIQNSGN SSYLVVGGKT
AEPETDDSVY SFDTDVFEN

> RXA01357 (1-303, translated) 101 residues
MSAEELDNYE AEVELSLYRE YRDVVSQFSY VVETERRFYL ANAVQLIPHN SGNDVYYEVR
MSDAWVWDMY RSARFVRYVR VITYKDVNIE ELDKPDIIMP E

> RXA01359 (1-1182, translated) 394 residues
MIDSRLLAWA YLSKVVEGPN AHLQKLLKEG HDVERIAFGI KHREEWIGEG LLKNTDSRYS
IDTAQTDLET IAKLGGRLIT PEDDEWPMEE LDHAFGFAAS GMSDHVRTYQ DDALPPHALW
IRGGNLRTLS AQSVTLVGTR AISQYGTEVT REFTQNLVSH QWTIISGGAL GVDSVAHSEA
VRAQGSTIAI AACGLDRSYP SHNRDLFNQI AKSGKGALVS EYPPGTPPQR HRFLTRNRLV
AALSQGTVVV EAAWRSGALN TLSWCAGLGR IAMAVPGPVN TAGSLGCHER IRNGSAQMVT
SADDVRSLLG AVGAMDSQTQ YELNFAATPV QGLTRNELRV FDALDDRGEG REAASIATEA
GLTLQLTIFL LIALNKRGIV KRDGTAWSRN AEMP

> RXA01362 (1-1395, translated) 465 residues
INELILFDVH DLVKYGVHVY GAPQESINFL SAASLYHPQT VLDSFDHDGS GNLPGLKDDN
GNWDRRPHKD RIQLVNADTL TVWKSILEDE QTPYLDTRMV YTVNTEAAAA LEKLASAPRI
KELGLQFSSG WNETTDKKKG YFDVGWGYPA SWSDAILQGP HLGVATPMIK QPNPTMKHNQ
DWSEIDFEAI PANFIPATAY QPDRQTKPTY DADYGTWTFG DKQVPVADTF RIAWREMAAT
TGFRTVYPSV IPPGANHVHT VNSAASRSNL KTILVGAQLG AILSDYFARS SGSSHIFNDI
VRKIPLPNFT SLEKQFARTY LRLNCLTSAY APLWEEITGE PWDVQVPLRN AEQRRAAQND
IDAMVALSLG ISADELCMIY RTQFPVMRRY DQEDHFDANG RKVPKEIIKL QQKLKDGQEL
SVEKRTWVHP QSEVSYTFEY PFRVLDREAD LRAAYAKFEN QLKEP

> RXA01364 (1-1866, translated) 622 residues
TGTHLYDSLQ LLFTLVDKGH HPTDAKAVAF DAEAGEEGLH FRNLSADLFL PAATELIDRV
GLSNEALNKV LENLLLSRVQ SGKDRGFISY ATLGVTELGQ VYEGLMSYTG FIAQEDLFEV
APHGKADKGS WMLPVSKADE VPADSFIEVD QEAPGGGVIK VRKRHPRGSF VFRQSSRDRE
RSASFYTPQV LTSFTVTQAI EELQASKRIT TANDVLSLTI CEPAMGSGAF AVEAVRQLAE
LYLELRQEEL EQQIPAEDRA KELQKVKAHI ALHQVYGVDL NSTAVELAEI SLWLDTMNAE
MDAPWYGLHL RNGNSLVGAT RSLYAPSLLN KKAWLTATPT RYRLDDIAQA IDENKAEPLF
NHGIHHFLLP STGWGATADA KDLKDLMATE IKELKSWRTS IRASLSKTQI KQLNNLALRV
ETLWRFVLMR IRIAESQISR STTLWGQEPA EVSEVVTREQ IEQDLFGNID GAYNRLRLVM
DAWCALWFWP LDAVATAEHP ERPALPDLDE WLATLTEILG IDLPLKSKNE NQIVLGPDTN
WLAINDAEAT DLGFSGALSF ERVSANHPWI NVARQVAKQQ SFFHWDLDFA HVFAKGGFDL
QVGNPPWVRP DVNFEDLLAE HD

> RXA01366 (1-390, translated) 130 residues
VSQFRRCSRP GCGKPAVATL TYAYSDSTAV VGPLAPAAEP HSWDLCEHHA ERITAPLGWE
MLRVNDIKVD DDEDLTALAQ AVREAGRTVS GLVPEDEVGG NHPVNRSARI AEQKVHRRGH
LYVVPDQDES

> RXA01367 (1-402, translated) 134 residues
MPVEVPRHAS RRQAFDRAVL EAYSPLYGIY QKELSNLDIA VDTVPRMRLS ADLAILPDEI
TADGPVPLGR VIPPAIDTKG NPTRARIVIF RMPIEQRVTN AVERHELLTH VLTSLVANYL
NIDPRDIDPG FQDL

> RXA01370 (1-351, translated) 117 residues
MGAWDDAILT EEVNVDFLDE ISELDTQDIL EALEDACLLV VNQDNATEDE HLNGQAAATI
AAIMFGAPYS AGQVLENYPF IRELVGEGSE ALRGAAAQVL EEADVEYDLE AYLEALN

> RXA01372 (1-591, translated) 197 residues
QDTFVLPTLP TAAGLSPARI VASISTLLDL LEADPSIISD RLEHLADCID EEVESLSPER
DELVNPGRKL RAYVDHARIV HTGRTDVGLA IANVIAPIWT RRGLVSAVLD FPELMESLPE
LRGPEPITDD IFHDPFIDDE PGVVPFRAVV WAEEEPGIPD AMAQSCDGPS KGALTQALRL
LVRGQSATTY SIEEKDL

> RXA01378 (1-1278, translated) 426 residues
HVWISPGASN PIKDRLFPWT LVKAFLSSPA ALGETVSNRL KKASAPEEKR ALETLSQLNS
AITPQTSQKY QSLLSYLGDI GVKKNSDTRV VIFSERVATL HWLQENLIRD LKMPPNSIAV
MHGGLPDQEQ MRLVDEFKKT DSPIRIMITG DVASEGVNLH TLCHNLVHYD IPWSLIRIQQ
RNGRIDRYGQ THNPSIVTFL LDPAEDSKVG EVHVLERLME REHEAHSLLG DAASLMGKHS

ERLEEETIRE VLRGAQNFND AVADPAEVLE NPAGLDDIDW LLAQIAQADA KAETEAEAET
ENQTAPDAAS NSTQHAQRRL YAQESSFLYD CLLEGFNNVP EDSINRGGVG FKKHDNDIVE
LTPTDDLRRR LDFLPQDYVA ARKVKEDLLL ASTLMRGQER LNAARTGEDG STWPSAHYLG
PLHPVT

> RXA01379 (1-921, translated) 307 residues
LNVEEWISDH YLTNDDAKGA SFSKRVRERI KEWKTTEDAT QQSGPLTRFS SNRLQLQHAL
SELDDATTAA SLVASALGYG VPSARHAQRG SDTISYSSWV GNAGSVEFLA ATPAESFEEN
FRSLPLEPVA VNDKPQDITA AKLVGQIFLS DTPPAFVVIT AGKWVVLAER ETWPLGRHLA
IDISLVVERN DTKAQGEMQQ TVVALARENT ERAADGTTWW EETIEQSREH AVKVSGELRS
AVRESIEILG NDVLTRYEAK ELSTAEIDGG ELAKQSLRYL YRILFLLFAE ASPELEILPT
GTPEYDE

> RXA01380 (1-2016, translated) 672 residues
SLILGCDTKA RLEDLYLPFK KRRKTKADIA REAGLEGLVD KLIDAPSLDA AAQAAAFTTE
GFEDSKKVLD GARAILIDRF ALDADLVGEV REQMYRAGSM AASVVAGKEQ EGAKFKDYFE
FSEPFDKLPS HRILALLRGE NEGVLSLNLD AGDDIIYEGL IADRFSLDTH TSSWLAEAVR
WGWRTKLYVS SGLDVRMRLK EKAEEGALDV FATNLRDVLL AAPAGQRSTI GLDPGFRNGV
KVAVVDSTGK DVATTIVYPH QPQNRWKEAV SELANLCATH GVELMAIGNG TASRETEKLA
GEVADMIKAA GGTRPTPVVV SESGASVYSA SPIAAEEFPD MDVSLRGAVS IARRLQDPLA
ELVKIEPKAI GVGQYQHDVN QVALAKTLDG VVEDAVNAVG VNLNTASAPL LTRVAGVTST
LANNIVAYRN ENGGFSSRKE LNKVPRLGPK AFEQCAGFLR ISGSTDPLDA SAVHPEAYPV
VRNIAKATGL DVSGLIGNSA VLTKLKPADF ADERFGIPTV TDIIAELDKP GRDPRPEFKT
ASFKEGVEKI SDLTPGMILE GTVTNVAAFG AFVDVGVHRD GLVHVSAMSD KFISNPHEVV
RSGEVVKVKV MEVDVDRKRI GLSLRLTDEP GAPAPQKRGN RPAKQQRAPQ KQSAKPATGS
MADALRRAGL GG

> RXA01383 (1-1143, translated) 381 residues
MNLHSLEIRQ ISSGTISERK TWIFPTAARS FNQNLVHPQS IEIDAQTGVI LAMENRLQRT
EVESVEYPTD LPNPAWTGPA ISWPLKDPSI DFPDPLPHSI SELPPQSDNP RHLRVSISLD
AVEGAFPRYR IGDSIRIPLV FARDTPFMSG LETTRRAWIE AATEMDIHNT WPIILTGDGW
TALSHSDKPI RHEAELKGWF FHSLFGSEMP LTDLKIERIY GGLGTFDSGA TRWQELTDTD
DAYTENGSWL LEVIVDATLD GAIPPPLQPQ QFEASITHIV DEQLWVLGQM LPVLRCWDLE
TGKYLGQTYV PISVSHSSRL QFSEGLIHDY ENAWSLNPGV RMLAEPQPWI EPVIELDVPA
PWELQESFPD GLYFLTDGKQ T

> RXA01384 (1-1716, translated) 572 residues
MRSLQSVLDL LTSKSKVATK IVVERIEKHP VHGLGWMMYP PFHPWTDAST LTIERNGTSR
RASQNGVAVL HQHEQVQTIG LASYFIDSKI WVNELAGLDR INISESEVAG RDVLVLPLSD
LTLSIDAKYG VVLAAEDSDE SVRAVSVEFL DQWVDEEEPP AEEVPKYTET REELPPLEIP
PAPSGNRNLR VLCTWGAMEG IIPEWKPGDQ VSLFLSFDLD DPPFEQLKTT RRGYTEPGEI
YGNQRSYKFH ADGWNAVISA KVPLRTEENL TGYFTHSSYA DTSRRTSAVI TAVYRHGKDA
IIDVTLDGAK PPRYQESLDW SSTSTCDGET IWLSDKSLPF VRGFNVSTGK LVHEISIPTF
NEIALESGNR ARAAKKLWEL PDLKEATDPV PAIPAGWKLH KRFGKNFHIV SADNGTWKQT
ILRIKPFKAI ELDLGYAKIS TIYQYGERIY LRSDLHQITF NQDLEILSVE VHGNPDAGYW
PLSDLPPGDS PTLGFPIGSL MMFHEQQDIY AFHDPKTTKQ LTTVNLPKRQ FEVEYASQNR
IVISLKNPES RLIDKLLVWE PQTRWREQNL ES

> RXA01390 (1-657, translated) 219 residues
MFRRSLPSNK TSSASSASSA DTSYSVRLGR PEEPGYQPEP SYSEPYTDSD FAPAGAAAAA
AAVAPPMIAE QPQIVEDARR GTLDFGLLII RAVIGVYLIV RGVFTFFTLG GSAGLAGLEA
EFAGYQWPEI LAILLPSIEL AAGVFLLLGL MTPVAAAVAT VATSFTTLHQ VNTHEGGWGE
LSEPLMLALI LTIVVVGLQF TGPGKISLDS GRGWQSVHW

> RXA01391 (1-690, translated) 230 residues
VAAVAFAAYV IDGGVEEASG TPTSSESSVA ATAPAASSET AAEYRAMLAS LDVKGRAPGT
GYDRELFGPA WTDTVSVEYG HNGCDTRNDI LQRDLDDIQL REGTKDCIVT SGLLSDPFSG
ELIDFVRGER SGDVQIDHLV PLHDAWVKGA QQWDEQTRKN FANDPDNLLA VKGTLNQQKG
AGDAATWLPP NTAFRCDYAK KIITVKDRYN VWVTEAEASA LERQLDTCAA

> RXA01396 (1-258, translated) 86 residues

LKAFNTNFAA TLATGKVGDI TTTVLVAGDD EDAKNALITD VNAGGLDALD AGSLKRAHEL
EAVGFLQLTL AGSEKIGWTG GFGLVK

> RXA01397 (1-420, translated) 140 residues
VFMIKELLNK LFGNKKASPA MTQSETISHK ENNTMTTYTI FGRGNMGTAI AGVLTKGGAT
VEHIGSADSD IATINGDVVI LAVPYPAVES IIASHKDALA GKTVIDITNP LNFETFDSLV
VPVGSSATAE IQAQLQPPAF

> RXA01400 (1-1500, translated) 500 residues
MAISVSMPKA ISREELERAW LEVIERHGTL RTVFSTGMGG EVQQHRIDVG PGKWIDHAVA
PGESINEALR AVLNRQCSPY SRPSHSLCII DAHPRPTVII GSDHSHVDMW SMLVIVRDLL
AALDMELPVE PPLAFESHTA ELLAAPPAPE RIHQRWREIL EAGGGKMPQF PLPLGDAISM
PERVEVRDIF GVNGLAIYSA RARAQQVSSL ALTISVMADV TAALADLPLR AVFPVHSRFD
QRWHDSVGWF ISNSVIEVPD SDPHTAAQAV REAVSLGSYP LAELLEPWGG MPETPGMFAI
SWLDLRRLPV SIDDIGLQAQ YVSASLRTDG VMLWFILDRS GAHLRCRYPD SLVARENVGR
WIDAIVAQMR AEAGTVNLQA GGEQLTLRHG TRADISEIAP LLARNAADPC ELVDLEHALD
LLTHESSHFL AVVRNARGKI IAAMQLTIVP EFSRGGALHL HIEGPFIIPE YRTTDLDKKL
RAWAVEHGRA RGVKVEEVVG

> RXA01401 (1-261, translated) 87 residues
MNSPLQHSAF PVPGAQLSTS YSDEHGQAVI QLHGLTSSRQ RDRLLDLDLG RGLSGTRLLR
YDARGHGTST GRAASTDYQW DTLAGDL

> RXA01402 (1-474, translated) 158 residues
MGCATLLKAA VLNPDRFSGF TLMLPPTAWE SRKAQASEYL SRAEFLETHG MDAFLNAEKL
HAQPPATVGT PDTVPDISAE LLPWAYRGAA QSDLPSKKEI AKITAPTTIL SWTDDPGHPV
STAIELTRLM PNAQLRIATT PAEVARWPQH LRDDLQLD

> RXA01403 (1-414, translated) 138 residues
PITYIDGHPY VDGAVGETGG LMLQPAIDAG FTRFFVIASR PRDYWRKEIG RPGFIKAALR
RFPTIADLTI ARPALYNSVK QQILDLEKQG SAYVFFADNM NIQNTEINLK KLRASFDAGM
QQTRKDWPEI MSFLNQTR

> RXA01405 (1-456, translated) 152 residues
MSKIVDLRYG TRRSSELSKR SAEVFAEAEE HPITVTRRDG EALVLMSQRE ADGRARLLEL
AAQLITVATD HQGTLAERMA KVFPWMLALS VADREACARE ILDAARASFA TEQPHLALTE
LTSWKETAAA VAAGLSNTDL QWYDDPHLVE RP

> RXA01409 (1-816, translated) 272 residues
DFPDVTARLG YEYMQLTPHV DFGPFFRHPK ADDDLVAALK KRAKDAGVTI PALLPVQRIS
WPEETQRVAA VRNIKRIIQL AVDLEVDTLN TEFSGRPERS EDSEDAFYRS MEELLPILEK
EGIKFNIDPH PDDFVENGIE AWRVIRGLNS KQVGFVYVAP HSFHMGDQAE AILPAVGDRL
GAVYLSDTFD HHKSHGLRYI TNPPGNAVRV HQHLKIGDGD VNFEEIFSLL RSTGYLDRED
ALLVSNVFAE DEAADEVSRY QLEKIRSLIE NA

> RXA01413 (1-600, translated) 200 residues
LTHLFLELDE RLVLGVQQDG YQWTEHLFRL PLQHLRNSPN DLQGLKIRWC ELYSTTGKDQ
GVELLPQATV VTPNNFEAST LSGLEKLETV EDLKEAARLI YEQGPQYVVV KGGMDFPGEN
AVDVLFDGSS YHVFSEPKIG EERVSGAVCT FAAVITAELA KGAEVVDPVA TAKRVVTRAV
QDAVASNAPF TSVWLAEDNK

> RXA01414 (1-507, translated) 169 residues
MAVFDFPNPV NEYAARCTAG LVVLLSAATL FASGDLRIIL ASILTFGFAL RVAGGPRYSP
FGRLSVHVLV PLLKKAPILT PGPPKRFAQT IGLGFSGTSL ILMAFGFNVA ASVVLVMLIA
AATLESVFGI CLGCWGFGKL MRYGVIPEDV CEQCFQKESS RTGWLVSLK

> RXA01417 (1-597, translated) 199 residues
MTDKFDRVLA VEVCIQEWID EQNLTLEVPL MIARLQLRDV AKDITAVHEE KFYDLTDIDT
DAFVKNIKLG WNERLIKKSL FPQPDVHKQH FTETEHGIDA TVTVWSKGFD PESGPDFLVS
YVDGLWSADI RNRITKFQNR EIVSKFYFTP EHIKEDGDFS AEIFINRPEN DDDSQDLVEV
WTDQDTRYCG EMIIYFKWL

> RXA01421 (1-387, translated) 129 residues
MTSKSISGKR PNLPSLTGAR WLAALAVYFL HALVFLSVYP FQQSELFATI HKFVPMQLGS
AGVTFFFILS GFLIYWSNSQ LKGMKNVLYY CKRRITKIYP MHLIALPMFI EASAKFTTTG
ITWVLILRE

> RXA01422 (1-783, translated) 261 residues
FGDSHTSGTN APFRTDERGC LKGANNWADQ LQSQLGLGAG DLIDVSCSGA SINSDGFHFS
DEVRHAEARG AIGPNTTDIF VQLGKNDQWG LSNVNLLQSV QTCLTDVFAG CGDAAVAAGK
MQDPNAVTAE NYAERMKPVI DYLKYYAPNA EITLVGYQEY TARSGSQVCV RLGGTPLVKN
DAPALVSFMN KLDMAIDGAA GILGVSHVDL RSATEGHDSC SNDPWVNGVF DARAEIVGGP
WHPSVKGDSV TAGILRDRVN A

> RXA01425 (1-885, translated) 295 residues
VLSPDSGITW ALSIMFLTFT VRMVLVKPMV NTMRSQRKMQ DMAPKMQAIR EKYKNDQQKM
MEETRKLQKE VGVNPIAGCL PMLVQIPVFL GLFHVLRSFN RTGSGVGQLE MTVEQNANTP
NYIFGVDEVQ SFLRADLFGA PLSSYITMPA DAFDAFLGLD VSRLNIALVA APMILIIVVA
THMNARLSVN RQEARKAAGK QQAASSDQMA MQMQMMNKMM LWFMPATILF TGFIWTIGLL
VYMMSNNVWT FFQQRYIFAK MDAEEAAEEE EKRAAKRTTA PKPGVKPENP KKRKK

> RXA01429 (1-618, translated) 206 residues
MLQASLFPIV QEHIDFLHPQ ARKSVFWELA PEVAAKADPV FEKEAWLSTT LLEYESCGFN
IGYRNGTPAL ASVIFCERDA APGAKALPTA PVSSDAAIIS SLFIDEVFRG TGMESALLDA
SLMELIRRDY PAVEAFGYRS ENTEADAIAA RRLEIGLIDV EALESAGFEV VADHPVLPRL
RMELPPATVL LTAKDAQRLL QEMGAI

> RXA01434 (1-366, translated) 122 residues
VTDGNTSTAW TSTGGDGLLV DLSTPARLDR VILTTGTGSD SNVTSTVKIY AFNDASPHSL
SEGIEIGTVD YSGRSLSHSI RDSSKLPGQV ESVVILVDEV RSSQTSDTNP QMQIAEVQLV
GW

> RXA01439 (1-546, translated) 182 residues
MTRYFAVSNL QELGSLEVHK LYKLRVDIFV HEQQTPYAEI DDTDAAPTTN HILVWERADA
TPTNLIGCAR LAPITAAELK AYTGKGISLD DATPLSQLGR VAVAQEGRGS GLSGELMRNA
LRLAYEQYPD RDVVLTAQKP LVDFYAEYGF EVLGEEYLDS GVPHLPMLLK ADELERFSDL
DA

> RXA01440 (1-1008, translated) 336 residues
MKTKWLAIIP FVALAVVACS DTQPPVTETV TETAPQPTSE TAAQPPQPTT PAETTTQQAE
GINLTPRYTR QNVGHFSSGY QPGQVSFSSA DGTIKCEFRP MEQDAPINRE PSTDWRLSFV
QGACQFDDGY VVADTNVENR PGFAEYTTAI SHVMPENYTT LPPGTYIDLH TMACFTESAD
EISCIKYATN ETFRISAQGF EMLSNAQRDA ELTTQGGLYQ AFSNIAELRF SDGNAMSCFF
DAPGSQDFWC QTLSTPGWDD GSNLIHLTVT GGKLSLMGTQ VGNPGLDYFR GRQLIEAPNS
LLDASLSVTL DGDRVRFRTA TGEEMWVSSS DYGLGV

> RXA01441 (1-1029, translated) 343 residues
MARTTTAHAV LMALSSVGLL MLQACSEQEQ TPEQTPAPTL TSQAPETPQA STTSSASSTA
TPIATPIAAT ELDYLHIDPA TYDIGVQDQE TAVFTTGDGI TAQCFFEATP GETSYQIKEF
DFDETAGTCA FGDQHISVTT DENVRERFAE LSETEEELPE AQATLDVGEM VHLGHMGCWA
PSVSEFSCLD FASNQAFTMN EQGFHELDPA KATEQLINSS GQVQTLSKMT NFQFTDGTSI
TCVSELQAEE FLCHNSGPGG WSTSAGPANT LWWNLNQADS EFEGARPTNP TQSVYKSQQI
FGPGSYLLAN GVSAEFDGTT LTLTTPQGNQ YWANTHDFGA GTH

> RXA01445 (1-993, translated) 331 residues
MIPLINVRFP VAALPLALVA TVWLNAWADH LLLTGFIVYL AVEYATSRGR FALALILGVE
WILIAYGVAL ERPLEAKDSP SLITEILLIL VAAGTGAGRW KILSERKQRA ITQQEIIKKI
RTDIAHYLHD SMARSLAIMI VQSKLTELEP DPKKIQEKLN SIAKIGQEAV ADLHQLVRHL
VVEESAEKAT AFGAWAAVSI HDTVNSAIQL LVDAGHVVSF DSRKKNYKLD HIAETAFALA
FNEAVCNAIK HSPPKANVTI RITEKAQSLQ ILVMNPIGDW HANGESAIPG VGIGVESLTR
RIRNIKGQVC VTSLQGYWKV VISLPLKCED S

> RXA01447 (1-849, translated) 283 residues
MRLLVLRCDA PHINEFPALS TSVEIHDLPA VPTRKDLKIL DDVAFDVLPQ DPTPSLDEIA
KQPDVEHLSS PKFAPQQPET RLRIVVIGSD AALSAVLTRL MRADNLWAEI GFVPVGPSTA
AKNWGLPADE AAALELALTG LVNPAPLIRD DVAVAVAGSA TITNWEPGEI TGEVIVDDHV
LIRHEAASKA PRRGVYGARL VPMLDAPGIA AVIMDTPLPG EVPSRSLFPR PSGSVIPESF
STGRAMQAGG PSLQIRVDGI SRKRKVERVT FYRHLRDLQI VRP

> RXA01448 (1-780, translated) 260 residues
MAIGGILIAT MFPPGDGGSI DRMIDAFIGG GVGILVIALL PSSPLDAGRH QVANVLGIAA
SVLEDVAASL KAKDAAKLNN ALEALRRSQA SVNKLETAAS SGKEATTVSP FLWGDRARVR
SLYRILAPVD NVIRNARVLA RRAVVLTEDN DTVSDEQIHV IEEIADIALR LSDLYEHHKE
ISEALEIPEL VNRLRQLGSE VGEDIAEDRV LSAQVILAQS RSIIVDLLQI CGMSRESAVA
VLVPTSESPA YPPELWDDED

> RXA01452 (1-279, translated) 93 residues
VIRSFADRDT ELVWLREGAK RVDPRIHKVA NRKLHLLDAA TTLDALRVTP GNRLETLEGD
RVGQYSIRVN DQWRICFRWN DSGPENVEIV DYH

> RXA01456 (1-522, translated) 174 residues
MNDSIFSPQA LNKAMLEAVE FIHAEGWDAG PTLFALVPTE MLVDTLDEAA DDSPLTLVVQ
DNLPDNLLPG SEALGDYVSR LAWPAEIAGA VLAQEIMFTD AAVAGSEPRP ARLFSGVLRG
EAELTLLQLR PTEEELAERG PFAEDEIELR GGPGVAPGVI AALRYTLEAD PDEI

> RXA01457 (1-675, translated) 225 residues
VASTPHKHVR VALGLVALIP LLAACTGGGS TETSTESTAE TTPATTTEAT TTPATTASSS
VIETTESSTA ETSTKESGET STSKPRMTKD VEVAYKAFSS LAPVELFEQF ETCDPSGVED
SFACNGPEVG QFQFFDNASK ATSTTQLLTE LRSSRVVEDS GSKVVGWTTI GTMSIITVVD
NDQGLVLQQM VSSDKIDPEE RIYELGLSTP KDTEESSEET SASKN

> RXA01459 (1-810, translated) 270 residues
MNSNGFGFSF GNNDDDDDKN RNNDPFGLFG GNFGFGGQGG AGGPGGLGDI LNQFGQMLSG
MGDSMNSPEA AGPVNYDLAA RIARQQIGRV APVKDSEKEA VEESLRLAEL WLDNATQLPT
SGHRVEAWNP ENWLENTLPV WKRLVSPVAE QMNKAQLENL PEEAREMMGP MSSLMNSMSS
MNFGVQLGNA LGDLAKQTLT GSDFGLPISP VGVSAVLPGN IAEASKGLNV APQEMLVYIC
AREAAANASS STCRGLSSAS FPPLRNTPSA

> RXA01460 (1-294, translated) 98 residues
VPWLVERLVS SVEEYAVGLE IDTSHIQEAM GNFQMDNPDP ERLQEMMNEL QGMDLSPRIG
SRNANAVSRL ETLLALVEGW VDIVVTQALS ERIPSPTP

> RXA01463 (1-1164, translated) 388 residues
MEMSYFSHQD PNNPESHINF TMAQMEIQRW TLLISNPEAD ASTLVMELKT VTGESKHFIN
QAINAMWALM KLPILRVVVE THFHVRIPYL ARIMQAVKQA KPELWDELDH RIAEKLTPRI
AGQALMEASA LAGLITRWIK ELDPTFTGKK RGPKGSDGTL TFRHVDGRTY ISGNIDGVTG
KLFQKALEKV KQKGEDLARA LVTFLAGRTK VKIVSAVYTP LVGGVSWIPG VGFLSQEESR
KLGKTASKVI DLDTIATRVE NGYTPSPELR LYVMGRDGTC RHPGCTVSAD NCQIDHVIPF
GEGGLTVAWN LQCLCAHHHN MKTDGRIQAA IDSMGRVAWI GPCNRTVVTE PVGPLAQEMP
TGQWGQTLEA RMEKTFEKLR SSLEVLDD

> RXA01469 (1-1032, translated) 344 residues
MAFADIVRSV ENRTNAATLN WSIKNGWKPE VTGFSGYGSG RRVRVLARVL MSNPENLLVD
APSQSITQQA QRGWRQFFTI QVPNLPVTVT VGGKTVTSST NDNGYVDLLV EDHNLDPGWH
TIQIQAEGST PAEARVLIVE NTARIGLISD IDDTIMVTWL PRALLAAWNS WVLHTNTRKP
VPGMNRFYEE LLKDHPDAPV FYLSTGAWNT FETLQEFINK HALPDGPMLL TDWGPTPTGL
FRSGQEHKKV QLRNLFIEYP DMKWILVGDD GQHDPLIYGE AVEEHPNRIA GVAIRELSPG
EHVLSHGTTA SLSTITTNGG QGVPVVHGRD GYELLQRYET KPFA

> RXA01470 (1-426, translated) 142 residues
MTNNALTVPT RTRHQADLLT ADFWEDMGLP QLKTTIEESI DDVALPMHTA VLEISGMPKE
LRQTVESAMV VCIPSPSELS GSNRDPLTAR WFTAWRRDPF ELGLTECREV ITGTPRELDK
LRGVLESLAD EYRFEVELRI VD

> RXA01471 (1-807, translated) 269 residues
MQSFKTLESW PVDNVSASVI SDGAVHFYGD VDRVFELMSV TKLLATYGFL VAIEEGVFEL
DSPMGPEGST VRHLLSHASG VAFDKPVAEK GVGERRIYSS AGMDILADAV AAEAEMPFAE
YLREAVFEPL GMENSELWGS AGHEARSTVA DLTKFGQELT APTLISPETL AEAFQVQFPE
LIGTVPGYGM QKPCPWGLGF EIKGQKSPHW TGDLMPENTA GHFGQSGTFF WTVPGSGQVG
VVLTDRNFGP WAKPLWTAFN DEVWAELNS

> RXA01472 (1-456, translated) 152 residues
MNQANLPAEI ADLSDETALW EIINEYNWDD GFAVPLAVVR HPKCDRALAL RLFWDIDETA
QIHHSDEESA IAELYASTAE NDPAEFDRIM DYCTTLVEGL RKQTYPRGAN RFDTGFFNLE
DPSLTDRQRK IRAGKTKFAL KNFEEAFLQP EL

> RXA01473 (1-765, translated) 255 residues
MTDIGDVDQI VWEFIHFHDD SINPFFEFIK SDCINDEAIE RKTQILGIIL GNEPCGSVIH
ARQNTIKPMS HTVSFGDGWI QVLEDAAETV SITDTLDALR FSPEQAEWAA EFGPLLCGPA
NQPPAYLTAL DGHTKLPLSP QLTEFYSYAR SWTNSEALGN VIDPDDYLDH LTDPRLHLQD
LLDNEFERVG VLVDKQNRPL DPARCALFSL DALARAPYNR AYFVFAAPEP EIWAFENEHV
HAPDLRAYLQ ARLST

> RXA01474 (1-546, translated) 182 residues
LVGIAYARFP DTRDDSISRG KARSALEKST GLKERFARHF PAISIPVDTG DAADILVSGW
WLSGSKKKIL TAAEIQTLFI NRLATGPLST QLETATGLKL QVVTNRERMK ITLIEPKGTS
GHAIDPQAGK GSRGGFLLDN GQEDEYDDVD TVTIPDALNV IGYILTHGTP PQEGWKVDVL
ER

> RXA01475 (1-426, translated) 142 residues
MSIQGFSAGD YSACFEPRID AWVDIRGPRK PEWLAENIDN PLRHWGDNPH IPVSAAKKAG
NIYKETLRTM RASTKTPDQD PLKETLRSFI ASINQLAAKK NFIDAGVRED IVVALEKLCE
AAEASPEEIQ QAIVMGEEFI ED

> RXA01476 (1-342, translated) 114 residues
MSDSPCTVVI LNRTATATSI LRDIKALTGY GLSEIRSRIV AGLPVVIEEM FSNAWYDERA
QLLLALLTKW QNEGITFEIR EVAEDDPIEA GALISLEVLR NIIEPDDNES RDGI

> RXA01479 (1-228, translated) 76 residues
VIGAAAGYVL GTKAGRKRYH QIKKGYEAAI NSPATKSAVN AARKAIANKL DPQPRMKEVK
NLRTADGHEV LEQDQD

> RXA01484 (1-546, translated) 182 residues
VLGTAQYDGV PSRQFAARLR HAAKLWRLHE IQHVYTVGGK LPGDRFTEAE VAREYLIKEG
VDPDLIFVSA VGNDTVSSYE ALDPEKLGRV LIVTDPNHSY RAVRIARRMG FDAKPSPTTY
SPAKFPSIVY FLTLSHEWGG VVVQDVSRLL GERVPDKVKH LCAQSKVCCA LRGVHAMSNF
GG

> RXA01485 (1-2052, translated) 684 residues
MNFSLVHLRE NVRRVSVTVA IGAGALLISG PFFTAHTAEA TETYVLAESP EFYQDNVTDY
TGQISSSDIT NIQAAIDDVK ASEQKVIFVV FLSSFDGVDP ETWTQQALQA NGGGNVLIYA
LAPEERQYGI QGGTQWTDAE LDAANNAAFQ ALSQEDWAGS ALALAESVGS SSSSSSGSSS
SSDFSGAWLA AAGVGTVAAG GGIWAYSRSR KKKTSAATLE DAREIDPRDT NRLMQLPMET
LEHLAQEELT STDDSIRRGK EELAIATSEF GPERTRSFNR AMNHSTGTLQ KAFEIQQRLN
DSIPESEAER QSMLVEIISS CGQADDALDA EAQNFADMRN LLINAGSKLD ALTQKSVDLR
TRLPKAQETL AGLRTRYSAE VLESIDDNVD LASASLDEAE EVLPQAYEIE SMPAGEQGGL
IDAIRHIEHA ITTADKLLAG VEHADENIST AKANVADLIQ EISDEINEAG QLKQSAGADG
ARADWASLDD AVRAASAALI TASADAEKDP LGTYTELVDV DSALDTQLDT LRATAADQAR
QLRVFDQQLQ SARSQIQKAE DLISTRGRIV KSEARTHLAN AQKLYAMAQQ NRTRDTRAGI
DYGRQAAVAA QRASKSAQND ITTYNNRHNS GGGTTGAIVT GMVINSILNS GRGGGFCGGG
GFGGGGGGFS GGGGGGGGFR GGRF

> RXA01488 (1-831, translated) 277 residues
VLLETGAVND LALLDLFGAP EVPVYLGEPH AQTKDGFEVL EISAFIHGQN GIGEVELPAS

ESKALPGAVD FLIDSVNTHG DDLVIIATGP MTNLSAAIAK DPSFASKAHV VIMGGALTVP
GNVSTWAEAN INQDPDAAND LFRSGADVTM IGLDVTLQTL LTKKHTAQWR ELGTPAAIAL
ADMTDYYIKA YETTAPHLGG CGLHDPLAVG VAVDPSLVTL LPINLKVDIE GETRGRTIGD
EVRLNDPVRT SRAAVAVDVD RFLSEFMTRI GRVAAQQ

> RXA01492 (1-804, translated) 268 residues
VTTTLWAVSD LHAAVKANAD PIENIQPKDP SDWLIVAGDV AERTELVLEI LARLRRRFAK
VIWVPGNHEL FSRSADRYQG RDKYSELVEG CRKIDVLTPE DPYLTFGGVT IVPLFTLYDY
SFRRPGFTVE QAVQAARDRQ VMMTDEFSIA PFVDIRAWCW DRLAYSIKRL SKINGPTILI
NHWPLVVEPT YQMRWQELAL WCGTRHTRGW AERYNAEAVI YGHLHMPGIT NVNGVKHIEV
SLGYPREWEH WSGQHVWPYP VMEVDNAG

> RXA01494 (1-996, translated) 332 residues
VTDNSQFHAA SALVQAAHTV SVVGHLRPDA DAIGSVAATV AALQQLGKDA VGAIGQLDSM
PENLYTIPGA SNIKFGDSLP ESDLIIVVDC GSIERTGAFE SIIVNNPDKV LVVDHHATNP
GFGAVNLIDV EAESTTTILY DWFDAMSVQI TPDIAHGLYA GLLTDTGCFR WGRPVMHDMA
KELMEFGLDI RAISSALLDQ TSVDDLRLVG QIVSRIELRE AGPYTLAVLV ADFDTINGRS
RAVVEGLIEM VRAVEGADFG AVFKEYERGV YTVSLRSSNL SVASLAVHLG GGGHIPAAGY
TARGTEIEAL DTLIEATVTL GESLRSSAHV DV

> RXA01497 (1-918, translated) 306 residues
MVGKLPIMAE TNENDLPVID LAQIEGYVVD DSDEDDPVLL RPDGTPIETW REDFPYEERV
TREDYEKVKR SLQIELLKWQ NWTKETGQRH IILFEGRDAA GKGGTIKRFN EHLNPRGART
VALEKPSPRE STSWYFQRYI QHFPAAGEIV FFDRSWYNRS GVERVMGFCT ESQHAEFLRE
VPMLENMILG SGISLTKFWF SVTRKEQRTR FAIRQVDPVR QWKLSPMDLA SLDRWDDYTR
AKEEQFRYTD TDESPWITIK SNDKKRARIN AMRYVLSKFD YTDKDYELVG EPDPKVVLRG
RDQIGD

> RXA01501 (1-288, translated) 96 residues
MKEVAVNEVP AGAQLIDVRE TDEYAEVRAQ GAVNIPMSEF VGRIDEIDLD RDIYVICKLG
GRSAQVAEYL EQRGIEAINV NGGTDGWVAA GLPTEA

> RXA01504 (1-609, translated) 203 residues
MNITWLILAG VLAIIAVVFF YLSAQKKKSE PQPPRQRQDP LKFADGSDTF NARILGPGAI
ISRGGVDYVC RGAIQFRQGQ YIWHEYLLDG GKGSEYLSVE YDEGQLNLGW WITRPDLAQQ
PAHDVTVEGV RYRKTESGVG TFTSEGTTGV ADQGEFEYWD LAEVGGNRLL SFERYGKDSP
FEVSLGWTVL PGELTVYPAP EAS

> RXA01505 (1-498, translated) 166 residues
MIHHIDCMPT DVSAEALGVS WNGESPEVLV DKLIDASPHP STCHLAVIGG SHVVTVETPD
GRFREEISCH AQEAEDSRWP LPDSITRENY LLQTNVAVLS EEDFARAAEE ISNGDDDWLI
ASFPGAGEHH LTALTAEFLE DVWEWFSHHL YPEELTIVST RSIYKP

> RXA01506 (1-411, translated) 137 residues
MSSRNYRSIG FILLFLAVLC LFAAVFAKPA VGSQVSDRWP GNNGTYSCAG ESGVVDEIVN
MSTPTDRATD PATGDTYLRY SKNLIIISGE GTPECTITVE GLDRVNSGAF IWLGGGFGPS
SPSSSSGGSS GSGGGVK

> RXA01507 (1-423, translated) 141 residues
MSQYLVDGVL GTLSYFVLAA VILVVGFVIL DLITPGKLHE LVFVHHLPNA AVITVAQQVS
IGIIVVTAVL TSSDILSEGL LETAVFGALG LVIQVVVMAV LEAVIPGRFR DLVEDPKLRS
GAVVAAVILI VVGTVNAACL I

> RXA01518 (1-474, translated) 158 residues
VAFMQKTSAG WLIATGGFLA AVSAILTWRF YGSMTSISIT VSITFWLLAV VCGFAGVKVQ
GRLDEGLIGQ DKSQMNPVTI AYLAMLGRAC AWGGAIFGGV YVGIGSYVIP RAGELSAASN
DLPGVIACAL GGIALSAAGL YLERSCEAPP PQSGEAIS

> RXA01519 (1-747, translated) 249 residues
MNQDLSHEDS GDGNSVDRGQ ILLAVLIGLA LIASVIMLLA NSDGAMKIAL LAALWAAIIG
FFLVYRSRKQ VEAAAREKET LEYAHQSELN RLEAELVQEK MEISESRRAR DQETLEEIKL

QLEEMRTQLS ELSGREWGYE PTMLRAEARR ILELESQQLS QQFQAPQPEV PEPVAVPEPM
PEPAPVPEPV PEPEPVEVAV EAEEEPAPGR RRRRHAAPEE TGGRRRKDER QGGLSVADLL
AAARKKENN

> RXA01520 (1-384, translated) 128 residues
VASALDELGE TIVGLLVGEL GGSIVEIADD KRAQLAAALT YAGFLSTLQR DASYFLDEFL
GDPDVTSDIV MDSAQQFQAL PSLDEVIAQY DSINNPGRQR LFRDLARRQA EISRAQDIEL
WAIQKEDR

> RXA01523 (1-951, translated) 317 residues
MKNWQEEFQL VNLTKLLHSD TETSAAISNG QMIKLTHEVA INAEKYRSLP AWDKAAARAF
AVGMTVDKAV VAGQSAARLW GYQTLTVEKT VLCLLPERLR SKSSKHWPSG MRYKDRYLSS
RDIREVHGIR VTGAFRTFLD IALDDGVVAA VVTIDSARRQ NPSLTREKLM HSAESFPRHR
GVKAYRQAIE LSIPNSDSAQ ETRARLILRE AKLPEIQSVK VQARFDQSHN KYFLVDFLIN
EWIIVEIDGR SKYDSPELNE VLMAERDREK FFLNQGYAVL RIDPKQLDLN QDGECEFIGI
LKNTLQKTPP EHLKQAA

> RXA01525 (1-1722, translated) 574 residues
MRSFQSILDL VNSASEVATK IVLKRFEKRI TSETDWVPYQ RFSLWSVGSP LTIERKGPDV
RVSKDNTAVL QRYQRPEAEG LISYFMDPKP WITELAGLNL DDVSEDTVAG RTVLVVPLSN
VILSIDAEFG MILTAENDIE KIHAISVELL EKWRSSHYPE PHFPAAVLPP ASTGNRNLRV
LCPEFSIPSV NVGDQVLLFL TFDQTLPPVD QLETTRRGYT DPIQLDYDHR QYRFHADGWD
AIISTVEPLH DEEELTGYFL HRLDPDSAYP TIAVVTAAHY HGTDAIIDVT LDGVHPPKNQ
ETLEGISTST SDGDIFWLSD ESLPFVRGFS VSTGELLHEI SIPTFQEIVL DSANRARVKQ
KQWPHDFSDC KGKTWELPDL KEVFEAVPSI PAGWRLLDSF GKNLHNVTRE NPRLNDNFWL
QTILRLKPFK AVDLDIGRSI ITAIYPYGDR IYLRASNHHI TFNQDLEILN VEVFGDPEVP
ESGLIYLPPG DSPTLGFPTG TLMMFHEQEG TYAFHDPETT EQITTVNLDR NSFSVAYSSR
TKIVISLKNP ESRPTNKLLV WEPQTGWREQ NLER

> RXA01527 (1-2511, translated) 837 residues
VIPNPNPNPK AKTLRLVSAL TAITVVGFSA SPVHALPIPL DPSDPAVSEL WVNPNARADD
ELSGVDVEIS DFVMPNSNLT VQVGESFKAQ VRVTNRSSET LSNITLQARR AEASFDMASA
RVAATDNNYG YFGAMVTLDD ELEPGESVET EVEISTDSLS ISQPGSYPTM LALSGQLDGV
AQHLDSQRFL LPVLSDTTDT EDTATPTTMI YPISAQTNVL GGETGEAPEE PPLLVSSDAL
AGELDEGGRL QKLIDAYLQS SPAVQQATCL AIDPQLLDVV DRMTGGYTVT DTRPSTVRQN
QRLRELWTAD NQPTNGVAGT GAENAAIFLE KLRQATATSC TVALPWANAD LNAVSQTGNQ
WLMREALQRG VTTFEEVLGV IPESNVVIPG NGFVEPSTVG DLGWAEVTLN PDQAWEVQSE
ELVAAPDATE QSALDNPKPT PGTVTPPTPM STVSVLVSDN TVWRTTSADR FHSLAPGITG
VSYQGSLSAT LATLGQNPET VGYSNPDSRY DYAMDSESAR NLTGQAALRL TVDNGDEDSP
VLIMPSAVLG AEDGAMLLET TGALLADGSA RPFSLQQYVT ANAEQRNTLA TATTPPDDTA
FGAPYDDPAS LTETEILRTT QQAEYIDDLT GIMSNDPSIA LTRYGFTAPL RQDLLRALSI
SERRSLARHT QATSAADKLL NRNRDTLQKL RSSVALLPPG NVYTRTSESS PLLIVAQNGL
PLPAETQILY SGNQDAHINT PGVVRIPAQG SITLQMTADL PDDNLRTDLT LWLASPDGAT
ISEPVEITVQ PRPNLGTTLF FVAAGILAVG GLLFIRKKRN VEKRSPGTGS PKPPPTH

> RXA01536 (1-1242, translated) 414 residues
MAFGFFSRRK KKNKDKNPNE NSAVPAHSED SPQEVFEGNG RQVGDPIEQQ VDRDAKGRLT
AADFLPDADL PQLNRSRANM LRRELEYRFS LQNAHINIDG NTAMIQRSDG GAAHVSLRTL
AMNAAGLDNF DQLPELVESF VHGTLADATL NDLSTADLYK ALRLRLLPTP GEGDDLVEHG
LDRESQIRDD SILRTFTSDM SIALVLDTEH AIRIQPLKEL EEFDDLSALE RAADRNTWQE
LYDANVDASF VDAESDSEGS SFWAFESNSY YLGSAPLFLN DLLAKWAPDL DQSDGVIFAV
PDRDLLIARP VTTGEDLMNG ITAMVRIAMR FGLGNPTSIS PRLHLLRDNQ VTTFTDFRVV
SPEMEAEWED SAFDAPPAGA IGIEVRPDPY LMERLQQGGF GDFGDFGKPR DLDM

> RXA01539 (1-1923, translated) 641 residues
MSSSDLASII GVEQQPVAYG ESEEPETLRD VLPRRKLHPS EITPSYEVAD GEQRSIFGES
APSDFDDLSD VEEFDTSHWV RAGQDDRSDD DRLADEAGVP PSGAQDVADN EANLSGVDEQ
LHMREVHAQS FDPIDVAKKE RKAAEKKYAK PPKSDNPYLA RDAKDAAARK RKINAAHDNF
AQEMAQAAMG PLRKGVNTQT VMAACTTAAV MWCMSPRMTG VNVDMKRKFN KDLEQAKDTK
LSKYVSKDFW KSKLTRDKTE KEAKSLSDAF MQQKTAIISN RERIPMSVAS AAQTVVRLSD
QAYEAMREVD TDGQAIVDAK DVSAQVAEDI DMVVKQGEEH GLKSKDIYGA ARDIVGRRME

RDPGYAARFN ETAFGTVRLG EQRRGMVISK TPTWQFPDGA GLSKNAGWFS VREPMGNAQN
FADNLAATLA TEMRVAGEQY GSDGVRDVVA GFMTATDVSE SGLASAKKLL PDFDTRGRSA
SRVRQIAMAQ RTQAAIKVLQ DDGNQTAMTT EQVKEVQVWA MDQAEKVMQR DHPAILDKFV
RKHGQTFGQD ADAFVKSITM EKDTSSEYTD AMVRPQENRG SGRELAARRR VQAAQINQAA
QLDMNVHDFR ESNLPEERPA NPYEAYVRET EAKTNDPQYG Y

> RXA01540 (1-702, translated) 234 residues
MTFAELSSPR TIIAFNGRAE SGKDTAAQYL THMHSFHRIA FADGVRDALY ALNPLVCVEQ
AITTHGAIYD RVATVVDTLG WDTAKQIPDI RALMQRIGTE AGWRIHGEHL WVNLAIKKIN
ELPADHAIVI TDLRFPNEIE WLNSLKANPM NTIQTVKVIR PDHESTLTAG SFGTTSHISE
SFNLTTDTVL RNDGTIDDLH SKLADFLSTS PQPVLSRNAP VPKHNAPAPT TDAM

> RXA01542 (1-5061, translated) 1687 residues
WGQKDHWGKA PLGDHDAVRI YRQAEALMKQ RAANNKGLDL NDEATYGAIM FASFDDAFAA
DAEAHGCVHR PQFAKVTRRN ILNSPQYTAI KSSYDALVQQ DLVAQQQQAQ ALQQAAYEQE
QAAIFQARDQ ATFQAEQTLA QESVRQSEGV GLPVIDPMES YFREYAFYEG VEMFGTWGTH
VDAGVSQFST SDGRAIRALV DEHLATYEPV EQRGSTQAFF ASVNAAFAEV APHAAPMFSA
IAREGEGSKG YQALRHRFDK MVGTAIGPNG LPEGPDLGGR RLPISPYDPR WSDREVVRVH
GTKLLSLSEE SVGMIRDLDL ATIHLQDNDV YEGTHREDDT KGGVRPLTQW VNGEAIAWRT
ITENDQMRLP NIGQFMTAKE YRAAASWLRA GLIDTADVAS QKIDPNKVMS DEGIARSEAI
LTYLSDEGVD FRIEPDREPG QLKVRIEGTR IDIRLTDTRA NEQWVGRVYD SGTVIKYSAE
QTAEERLRAR ERMENGDGTW TPATDYEPSP TEVVDLVKFA LGREVERQDG KGLVGVPNAR
HPRALEQAQD AYFTKNRSAF MVREGLSIVQ DARDRSAGPG KWFDNEAKAS EWLGNNIALT
RARVAEELGV EELIALSAQY ADDPDFMPAF AGEDELMAIK QDYWAMLRGE ETDLLNPGVN
RDDYMAAIRD GDHEQIAAMT SAMNAVTVED RVRQHAALVL DDYVGTVEPD PVTGLRFNPV
TVAQHMPSAK SLWSNHDDII AALRATSITG DELRGDEFYN DVINQQLLKF NPETAQKMVN
NPDLDPQLAR FGTVIAETIS RNGADVVDIA VDDNGVVRWT AQRRVGAKDS RAVDSKGQVR
GERTRHVQGE IGQIFTRGEH GEIVTKFNGG ENYMFAPGYT ASVVPQKPGE TKSLEERTKL
KGYEQVMSEA LVYRVREDLM FTERSRVGAT TSINSAYKRL YDNRFPVDFF ERSAEEGLSD
EWRAALLETA SLRVRYDNSI RDGANVMEDI RAQQRGFDAR NDNSRDALVL TGGRNISVLD
VDAGKGFFDP MMTGMAANQG SVRYLLPSAK VGADGMITPG DPADRVPVAA HPESWAMGFD
PHDRQNMTFS NIMQASAVTG GARTAMIQLG GWNFEDGIIV SADFANTHVI RDTEDEMRPL
VAGDKLSDFH GNKGVTALVV DPAMSDADAR AAGLESEVAF FRDNPDLEVV MSPFSAISRF
NGGTARELMT NPQDVVFRNN DGSTRVQPGA SGDLNFIVTH MAVDAKTNVY DEEAVREGQG
RKASSQLAWV LQAQECHEIM EHFYGNNVSA LANFQEYLRV TGLDVTPYGE LREGFSESNE
QRNIIEMPSI YDENGELNNR VNRAQVREAF VEQISRAGGV MEIPFQLQLR NGAQLEESPN
NPDMYQLPLL SPHLRSDEDL ADGSTSRHEY TTRYMAIFDT CYKLAEEQAK IDALRQEEAQ
HGTLPRAAEK RLSESQKFVD QAQKKVQASF DGIANDIVAS RIETKNNVFK DGFMSARQSH
SATAVWTGDP RLSVDEVAMN SSMARELGVL DNGYAMVWRD PVIRDGGVRY LRVVINDDLH
GVAVNPVSVK SFDGDFDGDS VGLVGNLPKK AHEEALSRLT VEANMLDLGD GKRMEDGTMF
YGLTLHDSLD VQVAQHHDPA MAENMKVIVS ELNRYQREYE AGEISREELL EVNRAHMDDL
NEHYAQA

> RXA01543 (1-2766, translated) 922 residues
MSLKQAIIVR NEYTIKQANG KGSRGSSPGK YISGYMARSD AVEAVAPIVR NKLDDFIMRY
MARDSAVEQL TTDSNADYDQ QPEMNSRRGR QGRRATLKQR RAERSARRAA LRAGVNTDSD
TTNPSQPVHP RELAEFTTQD GQRVHDLMLR AQGNGGVAFG YGDVSLSHDD LHAASNNVQE
LYENRHTVMK VVLSFTQDYL TAHGLIPEDL DIKRAGDYRG QVDQMKLRMA VMHGVDRLAQ
RHYDDLRYVG VIQVDTKHVH AHLTMVDAGY GHRAADGTQK GKINKPGKAI LRRGIDAWLD
QHQHMAHLSA AVGYEKRNVT SYVKRWAFHQ LTQESAAQFV VACLPEDKRL WRASTNAKEM
DKPNRLVREL VEARLGETDS PMPAALSQVY QYAQKRRVKE GLSKQDTQRL IDNGREKIIE
QAMNGVYSVL SAISDEQRDV STAMLTVMRQ DYEDLLDGIA RKKSKDLDEQ GSSGSQEVGK
EEPEPSIEEF GLRLRSYSAR LNHHREQREA FAVKKRSWED ANSQGLADPT SQVMWSFYDT
EEQYHAMCQS KYQHFLTFAP PVGQWEKQWA EVADYGKRVV GLRALRADRS LARMSDERAA
EALGRQLYDQ PGGGLLARTG AEGKAGRAVL DGRIERMMVT YQQKIDDLRR EWAQLGARLE
VEGDAVLMDA ADLRESGGEG ADERQIQQQT IELPVADVSD SVRTYLDEEL RDSRDVSAHD
PVHTLRGRFQ VVFRPEHDFE QVGGPDLRDL HYAWFSDQKV SQPIVCSYGE LVTQRRYAFE
RAREWMISSQ QEPEAVAEEL DHAGADITRM EATSSEVSRT GILRSAMLAR IREQARQRAQ
RAAEEQARRE RELVAQRQQE IDQETTQPAF EVVQRHVQPE SVQIKRGRTV ALDKRVQPLI
RDAVDRAVLD SQLRSTRDGG LG

> RXA01544 (1-600, translated) 200 residues
VKLDDAMVMI EQRLVKGRGA TKTQLAPYEH IQRNIAARGL RADDGGSCFG YGDASLSNDD
VATAAEDIQD LFACGHTVIS AIVVFDKSYL SEHGIMSFDP NYFGQDIYAD THPEIDLMEL
RLAVMNGLLG LEGTFFEDMR YVASIEVSRS YVYAHIMMAD AGVDDARGNA QVKITDTERV
LFRRGVESRF VEQEARNVVL

> RXA01545 (1-1251, translated) 417 residues
MKLAGFNTNS PAAQRVAEQG EKVQLDAPVY AVFTPDVVEV EFIGTQHEPV LHVEGAIDSV
TALSQLPYDI QKITFDSENQ QRFSGFYKFS PQQHKELIDK GLYLEGFQPP REMMTSLPWE
LPMNADVTVV APESQDAPPI VLVGLSEIHG VDFSQESSGY ELTSMFEDYR SQREAGEADK
DFSESISRAE IEGKDIFADA NRTRTGVSAH AQRLEQERAL SAAQLMAKLA GISFQTEPVL
VGAEESFDAE QFLAHDLDDT AGMSEWEREV TEFYNEKIRA QEPVVEREAE RDSDIETEVD
AAPTVSAAEI NDVIHDLDEL EFDDVIDLDA DDVVNTAEVE APASVSAAEI SATELDFDRE
SRAKTAQREA SRRVAQKIQT QESVREAYIR EQKHGYDASP AEGRKFDEKI AERGLDL

> RXA01546 (1-696, translated) 232 residues
MARAKNKKQR QLQHAHDAAQ AEIAEAVAVN TVEPINARTG GWPSWVDKVW KLTGSLGGWF
AFLVFAIAVW PVAILAAGTV VTIIGTWGVS VLPSLVISSI GASAGVIIST TDGFLFSWVI
PVLFLMIVLA LVVMKVLNLI FGALWRFTMT LRQGLYAGRE KISRDDAKRA RAEKKLTKQQ
AKEAKKQRKL DAIYSAQQAE ETLAQQAQSE PEESDDKNRH DALNDAVAAA RN

> RXA01547 (1-663, translated) 221 residues
MFDQVKRFFV RNIVMIIALI LAVVVIIVAT STSADRHAVL KRQTGEIMAL QQERDALNSK
LEGQLEQVVR DATGGMDIEH KAADDAVVRE FLSMALTWDS VRDYLDVREQ VMRVYDLDEE
SQFMSVFMPG EMAGIARTDP TGEVHYAYDA DLSNRFSSLE SVVTRINGTE YSYVSTVTMK
SKRSGGEAET TSTSRLAYDV IDGKIRNLEA RTVPGGVKYS G

> RXA01548 (1-1008, translated) 336 residues
MAENNGGSDD LKPISVDGVV NGEVRSDKEK QAFEKITGDD LRRRAEQIRK RRLAKAQEDA
RKRKPLFGLG RIAVTVLAGA VFIGTTLWIS TTSGGFDDKV SANNEQIVTL RNEVNDLKNT
AETMPKKETL ASQFDAATSR AQNVADLQNQ LAGIITSVDD DAATEQFKTI VDELKPKFTV
SAGTTGEFPA AGRWYQPQEV VVGDNNRPTW APMGAESWGW TVTPTLSMSD TEHVVVMWEA
RLTGGERYGA LLAWVTADYN INTGVFSSLA LAHTYEGHQR IGATTSPSEF GAHGTNAEAS
AARAGSEGGG LEGEAIFVDE LQRALEIAQL NKQENR

>RXA01549 (1-861, translated) 287 residues
MVDNKNSSSN SPTAASEYFL REWERPADVA GNAPIRAEQA SKWYAQMGGW QKNSTLGESV
IAMADGAAAK STARDEQDAL NDCPEEDRTS GGNTSAAEAM VTISHPYLAD SRGNDGTDIY
RYIHDEVLTG DPYYASCDRG VATAIRWSGT DDTFPAGPTA AQYEYVVGTG SGRWEEIGNL
ATMSENDLLP GDVLLGAPNH VAMYVSNEVV VDMLGPGNAE PNAAIGHASL NDRSPGLDTL
SLDGWGVNFK VFRNTQAETN SVFSGVQIPA GKEIGEMTNP TRTTPAG

> RXA01552 (1-978, translated) 326 residues
MYLGMKEDSL APPQNRFESH KTVFSLKQKN IPIKDAAKSD QVNLTWHDYP GEWFEGGAVT
DSEKQDKVET FRNLLGSDVA LFLVDGQKLH DYANEEERYL SYLFDGFIEN LNQIKDAILE
GGKQLQQFPR IWVIALSKAD LWPDLQVKDF ENLLNKKAGN EIIALRSKLL EFIDNDEAFS
FGKDFLLLSS AKFTPGHIDI SQRKGVDVLL PLACVLPMQR HLWWQELKVL PINLADILLG
NEIAQMGFKI VSKVLKNKVS GTNNKAMAAL VFAELVRDMV DQPTELLQKA REEAVGRREF
LKAITAEFTR KLNQAEADQV LVRDFA

> RXA01554 (1-2142, translated) 714 residues
LKKHVTSAVT AVVTAFSTAA LGLSIAVSPA VAQVANPAPD LSAPYTWVEE FDSEDALKGW
NIFRQPDYGS DKVLYTEDAL SIEDGKLTIT TQRHCVDEDF AISDPVNRGK LNDSTAQVEP
CAPGQFEKFT SARIVTPKIA RGEFDLSVTA TLNTGGVEGV RSAIWMQNGE QACSSATNNG
LYGELDLVEH FSYDLRSPWS PSNTHLGCDP ESVNGTNRAP RELKLDESLD GVEHTWTVST
TRDGVEYFID DEAINRQSWR NDVTLGHAEI DDFGISAQTF DEIVDREWTL TLNQKVESAD
WAKPRSSEED FPVRSMVIDR IEVTGSPAVS EDTPMPDTTQ LLTQDTLEYL GRMPVLERYE
PASADFADGR RPSWNYFNLK ESWQNPELEQ RPEAVEFVDG RMDIVTRRHC LATTDDIATP
ENAQEEPCAP GEVTRYSSAR VHLPEIPAGN FRLTVRARAQ SEELVDGVRP AIWMQNNTNF
CADNDGRPYG ELDITEFYSS RVNTQYSAVH LGCAGNRPEM KLRQMEMEES MFGDWHDWGV
EVFDGQIVFT IDGKAVTSSG KDVFGNSVTP AAAPLRPAHF KLSEEEYREV IGQPWHLILN

TMVEQSGKDS WITAVDNNEA FPEHRFQIDH VAVDIESDSV DNVWPDAANE IPDNVGIEDS
DDGSDLEVGS TGSSTAETVS WISLFTALSS LVFTLALNQE ALQNLINQFM RQFK

> RXA01557 (1-816, translated) 272 residues
VRSSNPVFSS LKETQRPQGQ NPYGGYDNFG GVYQQNVAPQ KAERPMTVDD VITKTGITLA
VIIVFALVTF GVWLVSPGLG MILTLVGAIG GFITVLVSTF GKKYGSAAVT LIYAVFEGLF
VGGISLLLSG FTVGNANAGG LIGQAVLGTI GVFIGMLFVY KTGAIKVTPK FNRILTGMMV
GVLVLVLGNV VWALFTGGAS PLRDGGIIAI IFSLFCIGLA AFSFLSDFDA ADRLVREGAP
SKMAWGVALG LAVTLVWLYT EILRLLSYFQ NR

> RXA01560 (1-330, translated) 110 residues
VGVSYIIAGD EQLDMAEAVR KIGETFKTEE IILGGGGTLN WSMLRDGLCD EVSIVMMPIA
DGEKHTHSLF EADEKYSAPL PIGFSLASVE PLEDGSVWMR YGVNGPVDAN

> RXA01574 (1-1035, translated) 345 residues
MSNKRIGVVI VSYGHEQDVA NLVDTFADQL KTGDRVVVVD NRKPWVLKDA VGERLEKHGA
EIINHDNGGF AAGCNVGAAH IVDDVDLLFF LNPDTVIDDP TLFNSLRRVD EQWAAFMPYL
LLPDSTINSA GNALHISGLS WVTGLDEKPV EGSSEVTDIS IASGACLAVR VDWWKRLGGM
EELYFMYHED TDFSARLLLA GGRIGLLHSA YVTHHYDYAK GDYKWIYIER NRHVLLLSVL
PLPLLFVLIP QILGVNLGLW AIAAKEKRVG LKVKSLRLLI RDLPAIFKLR RSTQELAELT
PSQYLAKMEW RLDNPNLGNI GSNKIVATGY KTYYKLCMSI LKLLA

> RXA01575 (1-1020, translated) 340 residues
MKSIDLEQLA GTQSRTYQSR KITDEMVARP VHVAIALWEV PWESAKSGKI EGWVIAVDSP
RGRFVRSGQT KNGDAVNRTV SMLKSALKGV RGKAWIVTGR RQAALRAALV RENYLVTGSF
AEQNRAGVKA SAISRRAEQS ALYKAKKIGE FAERAPRVKE RQEAHWWPRL SRTQGTAGVL
RLATDASTDG VFRGAMCFVA SNGDYLLETQ DTTASSDELE LESITHALIY LKTIGATQAI
IESDSKAALE AIDFILNNRP RRGRWRGITA CARNRFRDAW EALIDDCVVE LSRVLGHAGD
PLNQAADQIA YMGMRAVIFE QKSAHPTLLK GIDKALRKAE

> RXA01577 (1-375, translated) 125 residues
MTQTTTQIII QILLLLATAA LALYFLRNRR KARAKAWVKI GFVVFIFAAV WAVLRPDDLT
QLANFVGVDR GTDLMLYALV VAFMFTTLSS YVRFREQELR YSKLARAVAL QNVVLPEDSQ
GSDPA

> RXA01579 (1-384, translated) 128 residues
LTEVFNTDQR VLNALFNVVE EDDSGDTDDE QHNHQNPVRG TEFAGLVESH EQRSNGHRQW
QHTKPVHLRG FFSGGFLHAE RQCEGSDSAE SSHDPEDGTE TKCFSQPATS KRVHAADTTV
DRGNNSEK

> RXA01585 (1-627, translated) 209 residues
VVETLSITSG AAGLQALVAR AVGLNELASA RFRQLTPEVV DVFVTTPFNV TASRRVFGVA
GRDGAAVGAK DLLQALSEGR EDVGTSRDAS WPGSLPPATG FTLVDELPTH VVRTLADQGQ
ALARQFSGPL GPPASLMDQE VISAEGNGKK AGIPMRTVFT CTSLGLIPGF EAANDVPRHL
RVSVNGRWTR VDAPYGSVYH SSGLGLSVF

> RXA01586 (1-369, translated) 123 residues
NNAAFIEIAQ EARLAFAEDQ FRERGYEIPA VFVRHLEVDY LRAILPDTTQ AVVETQVTKI
GNTSFSTRQE VKDRNGRVCC VVECVQVAVN VQTAAPRSIS KVERKVLTAV ATDEVQSQEA
LEK

> RXA01587 (1-1983, translated) 661 residues
MTDFFGLIYN WSVTVGWLIG IPVSIGLFMM GALMFRRMDK GSAFKKVVIR VVYGVVGLPL
LGVSYTGALD SFLDSGSSTS AGSNATKIVL STYVDFQSWA ENTRMRVPDK VTLAWSLEDQ
APTGQSMRMV RNSALEINAQ SNESFTTFKN PGSMDLGYSM DWMEKMADPA NSGTDGTSSS
SATTIFQGTI ALLSRYIDND SISSGSFETS IRSAMESLTS KEGSGEAVAG GDVMAWVTGY
NTASGLNEIT AAELADANNP LLEVSDSAGL QGRPIDRNAV SFKSGDATAS CNNSVVTGSR
AVVGDYRSDC NMSPLTMYNF LNTSFHPADA SVFSTSTSAS SYTRASHSAV SLIGSGAMNF
VYWFSAMSLM GSFIVIGIGY AGAMLFNTIR RTLSLIGAVP FAAMGFIAGV AKVIVYTIAM
LVEVIGTIIL YQLITRFLMA VPALFEQPLA DSLSSNESAE LVAGAGMGLV GMALATSGNW
AIAGMVITVA SSMGVIIFTI IAMKVRGSLV SGVDETVTSV INRFLDTQVS SAGATSGDGM

MRRAAATGLG IGATHMVLNR DGDGGGSDSG SGGSGGGSDS GLGEKAAGLA KVVTTVAGAG
LVGKYATDAL DNYADGVING DGDGAFAAGG DATVDGDYVA DGDAIASADA NADFVDGVAD
G

> RXA01590 (1-1284, translated) 428 residues
GKLKEYATYI GADPAQGFKD VGQPTPEALR SHYEGSQKAT AIKVLFTGVA GKKEQEMVAL
CRNLGLTKEA MAASAPAQQS ILQAKHDPID ALYRAETLMG PVGDLYQGRK MRRGENEQGR
YEWEVVRDEN HQPIQATKDE WVQQYMEMYA DDKGMGVSVG VDQVEKIAEE FSDEQGYMRV
LSHDELPTEI KPLALDQLAY GDKKNRFDLL CEMAKQQVNI YDGDAYDFAP RVVRANMKAM
EDAARFGIPD VEIQSISAQQ SLASFERVPQ RSGFRIERRV PAEVGTGIAA PAPLPDAGVQ
GNYVQQQVPA TPPVMPVTPP AQQPVSPAQT DFRGVGQPLD QGGKIGNYGH QGPAMGAQQP
VVPQQQNIPP VHNPVPQNSV PPTPVVPKPG TGNPFTHGGA NNQFMGRFDT SRYNQQEPPQ
RQDGGFEL

> RXA01592 (1-1293, translated) 431 residues
NFDRSRDNDR SSARTPRGDR GDRGGYRNSR GNDDRGNYRQ NRDGESRDRG GYLGDRRDNR
SGEYRQRDDR RDDRRDNRSD DRRGGYRSDR NFDDRNSNMR DDRRGGDRSY SRNDRSDRGY
RSNDRYDRND RRDDNRDTRG GDRGDRRYDR RDDRRDDRRD DRRGGQGQGR PGGDRRHANR
AGAGRDQQRD SLHPQRAGFR EERLNTRLNE PDLPGDIDIK DLDPLVLQDL KVLSKDNADA
VAKHMIMAAT WLADDPQLAL RHARAAKDRA GRVSVVRETN GIAAYHAGEW KEALSELRAA
RRMSGGPGLI AVMADCERGL GRPEKAIELA REEDLSSLDQ DNLIELAIVV AGARHDLGQH
DSAIVELQKV NPSLKSTGFT HSRLSYAYAD ALVLAGRGDE AREWFQHAAT LDEDGYLDAE
ERIEQLDNGN N

> RXA01595 (1-960, translated) 320 residues
MTAPTNAGEL RRVLLVPHTG RSSNIESAIL AAKLLDDAGI DVRVLINDAD DPIAEHSVLG
RFTHVRHAAD AADGAELVLV LGGDGTFLRA ADMAHAVDLP VLGINLGHVG FLAEWESDSL
EEALKRVIDR DYRIEDRMTL TVVVLDGGGE EIGRGWALNE VSIENLNRRG VLDATLEVDA
RPVASFGCDG VLISTPTGST AYAFSAGGPV LWPELDAILV VPNNAHALFT KPLVVSPKST
VAVESNSDTS AAMAVMDGFR PIPMPPGSRV EVTRGERPVR WVRLDSSPFT DRLVSKLRLP
VTGWRGPQKQ AENKDPRSAG

> RXA01597 (1-1182, translated) 394 residues
MSLFNRKADL PGLQGATRIC TPQGKGLKRL SEGDLAIIDA PDLSRTFAQR LLAAKPAAVL
NVSRFTTGSV PNFGPQMLID GGIQLVEGFG QELLDGTKDG KKGRLTEDGQ LFYGERLISN
GSVLSGPAAE NAFADAQQSL LDRMEAYFGN TIQFIHSEAP LLIDGLGIPD TGNAIEGRKV
LIASPGDNHR SRLKELRSFI REYDPVLIGV DGAADTLVEL GYKPALIVGN PTGIGADALR
SGANVILPAD PDGHAVGLER IQDLGIGAMT FPSSVNSSTD LALLLADFHN PQMIVNVGGP
VTLDGVFENR EDSDPAALLT RAKLGTKLVD GSVIASLYTV RSSSNLGWMW ALLAILVVLA
VVIVIAGTAG SGSFTDNLID TWNSFALTVQ GWFK

> RXA01598 (1-963, translated) 321 residues
MAKRRGRGAA TFAALGFGAA AGIAFGTYVL APNLPENIDP NAPTSAELVE AETLAEVNAV
QADQADSIID HIVEDVVAGT LTDRPVLVMR TADAEESDVA DVSWLLQQAG AINAGSITLE
ENFFSQDGAD QLKSIVANTL PAGAQLSETQ LDPGTHAGEA LGAALLLNPE TGEPLASTAE
RGLLLNVLRD NGYISYEDGT ILPGQVIVMI TGDSDGSGDG AFAAETQSLF ARALDAQGSG
VVVAGRIHTA ADTGVIGRLR ANPDAAENVS TIDSVNRTWG KMATVLSVRE ELAGRSGAFG
SAASADAASP SLDGTAAAPA Q

> RXA01600 (1-669, translated) 223 residues
MVSKMHIPGT HEFTVTDTEL LLESPILGVR RDSLIMPGGS TARREVVEHF GAVAVVAFDG
ENIAMVKQYR RSVGDSLWEL PAGLLDIADE DELTGAQREL MEEAGLEASE WSVLTDLITS
PGFCDEAVRV FLARGLTKVE RPKVMGDEEA DMINQWVPLH EAVGMVFSGQ LVNSIAIAGV
MAADAVIAGR ASARAVTAPF TYRPTALAQR RKAHGIVPDM KKL

> RXA01602 (1-1530, translated) 510 residues
MAKTHIRLQD LSLSYTSTPL ITKLNITVSS GQCAVIVGEN GRGKTTLLRA LAREFPPSAG
EILTHGTVAI AHQHMPAGDL SVGEICDEAI RDSKNALEEL ERAGALLETN TAHALDGYQQ
ALDAAEVLDA WNAEHRLEKA LRSFGAITDR SRALSELSIG QRYRVRLACL IGGDADILLL
DEPTNHLDRG ALNYLTEAIT SHKGVVLVVS HDQALIKDVA DFIIDIDSTP DGLPRIYHEG
FDSYRRQRSA LLETWRQDYA AAQTVQQQLQ EDLEHARQRV NSSWKPPKGT GKHTRASRAP

GVVQALKRAQ DALDSKALDV PPAPAPLLLP TLKVRPDKPM VDFSDLFVPH RLRLPGSHSV
VSGDKIVITG DNGAGKSTLI EVLSGVLTPA SGSVANHART GVLGQESLVG EVPSIARDHA
VKWGLLSVEE SRFALQEFSI GQRRRLDLAM SLAGNPELLL LDEPSNHLSM HLVSALTEWL
DTTAAAVIMV THDRQLLRDT AHWRHIELKS

> RXA01605 (1-1515, translated) 505 residues
VTSDSPAPAT VNAVFNNSNG FIASMLGNQV VNTVVETMDT EFGVRIVDNM LVGFSTLGDG
MNQAAEGATT LSDGVGSAND GAVQLADGAV TLRDGIASAN EGAQSLADGA SQLDTGLGSA
ATGSQTLADG LSSLSAGTAQ LGQGATQVSD GVGQLVDQVA PLTAYVPDIN SQLITLRDGA
ATIASELSDP SSTYRSGVDS AVSASQQLAA GLQTLKDGSS QLSIGARTLA DGTSQLAAGS
EQLVVGAQAL RDGTVQLDEG SSELALKLTD GASQVPTFAD GADTTIATPV ETEQAGDTTP
LFGIGLAPFF MAVGLFMGAT VAWMILHPIS RRALDSRMGG FRGTLASYLP STVLGLGQAT
IMWAVLYFLL DLNPAHPAGL WMAMVAISWV FISITHMFNN VAGPSAGRVL SIVMMSFQLV
SSGGLYPPET QPAFFHWFHT YDPITYAVNL VRQMIFNETP SNDPRFIQAI WVLLFIWALM
LAISTLANRT NKVLRMKDYH PELKV

> RXA01610 (1-729, translated) 243 residues
VSGFLTPPAT PHIRTATASI ATAVAVALSV FAAALIPGSA LYSVLTAGGV ALGAASGVAA
LRHRGGLRIF QWLSALGGIV ILLIGIVVAV AKFGASAKLA TLGLVTSYYL MPSAALACYI
GGLGQLPAKW IAPAFMATAG AGAAGWFSLG AGTGFERFLI AVAAVFSLMG CVYPVWGCVV
KRPRQVAAWL VALAALVLGA LMLFMVSMVV APGLLWLQPT TVAWGFMIAG VLATVAGLWP
RRF

> RXA01611 (1-357, translated) 119 residues
MRKFRNTAIA LVSAAAITLG GVTAATAQED ETPPAAETET TSPSGSSGSS WNDYNEEYEG
DQEGYGIDGF GSSRDDSGEE VPRWLETWGK VFDALTITSV LGLVVFPVVN FLKYNGLIK

> RXA01612 (1-345, translated) 115 residues
MRSFRTAAVA GLTAVALSVG SATVATAEES DQNLSSGFSA LSSGGAAAVG EDWDADQPVT
GEDIFGEEHE RDNENTPAWA KNMYDLTVLG GIASLLGVIV FPAYNYLVYT GVIKG

> RXA01618 (1-384, translated) 128 residues
MIIIGAVFAI LAVLLHVFIF YMESFAWTSE KARGVFGTTE IDAENTKEMA YNQGFYNFFL
AVIAGVGVAF LFAGSTGIGA ALALAGTGSM LAAAAVLALS SPDKRGAAFK QGTFPLLAVV
FLVIGLLV

> RXA01619 (1-975, translated) 325 residues
MRAITHNTFG DPADVLQITE KEIPTPGPGQ VRIQVTLATI HNHDLWTVKG SYGFVPDLPA
AAGTEAVGIV DALGEGVEGL QVGQRVASGT SFGIWAEYAL VDASGLIPVP EQLSDESAAQ
LVAMPFSAIS LLDFLDMKPG EWLIQNSANG AVGRMLAQLA ESRGIHVVGL VRRDAGVQEL
AAQNISGVVS TETPGWEKQV EDITGGASIA VALDSVGGSS AADLVKLLGE GGTLVSFGAM
GNPIMEIPSG PVIFKHITVK GFWGSKVSRE MPAEKKTQLF GELIARILDG TLTLPVDSTF
DAADIVSAVR ASSEPGRAGK VLIRF

> RXA01622 (1-603, translated) 201 residues
MSDFYADRLF NAMERNEVAP GMLLVAAPDM ASEDFERSIV LIIEHSPATT FGVNISSRSD
VAVANVLPEW VDLTSKPQAL YIGGPLSQQA VVGLGVTKPG VDIENSTSFN KLANRLVHVD
LRSAPEDVAD DLEGMRFFAG YAEWAPGQLN EEIEQGDWFV TPALPSDIIA PGRVDIWGDV
MRRQAMPLPL YSTFPSDPSD N

> RXA01623 (1-711, translated) 237 residues
MSSENLKEIR GGIGETLTVG LGLIPLGLAF GLLMVQTGFA WWWTPIFSFV IYAGSMEFLA
IGMVTAGIGP FSAAVAGFMV NFRHIFYGLT FPRHRIKSGA GRAYSTYALT DESYAIVSAR
PPGDISGTRV LTVQILCQAL WVIPGIIGAL VGQVLPDDLK GMDFALTALF VVLAWEAFKN
NKDYSLPLFA VVLALVSGFV APEQMLVIAL TTYFLILLLR VRFPNLDKKL EIRTSHE

> RXA01624 (1-345, translated) 115 residues
MSEFGLPEGV TLLNVAAVLI PIAIITLLLR IFPFAAMKRV NSNQLMGVLG RTMPVGVMVV
LVIYTLFGQV SAPGGVGASL IAVAFTALLH WLKGSAGLSI VGGTLAYMFL VNVVF

> RXA01627 (1-495, translated) 165 residues

RTYSPSLKDY NSDEPSLLGP AEDPNMYQEF EVSYEQLGIK PEGRTLIGDS FSADFLTSNE
IGIVDEVPSG TIAFTNWKDV TEGRHSWYVR SEDPFGGVEI SPVQSFIAGE EAGGNAPGTG
SSNGGSSHGL WGALAEFFAG AAALAGAAIA FVPGIWDYVT NAFKR

> RXA01628 (1-1014, translated) 338 residues
LVLVGCSNTA ESTTTDTAGS TETSSQISPT TPVSTTEAAP PEDPSANALE EYAQILANPS
IYPLTEISQF VPTGTYAYTL VEATSDSIPE LLLRADSHEF APILVFTYDE NTQSATQAGG
VLIDGVASAG GSRVKVRASN SGAGIYQLNW YSIQPVGESS LYGIQGNSLT QIADPEDFMV
RELLPDHHEI TWVDSNDPSG LSTVQTGGAN IQQAAPTPVQ QPASNLHYFS GVVTMQTAGE
LMRGERTPNG EPATDLYLVL VLDSPIEITA RNAATDPQTR TISEVSLGRY IPADGDNDWI
GYLDTHVEIT ATTDQVWFPT DTGLPLGMLR LADYKSIS

> RXA01630 (1-1077, translated) 359 residues
MSDQKIVVGL LGITHPHASA RVRALREIDG VEVVAAADTD SRLQYFTDKY DVEPREIDDV
LNDDRINAIM VHSKSKDMVP HAKRALAAGK SVVVEKPGGG TVADLEELLA LKEAADPQRI
VQVGYNVRLS ESVQRLKELL DAGLIGEVVS VQARGAAKVG EHITEHLNQP ADMGGVLWIL
GCHMLDALVE VFGAPESVNA RVHKTAKLSD DTSREDSASA LLYYPDFSVS FSFDGHDDLE
WFESSRLTVY GTKGMIEAGI LPQTLRVYLN ESRQGWPQGW TEWTQSYFTP PFARTESNKF
SELPELENIS NFRTEMQGWV NSIRTGSRNV APVEDALTVA RIVSACYESD NNQGISVNI

> RXA01634 (1-552, translated) 184 residues
MAVGQETDLL NAMETLAGVP SDLVVTEILP DTTSYDNFEF FEVHNTGSAP VTIGEGEYTF
AYSFDDSADT SRDKALDLGG EVTVDAGETI VVWIEYSSST VDTAAFSEQD FRDFYGMDSS
ARIFRATGQA GLANGGDRGI RVLYNGEVSG WSHYPSDSAA VQKGIDFALP KVGEQASIAS
AHQN

> RXA01635 (1-741, translated) 247 residues
LIPGGLDTPE EPEAPEDSLF EGRTPPRDAS TRLILTELMV NSTNMGSSDG FEYVEITNTT
AEPIDFSDYT LNYLYPQDEF TNTNEAVWAA EPGDVIIQPG KSLVFWIKNG PNDEATAADF
NAEYGTNLEA GKDLVEISSG GMANGTARGM QIQTNTGHIV NRGFYNMAGA SDVKANEGLH
FAVDESDLLK QTLVGSGAPT PGTVYTSQIP NPLSAVIADS SVPLITDNTA TSINPAEPFT
FAFKYHR

> RXA01636 (1-573, translated) 191 residues
VRTATLHVTS SAGEAATTIN LTEDDGSFNW ALPAADLTGK SWFEYTVTAT DGFNSVTTEP
VRVTVDGANT DPLRLNLEEN QWVSGTTDVI GASDVFGDKL ELLIDDAPAV TNSSLSAAPT
FAMEVTQTDV FFRNGILAGG EELRIFDQGT YANTETISTP VPLYHINEDG TLTVSVYAGT
KAAPEIDLNE N

> RXA01638 (1-390, translated) 130 residues
VLVTEDLLIE APFGFEMRSD EQSRYLEGPD PNLRIHVGVD PLHGADAALV AEELRRLITE
DPSLEEIPAG EWGEKTTIDY RETPGDGSHV LWVTWFDTDR QLNVGCHSKA AETLVHKAQC
RNVIEHLTLK

> RXA01639 (1-438, translated) 146 residues
MSTQTITITV LETATIFDGP ETIYRYDLAA EGILDGWAHS AVLDQVKQIA GENWPTVEIV
VDGTDNVVNA LTSMFASKGV TCGGVGVEAP PVAEEPPKIK RPTSGKQVRQ FYGIKPLHLL
LVSILVGSIA GIWGFRVSLG QWTHGR

> RXA01641 (1-1371, translated) 457 residues
LAIDNALRVS IRIDLTVGDA PAAVADVALP AGSSLADILD EILELTDAPR ISRPWVAHTA
AGSPIDCGIP LAETQVEQGS VVVLSPERDL EAPVLRDVAE ALVEFSSTNR AGHLVELMTF
AGLIGAAVLM TSPAASGIIV PGRMGIFVAI CALLLLWLPP AHTPILRNVL PITLILGAGG
AVSVLVAGTS GTSPGALTWT IFAGACTILA SSLLVHVVYR PAILLVATLS TLGLGLLVLA
ATTTLWKLKA TEDFSGPAAI TVTASTITMC FAPKIAASLA GLRVPSLPTA GEDLSVSDLT
MTDPEKRIKT TKTLFDAQIL GLGVLSGPLA LLSVTPGTWT TTVFSLCIAV ASLLHANRHQ
APIPTWTLMG LSALGFISMA LSASRSGSLI ALIGSVVIIA VLVSVALWIS TVPTLEPTTI
VWLERLESLC LAASLPLALH LLDVFGMLRG LDIGFGG

> RXA01642 (1-1242, translated) 414 residues
MRRLIAVSLA ALFMLASTPA TRAQEVEALA CPEVAIADPS SAVLDEHLSQ SLSQAHQLAT

GAGVMVAVID TGVSLHPRLP HLIPGGDFVG AHQSPDVPGE LIDCDGHGTI VAGIIASQGN
PGTGWPYDGS SDPYIGVAPD SGIISIKQTS SYVRTREDSN VGTLSTLAES IHRALDSGAH
VINISVVSCL PQSPDEAASF QPLTDALNRA ELQGVIVVAA AGNLGQDCPV GSTVYPAHSD
TVLSVSARFD SHTLAEYSMP GNQQILSAPS HIQAGLSPRG DGFASHMITT AGESPFEGTS
FAAPVVSATA ALLRQHFPFA TPYEIRARIF NSIDPARGAI DPYLALTQEI YPTTPLVHEI
ALSVPTPPDD SPRERGILVT AIIVGLLAVL AVLMGLRRIH HHSAFQKASS SVIT

> RXA01643 (1-426, translated) 142 residues
MGTMREMVSD RIDRLQEAHA RSKQKKFGFL VRPGTLILGW LVTIIGLITI PLPGQGWLTT
FIGVGILSLE LKWAKNLLAW GVHQYDRFFT WYGKKSFRFR MAMLALMILL IWVVFIVTFW
LMWHAGTIPW ADEFFTWLGL SR

> RXA01645 (1-606, translated) 202 residues
VVRKLWPRDL LRSSFYWKII GWDRKYSIAD RLEERKGRPA RERVVQDVEV TIDKLPEFLK
WFFESSDIEP LWLCPIKLRE VPGSSVGAGE ILSSAEAIDS GAAEHPWPLY PLKKDVLWVN
IGFWSSVPVD LMGSDAPEGA FNREIERVMA ELGGHKSLYS EAFYTREDFE KLYGGTIPAL
LKKQWDPHSR FPGLYEKTVK GA

> RXA01646 (1-819, translated) 273 residues
MSGLVDPDST FLKTIGKLSN SLSIGRGVDQ KEVIPKGWNA HWEAITKLKR SFDAIPAGER
VRLAKKTSNL FRGRSDAGHG LDVAALGGVI AIDPVNATAD VQGMCTYEDL VDATLSYGLM
PLVVPQLKTI TLGGAVTGMG VESTSFRNGL PHESVLEMDI FTGTGEIVTC SPTENVDLYR
GFPNSYGSLG YAVRLKIELE PVQDYVQLRH VRFNDLESLT KAIEEVASSL EFDNQPVDYL
DGVVFSPTEA YLVLGTQTSQ PGPTSDYTRD LSY

> RXA01647 (1-888, translated) 296 residues
MPRGVPVGVP DAPGLFSSTE EPEQDWFVCQ DVGTGDLHIT VPRGGLGPTL IAEGNGWLGA
SKSETGEVTW NLITADGRRE LPAWGSEHGR IMRRHLGISE DTPRVYLTTE LLNAIPEHDA
VRFPAPLPEL VDASTRNWLR LDGALAEITP LQRGLLIDAG SGVFPDPTAL LGVHEETANT
LTLPEQTVSW QDLDGGFACA DGEGQIGFLE TLESGVALSG DSRAKSFSTN AGGAVGVDSG
FGYYVVSDFG LMHPVSTGES MVALGITDVQ VVPWSVLRLL PQGSELAKET ALAPTY

> RXA01656 (1-897, translated) 299 residues
MTETQETYQA TTRVKRGLAD MLKGGVIMDV VTPEQARIAE DAGASAVMAL ERVPADIRSQ
GGVARMSDPD LIEGIVNAVS IPVMAKARIG HFVEAQVLEA LGVDFIDESE VLSPADYTHH
INKWKFDVPF VCGATNLGEA LRRITEGAAM IRSKGEAGTG DVSEAVRHLR TIRGDINRLR
SLDEDELFVA AKEFQAPYDL VREVASTGKL PVVTFVAGGV ATPADAALVR QMGAEGVFVG
SGIFKSGNPA ARAAAIVKAA TLFDDPSVIA DVSRGLGEAM VGINVSDVPA PHRLAERGW

> RXA01658 (1-1485, translated) 495 residues
DPQILSPTFT QQQQLRNFYG FPDQLAMDRF EVDGKLRDFV VAARELDPNA LQQNQQDWIN
RHTVYTHGNG FIAAQANQVD EVARDVGSTR GGYPVYTVSD LQSNARAAES EDAEELGIKV
DEPRVYYGPL IASATDGADY AIVGDTGDGP VEYDTDTSSY TYEGAGGVDI GNMVNRAMFA
LRYQEMNMLL SDRVGSESKI LFERDPRSRV EKVAPWLTTD SKTYPTVIDG RIKWIVDGYT
TLDSLPYSTR TSLTEATQDA VMPDGTPQPL ITDRVGYIRN SVKAVVDAYD GTVELYEFDT
EDPVLKAWRG VFPDTVKDGS EISDELRAHL RYPEDLFKVQ RDMLAKYNVD DSGTFFTNDA
FWSVPGDPTA AEGRQELKQP PYYVVAADPE TGESSFQLIT PFRGLQREYL SAHMSASSDP
VTYGEITVRV LPTDSVTQGP KQAQDAMMSS DQVAQDQTLW RGSNDLHNGN LLTLPVGGGE
ILYVEPIYSQ RKDQA

> RXA01659 (1-486, translated) 162 residues
PEAVTAVWME SDWVLAETIK GSTPSDWEEI LRPLALLTDA SFTLPPRSTR AQTLDLKHLE
PSRLKPEQPE KPAFTPNASE EDLSQPLVIR PEEPLQMPVR GVQESRGVVE PRSLGADDVE
SIAEGDPERP SDLYGTRVLR DLNGQSSIFQ DSTDADEPPK KW

> RXA01663 (1-435, translated) 145 residues
MEISVLIIAA LILVAGIVLW RADSSKQAAK KAESPVGSVA PAPVLVEEEP DPEFEPELDP
EPEAQPEPEL EVAPRFAPEP VQDLEPDQAE DIYFDDSPEL DADVENALAE LTEVEDYPEE
PVQSEQPQAP ATAEVAADEE QRGVD

> RXA01665 (1-720, translated) 240 residues

VKIDELIALA AEQPTRISRR SGVSRSTLKR VGDGTSEPTL STLREVALAL GLDIKVAAHH
ACDPFAAAAA RTLIDASVPE NPHNQEILAW LHRFERWNIN DPLTLVSEAG TLQGITHRQD
AQFVKLNPRG IAELPELFQQ HKTKWALSGA AAATVIMGQI VLGNSIVWHE PAHDLDVSAL
GTIVDVAEDA DLILLPATVT ELVGSYTQDR LNFVAPVQLV IDLHSLHMFE EADYLTSGWR

> RXA01669 (1-732, translated) 244 residues
HNLSDALTAI PLWIAFILSR RAATQKYTYG FNRAEDLAGL FIVAMIALSA IVAAWQAIDR
MINPRPMENI EWVIAAGVIG FLGNEAVAMY RIRVGKRIGS AALVADGVHA RTDGFTSLAV
VAGGVGVFLG FPLADPIIGL IISAMIATLL VGTIRSVGRR LMDGIEPELV EKATHAIWHV
KEIESIDRLR LRWVGHRLHG DATVSTSTSS LSEATAIALE AELSVKQHLP NVDEMTVTIT
PSKP

> RXA01671 (1-615, translated) 205 residues
MNHVVNFASH LEDAALKQAE ATATMPFIYP HVALMPDAHF GLGSSVGTVF GTKGAIIPAA
VGVDIGCGMI GVCTNYTASD LEGRDLVTLR DYIERVIPLS PGNYNSTTLK ETAKVKVAEL
EELAERDGVD LSHSPTWKRQ LGSLGGGNHF IELCLDELDR VWMFLHSGSR GVGNKIAHKH
IKNAQAQCKN EELPDKDLAY LDRGD

> RXA01672 (1-309, translated) 103 residues
SPLATFRVAL AMSIIGLVAW IICVTVLYFG LNVAGVWQNF NDVIGGVGAE QTITFGLVLS
ISALLGAIGA ITVAVLAPLC AIIYNSIVDL FGGLQIQLQE EVD

> RXA01673 (1-1035, translated) 345 residues
MSTNLLESTP PFTQLRTGVL QKYTPGLLLC SIAVLIAMIV NHFFSGVSPL IVAIILGIIL
TNLIQLPAST SPGITLASKK LLRLGIVFLG LQLVFSDILS LGFPMLAVIV CIVAGGIFGT
ILMGHLLRMK PTQVLLIACG FSICGAAAVA GVEGVTDSEE EEVVTAVALV VIFGTLMIPF
IPFATKVLGL SPEIGGMWAG GSIHEIAQVV AAGGVIGGGA LGVAVVVKLA RVLLLAPIAA
ILSFRQRRQG YTSPDGKRPP VVPLFILGFL AMVVLRSTVA LPDEVIAAGG FLQTALLSAA
MFGLGCGVKI QNLIHVGVKP FILAFGSTTL VTSIALAGTL LTHLG

> RXA01675 (1-411, translated) 137 residues
MNEIPEWLTL VSVEAGKRLG RPGPLVFPPE LVTLAVEGIE LIELEPSWTS DLPLPEFGFL
AADMVDFYDD YEFSEWIPGA WPLALDGGGG FFCLDLRAAN ADGEIPVVWV HASNLGWGDD
EAVRVAASLA DLLSPSK

> RXA01676 (1-756, translated) 252 residues
MILHGVVFYA GLLVLLVPLG LGAGILGELF ITQRQTIIVV SSIVLIILGF VQIFGGGFDF
GKALPGLDRL QSKATVTSGL GKSFLLGMTS SIAGFCSGPI LGAVLTLAAT SGNSITSALI
LSAYGAGMVL PLMAIAALWA KLGQRGQQML RGREFTFLGR QWHIVSVISG ALIIAVGILF
WSTNGLVSMP ELVPMDTQIW LQEATFSLGS PLFDIALIIV AAGLFLYFWN KRQKRKEEAQ
RPKESGWVIN PR

> RXA01677 (1-744, translated) 248 residues
VNQQSKKWLV PTLVVIIAVL LIAVVLLMYR GNASDTAEGV SAAATSDSAA ASTAASGSAS
GAADSDLTSV EARDPSDPVA VGDVDAPVGL VVFSDYQCPF CAKWSDETLP QMMKHVEDGN
LRIEWREVNI FGEPSERGAR AAYAAGLQDA YLEYHNALFA NGEKPSEDLL SEEGLIKLAG
DLGLDESKFT ADFQSPETAV AIAQHQQLGI DLGAYSTPAF LLGGQPIMGA QPASVFEAAF
EQALAAKE

> RXA01681 (1-633, translated) 211 residues
VEVLLLIAIV VGGGVFVASK MGSNNNKKQE EAKFADAQAD ARRWIERLGS QVLTIAGTDA
ASTQAIADAS ERYTAASSQI SSATTPRQAE LARESALEGL HYMNAAREIM GMTAGPELPP
LEGQRNAGRV TEKRTIEQEG RQITASPVAT DETPNYYPGG NVAGRPVPAG WYSEPWWASA
LRSGLWTAGS VMMFSAMFNG MAGVGYSAAD L

> RXA01685 (1-579, translated) 193 residues
MSFAIGITVH AGLGTTTISS LPVVWTAASG LSLGWTTIYF NGFMILCQII VLRSQFKPQM
LVQILWAFLF GFLCDLSLQL TTWAQTDNYF VAWIWVIVST ILMSIGVFIQ VLPNITFIAG
EGIVSALVKK FPNVEFGTMK QIVDWTFVSV AAILSWITMG GLIGVREGTV FAAFFIGFFV
RQWRKLYLRS IGH

> RXA01686 (1-441, translated) 147 residues
MTSLRDLLVS TNADAAIADM SAFIEETVGK QSGISGIALK GAMGAATKID SDIVAKGSRR
LLPEIADSLD GLWQEYQNGG TAADFGAHLE ANSSTALDAI LSVADKNAES INVPGLGKVY
KGVRGKAAKV IEQELPAIGQ LIEKNAQ

> RXA01693 (1-1422, translated) 474 residues
MNTAPFKLEA DFASALPTMA APWQGEEAPN PELVILNDDL AYSLGLDPTW LRTPEGVQFL
LGLNPEPLTK AVAQAYSGHQ FGQFVASLGD GRALLLGEAR SADGVLHDIH LKGSGRTQFS
RGADGRAVLG PVLREYIISE AMHALGVPTT RSLAVISTGR KIQRGSVAPG AVLVRVATSL
IRVGSFQYSN ISGGIELSQH LANYTITRHF PSLVAELSAP TPATYVSLFK AILQRQADTV
GKWTRLGFVH GALNTDNTLI SGETVDYGPC AFMERYRGDA KFSSIDTYGR YKFENQPMIL
GWNMARLVET LLPLLGATPD EGMTAAQEAL VEFDDLCEQA IRKEFATALG LDESDTGTVE
QFRELLYLHN PDITTLLRAL TDNTAPPSGF EAFVHDWKTQ DPDIEAMRAV NPLFIPRNHL
VEAALADAVE GNLEKFHELL AAVTNPFDPT AGPDELRLPS EEGFEEDYMT FCGT

> RXA01694 (1-900, translated) 300 residues
MQKITPNIWC QGTADEAAEF YVNAFSEFPG GAEVLTTVKY PEAGLLDFQE PFAGKTLTVE
LAISGFKIIL INAGEEFTPN PSISFMVNFD AVRDENAKEH LDAVWEKLHE GGSTLMPVDT
YPFSEYYGWV QDKYGVSWQL MLSRPEEKPG PAVIPTLLFG GAAQNQAGPA QENYVEVFPN
SQLGDRAPYG QQTGPATPEA LMFSQFQLDG QWIFAMDSGV EQDFTFSEGV SLMYEAHGQE
ELDAIWNALS AVPEAEACGW LKDKFGVSWQ IVPDNMEELM AKPGAYEKLL AMKKINIAEF

> RXA01696 (1-597, translated) 199 residues
HSDPVLMVEA YRQLAEQSDY PLHLGVTEAG PKFMGTIKSS VAFGALLSQG IGDTIRVSLS
ADPVEEIKVG DQILQSLNLR PRKLEIVSCP SCGRAQVDVY SLAEEVTEAL DGMEVPLRVA
VMGCVVNGPG EARDADLGVA SGNGKGQIFV KGEVIKTVPE SQIVETLIEE AMRIAEEMDP
EVLAAASASG MKAEVKVTK

> RXA01697 (1-726, translated) 242 residues
MFQGLKELTA AKGRTLLITV TVGLIAVLVT FLSALTAGLG HQSVSALKYL AGDNELILAD
SGSTTLSAST LSDQAVAQLE DEGAQMLWQV RDRVADTPTM LLNSPDLAPG EVSLPAELAD
SELATAHDVV DSSNDLYLDH LPVVLMNTSD LASLAQVRGV TGPAGAFASD VALPSDTVAL
SGSERWNASA SYQGEQMSLN LMIVMLYVIS ALVLGAFFTV WTIQRLRGIA ISSALGAARR
VL

> RXA01701 (1-333, translated) 111 residues
MLSHEEIVAI AEDLLSKRYG GVQTLSDVEQ LNGSGTSAVL RARVANSPFL QQRSVVLKYV
PSTGDVFDDS ALVREIVSYQ FTTSLSEDVR PGPVILAYDI DKRILVISDS G

> RXA01703 (1-471, translated) 157 residues
LKYFAHIHAV VQAVSRKMTN FHGVIDWDTG DGDGGLFKGI LVRYLADVAI RLPDDSPTNR
ETKKIAARLV LESAESVWNH RLEVDGLPVF ATDWTTDARL PQNFGLSSSS LSDLVSVVRV
DERDLSVQLS GWMLMEAAAK VAEELENNGN SYTGRSR

> RXA01709 (1-330, translated) 110 residues
MRSGVDMILN ETGGEKMLAQ ADLVITGEGR IDAQTLSGKA PTGIAKRARA KGIPVLAVCG
QSLLGPAISN ELFEDIYSFT DFESDINECI RNPLPILEGI GFNIAKHHLS

> RXA01711 (1-1158, translated) 386 residues
MLLMAHRFFV LAINGAVTDD FTTVYSALRR FVEGIPVYNE VYHFVDPHYL YNPGATLLLA
PLGYITHFTL ARWMFIAVNL LAIVLAFGLL TRLSGWALRS MVWPIAIALA MLTETVQNTL
IFSNINGILL LMLAIFLWCV VHKKSWLGGL VIGLAILIKP MFLPLLFLPL VKKQWGSLIL
GILTPVIFNA VAWFLVPGAS EYVTRTMPYL GETRDFANSS LPGLAIYFGM PTWMEITWFL
IFGAMVGLAV LALLRFRNTE PYFWAATTTG VLLTGVFFLS SLGQMYYSMM IFPMIFTLLG
SRSVFHNWVA WVAAYFLLSP DTFTSQRLPD VARWMEFFSA TVGWGLLIVV TFVSALIWFI
GDIRAKGTPS SPITTDPTHD HLERTA

> RXA01714 (1-615, translated) 205 residues
VIDSEATSQH KTSATPAEST PAEFSEAVES MHRARLRPEL TLGTIRPPQR LAPFSHAIGL
EVGNQEESDD VSTNSEGDSF GRLILLHDPG AEETWEGAMR LVAYIQADMD HAVASDPLLP
EVAWQWLNEG LEQAGAGFTN LGGTVTSTTS VRFGEIGGPP SAYQVEMRAS WTATGTDLTA

HVEAFAAVLA SVAGLPPEGV TELRR

> RXA01715 (1-696, translated) 232 residues
VSELDIKQLN KLQRYSQWAV FRAIPGALDD DRTEVTDQAA KFFADLEAEG KVTVRGIYNA
SGLRADADYM IWWHAEEFED IQKAFADFRR TTILGQVSEV FWIGNALHRP SEFNKAHLPS
FIMGEEAKDW ITVYPFVRSY DWYIMEPLKR SRILREHGQA AVEFPDVRAN TVPAFALGDY
EWVLAFEADE LHRIVDLMHK MRYTEARLHV REELPFISGQ RVDIADLIKV LP

> RXA01729 (1-519, translated) 173 residues
VKLRTIPALL AVALLAGCSG ESADSQAVSA EETMEVTTTS TPVFEAKEVS PITVPSGDIR
VEDPGLNVEF IFRGTRYGTN GGSIIHIAVK NLNDVALPAD AIDPPTLDIE DYNGNKTNIE
TLSGDDNIPL DLPLGAGATT NLQYAFNTSN GSLSNAKFQI GNVIYSGNLN SLA

> RXA01731 (1-699, translated) 233 residues
MNASSISSRF KDLFVTPSIV FDFDGTLAIG HGPVLAYALC VAPEGSKDFL ERVRRELRRY
DDGQSIYRDG YDIVAKLASE LGIDDGTMSV AYGESRKLLG SDLAPVEHVR GIKDILSSLK
GHARLVLATN APENGVHDLL RQWGVADLFD QLHFVVGKPA GLISIISDLQ LDGPVLAVGD
IYEFDLSPAA QLGADTALVG ATATISEAKV SMRGDSIADL PLLAWVCSRV SSS

> RXA01734 (1-534, translated) 178 residues
MTDPIEQAFE RIRAEAMRRN GSVPDLNKND AFRRPPAPKG GVEKRKKGRA SGLDGRQKRY
VRGAESLGSV LNKEIQRRGW GKDIAGGWVT SNWEELVGAK IAQHTRVEMI KDKKLFITCD
STAWATNLRM MQRQILQVIA EKVGPNIITE LRIFGPQAPS WRKGPLHVKG RGPRDTYG

> RXA01738 (1-714, translated) 238 residues
MRILPIGPHD EIAVNGSIVL LSEHDGDIVS VGPDLGTVRV TLEEIESLGT PTAPRDLGSR
EVDACVSLLR NRELVRFDPH DGSELTYREH SVAYGASGKP LFPRLDPAVI GIVELRGEDR
LLLGMNAQKR QRYSLIAGYV SHGESLEDAF TREVFEEAAR RVSEISYVSS QPWPISGSLM
LGMKGFTEDE LPQGETDGEL AETIWASPLD IIDRKIPIAP PGSIAYDMIN AWARDKQN

> RXA01741 (1-798, translated) 266 residues
MTHIALANSA QVLIRPDSAI QFGIDATRAG VLNIDPSLSS RVVPVLRNLR TARPIVDVIA
DLTTAGLAPT AASSLLEDLL EFGVVRESAA AQVLLFGDGS LVDVTSFLLE TSGFVPRPQI
IDESPREFFE LPSSHILVLN KLAHSQRLSP LLHKYAPTYL CAAIVDNRGI IGPGRRSRSG
PCLMCVDLHR CDIDPHWLSI INQQPNGPTF PDPVTEMATA ARLVAWVTAD TWLPGVVEEV
NPHDRTNSVR TLPVHPKCPM CWSLGS

> RXA01742 (1-504, translated) 168 residues
MQEKPEMPAI EVIRSAKRTK TVQARIVDGQ IQVRIPARMS KAEEEKAVGE IVAKLKRRTQ
SAVSSDADLI ERAHKLNKTV LEGRARVESI RWVSNQKGRW GSCTVATAEI RISDRLKHVP
DYVLDAVLVH ELTHTFIAGH SAEFWEWADK TPLAERAKGY LEAYQRWG

> RXA01748 (1-780, translated) 260 residues
MADAKKQADK AAKKQVRAAK KAQRKETRSQ MWQVFNMQRK QDKALIPLLL LAILGIPLVL
FLIGLIWGGQ WWMLPIGIAA GVVAAMFIFT RRVERDVYKR AEGQQGAAGW AVENLRSGVG
MTWRTKTAVA VTTQMDAVHR VIGLCGVVLV GEGSPHRLKP MLAQQKKRLN RVAPGVPVYE
IITGNGEGQT PIAKLQRELV KLPRNYKKND VAALAARIEA MDNVGNAPGG SLPKGPLPKG
ASMSGMNRRA RRQAERKGEA

> RXA01749 (1-1617, translated) 539 residues
VSFLVENQLL ALVVIMTVGL LLGRIKIFGF RLGVAAVLFV GLALSTIEPD ISVPSLIYVV
GLSLFVYTIG LEAGPGFFTS MKTTGLRNNA LTLGAIIATT ALAWALITVL NIDAASGAGM
LTGALTNTPA MAAVVDALPS LIDDTGQLHL IAELPVVAYS LAYPLGVLIV ILSIAIFSSV
FKVDHNKEAE EAGVAVQELK GRRIRVTVAD LPALENIPEL LNLHVIVSRV ERDGEQFIPL
YGEHARIGDV LTVVGADEEL NRAEKAIGEL IDGDPYSNVE LDYRRIFVSN TAVVGTPLSK
LQPLFKDMLI TRIRRGDTDL VASSDMTLQL GDRVRVVAPA EKLREATQLL GDSYKKLSDF
NLLPLAAGLM IGVLVGMVEF PLPGGSSLKL GNAGGPLVVA LLLGMINRTG KFVWQIPYGA
NLALRQLGIT LFLAAIGTSA GAGFRSAISD PQSLTIIGFG ALLTLFISIT VLFVGHKLMK
IPFGETAGIL AGTQTHPAVL SYVSDASRNE LPAMGYTSVY PLAMIAKILA AQTLLFLLI

> RXA01750 (1-1641, translated) 547 residues

MCINDPKGEL LKKNYVRMSK RGFQVVQFNL INNLKTDIYN PLGLAAEAAR EGNGMKCATY
VENIAEVFFP VDGADDPVWP NAANNAFKRA AYGLIDFYLE EEREMRKQAA AENWDAKVLD
TRIDQMWGKV TLYNCYQLFV QLSAKKLKNP VERLNERARA GEFGNLETDE NAAMMFQDAV
TEAEENEMFL WEGEKEKDML TLFFSATDGL PKSSVRTLVG NADKALKAMG GAEKMMASVY
GIAITAMSFF TDPTISTLTS GTLSQNVDLA GLSFPRRMGV RFAAPYVKRY NLVGSQVKWD
AYSDAKFTKP LGKNFVHDDT LSVEGWARFY IKDSFPSNTA YLRLRILNGT SGTLIKTLYF
KFTKGYQTNL KGRAFITDPV TDEKIIKNGL LIELVKNDAG DFVPGHVQFK TKKLNLDQLT
QEQINMPGHD MIKQVDAMVD AVSALNVRYS EKPKAVFFVT PPHLMKYAKL ILILIKQLVD
LNFDSSYMTR ENQKPDYKTR FMLDELGNLQ SEGHGIAGFE TMLSIGLGQE QQFSATSCVA
KNYALAA

> RXA01752 (1-552, translated) 184 residues
MMEQDLSYRE ILPLNASEEK KKAALIDAIE GLRVRDPLLS ASIAFTRGQK VAFIAVVVGF
ILMLIFARQA ALIGLSATCT FMYLITLLDR FIMFSRGIRA ESIIQVSDED ALAFPEDKLK
TYTVLVPAYG EPEVIAQLLA SMHAFDYPKH LLQVLLMLEE DDLPTIAAAE AAGVDQVATI
IKVP

> RXA01753 (1-1539, translated) 513 residues
MSNPSLEPLE PIELSDGTEI EVSDVDPEPQ AGNAQMEVPS LRTYVFRGII AIACLIIGFY
ESFVLMWQNL RIGVANYSLL VVLMAIVLFI GLDRKRARAL NIHDREVDYI IGGIVVLIAI
TIKSQLLPRF VDWETLLRLD MFALLFFAFG ISGLVFGMRS TFSFAPGWIL LFGYNAVAHL
IISVIFGGGF WGPVMANIIG LSLAVLVSSN RDLVQATYLA LMTVLFGVII AIIVWALTDG
SKFLTLVPAV LATITVVLVS SRWRLGQWKI RRRQPTVEKA GPALIAVVVA TALLAWIPTP
YVERVNNLPG LQMLAKPAPG VIAPIGWHID DVQYYNWASR YFGPGSSLLR QTMTADHYNE
AWDPDGLDRT VVVDTLQSAE RFQQRAFGDE TLYSTLRGRK SDTVQVDLGY GVDGRAYTVL
DETDFLTYTK LVFEWQTTNN TVEKISVIAV DDHRAEAKFP ELAPSVTRMF IQVATILFRG
NDVTIDTNTQ LKDLDLVSQV GRQIVAEQQV GRS

> RXA01754 (1-1941, translated) 647 residues
VKIKSVFLST ALSASLLLGI TPPVLGATIN PSLPLSALSS SDDIAVPNFA KELPLAFDVP
AGTVPQSLSG TLQIPAEFSG GVVEFYDGDR LFHTLRLEVN DSRAHIEVPL QSVPVEDGRA
TFWLRAMLDP VNNQWCYEEQ EVRFLDGNVT FEGATINPAV VADYFPSVLR ALTIYVPENP
SEAVQEATLE VATSLDSVYR RSGLDVNVET LPTGTDAPPT RPQDFERQIV LVDEATESNT
QKTELVNPGQ DNAFLRLNGN ADELYDQARL LTDATLPLAV DTEVTASGFG DVPNLSTDVA
TLQELGITQL TSESVARTSV TLGIERSRLR TYSQSMDLHI TGTYTPLPPQ NAGQITFSIG
DTVLDSLTTD DTGIIDREFN VPGDLVNRYT AIVVEFTSTG DVNCGVTQPV GLNIDSDSLV
TSQHSDVPVL NGFRSLPQSF QPRVDVAFAD PSVQELSRAV SVVLGIQSMS SQRIRPHLVN
WDEAVASERP TIFIDAAGAK TDQVPSYLAQ QGQTLEITSK NDQNADGEQL TRSLQTNAAL
VVGSIQAVWD ADKKRTVIVA SSQDNPPDLD ALISWMGEDR ERWSDLNGDL IVKVRDREPV
QLTTVEAPDQ PGRSATAFIA IGVSLVVIAL IVAAVVSVSR RSQKGYK

> RXA01760 (1-282, translated) 94 residues
MAAFLEITLK INDEGRPSAA GVYQEYKQPF LSSIAGATSK ELLIREEDVQ VLHGCDTVAN
AEDYLVSELF TADVVGGLAP LLQADPEIRI YQVA

> RXA01761 (1-1518, translated) 506 residues
ADANADFVDG VVDGAGRASF SNAAYSSDGT TLDGEGASVD AQGNPLHADG TPMSAAEAEM
KMAGLSSSGT MMEKSGVKSS GITTAADVMD DQSLASSVTE SGLSKIPDTY GADVSGAAGT
VGTTGADYSA TDSSAGLNMS EAALQSGTPM GALAGGSVSS SDQAMNDAAL QIAASQGLAP
AGSIAGMEQL SAQATEAPAG KAGKQLGDLS GSALNTQLAS MGQQVGDSVN SAYAAGGMGG
VDVAGKVTEA AQHLSQVPGQ IQNAVTNADA GSSGASFGQM AQGAAGIAGV AGVIGAAGAA
SSAAQGAGTV QGAMGNAAAG AGMINNAVSG GATGSTGAAH VVNASHGPVA PGQAHYQESG
HAQAFVQNNQ ANTAHTANTR APSSAQIMGA NVAGSLASQA VRGIGQPGQM GANVRDAMGG
SGRSGGRGGA TQGGRGAQRS GVSAKNGIRA QRGQKPSVTG QAMNAAMRSA AVSGRMANMD
GNSVGGTEAD PQQGSGVTEK GDKGVK

> RXA01765 (1-942, translated) 314 residues
MSNNVVKYEC AVDADNIVAV DMHVHLEVDS CGHKSMPADI MAASSKYFKT AERTPSADAI
ADIYREHKMA AVVFTIDART QMGHLPNSID DLVASCARNN DVLIPFGSVD PRTGEDALVE
ARRQVEELGV RGFKFHPSVQ GFDPSAPEFY PLWELLESFG LPCVFHTGQN GMGAGLPGGR
GIKLRFSNPM LLDDVAADFP NLTIIMAHPS VPWQDEANSI ATHKANVFID LSGWSPKYFP

ESLVRQSNNV LSKKVLFGTD FPLITPEKWL AAFANLPLKD EVRPGILKDN AVKVLGLAAS
TERGSQAEKV VQHA

> RXA01767 (1-336, translated) 112 residues
MIDHKLWFNT VTNNASVREA AGKCDIPIRT LNEQLNRRIL PEKTVIALAR AYDLSPVDAL
VRTGHLTEEE AGSREEDASP DSADDYPTWA LNSHLDYGIL GAFGDIAEEV NS

> RXA01768 (1-378, translated) 126 residues
MSESTSSANS TTILNDTFNP KPGVPYARVD NLEFATRDEF RAWATAEMEA GNVISATIAN
APREDRIKSF VMDLVRDGID DAAEEIVSRI DSGDFTMKEA LTAIAASIND LDADDVVSDI
VENHFN

> RXA01769 (1-429, translated) 143 residues
LGRAPHSLFF PIGFYYTPMT SITTTDTPLY TALPHTRISD AELLTPTTTV HEILVYGPAE
CPGCTATLDF FARKNMPATK VTVAAGDVAH TYITQDLGYL QAPIVTVRIS SSASNHDNEH
NTQILHWSGV NRYLMQALSR THF

> RXA01770 (1-3765, translated) 1255 residues
MPIIIDNLNS DDDSTIGTAT EYNPDTDADL LDAINADADL DGDATISTNA TEEGVDAAAE
KPKKKRKAPA LKPKGLTAKF FHRDLTGVGG RTGRLNKNVH PTNPDLSYQP VSDVYTPQSA
DHKGIKTRYI LTHPTPAVVL SESISNAFHV STLRRNNNVN NSDSELAAWP YLYQLDIPQL
DQMINVADIC DYHFHGYNLW VDFTPQTIAL RSGKTVLDDG TTASDNTTHV YYRVTVHVIA
GQDHGSTLLD DQGNQVLDRD DNPISTPSIK RIGAVTDLFD HNPFGFASVN SFAFVDFSWD
PATTLVDMLN NLDSYLSNHI NIASSPTPIA LDMVVLNEWS EKSYQLCERV VAQAKLINSN
KITAHVSDVI KQNAHNILWF TEQMNPGTTN LSEVPISKKS MLPMSRQLRI LEHYDVPLTA
YSALFWTVSA IKNESMVQYL VRQNMQLTLS SNLDALNSIV SQLPVPDKDV VAASGYQIQP
HFSTQQREAI TTDNPLAIIQ AGAGTGKSTV ILERIEYLCA AGTNPEEIAV LSFTNAAADN
ITAKNDKVTS MTISKMVHEI YAHNFPDHEI STIDTIINTL DIEYGDQMVT SDYMIQLRDL
LYKVMTQGGN ANLTALSIFM ESHIEAFISV LDQIKQTSLE LEIIICYLLL DKLIEPHASP
KYLIIDEVQD NSVFEFVFAL RFAAKHNTSL YLVGDSSQTL YEFRSANPKA LNSLEASGVF
GTYRLTTNYR SNQEILDFAN IHLSDIEANQ FAGIQLYANS FDAPTADSFK EKVELDMHHV
SKQSEFTDSI PYFMESNKAR FDAAILNNEQ TIVLAHSGRE IRAAQQALAE MYPSITVRNL
QSDKGFNNTV FSTFIKDFWF EVTAVDPAHA AFTFTSQVTA HLDKLVRGKR EQMEDRVIRS
MAAWWRENER DIQGWVQQTQ SGAITNEEFF YRLRQCILDY EIRNNRARQS MLNARNNANK
EAVAQEKPLL MVSTIHSAKG LEFDNVIVLQ KPSSDAEMTE EGKRATYVAL TRAKKRELII
AGSTRAYPRI VTDYEQIVDL LEKRDEERKI KEEEAAALAT LEAEQETRAL AAAEAQAQAL
LLEHNPWLRD LSDEEVTALT EQEIINNVEP ALQIEEEEEE ARALAAAEPA IQQYLSQFAF
DEFPDDDNVA NTVVHVAPQP ILHQAVPADV TVQSSTAPVT PVVADLEVTT VAADPVEPTI
VAAQPEVDDN LVYSTSTPNS HSDVIAVNSD TSENAAVNPV LSDIEALRAI FNNQD

> RXA01771 (1-702, translated) 234 residues
MHQAGQLIND PSQGLWRTSA LRSPVARVGH AVLRQRAGEI SRMQGREFSR PGDQFRQVDL
RRRLIQVHPQ SIPTADAMAV TITMALTAAT IDPVKFVADS QNPDEEIYLA AQIALREMVI
AMPLEDFIGV RIDLEPVLVA AQAAAKNVGV EVSSILLKDL NLPQEYSGAL QESIVAKIQA
ETDLERARNE VKTTRARLAS AKVLEQNPIL AKIRMIEALP PGSTIEVREG DSKA

> RXA01773 (1-411, translated) 137 residues
MITHIQAGLH LGGCRAAGLL PIPAHIDHIV RLTAADFYDT QSAPQLLSNT VLDVLDTTTQ
DLKALWPVAE HIATTIPESE NVLIHCQMGI NRSAALMTRV LMLRNDCTAD EAIALLRDRR
SPFVLFNEHF VEQLRAL

> RXA01774 (1-783, translated) 261 residues
MSPNFQARGT TAPTVALSMR QIAHIREEIK KSPLAASVFI TPTTKQMVVR DLESLFQQLY
HTDLPEPSIK DSGLISAIGS SAGNTNNPAL ALETQMAYHL VLAMHHTDVA TWHKVVTKNI
TESAAAQDAA VEHSAKYDAV YDAAQLMGIT VEEGNVGSIA IAFSTARADG KSDWCVSGIS
RYIEVTEALD AARAVTKNTD ALNKTALPDV QPAPVVHSAQ FMNKSAHDHG VNTAEKDQPT
CLKTVHLQPH RYPRTGFKAI Q

> RXA01775 (1-564, translated) 188 residues
MSYSLIISKA PTHSMPFNEA ELLELVDELH SDNTVKKPVI VPLPDDFSYT VDSAVRLHDL
GVDQELTDWI TAQVAAAYPN QIVSEIAAAP DPQAKTLFSA NAYNTRSFGT FWTEHPITQL

QYKRCYQIVI ENVTGVYHPL PVDNYRYVPP VTPSLPQPVY HEAIALNESD VADHGTRAAK
HAMINRNV

> RXA01776 (1-1452, translated) 484 residues
MTHTDTPAPA HGVTPSEFAV TSHELTTSPT PSPTQVAIAA QEKIRQRKLE ELKAKKRTDT
TAQPLLPAPV LHTRPLPSPN PPRPSPPAPT TGHWELLIVR SQQKKMTAAN PFLKFLHLGK
AFNVKDLGLT CDRTTDVDLS RLGKLNPPSS LILELATALD LHPFLSVALS SHSAVNARRN
QLELTLHNHD TQGTALGHSV TMVQLPEVIN RAAVEPYIKP KGSGNDPLDQ SLNHRAPTVS
DVQKALVQEN TGTATDSNNY LLPFDPDSGA PKTTALNAPN KDLLQARHEL AYIPEIPAIA
SWLDHLDPIM RVHRSLALSI FPVQLLRAAV ENLPHNVTDL HNHLDPEDLL PEELTTWLDH
LFDADLTALA SCPQLAPPIV RSHNHAKAIA AITVTSVMDA LIAKTLDAHD DPLPSLPEFV
ELLRDAVAQL AAHFKQQRGE VLPQPNGLRY ATDFGLLSYI ADGLHEYALA IDFGLIYPNE
LITE

> RXA01777 (1-459, translated) 153 residues
MSRIITAPVH KPYIIAREVK GVSHVHDTVG GKWQATLHTL KPGPSWPKPS QFTAPKSTSI
WFIAVATHPR NPRARKGTLL GRGGLYELKD TDLNFLTERQ DLLATSTSRD PEDCRLRFNS
RHDAAAFLHA NARHINKLFH PALGHARYDL IDV

> RXA01778 (1-1137, translated) 379 residues
MLYQHTTRGL IISDAIIAKI SQVNQLLLLR PTLLQDKDMH HATLSSDTPS IRSRRRSYRE
NKAAYATTST IRNRETFFST SDIDFAILMI QDVQESLVSF DPTLAQDMKP RTNAVISALN
ELREPLDTFY RAHEYGDIIS DGAYEFDHAA IDAQHSLSEL VAGLHNYDNL MFPQETAPLM
SESNGIQLAQ YYKSTKLDES QLTVEPNEPG ISIMWHAHDF TWSCLVRYDD MNRYPEHFSI
SFKDMLIPEQ IYTFHFTPRE AMQLRKGLFN AIAAYKSQTW GDENTDLTKA ELEFGGTSMT
FRAGLSQLSV TGPPDHRQVF CLSSSGREDH NTPPNMRDGH VIDIAVTQLS TLRNLIRVLC
TTHPDHSPAL LPYGQQYTI

> RXA01779 (1-1419, translated) 473 residues
MRYTPRTHRA LGLAALTATA LLLSSCSTTA DLLGADSVAQ AVTDGGSALD PTAAHVLTIT
NATAMTLAEL PENTDPDAAN NTEPTMAQSA LKRIYGLEIA ADGTLIAVAA PLTSRNSGSE
QPTVAAMADP ENNAELTTAH ILEIDPATGT ATPRQDIALT EDFQTMASSF SQIRNGWGTT
QLIGQHPDDP KQPIRSADTW TVTGSTQITG FNTNTPTGTE DAAYTMPATE PAVGLCALES
GSDAPLDEHR ELSTSALRTA SVLSSSGSAT LKLHDPMVMS ATGIVQARAY VDGEVINQHE
IGDLREQLGI TIEESEAAQA ESDAQAATDH PLAALGLSNP TSSALVPGLA ELDCLSADQA
ATWHNRDTSI GTGKPSVLAV INAEMADDFT LQLLSSGATT AETQLAQLPD ETAFVLIDPS
SGAVTDLFFI QSLNTDLPAP TTQINSIAVD ERDPNIIYAT FSGDDHLYQM MLG

> RXA01780 (1-375, translated) 125 residues
MTFLHPKAAF YPLTMDHLTD LGLDPEQLIN ELPTITYDVQ PHNVFVLQFS TADVRVYQEG
NTLFIRSAEL INPELRQRQR TQLNDDLNNP ASLRVCDEIS GRSTVFLKDK SVVTHDHGTN
CCDSA

> RXA01781 (1-261, translated) 87 residues
VLSLTITGPI AVIPHNPDEA SAKAVATKHK HTLSGATSDH PYAGMTLKDM IEQGFTLTPL
EFPLCAVDDP TDSDRTMHVI NVREHSM

> RXA01782 (1-396, translated) 132 residues
MTTFALIASP NNVDPTAESP LAIEIHTDED SSYPLGLIDS DHLVPAVIYG DMVIYTKTLL
AQTPPDDVST ASAFFDKLTA LDAQGRTRDL VYSATYSQLV IAGHNRTVLT DDSEFYDEFY
QVIEAAPGVI LK

> RXA01783 (1-237, translated) 79 residues
MINLFAAALP AFEPLSITSI LVLGAVALIC GLPVFLALEK SAELDDLFAA LIIAVLLGFA
AYTFVLPKLV ELGCTICQL

> RXA01785 (1-576, translated) 192 residues
VDQFVEFGGG QANINPDGSA TVDWEGSFSI NFYDGLVPFT ITNPHLEVSV AGTGVLTGDL
TSYAVEMSNP NEKTPLTDLY EDVTITTFGG VNLDPEGVVT SNPDYDGVIV DVPLDATSQV
TSGAGWGAWP QGFLDFHFDT NLPSYWYSSD GAGDPKKAPM SFNVDFTNGP GLVNSQLLHR
QVISMPETKA VS

> RXA01787 (1-354, translated) 118 residues
TEKIDKAQPP VDQLGSFLHG LETSVADLGV GDRVFLPRFS TFDKKLGRYR IHTVLGFAEN
DPFNPMTSSE RFKGKPYVDM FDNQDNAFNP NSYITTDTVR IVVDPVPETN PDDEKAGR

> RXA01788 (1-441, translated) 147 residues
MSRSYPIYII SFAPADDLHG VGGFEWVPAS TPENKAAAFT TFDRQFDDSR NNGGSHIVRL
LNISDPNITA DMTQDDITAY LDSNIDRWES TEHALKQFVP LNAGADRVPT GGADEHITHA
CRIITVQRSC TRIHLRCGCI PTPQHRP

> RXA01789 (1-642, translated) 214 residues
MPHNPIELHT NDVLDALDID AICDDVFLYT DFEHTPGQLD RFEQLAFTKI YDMLETAAEK
FPDVAINDTL STGNHAAEQY FLANPGNIIV LTSFALNQTD LRDLIISPCI KYTAHARALM
RAVTRTLCTA NNPVERATIF PVSVANALSI EALCSEYHAF RTKQVLNTAA LINPDNTLIP
MLLSKAYEAY AWHKGVESAQ RGSNLAREYY AGLI

> RXA01790 (1-60, translated) 20 residues
VLIAEDIRDM DDYGEDHPDL

> RXA01791 (1-363, translated) 121 residues
MTSPTTLKPW SIRGPIDGEY TMLEAYPFQY VANTRPAIML YALDENGVPE QYADLTINLA
DVELKQLNHV IINPDLHADV TELCISAGLL RPGVLGQHQV GSTTAKVYRL TERADGWLQL
F

> RXA01792 (1-273, translated) 91 residues
MPQYTITITD EQKAVLHSLT NPHIATAEHG AITAIEIHDD HDVVVYHVQP DGTLTYERLV
EGFHYGWTRF DSEGFEIDSD NNRVVDGLRD E

> RXA01793 (1-234, translated) 78 residues
MAQYRVSFIA LAESTIEVEA DSPEEALDLA NAEFDYPVTL AGDPYELHDW EARAEIEWLD
TSSTPQQRLG EHVVKIED

> RXA01794 (1-234, translated) 78 residues
MATHRVHFVA TASAYIDVEA DSPEDAIEKA YDLAGDLPGL IADNEFDLGE WEVQADVQWP
DNSVPREQRL EEGVDLLD

> RXA01796 (1-483, translated) 161 residues
FYCPSDQDAY VDLTLFDQMR QFGAENAPLA QMYIVAHEYG HHVQNLEGTL GLSNYNDPGA
DSNAVKIELQ ADCYAGIWAN HSSEGPDPLL QPITESELDS ALLAASAVGD DNIQQRSGGD
VNPESWTHGS SQQRKDAFLA GYNTGQMSAC DFLGRGVYND A

> RXA01799 (1-1194, translated) 398 residues
MEIPLPTSLI DVITDGALGQ TCIDQAFAAQ LGRVTGVEFN LSDDKTAAEV RINKASGSPF
DTTGEVIAWI NNQEFEWVST RGEDLGLPEL QGIQPLDDDL ITAARTLYSN APAFIAPLRD
GRRALVAINH TPKLVGIRRT LIEGLQALKP GTDLKRALTS FAAFCELGIR FDDNRISFSD
GTSLLLRGGK VIEIAGGLSL RDVRADAAFM SAEHQLLFDA ISSSHNVTFD PHTNVATVAN
EHQVHAIPLA VIDGTRWVWT WSLKELNGQA TEGLARFGFD NGLLLLTNAE ILAEEATAFN
LIDVAKQVLN TWTHTIVQQP DGTGIVLLLD HPRLQLPPAS HAAVEATLYH QLPGDIDARR
AVASYAAHRQ LPFDGYALTV EGQQVGVTFD GEHLTKVG

> RXA01800 (1-720, translated) 240 residues
VKPLGKIAVP WTWYLGIVGV IIFDVVAAIT MLTLVPNKMP ERVNSGLVAL GGSYAPPMSR
ETLIARVIAG AVLVLVISLG ISLLISAQSK NLASDHPDAS AIQIARRWAF LNNIQSCIGW
FSFFLAAILS ISSLRLNGPG ATTHLEMAVY IIAVSVLAWA LMISLRRGQV AIDRAIPIRE
DDSELKWGMI YHDASDKRVF VELDDGHTTV INMARGGAWL LIAVMVLPAL AIVGWVLLEN

> RXA01803 (1-960, translated) 320 residues
MRKKKDGQNL PDFRKNPPKL DKKAYEKELK RLQAELVDLQ QWVVETGARV VIVMEGRDAA
GKGSAIKRIT QYLNPRSARI EALPTPNSRE KGQWYFQRYI EKLPTAGEIV IFDRSWYNRA
GVERVMGFCT SQEYRRFLHQ APIFERLLVE DGIHLRKYWF SVSDEEQIER FEDRLSDPLR
RWKLSPMDLQ SITRWEDYSR AKDEMFIHTD IPSAPWYTVE SEDKKRSRIN VISHLLSTIP

YEKIDRPLPE IPHRPDSESD YVRPPRDEFR YVPDVAAHLE EERIKKEEKA KKAKKPAKAA
GKNSDKQKSS GGKGKKKSKK

> RXA01804 (1-321, translated) 107 residues
MHIVNIRFKP KAKYVDTFRY TVDKFTESTR TEEGCLYFDW FRNTDYPGEY LVIGVWTDEG
ATEHKKSEHF LRAQETLPPL LQQTPMIIQS EFSKKKGWER FSDFTVY

> RXA01805 (1-330, translated) 110 residues
VVVVILINVK FKPLPEYVDT FREQVAEFTE KTRAEEGNIF FDWSINTDNP NEFILIEAFQ
DDAAEAHVNS DHFKAACELF PTILSETPEI INTLIEGKTE WDRMAEFAVN

> RXA01806 (1-480, translated) 160 residues
MSSLDNAPLL ELDVQEWVNH EGLSNEDLRG KVVVVEVFQM LCPGCVNHGV PQAQKIHRMI
DESQVQVIGL HSVFEHHDVM TPEALKVFID EFGIKFPVAV DMPREGQRIP STMKKYRLEG
TPSIILADRK GRIRQVQFGQ VDDFVLGLLL GSLLSETDET

> RXA01809 (1-636, translated) 212 residues
HIRHEQAMRD GHQDLSVFVG ADGAIMLEEL KNRYQRPPEN EPHDDDVTEM IKTTEETEKE
NVEMDQDIAV VDNVDEQVVV TPAHDADSVA VVAEQVVASE PTPEPVPKVE HVEMSVDLAG
ETITPIDQAI RSFMQLNGIE HSVVLRRLGL MTQVAHNKEL DEVYAKALAE GESHAQQQHE
LEAENERLKK EVDALAAELS AALMGEGGGD HD

> RXA01812 (1-1230, translated) 410 residues
SFNDVDPAVT HPHLTVIYPP LTPASEEKFN KITSVAAVSK RPTTLPYFRA DGSPTRGFAN
FSTGGIHGAE YNEDRFDHDQ DLHTVATREF FAILDATLAA LYAAHQAEPE SADYQIAQDA
LAWAKNVLSD QKLIAKSPQL YNPETGVTYE WEFVAQAAWW IRNKPVEVIL PTGESMTVKH
KSVLASASYP LRDNVAYWRS EPKTPQLFPV AKSGGSSLEK KYNYTSVGTA IHEDFSSYYP
LLLTNMAAFT NADLGIDEKT GRPRDRYREI YEQKEIYGAQ RKDPSIDEET KQRLGILREG
TKLILNSATG AADAGHDTPI LMNNRVIAMR IIGQLFSWRI GQAQSLAGAT IISTNTDGLY
SVLDMGTNQR VLDEHATAIG VQIEPEELDI VSKDSNSRAE FLGNGYINAA

> RXA01813 (1-630, translated) 210 residues
MVAIVVVAIV VVGFIVIQGQ GSKAAKLGDR DYEDTSLAME VGSDSITLTS ANTSADAKSV
QLFEDFSCSH CSELSLATDA DMKTQIEDGN LVVEIKPLNF LDRENIDGHS THALAAALAV
ADSNDATLYW NFRAFLMEDQ SEIYNQWSDD DFADGVEALG ADSSVVDAIR TATTSSAHTT
WQPQTVKNSL KKPAACSYHA FFKTARMLKA

> RXA01815 (1-792, translated) 264 residues
MNRSTISPVE ARQQFRAGLI QPTSGWSAGF AQANLISMPQ DLAYDFLLFA QRNPKPCPIL
EVLNAGETFG GIFGSNATEA DIRTDAPQYR IYAHGELIDS PASAVDYWRD DLVSFIIGCS
FTFEHPMVQA GVPVRHLEAG RNVPMYETSL ACRPAGSLSG NLVVSLRMIP ASQVADAVRI
TSRYPAVHGA PVHIGDPSLI GIDDINNPDF GDAPLSEPSD VPVFWACGVT PQAMVMSSKP
PLAITHAPGH MLITDAPDLG FQVP

> RXA01816 (1-732, translated) 244 residues
VQLLHTPAAI SISFDDPNLI STAGLVPTMA LAEDRLTVPT DKGANPGAKI TTLIAGMVAG
ADSIDDIDAL RHGGMHRLFD WIYAPSTLGS FLRAFTFGHV RQLDAVASRF LVGLATQAPA
LVPVDASTSD YVFIDVDDTI IKVHGHQKQG AGFGYSGIRG LNALLATVTT PESAPVVVAQ
RLRKGSCGSP RGAGRLIADA VATTRRLPGM EDEKILLRAD SAFYGHPSIS AAIKAGADVS
SRCG

> RXA01817 (1-633, translated) 211 residues
MTPNVKKAIA QVPDDAWQTI KYTNAIFDED TGRWISVAEV AEIPFTAFTS RKKTDHIPGL
LVVRRIPELN NKDVDQPGLF DLHRFHAVFT TADPGILDTV AADKTHRQHA IIEQVNADVK
ASALAHMPSG VFTANSAWLV CAVMAFNLTR TAGVIAAGAM ARATTATIRR KLVAVPARIA
RSARRLILHL PRNWRWETQW SRLCDHGRLP P

> RXA01820 (1-1374, translated) 458 residues
MSASFDDPNL ISLAGLVPTM HLADAASLST LAQDRLSITG DKGANAGAKI ASLVAGMVAG
ADSIDDMDVL RHGGMRRLFD RIYAPSTLGS FLRAFTFGHV RQLDAVASRF LVNLARQAPH
LVPPPPAGSG GNGYVFVDVD DTIIEVHGHT KQGAGFGYSG IRGLNALLAT VTTAQSAPII

VGQRLRKGSC GSPRGAHRLI ADAMTTTRRL PGMEDKKILV RADSAYYGHP SVSVALRSGA
DVSVTVRMTP NVKKAIVAIP EDAWQTIQYT DAIFDEASQS WISLAQVAEV PFTAFTSRKK
ADHVPGRLVV RRIPELNKKD VYQPGLFDLH RFHAVFTTAD PGVLDTVAAD KTHRQHAIIE
QVNADLKASA LAHLPSGTFT ANSAWLVCAV MAFNLTRATG VIAAGGMAKA TTATIRRTLM
AVPARVARRS RRLVLHLPEG WTWQPQWQKL FDHGHSPP

> RXA01825 (1-270, translated) 90 residues
MPKARVTKNE TAPVSSNPSA NRTPVKINSA GTPMWYKVIM FAFMIVGLAW LIINYLVGPQ
IPFMADLGAW NYGIGFGLMI IGLLMTMGWR

> RXA01831 (1-462, translated) 154 residues
MDSLVLLGLR IALLVVLWFF VLMALRAMRA DLKVTGQAST SSSSVAAPQG LARAFNRSSP
PRLLTVVEGP LAGSSIEVSE DMTMGRSPEC TFVVGDDYAS GMHARVFKRG SEWFVEDLDS
RNGTFVGGTR IDQPEQIAVG TDIRIGRTAV RLVP

> RXA01834 (1-702, translated) 234 residues
MLGGGGAILA IPLLIYGFSF SATQATAASL IIIGLGALIG LISQYAAGHV RLKEGLSFGL
LGLVGSFVGS HLASNIPDSL LLSGFAILTL VVALTMISKL RSTREYITRR PSILAIALSA
TGVGFLTGFF GVGGGFAIVP ALIFALGFSM RQASATSLVV IAVNSAIAMG FRYSDLASID
WSVISPIIIT TVLGAFSGVK LAKKVKASSL QLGFAGFLIF ISIYMGFQNF PDLF

> RXA01842 (1-918, translated) 306 residues
MSKVYVSNEY GGPENQELIT RNTPQPGPGE LGVKVHAAGV NPLDWKVRSG VAGTPRELPA
PLGEEASGIV TAVGDGVEGF AVGDPVLGLV APGVGGYAED TLLVAESTVL KPEEISFTDA
AAIPVAGASA YAGTHQVELE PGQSLLINGA GGGVGLMAAQ IGRVHKFQVV GVDHEDKREL
IESTGAIFVA TGDAVAEQVR ALLPDGVDVV FDLVGGEALR VVAPLAKNPA HVISAADAAT
VGELGGQVLR RTPEMVGQIT GVVQYGLVDP KVDTTYPLEQ AGKALAHVEQ GHARGKIVLE
LITSQD

> RXA01844 (1-180, translated) 60 residues
VVSIAQELEI IEDGTGAVLV SEQATTFDNG FIGYSYFTTG TDGATCITDL RLRASPLPQV

> RXA01845 (1-408, translated) 136 residues
MISNSWAIET TCALYLPVEA LAEVVDAYPQ LALAIMRMQQ DQLVRSRERE TAQTTSTVEQ
RVAAALQHLD AKLGQIRQDG SSLLQVRLRR DDVAGTTVES ASRAMARMKK TGVIDSGREW
IAITNHQALA DLVAGL

> RXA01846 (1-258, translated) 86 residues
MSIPGNVSYV AQGGTGWDGA DQYTTGESWD LQSFLENSTD YLMIIGGSLL ALVGGAAVIW
GFVNVMRKLF GGQSGQQIQW FTTILL

> RXA01847 (1-735, translated) 245 residues
MLIVLPPSET KTHGGSGKPL DFHHLSFPSL TKARQTILAD LQALEVDEAL KVLGISEKLR
PEAESNRALE TSPTMPAIFR YSGVLYDALD AATLPEKALE RLAIGSALFG VIHATDPIPH
YRLSGGTKLP TKSGELPTMK ARWGTSISEA LIDVNQLVID LRSGTYQQLG RVKDAVTVRV
ESVMEDGSRK VVSHFNKHYK GELARVLALS EKEAHTAEDV MSIAQAAGLV VEENPNHKET
LTLVV

> RXA01856 (1-546, translated) 182 residues
MNPFLSDTLI VQQTSSFLSN NFEIYNPDGE VVIRIKTEGS LGSRLVKGDR RFTLEDAFGT
PLMQVRDPMN FVRDTYEIDD PNGNPIAHVR KRFTFFNKRM DIELPGDRVI EMHGNFLGFE
FEFRMGDRIP AKVTRKWSGA GNGYLGRSTY ALIFDEEAPD EIRKVIIGGM VALDLIREKE
RN

> RXA01857 (1-651, translated) 217 residues
MASRRFRMML TASITAASLG FSLTPAIADE AVTVATAPSV GFDSGVERDA PFTAVPHDVV
LGVGATQSEL IFNWITAQGL TGQVAQISLD DTFASPITVD AVSENVSIVN TEGDSRDRAE
GEYVEYRDGA VNRATVDSLA ENTTYSYRVG SEADGWSEVQ TFNTGTYGDN WNFLFFGDTQ
LYNTHSNRAE EVQNWANNLE RRPTNRKPRN LLHPLRG

> RXA01858 (1-573, translated) 191 residues

MFMTPRALTE DNELTLALKS LGGLMVSPNE CSVVTEVMPT WRELWHQRLR WQRGALENLG
AYGITPQTTR YWFQQLGIGY GALALVAYFA VIIITFLARD QWIWYPFWML LGLLFMIERV
LTVWRSTWFA RFVAALLIPE LIYASYLNLV FLKGVVDILL AKQAHWGEHG DKTMQVADAA
AEINDEGEER R

> RXA01870 (1-675, translated) 225 residues
VGVAVVLLLL PTLINLVVPD KANDYKQLEI DLLGVDWSVP ITTEESAAVL CEETSDEITQ
KYWDCNGDTT VVTMIVEGVK DPSNTLRRMV GSSLITSVDD SLEAVSSEDG RAHALYVPGQ
QEGSLWTLPI VALSVQGSGD YEDLTAIAII NGTSLDYYST HIWSSMAADR GLPYQQDFPL
MLEEEPWQDT PGGDRPFELP NDFFDQYPDL FGPGSVIPNL EGESL

> RXA01871 (1-963, translated) 321 residues
MSRMFSITLW VAILLSTPAL FLSLATFIFV DGISVLVNIV FAVLYLVVIV FLLSRTPLWP
RFKGSGSKKG GGFAWAASSL LWGAFVGFGI VMLFAGPVMD LTDKLGWDFV AMSFTGAYPE
EIAKALGVAI ILLSFRQLNR PWHGFITGAL VGLGFEVNEN LLYGATGAIM DPNADLDGVL
MMWQYRTMLG PLIHTLLTGF AGYGIALAFF RARKTVAWRW GVAIGWTLIA FALHFSWNLM
WENVIGSYVT IIVVSVVMYG LAIYILWSNW AEARNDSSYA FVPGIITNTK DLSLLDAPIP
VGAEVPESRI PQQIEEPKAE N

> RXA01874 (1-348, translated) 116 residues
VIAYVASACC LPFGAFAGAL LSKELSGHLQ ERVLLTHTVI NFLGFVGFAA LGSLSVLFAA
IWRTKIRHNF TPWSVGIMAV SLPIIVTGIL LNNGYVAAQA WPRTWQHGCW PWWGGG

> RXA01875 (1-798, translated) 266 residues
VDSLLNKGVA ASDIVAIVRN EEKAADLKAR GIALGVATFE DEAALTAALE GVDRLVFISG
SEVGQRVAQH TNVINAAKAA GVTFIAYTSL LNLGTSKLAL APEHIATEKL LAESGIDHAL
LRNGWYWENY ESSIGAAKAT GKVFGAAEGA RVSAAARKDY AEAAAVVITS DNQAGKVYEL
AGAPALTYPE IAAGIGEVIG SEAEYVNLSV EEYQNALEQA GVPAEFAALL AGMDPIIAEG
ALYSDSTDLQ DLIGRPSTSI VEALSS

> RXA01877 (1-1065, translated) 355 residues
LRLATGGVLA TLLIGGVTAA ATKKDIIVDV NGEQMSLVTM SGTVEGVLAQ AGVELGDQDI
VSPSLDSSIS DEDTVTVRTA KQVALVVEGQ IQNVTTTAVS VEDLLQEVGG ITGADAVDAD
LSETIPESGL KVSVTKPKII SINDGGKVTY VSLAAQNVQE ALELRDIELG AQDRINVPLD
QQLKNNAAIQ IDRVDNTEIT ETVSFDAEPT YVDDPEAPAG DETVVEEGAP GTKEVTRTVT
TVNGQEESST VINEVEITAA KPATISRGTK TVAANSVWDQ LAQCESGGNW AINTGNGFSG
GLQFHPQTWL AYGGGAFSGD ASGASREQQI SIAEKVQAAQ GWGAWPACTA SLGIR

> RXA01879 (1-588, translated) 196 residues
VKITAKAWAK TNLHLGVGPA HDDGFHELMT VFQTIDLFDT VTLTTLDEEL VEEGSVVKQL
SVTGARGVPE DASNLAWRAV DALVKRRAEK TPLSAVSLHI SKGIPVAGGM AGGSADAAAT
LRAVDAWIGP FGEDTLLEVA AELGSDVPFC LLGGTMRGTG RGEQLVDMLT RGKLHWVVAA
MAHGLSTLRY SKSMMS

> RXA01880 (1-408, translated) 136 residues
LGGGRDGAWP VHPEVFKKHD ELNPESHMDI SDLSAALLTG NTAEVGQWLH NDLTSAALSL
RPELRSVLQE GIRSGAHAGI VSGSGPTTVF LCESEHKAQD VKEALIDAGQ VYAAYTATGP
AASTADQRGA HILTVS

> RXA01896 (1-579, translated) 193 residues
ARAALHAWSP TVGVDTDVER WIELDKWGFA RFERGETTHL GQRRDRIRAY LNRELDDATC
DDIYSGYLKA YEQNWTAYPD AKGVLDRAVA TGAPVGILTN GAAPMQQDKL DRTGLGLPEL
VMLAASTLDS AKPRPEMYAR ALTHLGARTA TIIGDDWTND VAAPRELGWN ALYLDRSGTD
PRADIHSLDE LFH

> RXA01899 (1-786, translated) 262 residues
MSRTLWAVSD LHVTFAQNQN TVDALMPQDP GDWLIVAGDV AEKIPDVVRT LSALVKRFDT
VIWVPGNHEL FNRKTDRVNG KARYRALVGQ LRAIGVITPE DPYPIFGGVT ICPLFTLYDY
SFRPLGLTAK QALAQAKIKL DDELAIAPYV DIPAWCAERV TYTEDRLKAT KGPKVLVNHW
PLVIEPTHRL FQKDIALWCG TTATRDWAVR FNALMAIHGH LHIPAETRVD GVSHVEVSLG
YPFEKHPPHM KRPWPFPVMQ IN

> RXA01902 (1-864, translated) 288 residues
NYDAYNAMYP RPNQVDENYF FEYNNALFLS LDSNDYLDID DDIAFLRDTV AAHGDDKDWI
VLTYHHSTFS QAYHMDDARI KYQRERLTPV ISELNVDLVL GGHDHIYTRS HLMNGFTPVD
AGREAVVGET LNPKAGEVVY LATNSSSGSK FYDFYDFQLG QRYDTGLDFQ ETVDQKKIRT
YTAVWNQDQV QDYTNVELTP EGLTVTTKDA VSGELVDQFT LSKQDRDEES EVPVEDDKDG
DNATGSSNLG LAAILAPVLA IFGFVGGLFV GGGSLAEFFA NLGVKMPF

> RXA01903 (1-279, translated) 93 residues
AHLDDRGIYI IPAQYPWGYE EIINLPARAT STPAVAPRTE AAPATVSDAE VQSLLEYLRT
NAFVSRHDGD TTKADIFNKH ADTVNKLAAL RAP

> RXA01904 (1-423, translated) 141 residues
MSISPKNSGT PNENAAAAQV AANLANLTSQ ATGSMDETNE QVIKSNEHGS DAYLADIKAS
REMWAKIALD PNQSEETRKE ARENMARIDE YAREHDKDNK GLLQKLAKNK AELIGTVAVA
TLGVVAAIAN NGKIPMIQLK K

> RXA01905 (1-531, translated) 177 residues
MKASQTLTRN TRARKLGMGI LAATIMATGA LAGTAPQATA AVDTTAPYVS YVVDIPGKVG
EPIKPQYLTI SDQSAYTVTF KYMPSWLKYD ANKKMLYGTP TEVDVWTPEV HVVDAHGNKT
VRYFTVVAVP ANTGPTTTTP STSKPSTPQV TTPTTPKAPT LPKSTFDWTL WGSIFGF

> RXA01906 (1-465, translated) 155 residues
MSEFPTPTTF HVEPETLSSA TDLTVDAHKI AELLLSTTDY RVFYMPRLAG VTPIVSYLYV
YDGENFLIVG RSTHVPWEYY VHYPIKPSRE FGSAIAVPLD DSDDPYDAAE VVALVKQYMT
PTLTPGEGYM QGFYKGLTFT NHLDIHRPLT QIISD

> RXA01907 (1-612, translated) 204 residues
MSAFDELRKN YRYKFTDTWP ANAVTGTGYY ANPAFIIISA DAMTQNTHAD SNLITVKEHL
NTLFPYSVQR KDRAFVSEIY TPINLLEDNP ELAQEILDVL DTLSNNAVFN DAHYSELELE
RLNEYVIDTL AYDMKSDMMR ALVKARPEAD LEAMEELDIA NIQSWINLHS STVSEHNDGS
VDDAPFNSLA LAEIYLQQLA DHTV

> RXA01908 (1-483, translated) 161 residues
MHSDRFEHPD NGYGYTIRQD TDAENPMTHH DTKDAALWVH NRPRRGDTVA DKPEGNEILD
IFAKFICGQH DNDDNPFEVW SDGDSDASLI RTKAYVAEHH PELIFDISAK TITGYSQGDW
LDVVCVTTAA TCDELIPADS LIDIYRQWAF GDVWTVIPDS Q

> RXA01909 (1-879, translated) 293 residues
MANFRSKDKD GNVINPNAST KGVDLVVNVY DSAKHVTEKG NTVHFVDVQV AQIPIDADGT
RANANLAPQT MPHLHLDTKD GQRNTGVAYS DAQIQAMQTV AAQGRNHMTP LLSKDGETVG
YSMLVKADVM FPKTKDGKSL PAVMNTKSLQ PSGVPISDAM NIQQQQFMAV AMNRQAAEAQ
KAAQAQATQA QAPQVAPQPV MQNQQFQAPV PQGQQPAYAG APVYADAVAH ATAQQQAAAA
QAPQAPAGNP FNQPPAVAAA LAPQTQPPAV AAALAPQTQQ PAAQPQMDNE PPF

> RXA01910 (1-846, translated) 282 residues
MAFPLLAVAG TVAPVAAGWA KDKFLSNSQN NQQAQNQQMS FGQVNNSAQN SGSENSGFMG
QYGNLGAGLA GAATGAGLAY SDFEDGQSLS SKARNMVGKG LAGAGAGVFT KLANDAIQAE
GGSMKASAYS AIASGLGSYL KNGGPGVIKS AMASGAAGFG ADKVHDKLAE SGHEGLADSL
SGAIQGGGLG YSTLGGVTGA GIGGATGGLA GLAQNYFGGG DDYSNAGASA SGFSANQVNS
EISTEIPQFA NLGQPQRSEL EQLALPQESR SVDKSYDQGY EA

> RXA01911 (1-846, translated) 282 residues
VFIIGAGLPL LYVPIFVTVI VMVVYALLRY EQRMSGTVYE EADPVEMDSV IWEGIKCDIA
SDIAARAEAK KAKKPVASDA VAVGNYIASL RQHMLVETQR RYHHKLGREL HNDPAQLEDY
GSGLRDCECR ACVVAQKLGV TVHAHGVVQA SARKKDRVII GRADGIDVAG WWNHRQEARR
KTSAAKQLER DAQRKRTQAE RDKEIERKRK AQEFVAEQSG KAAAAQRRAE KKAAKQARVD
ELVAQKQAAQ EQKTHCKRDK QRAKKAQGRK VGAVDNSAVD DV

> RXA01921 (1-939, translated) 313 residues
HIDIQRLNEK QLFVGLKRLL GLLGHQILES DRLSGDDAHV DTNEDVLDLI AYNVSDVVGT

RLLAEDPVYS GSFDLRAGLL STYPETVFDH DGTFRQPSTQ MRKDRLTINT SSAQFAARIL
APYRPLRDVP DAIGDMPVVS YLYPDAAVAE ATGQKQVNVL DESKKFFYDN ITDPEARAAF
DEVFAFYADI EGRNFNSHNE AIDTQINQLR AYLNQVVAFD AAGYALYDVR TRFEQIFPKD
RSYINDATDM TPRAVSSFDD LVALCDDIRG VLDRGLEISS PNHHEMVDAM RKQLHYIQAF
TVPGTHQRRF NDA

> RXA01923 (1-429, translated) 143 residues
MSALIKGSGP HHVVVLNGWF GHAAGWGAFA DYLDLGNYTW HFWDYRGYGN RKDDAGEFTL
EEISADIVAY IDSIEAEKVS ILGHSMGGVF MQKVLADSAT PIASLVGISA VAAAGTPFDE
DSRKLFTSAG HNPDSRRAII DFT

> RXA01930 (1-951, translated) 317 residues
VISTNEIENI HSTRRDIEIA LDESSTSEPK RFSEISHLYL ALAEGKISFP ESPSELRELY
DHLMHGELGK ENELDGEIFR QGPVEIRDSR QKVIHSGFSP ESQIIEGINA IIKLAHSEEE
SNLVGIMMSH FMFESIHPFY DGNGRTGRYL LGIQLSKILS PATALTMSSA INQFRNKYYK
AFHAVEHRLN RGDGTPFVIS MLELLIAAQE GLIENIKQRI DFLASLEDAI KTLRGTNSFK
NHQINLLYIL GQIQLFGKDE TLSLESAAKF LKVSKATATR YFRTLREMEL VHEVSKRPLR
FALTDKGREI VGLEVKI

> RXA01931 (1-654, translated) 218 residues
MSTSFESIPG VTISARKALS TAGFKDLESL AGTNYEEVAG LSGIGARTLE RLQAALVEKR
MSFGGKVPEA EQRTATWTTL DSAAPEATET SESPEYFIQN LDIPRRITHG RLLLEIFNRA
TGQKPYVAGS SIVGYGRVHY RYATGREGIT IRVGFSPRKA KISLYGLTSA PASRELLKKL
GKHSVGVSCL YINKPEDVDL EVLEEMIRIS WEAEPGEC

> RXA01941 (1-435, translated) 145 residues
MALTSLLHQL ADKKHSDLSR EDIVPRAFTV PTSTDAHAIH QDLEKLRNSV LKEQNHLTTV
LGTWSEFLTS NSDNSDILRS SAELGLQLEQ VRDKALEVEQ RIKASAQVDL TDLAHEIEIC
NQHHATLISA IQVRLQSHTA ELRAG

> RXA01942 (1-600, translated) 200 residues
MLRIGLTGGI GSGKSTVADL LSSEGFLIVD ADQVARDIVE PGQPALAELA EAFGQDILKP
DGTLDRAGLA AKAFVSEEQT ALLNAITHPR IAEESARRFN EAEDQGAKVA VYDMPLLVEK
GLDRKMDLVV VVDVDVEERV RRLVEKRGLT EDDVRRRIAS QVPDDVRLKA ADIVVDNNGT
LEDLHAEASK LIAEILSRVN

> RXA01944 (1-384, translated) 128 residues
IRNLRLILPD GRTLTPAGIS DSNAWLNMGD SAGKLDFFDA TFALPEDAFT GVAHAWDTTQ
STDGEHHITI SREDGGEISR TIRVDNTAPE LTVSGVEEGQ ELRGTVEIDA QATDAGAGVK
SVETLLDG

> RXA01945 (1-1242, translated) 414 residues
VQLPLTTGSI ALDKGEHTLV IRAEDEVGNR TEKTITFSTP DENPISGDYA PSNGATVGVG
DVKLSARASD PSGDTVKMTF LEADSPKLDS GRVRMSSGTV EDAGSVSRAE AKMLERGDVE
KLSSLDGLGM EVTSDAALPY QLFEVDAADA LAADTEVRLN WAGSADGRAQ VIMYVFDGEA
WVEVDRHLTG DELEEFTLQG VVNAEKFAIG GTVTVLIQHS EGFAGADHST RNSDVTAAHP
DDVARSEYDF TLAWESDTQY YNEEFHEHQT NIHDYVLAER ENKNIQFMFH TGDVVDDWDQ
PAQWATANPE YQRLDDAGLP YSVLAGNHDV GHTSNDYTEF SRHFGEQRYV DNPWYGESYQ
DNRGHYDLFS AGGIDFINVA MGWGPDDEEI AWMNEVLAKH PERVAILNLH EFML

> RXA01957 (1-462, translated) 154 residues
MTTRTVSTSA PHVTVNINTA HNKTRTVTNG ARKTNAERGK SCISFRVGPE LFDEFKATCI
DNDISMTKAF EKELRTWVDE HNAGATKKRN THRTYVQAPV GTVATSSIPG LGLFTVFKKS
SDQMWYDLES SPLIAQEPMS NMDMHRNGSF ELHL

> RXA01958 (1-507, translated) 169 residues
MSKKRDHLTV IPDLESRTHH SRSTQPPTTL PAPQLTIITA PDKHQPQLRV VKNTTTPSSV
QPSPINYSFT DPVLREAHYA FQHSELARPT VLDSHWVRRA QEEFDTEHNA AYVRAADQLL
SPFDAYILDN GDVYTKTPRA ISAAEQEEIL EHLHEHHICW DEEAEFLLR

> RXA01959 (1-381, translated) 127 residues

MPHDVYDVEH IISKQPFCSI FFQLPAAALK PTIQKAATNR DLTKLNTEQI AENLQRYLDT
YSVMSHQRVT IEEVTHVRNP HEPDYEFSPQ YGAHISLIGE SYAVNTATNE PYATDSEGHP
LALYFEM

> RXA01960 (1-318, translated) 106 residues
MPQHFSQENY RKAPVIMSAP LTIHDLLSTN SKLNLKWLTC TVLNSPNLPE PCITVSVNHT
EGMSLVSFEG GHGLTEIANT QLVPVLELPK FNPFEALAIH LEAANN

> RXA01961 (1-480, translated) 160 residues
MTDNADNTTD NVTNNSDTNL DYSFDPLPDE PYAYGFELVA ADAHSDSTTT STDTPETVAV
ALKTREDTIN WVNTQRAEGK PDEIRINNPI RSERIAEFVH EMIMHHGLVA CMEDLAILIK
RDKLTQLEAE NAITAWHNLT KESLGQIMGL FYQYVENNTK

> RXA01962 (1-570, translated) 190 residues
MSDNTQDNPF SIRYAHPDHQ LALNELVDTA DLPAPTSYMK NPWSGDNTPI AEWRRERITQ
WQRTEIIVNQ RDDDDLIHVS FPKLGQHIQL NTDDILALVA ACVTPTANDI EATIEENLHS
YPHDTVIMFN ADDLDDALGL VVAVKDASGE HSPRAVWRTN TDHGALDETE LARLILKFGG
SFDDYGVLQH

> RXA01963 (1-684, translated) 228 residues
MKNRKKIMST LTTVCAVLGI VAAHPFHASA VIGGSVPSTD SVANAVAKIG PGALNCSGVM
ISPSWALTAR HCVDDINILG DIDTITPITP GIHRNEGNYM GEVYRAPSGD LALININGVH
KGTIAQLPTQ EYPLGTAAQS VGFGGGGVNI RTAESVNMIL TDIYSVRSGK FHHGVGRSHY
LLFDYDSAET GRIHKGDSGG PIFIGDEVVG IMSHGTINKN DGSFDDES

> RXA01964 (1-1326, translated) 442 residues
MTSAVNVQKK TTQKVLKPIN TKNYSATDAV QTGQHGSALG SNIGVYTYTA GLDIGNGYVK
GIIEATGDTT GTSVDVIDMP SAATRMSRPT EVPEPDDTAV AVTGADFFNH IDTNFNSPMV
KGNYRYLCGT RSLSARGSLE EFDLVGNRSK AEQELSKVLV MAVLAAKAVK DFVAAHGRIP
QVAVEGDPGV LRVHTYLALA LPINEYVGHR HGYKAQFMGD GAANPAVHVV TVNNFETPAT
VQLIFERVEV IAEGASAQYA ITAGGEVLMN GMLADVRSKG LALEGVTAGD VLQARHTIGV
DVGEGTVNFP VFTDGRFNHD ASRAYDKGYG TVLESAIQAM DDAGLAHNFN SRKQLADYLQ
RPPSALKRNF YTRVEQHVDQ EAVFFVQDVA AEFARVLSDV GALTEVAFVY GGGSGPLRDR
LHEALLIKAA EMGSEDTFPV LY

> RXA01965 (1-561, translated) 187 residues
MAQKQDTTHV SEDDAPWRNV RMRFPETDAI VERFLETQGA RGISLAMRQL IYLFVAEYGD
VEVATVIGLK LVESLQAGAE GSDLFAQLAA GVADVDAVTT RKKAPQQIAP PSTTTRAPDQ
VNEFVAEAES QPVEESVVEA KVPKQQVAPQ PAQKPEQKPE QKSAQPAQSE PDDGFDMDDV
MGQAFGR

> RXA01966 (1-657, translated) 219 residues
VSESENNTTP AVAARDDRLV WVDLEMTGLD LKRHVIVEVA ALVTDANLNV LGEGVDLVVH
ATEEELAQMD DFVTNMHESS GLTEQIRESA VTLKEAEDAV LALIEKHCDP AHPAPLAGNS
IATDRAFIRE HMPRLDEALH YRMVDVSSVK ELARRWYPRV YYKQPEKGLA HRALADIVES
IRELDYYRRS FFVAEPGPTS EQCADDAQAA VDRFAPYFD

> RXA01968 (1-1158, translated) 386 residues
VLAIGSLALT GCTIERSDAQ EQSSQQSTEV EAEEAQAPVI SVDDGDEDVD PSESVIVKSM
GDGLSKVTMT NEEGYEVESE LSDDGRSWTT AETLGYNRTY TIKATDKNGE TATASFSTAT
PAATTNVALS PLADSVVGVG QTIGFRFGSP VKDRKAAQDA ITVTTSPKVE GGFYWLNNSE
LRWRPAEYWE PGTEVTVEAD IYGKDLGGGV WGETDNATNF TIGDKVEAVA DDATKTMSVY
KNGELLRTMP VSFGRDTSEW ATPNGTYIIG DRNESMIMDS TTFGLGYEEG GYRTPVKYAT
QMSYSGIYVH AAPWSVGAQG SYNTSHGCIN VSTENAQWFQ EAVKRGDIVT VKNTIGETLS
GYDGLGDWNI PWSEWSKGNA DQTSAW

> RXA01969 (1-474, translated) 158 residues
KCQRRGLSQD PLYKNRNSLL TTQKWFSPRQ QESLEQLWAY DKAYGALKLA WLAYQAIIDC
YQMGNKREAK KKMRTIIDQL RVLKGPNKEL AQLGRSLFKR LGDVLAYFDV GVSNGPVEAI
NGRLEHLRGI ALGFRNLNHY ILRCLIHSGQ LVHKINAL

> RXA01973 (1-582, translated) 194 residues
SAMSKSQDDR KIAELEAQFH SLGLNNTELV TLDDAASLLG VPAGIHQIEA EVMLVNFGDG
ADGMGGDTTK FLHYQPDESQ PYVWVMKRVY SFEAMKKLMV GLFIGLCILI VGGPALGLML
GGFIGVLIGL CLGTSAAMIV GPFGLMRMKA YPPCMDSPWV YMSQEQWRTA MGAAQQTEVS
FVEHWDNIYG DNLH

> RXA01974 (1-1452, translated) 484 residues
MTQVVAGTLV GESINREIDE DKYPYLSSYA APVAVPVREI IGREEEVNKI MAALMRPEIS
NVMLVGPAGS GKTTLVQQAL VKDPERNYIE VDVAKMVADL STPAQMAARI KGVFEDAIAY
RKHEGHELVL FVDEFHQIVQ LSNAAVEAIK PILAMSGVLG VRVIAATTLE EFHEHIRPNQ
ALTERLQEIR LTPTDQKTTV AILRGMADRY GVSDQFYDDH VFEQIYSTTE RFMPSSVQPR
KSIRVLDAMV GWHRLSGKPM DMDLLGDVLH DAIGVDIAFK VDGTSIKDKL DEKVMAQSLA
TTVVARRLQL VVADLHDKSR PLSNFLFTGP TGVGKTELVK QLARVLFGDD TGRLIRFDMS
EFALESSLDL FRSELTRRVA DQGNAIVLLD EVEKADRAIA RLLLQVLDDG RLSDDYNREV
SFLNTYIVMT TNAGSEIFET ISNYATDDTG DGRAIKDFVK NIHTSIKNKG FPPELLGRVD
EIVP

> RXA01976 (1-1521, translated) 507 residues
MTQTLAGERR IVTTAELKAM LARGDKVFLP GVAARAPEIL DNFDPADRAR LDVPAADNEI
VSVEFSRRDT VQCISIADRD HLYITDDMIP THNTSNIIFL KSTDETMIKT LVDWSGERHV
VRRNSKTVTR DLAQLVMRTE GKVSYTSATE KEPVVSYNDL NTLPSQNAIV FRAGQYPVWS
RNETIWPMSF MLFANQIIQP GREYSLQTIP TLSSANEFDV NQNAPDFMAM LEKRMAQSIR
TQRAVDIYKK ATGLDDSDIA RLDMDVYSAE IMDIVDTMIA KDEYDDTPDY DEGDESVMNA
RDFMESEYDV FDDEFEDSAQ GFPVATGTKV KKKSLSEEAE VNDEFIHDQE NAEHKLADMR
LKRYAEGKVS RDMLADQFGH ILQDSLEDEL TAAYDESLHA FAQDPNFRVT ANNGLVNAVD
GTVLIEALSQ EDIALMRAQA GVEQSRVYSE GEEALSGTED DPLSAMGKYK TTRAFRIMLV
ELPHWRDLAQ GHFDKEVARA FRRIEDA

> RXA01977 (1-576, translated) 192 residues
MLRTLFVRKI RALLLVLMIA PTPLVEGLTS TAMIVSVVIL AIYMAITMYR VVHGRHEFAH
IARRMALYVN KTSSRFSVVI AYVVLIAIYA LLIPGLVYSV TFGFIVPSTP NTFSDAPAWI
MCVSLLLIAV ASFITSIMDD FIDGILTDFY DEDNADSPDS PAEDIATRPV ESATTSALAG
FAVGYICGRF NR

> RXA01982 (1-1158, translated) 386 residues
MATTSLPTTI TPDSEETVEK RHSLTPILDS LPCESVPYAL AAGEGQQHQL GPYHLTVMSR
PEDNGGIFSL ARVSAGKTPA TRFFSVAGPT FLYMMEGRLT LWFADGRQEI IAGGSATIPT
NTPWSFACEG LVNSALVYYS SSNAFLHAAE KLGTSSFSHT FRVSGEVTGI PYEELEDCGF
TFYERDHLAE LGPHFDRLPE DMKAFALNDG EGDRLEQFEQ INSFVCRPRH TGNQFLAMQT
KGAKTPYIPR HFHRLHTENF ICLDGRVKLH VNGQEIILSR GDYVHAPAGT IHSFAFAGHN
TQMLGVLTTE VFEKFFDYIN TPTNARVQLE DGGKPFFPAE AFAKVQAELD VVVVGPPRIS
TLDVVTNSRF EPINRTITYR ALDANQ

> RXA01987 (1-213, translated) 71 residues
MTFPAQSRRL ARSTTDKWIG GVAGGLAETY GWNPAYVRLA FVASVLFPLP GSQILFYALA
WLIIPSRENR F

> RXA01988 (1-318, translated) 106 residues
MIDPLTPVVP ITTGTSVAEL YADAREHLDN GATQVMIPVI SPSNLTLSVV ALGNQEVDAL
GHSEGQAVHS LLEIHTPKRS WPLSELYIDD NEGLAQVSRC FARLVG

> RXA01990 (1-999, translated) 333 residues
TSDHVAQFGM ATASAATLPD SIVTSVSYTL NGLSFSDPVE LGISDNDKRE ELLGDITKGE
LRLQMEFSIP DSATAEDEYV FNLTGDGLRF FNSNDRTVPV RNDAGIRVAD LLVSNGGTRG
TLTNFSSDAG TTSRTAALDM ELYGWVSSAQ QTGERPIQDW TVGKTEGQVE NKVVRYGVAG
HPWIISTVQH TWVKSTQTVS HFRSEQDWKI NQPPAVDMGA LAYAAPLGVV VGHANVVISN
NNGAGFRGAL VNTTPTTRDV ILNFTAADGA TLRERSGGGF EDFDVFSEVP RVEETSTRIS
YSYKNSFEYD EFVAAFPEYR RSCVGTNRCV FSG

> RXA01991 (1-795, translated) 265 residues
MTNLLPHFPS TDVAAWEPTV VYSADKTTAT ATFKNIPSDI SFSWTGIEAL EPFSPGKTFE

HKVQGSVGEP AGAFTRDNYF TEGELYKHRH ADDLLSGDGL FGPNITDGDG NLPSVDDGKD
GDDGSDGSDG RDGVVAIDVV DNADGTVTVT LSDGTTFTLD AGQDGKDGLD GLDGTGLTLE
SATPDEDGNI TYVLSDGTEF TVRNGVDGSD GKDGKDGVNG TDGVDGSDGK GLVEVSRVTN
DNGSVTITYE DGSQITTKPT PTNWL

> RXA01992 (1-450, translated) 150 residues
VYCPFCQHDH SKVIDSRVID AGSAIRRRRE CSKCEGRFTT IEKAVLLVVK RNGVTEPFSR
EKVVTGVRRA CQGRDVSDDA LKRLAQQVEE TVRSNGSSQV RANDIGLAIL DPLRELDEVA
YLRFASVYKS FDSADDFEKE IRLMRRRGRD

> RXA01996 (1-537, translated) 179 residues
MSKLTGTWTL DPAHTEIKFV ARHAMVTKVR GEFTEYTDSI VVDAENPENS SAKVVIKTAS
VTTGNADRDA HVKGDDFFAV DKFPEMTFEA TSFVIKNENE GTVTGDLTIR DTTKSVTLDV
EVGGVAEDPF GNTRLGFEAS TEINRKDFGV DFQAPLSTGG VLVSEKIKIE IDGSAIKAA

> RXA01999 (1-471, translated) 157 residues
MTLPTPTHST KGSSGRMKRM ALIGSSLIIS MGLITACGSA AAEPEAPAPT VTETVTATVT
TTAKASTITS TVTETTSAED LAQEIVKPAA VEEYSEPQVN TPQQFAAIPE PAPAVAPAQT
YYANCAAVRA AGAAPLYAGS PGYSSKLDRD GDGIACE

> RXA02001 (1-549, translated) 183 residues
TRDPIVAAVG IVQAFQTIVS RNHNPVEDLV VSVTQIHTGS ADNIIPETAY INGTVRTFNK
DVQAMVITRM EEIVAGQAAA YGVEATLTYN RNYPATINDA AKAAIAAEVA GEVGLGVNPN
GSRGMGAEDF SYFLEKRPGA YLFVGNGDSA GLHNPAYNFN DEAAPYGASF LARMAERPLP
LKG

> RXA02004 (1-207, translated) 69 residues
RVGRLMRQNG ILIIRSRKFK RTTGSDHTFN IAPNFLQQDF MASRPNQKWA GDITYVWTRE
GLGLSGRHS

> RXA02006 (1-495, translated) 165 residues
MTVAHKRSLT WIKRLSATTF AAFLGIQLVT PAHSIENTTQ IPESELHNLG LTDEEIQEFN
QYLIDESLFQ ETVETSPIVV SDNEDAAQDP GFGLFTTNPV KHTDEHIGAL YFSDLPGISN
LTCTANYIGG KFWTTAHHCV EGRSRFVGFI EQSDGQYAGI EHVYT

> RXA02007 (1-429, translated) 143 residues
GITANYAFKG KKVVAWKDLA GIGFKGARTF ARPTSDAEVT LPGVTFNSLP RLEAASHGRI
PDAITASKEA ADGKVVVVQE DGYSVMMSKE EYLERQKALG KPVQLNFDDD TDGNTTQTES
VESQETGQAA SETSHRDNPA SQH

> RXA02009 (1-123, translated) 41 residues
MTMYNAAKTL VPQIVAFDDT AIIALDQAAE DEFRKANYPE V

> RXA02011 (1-318, translated) 106 residues
VANDFIEPND APDAPDNGDS GSSGFVDEAK DKTRSAAQGL GYGALRVGFG TAALAANGAR
SMGNLAKNLW TPMMGLALSA GTGISAATGG MITARVGAML AGTGSA

> RXA02013 (1-549, translated) 183 residues
MTESPDLAVS FLAAFNDIEA HLRTQLRAKR SDSFRWMVRI AEKQHLISKE QAETLDAFAE
LRNAISHGQY NDLRPIADPR PDTVDTIEKI RSLLLNPPIA LNVLPEQKVR SYSLEDPVSR
ALEVVHTTEI SQFPIYKGTE YVALLTTNTI ARWVASDLHD NAQLDARSIK EVLDYAESSD
TAV

> RXA02014 (1-396, translated) 132 residues
ISLQLQAIST FPTDPEGVWT SFNQLLFDRG LGSLVPALAP ESLDDLPDEV SALRRTTEKN
TTTLINLAKQ HGLVHHDIAP GTYIVGLITI SRPPITALAT ISENSHKALL GLYLSGLKHG
MMANIGEHDG KS

> RXA02019 (1-492, translated) 164 residues
AGTKVEASDL GLQAIPTSLL PSTSYDSIDD VVGLVAASTL SSGEIATKPR FVGTELINSI
ATNVTDSSLV EEINMVPLSL AEPSVIPLLQ HGDTISVVSQ DPDTGLPENI AAGGTVILAG

GTDPSTILIA LPQSIAEKVA AQSLNTPLAV VLTGDRANNY TTEE

> RXA02021 (1-948, translated) 316 residues
MSENIRGAQA VGIANIAMDG TILDTWYPEP QIFNPDQWAE RYPLEVGTTR LGANELTPRM
LQLVKLDQDR LVEQVAVRTV IPDLSQPPVD AHDVYLRLHL LSHRLVRPHE MHMQNTLELL
SDVVWTNKGP CLPENFEWVR GALRSRGLIH VYCVDRLPRM VDYVVPPGVR ISEAERVRLG
AYLAPGTSVL REGFVSFNSG TLGAAKVEGR LSSGVVIGEG SEIGLSSTIQ SPRDEQRRRL
PLSIGQNCNF GVSSGIIGVS LGDNCDIGNN IVLDGDTPIW FAADEELRTI DSIEGQANWS
IKRESGFHEP VARLKA

> RXA02023 (1-768, translated) 256 residues
MAPKQTPSPE KNRNLVGPVL QRRQTEGTFD QRLLEMRADH NWKHADPWRV LRIQSEFVAG
FDALHEMPKA VTVFGSARIK EDHPYYKAGV ELGEKLVAAD YAVVTGGGPG LMEAPNKGAS
EANGLSVGLG IELPHEQHLN PYVDLGLNFR YFFARKTMFL KYSQAFVCLP GGFGTLDELF
EVLCMVQTGK VTNFPIVLIG TEFWAGLVDW IRHRLVEEGM IDEKDVDRML VTDDLDQAVK
FIVDAHAGLD VARLHN

> RXA02032 (1-570, translated) 190 residues
MPFLQISLLS IGVAADAFAC SVVRGTAIQV NLFKRALVLA GIFGVFQAAM PLIGWFIGRF
FAGITFIAEI DHWIAFALLG IVGTKMIWDA FQPEDDETIV DDGRVQFRPA IILGLATSID
ALAVGMGLAF VEVSILKVAL SMGSITFALS LAGAWIGHHG GGKFGKWATI LGGIILIGIG
ANIVYEHLSA

> RXA02036 (1-381, translated) 127 residues
VHIPFGHLAD TVSWDCGGGS CATNDLVSLF MPAAFMSTLA ACVFGAWAIG LIAPALFIAV
TAWAFRSGVQ AAIADGYTSA TSVGFEMTVS LILFIIAGLC FLGWIPMFIN NRQVARKVRE
RAAGLSN

> RXA02039 (1-810, translated) 270 residues
TSTSTTAPLW LVGTLVWLAV QAVMHDGELY HVEVPTIALV IGFGAQLLIG VMSYLLPSTM
GGGASAVRTG THILNTAGLF RWTLINGGLA IWLLTDNSWL RVVVSLLSIG ALAVFVILLP
KAVRAQRGVI TKKREPITPP EEPRLNQITA GISVLALILA AFGGLNPGVA PVASSNEDVY
AVTITAGDMV FIPDVIEVPA GKSLEVTMLN EDDMVHDLKF ANGVQTGRVA PGDEITVTVG
DISEDMDGWC TIAGHRAQGM DLEVKVAAPN

> RXA02040 (1-528, translated) 176 residues
YIPFVIWSDL GEAAEGENFA RFWSWLKSRR DKARQQGQTF GVFCYASNGE NHWMLSTARR
FFGKVKGVPD EQEIRSFISS DQWNDMFAVA RSQLVGPGGL GLKQLAPAAG FHWEEEDFAG
EDSLHAYLIA STAAEPEAEA ARAQLLSYNG DDCRATAAVR HWLRQGARTA PVLGNI

> RXA02045 (1-261, translated) 87 residues
MNFATIFGSI FEVTLVGILL GAGLPALFAL GIRFAHSPSS NGTNALGKIA STICFAIIAV
AIIAGILWVT KATIYQYSGF DIFGTEG

> RXA02046 (1-264, translated) 88 residues
MKETLTTGLT HQMTYIVPAN RTVPHLLPEA AEFETMPDVL ATGYMVGIIE WACMELLRPH
LDDGEISLGT HVNFSHAAPT VPGSTVTI

> RXA02049 (1-447, translated) 149 residues
VRYLTLATII AGLSGFVVII IAAWALGDSS QLSEEFTAYW GLFFAGTGVL TGLTQETTRA
VTAGSRGGSR GGRAGSVVGF RPFLFSFVVA AIVLVVLGAS APLWIGQLLS NLQGVGVGLL
AVGLASYAIQ ATISGIFVRL PIVEKSMPR

> RXA02050 (1-372, translated) 124 residues
LAIVWAVGLV GAGLAWLVGP WILDVVLQKE LFAVPGWLLA MLTLGATTTA SLMVSGCAAI
AFERHGIYLT GWVVATVVAV GFLLGPFDLG VAAGLALIVG PLCGLLVHMG AFVGGDRNRV
LTAG

> RXA02051 (1-498, translated) 166 residues
MVIRALQREE EIVLLSAGAL GIHEKTVERT IRGKRIPGTQ KTVHVQYSYT GKLGIDASDV
EIKSAGDNKL SITIPEFIFI GYDDLKFKTI AEDDGWISFS TDDIDTAEVV SEIMSQENFV

EQVTTNREML EDQAVDFYND LLHEFTEKLD TDRYEDTKIE LEFEFE

> RXA02053 (1-579, translated) 193 residues
MSLSVVEAIT NRRATRKYTD EAPTPELIDK IVDLALEAPS AFNAQQREIV VITDPAQKQK
LYEASHQKQF LTAPVTFIAV ARVENEPEDL EEILGTERAE RVAGFINGRS IQQAREATLR
DASLAAAFLI LAAQAEGLST SPTTGWDEEK VKEAIGLGGR EDRAIALVIA TGFPNEQPEH
PGRLQNRRID NSY

> RXA02057 (1-531, translated) 177 residues
MKRICAVAIS SVLLLSGCSS TSTTQLEGFD GRSAQEIITE LDQTPVADRA TNLMASIRAD
ELILSDQSGQ LSIDMPADEF YISAAPYTTT THECFYHSLT TCTGELANTP VKVTVVADNG
ETILEEDTIT YDNGFVGMWL PRNIDATLTI EHDGLKSTQP ISTGDDAPTC ITTAELA

> RXA02058 (1-552, translated) 184 residues
VQIVSPNGEI ESFVLGKLYE TALVERGRSA SVQLIDGDLD EQLSMLRDDS TDLVIACSGQ
LLEYYNPDLA SEFAVEYANQ TAFDKNSGEW REKVYDALQG SLPDSIVATD PSNAIGCKDD
TSLPQNIVPI YRKPNLDRDN RDTLNFVSGS LGTSDLEALV KDAQTTGTTS ETALDFLLSK
GFSR

> RXA02059 (1-495, translated) 165 residues
MTQPRPDAAS VSLEKKRPEG WPVGSFETYP EAQAAVDLLS DNAFPVTELT IVGVDLIEVE
RVTGRLTWGR VIAGGMASGA WLGLFFGIVM ALMSGFWFSS IAAGIGMGLV FGIVGAAVPY
AASKGKRDFT SSTQIVAGRY DVICSPERAR EARDMIALKT RDLRQ

> RXA02066 (1-492, translated) 164 residues
MFNSDTTANL QAKSRDRAGS KAKRSRPSFD SVARDVLDVR TKTAQVKNKA KEFSSVDHLS
ADAAAMFVDN ELSRGAMHRA RLHIVHCAEC REEINRQRET VDYLRSECKN EEVSAPMDLK
ARLASLATEC MPGPGAENLA MQRPESFVAK VESVVRAVRK NQGR

> RXA02067 (1-456, translated) 152 residues
VGWGEIFLLV VVGLVVIGPE RLPRLIQDAR AALLAARTAI DNAKQSLDSD FGSEFDEIRK
PLTQVAQYSR MSPKTAITKA LFDNDSSFLD DFDPKKIMAE GTEGEAQRNK QAADNNANVV
ERPADGSTAR PTQNDPKDGP NYSGGVSWTD II

> RXA02069 (1-579, translated) 193 residues
MADFNRSELD SPLFGSRKRF KFDDDTIGAY AEKVARFFGT GQYLFWQTIF VVVWIFLNIG
GWAWSWDPYP FILLNLAFST QAAYAAPLIL LAQNRQEDRD KHTILADRRR AEETKADTEF
LARELAGVRL ALGDTVTRDY LRHELEDLRG LLDRIEAKLD DEAASRIADR HEQHGSGPQD
LSDPTQGDVA DEF

> RXA02070 (1-1098, translated) 366 residues
MTQVTESAVR SALSRVEDPE IGKPITELGM VKSVSIDGSD VQVEVYLTIA ACPMKTTIVT
NTEAALKDID GVGQVHVTTD VMSDEQRRAL RVSLRGETSE PVIPFAQPGS TTRVYAVASG
KGGVGKSSMT VNLAAALAKR GLSVGILDAD IYGHSVPGML GSDQRPHQVD DMIMPPQAHG
VKMISIAHFT EGNAPVVWRG PMLHRAIQQF LTDVFWGDLD ILLLDLPPGT GDIAITVAQL
IPNAELLIVT TPQAAAAEVA ERAGTISVQT NQKVAGVIEN MSAMVLPDGT TMDVFGTGGG
QKIADRLTAV TGEEVKVIGS VPLDPNLRIG GDVGNPIAIS EPHSPTAAAI NEIAEHLAHR
KVSPTK

> RXA02071 (1-453, translated) 151 residues
MSNSPTDVST SAPRIMIAPD SYKGTATASE AAQYLGEGVL EILPNASITL APMADGGEGT
SSVFGGQVIT LPTTNAAGRL TEASYTLDSE TNTAYIDIAA ASGLPAVADD LVPTTGDTYG
TGVLIADAVT RGATRIALGL GGSATTDAGS G

> RXA02076 (1-534, translated) 178 residues
MKSPFIFDVA ALLRGSALPE HLTQSGPSPT RIGPEMIAIP EGGKVIVEAQ IIPLGGGLAV
EADIEAQLLG QCSRCLRELT PTKTLHVSEV FAADPDFVTG EDAADDEDEL PMVNQDQIDL
LQSVIDEAGL TLPFNPVCEE LGYGACQDDE TPAPDGVSEE VEDEEKVDPR WAGLEKFL

> RXA02080 (1-807, translated) 269 residues
MSIEWLQIVE LGAIFGAGFL AGSINVIVGA GTLVSFPILV FLGLPPLTAT IANTIGIVPG

SISGVVAYRR ELHAHVKTIR FLLPASILGG ITGASLLLHF SADVFTAVIP WLIGFGTLLV
IAGPSIKKHV GAHTSGGISA GFRQLPFPSR TTFIVSVCGA LLLGMYGGYF SAAQGILLIA
LLGITSTLQM QELNAIKNLT VAAVNLIAAS VFIIISPELI SWPTVALIAL GSALGGYIGG
RYARRLRPSV FRAFVVIVGI TTVIVMTIG

> RXA02081 (1-1629, translated) 543 residues
MTLSGLELLE FERRTAAMET RLGRHNRGAG GAFPEAVVSR SVELPLFVQA RNFLNNQQIR
AQVHRRILEQ LPTEGEIVLL GHSLGSVIAA DLLRRLPPEL TVKGFVTIGS PLANGQFNVD
DLFKLLRTPL SNVSWWVNFW SGSDPVAAKR GVSVAVPWVL DFRVKTSLVP GPGHSSREYC
ANDAVAEAIG FGLFGSRSKE IVLAEKNLQI PLNDAEIFVL QALRYCYLIL QRLKGDEALR
YEYALRETQD RLIEEIKSRN AEEGRPIPKE IARLDFDNGD PNAAAPVPGL SPFMPKEQAI
ERLLEIIGQN LLLPFEIEVP EKIQREALRD FTAETQLGST VGADIFDALQ MAVGVVSGSA
KSNWRKWGAF GVGAAALTAA TGGLALAAVP TVAGVATVAS TLAAFGPGGM MGGLVTAGTL
LTVGGGSLTA GVLSSVNTTE EIEALVVQKL SLAILWQRHE IDRTHEVWEE FAEAERLIVR
EHTRVKNVSD SSSPILKAFE QQRSTIERAL KYLSDHGMEP GWFEELEPPA PTPFLKLRAK
KTD

> RXA02084 (1-345, translated) 115 residues
VIIIASVVFL LVGAMLANAA AALFSASEPF GRISYLIGLP NEDDFVPYSL RFVAFFPLML
SASMAASFFG VWAVLIIPFG YFPSLMMVHK HNKQVQRTWD SVTVADFYED STPLV

> RXA02089 (1-471, translated) 157 residues
MSSIYSATRY AAHFKSVFPT ALDDIQSMMR HPRSLARAIP TWRPPSIPLP SLPGEDPLTL
TLSRHRAGPA ARQIIREFGE QREPAYLITI RITSPEGFKV STRLAEGWIR AILSTAHSGT
VHQLTDEPAP TFCWLVDAHF DPVRSPSFLF EYSKSAA

> RXA02090 (1-801, translated) 267 residues
MSFFEDIAAG LDSDGIESRV NGDTMFVPIT SDLEIQFVEI DSLLPAANVY IAAANVDEDD
DEFEAVLVSV VFSVEDAVAA VAKHVATDQV VTVLRDLLEG TDERIQDLEF FQDAVNANLV
RAEVGQNSEL QVLVEVEDGV PTATVNFIAI GESFEDLIDQ AIEELWESDG DAVLSDEDRQ
RMFADLTSEL EFVTDEVLDL GTFTDFDRLF DILSLADDQA EDWEAQLVPF EDEEFDEPDV
YDLFVDDSEE DDDDLDDDED DEDDDED

> RXA02091 (1-651, translated) 217 residues
MSIWKRLLVQ YPRFADTLTA GQPITLEELA TPEVILEAVA KGQEIFGIEQ PKHAAQLWFH
SLCTAIVGPA VTAMVEFDVI PSLDIRRGQL HNIDGYWFGF RPEEMLVDAS LHLSGTQFGE
SIRVVIDALC AATDLRPAPL WAVASDALGI AASGAGVEAF EEEHAREVAE ALIEGMNSVN
SVPSPRFNDD DYFIRAGCCM IFHSPRADFC TSCPQKR

> RXA02094 (1-717, translated) 239 residues
MAEHNAIITD AVHSDPAVLE DNAGFSGKYL IRALDKAAHM QTGAIEGYIS WLRKHNPEKT
PAQLQVLVDK HFMRLATGSG AGVGMAAAVP GIGFVTGALA VGAESLVFLD AAAFYTMASA
HLRGIDIRHP ERRRGLILVV LLGTAGKAIV DAGVGDLSKK NHAPGIAISR FNIGGLMEVN
GRLMRYAVKE VSKRFRSALI GKILPFGIGA VLGTMANRKI AKRTVGNAYD SLGPLPTHF

> RXA02097 (1-3372, translated) 1124 residues
MPAGIADMTD SLLGWASQTE LDLNQRLAGV EYFPQIQLRH DELERIHRFY GTFLSRQVGA
GASLGDLFEM TPCLTVTTLV SRASRISDPA DFFGEYIGGL GLSAEHAAVV EGLTEKLFAQ
AGLLVPEGIA SPLELLSIHA GISNHEVAAV LTEVENGTTE YPFMFDAVLR LTPEWAQTLI
GGVQELIEFA TTHRTSWSDR QRESSLPAMI DEIVVAELRE RPVGTADREN SVGVALRELR
PRLILDAERR KVCLRLPEQR VSDDEINWRV SLEGTTRIFS TRRAWGDTSG YSEALDITVE
RQIRETTVTD TSNQITWVVP VVDFNDPVLV FSARGENLTD KVSLHHQEIY VLAPAEAKLE
DMVTGQPVPV IEQFLVEGWN SWVCSRVDAR GLSSLKVNKE VRCIDPRRRV AFHHPAELVP
HVRSISGLPV HAQSLIAEFP PTLSGQDETW MLSISAFAGV GAAGEEIAEP EPLEVPADGG
LFAIFDPEIY DAPWVGEYLV RLRGPRNESF RPEFAIVEDM TTEFEVASGA SFRIPTTTGL
SEASLRVRSG EKHFTAEPRL VTVEATDPNA SFVVTTDEGD QMPLRFVPPQ IAIELPLTTE
PPTWRVTRTV CGPRDLDGAG ELRIRTGVDV GDPKVSVRNH HGSPLRTVKM VTPDNGRTWI
ASMKEIAAST FVMPRGSIEF EWTDRKVDRR VSVTIAVIDK TENFTGITIE DGKLVFEELA
AGRQLAAWVW PQTAPWVSAV ELAVTGPELE LPEVLVGAGN LIVQLHTADP FTTSVTPLSP
GKAAVTVEQE GYYSAQTEEY AQLSAFFGGE VEEPPISDAV VPALWDVSHI WTEQGNTEHL
PVVHAALRSS PAAALKGLSA SLVPAQALPG KVISSGLAAS PFTTESPATE VHRTAWIGTL

QLLGALPSAF KEAEELGNRT PLLPILGQLE EVAGKNILST LATGRDSTLD TACIDQSTVA
IAGMNETQQK ALLDMFFSNA DIVPGPLMED NTRLMAVFET FKKRDALREV LQTEGLIKTA
VELLRAMRGT QRQLYSSARI RFDKLDGVNT DNPENMWALT PVVSLVFALS SRLHAHELIG
KTRTLDRASA GWGRIADLVP DLVTGDLISA EAMVLGARNP GLVD

> RXA02102 (1-1158, translated) 386 residues
MTSPHSFSVT PIRTMADGTI KQIHPFTGTE VWTVPGRGNR PLSHPASTIV ELSAHDHTSY
CAFCSDNMLS TPPEKSRIII DSSGDFDILP GALPGELSET TPEFRRVPNL FEIVSFDYWH
QNFGFDMDSE TAMRMAQYLA IPEGREHVLA IVRTRLSAAG EDPAHMTDGE LLEKAPSYFA
GGHDVIIGRR HFVDDATTSD QLASSGTLTV KEHEAFIRLT VDGIRDLYHR NRYAPYVVAF
QNWLKPAGAS FDHLHKQLVA IDERGRLIAD ELHHLRGNPN MYNELAVDYA GYHNLIIAEN
DHAVAFAGFG HRYPTIEIYS KSAIPEPWLQ SDEEIQAMSN LIHACHAATG ADVPCNEGWV
HKPIDVDMPM PWHVMIKWRV STLAGF

> RXA02103 (1-396, translated) 132 residues
MPKIQFDVLV PDTDSIALAG RFTVVANLLI EKGLMDHGVV VHDPAAKIAE AVEEQLRQTY
RDEHEDADLE ESSVNRYLIE VDGVKGSVNQ VTMIFARLLT PPAELPKDAF LLEQELAYEV
PAVYPWTVEI LR

> RXA02104 (1-420, translated) 140 residues
HACAQLEVDG TKPGMGAAGG IAIGLTWLST LMHGNDQQIH ILPGAPLIAR SNGIEDALPE
TDLLITGEGR LDSQSFTGKV VGTLHGLAKA HDVDLAVAAG IVEGGIPDDF LAVEMIKSSD
VAAQLRDAGR RIAQEYVAQN

> RXA02107 (1-342, translated) 114 residues
MDLHKVAAAH AATLPLSTKE FPFGPEHEVY KVRGKVFLLL TILNDEPIIT LKSDPEIGAS
LRSGFPTIQA GYHMNKVHWL SISDGERITK DFIEGLVEES YELVISTLPK YKRP

> RXA02108 (1-435, translated) 145 residues
MTIYAPRSVA HSIPVECHIV EHGRNFTVGS LSVEVLGSEH AMLTHSMPIA ENVGYLINGR
VLHPGDTFQP IKDVELALVP VNGPWVKMLD VEGYLKKFPP KRFIGIHDGI VNDRGLAINK
KFLTHLGETY GSEYSPLEEG ESLEI

> RXA02109 (1-921, translated) 307 residues
MLAVLFGVVA GAIMPFQTSV NNRLRQSVGA PLLASFISFL VGTFSLLVAT WITSGHPYPA
LGNTTGQPWW IFTGGMLGVV LLTGNILLFP RVGSVQTVIL PISGQIIMGL IIDTTGLAHS
PQAPLTLFRV LGAAAVLVGS LAAVGVFSKK NIGQTQSQGA SIWLWRLFGV VMGMCQATQV
AVNGYLGTVL GSPIESALVS FAVGTTALFI LLLVTRTKWR GINGAGKKNP WWMWIGGVIG
ATVIFSTAYL GPIIGTGVTV VVMLLGMMLA SLMIDAFGIL GSPRRHIHIA QLLGLVVIIL
GVTMIRI

> RXA02114 (1-486, translated) 162 residues
SIGYAWTTAF HALTPGLGGI AIGIWLLGGV LGGLVIRKPG AAIFVEVVAA CVSAALASQF
GISTIYSGLA QGIGAEIIFA LFLYRRYSLP TTMLAGMGAG GGAIFLEMFF YGNLAKTMSF
NIIYSTTVLI SGAILAGLLS WYLVRALART GALDRFAAGR EV

> RXA02117 (1-474, translated) 158 residues
VSTDPEEFDQ AETLDQLAYE IILLTRYGVQ NTPTNKREAI MDRSALILLT RLDAQGPMTV
NELAESFGLN VSTVHRQLKA AIANGLIEVV DDQACPAKLH RPTELGKEKL QQELLARQQD
LTRILHDWDE EDIKTHAKLL RKHNESLEEY LDMKWPRP

> RXA02121 (1-705, translated) 235 residues
MITSPFEREL KLLNEGELGI VQQLVESSNI GFIVDLELDG DYGWAVYKPE LGEQPLWDFP
PGLYKRERAA FVISEFLGWN IVPPTVIMHD APAGVGSVQW FIENNGEHYF PLFDTRADLH
PQFVRMAVFD LLCNNTDRKS GHVLLDGDHI WGIDHGLCFS VEPKLRTVIW DFAGCTIPDD
LVTDVEQLLE DVPEELHQLL HPAEIDALQR RASRISRLPF LPQAKSHRQF PWPLV

> RXA02123 (1-1371, translated) 457 residues
VWGVSLPPNV QTVGELKAAG HIYRPLRVEI RDNLLAKLRS GEDPWPGLHG LNYTVIRQLE
RALIAGHDIV LLGERGQGKT RLLRTLITLL DEWSPIIPGR DVPEHPLAPN VEISDDQPIE
WVHRDARYTE KLATPDTSVA DLIGDVDPMR VAEGRSLGDL ETIHYGLIPR ANRGIVAINE

LPDLAERIQV AMLNVMEERD VQIRGYNIRL DLDVLVVASA NPEDYTNRGR IITPLKDRFG
AEIRTHYPLE LDDEVAIIRQ EAELVAQVPD ILVEILARYT RALRESSSVN QRSGVSARFS
IAGAETVAAA ALRRAAVFGE DEAVARLVDL EAAVEVLGGK IEFESGEEGR EWEILDYLLR
TATAEALRST LRSLDLTPLI AALDGSITVS TGTNITASEF LASLPELGES TLYDDIAQAF
GATTPSTRAM AIELALEGLY LSRKIAKDSG EGETIYG

> RXA02124 (1-1956, translated) 652 residues
MATSHSRPRR SRYGRYTGGP DPLAPPVDLS DALRDIADDV MAGYSPEQAL REYLRRGARG
QEGLDDLAWR AAERRRELLS RNNLGGTLAE VRKLLDEGLK LERAQLARDI DMDDTDRAFR
EMQISNLPES TAAAVSELNS YDWQSQEARQ KFEQIRDLLG REMLDQQFSG MKQAMEGASD
EDKAAIAEML RDLNDLLSKH REGTDTPTDF ANFMAKHGEH FPEQPRDINE LIDALAARSA
AASRMFNSIS EEQRRELMKL SAQAFGSPEL QELLGDLAGN LQGLRPDLNW DGSEQFSGDE
GMGLGDGTGA MQDLAELDNL AEQLSNSHTD LDIDAIRRQL GDDAAVSAET LAKLERALRD
SGLLRRNPDG SLKLSPQAMR RLGKALLDAA SEQLSSRPGS RDSRLAGANG EATGASRPYV
FGDTQPWDVT RTITNALQRT AGTDTEGPLR INLDDVEVIE TEARTLNAVA LLVDTSYSMA
AEGRWVPMKQ TALALHHLVS TRFRGDELAL ITFGRHAQNM DIEELTALPP VHEQGTNLHH
ALLLAERFFA RHPSMKASLL IVTDGEPTAH LEADGHAWFN WPTDPETMFK TVTQLDKVTK
RGTHTTLFRL GHDQGLEHFL NQLADRVGGT VVAPDLDGLG AAVVGEYLRH RY

> RXA02125 (1-801, translated) 267 residues
MVATSQFIDD SEAAQAVRAA IVAGYRNIDT ALAYGNERGV GEGIRTAGVP REELFISTKL
AAEIKDYDGA VAAIDESLAK IGLDYVDLML IHSPQPWSDF RGGDYSEGNR EAWRALEDAY
KAGKIRSIGV SNFLEADLEN ILDSATVAPH VNQLLVHVGN TPSELISFCD SKGILVEAYS
PIAHGEMLKN QQVKAIADKY NVSIPQLCIR YTIQLGTVSL PKTANPDHMS SNAQIDFEIS
EEDMAALQEV TARDYGEHSG FPVYSGK

> RXA02129 (1-234, translated) 78 residues
MKIIFKMASN KFIDNKKGLA MLVFAELVME MLDQPEEQLH NVRGVAIEKR EFLKALTADF
TSRLKQAQTD KILVWDFA

> RXA02132 (1-639, translated) 213 residues
VHNFSFDVDE SYAKKNNEIL RDAKRLQISA LCLGLILGGG AVAVYLFSNG AVWMWMIAIV
MVFLALLSFI MIPVIPRQMG NAQTLYDDYE LAPAIIAEVN PRDVVLLALV NRNVNPEAKP
EWALATRTIV RVGAHERRLG ERIPSVAITG RRTVKDQDHW DEISPMPITW GTTDKDIIRE
AEKTIPHELW AKLEKNRGKL EDVKKTPNNL FKL

> RXA02137 (1-798, translated) 266 residues
MVVLIPFNDE VCTPIPDLGG FPCSLLSVKL PWDKNKNNEG ADAAGQDASS TPETATPDAT
EQKLPKGHTA PKGRPTPKRR EVELERGVVG GQSLAPTDTY AQQRQKRKEF KASMTKEEFK
AYKQKERDAR VKRQRETQAA MDRGEDAYLM DRDKGEVRRF ARDWVDSRRF LSNFVMPVAI
ALLVVMLIGN FNPSFAATSS MVAMVLMLGF LIEGITTGRR VNKAARTRFP GTTETGFGLG
YYAYSRTIQP RKWRTPRARV EIGAEV

> RXA02138 (1-342, translated) 114 residues
MTAPSTNTGV ILTESAASKA KALIDQEGRD DLSLRIAVQP GGCSGLRYQL YFDDRTLDGD
KEDIVGGVRL VVDKMSTPYL LGAQIDFADT IEQQGFTIDN PNAGSSCACG DSFN

> RXA02141 (1-408, translated) 136 residues
MYGPTVFMAA MAVIYIFATM HVSDGGSVKG VEWVGSVALV LSAGLTLMLG VYLHFTEVRV
DVLPEDWEEA EVADKAGTLG FFSPSSIWPA AMSGAVGFLA FGVVYFHYWM IAVGLMLLIF
TITKLNLQYG VPKEKH

> RXA02146 (1-627, translated) 209 residues
VGKHRRNNSN ATRKAVAASA VALGATAAIA SPAQAAEVVV PGTGISVDIA GIETTPGLNN
VPGIDQWIPS LSSQAAPTAY AAVIDAPAAQ AAPAASTGQA IVDAARTKIG SPYGWGATGP
NAFDCSGLTS WAYSQVGKSI PRTSQAQAAQ GTPVAYSDLQ AGDIVAFYSG ATHVGIYSGH
GTVIHALNSS TPLSEHSLDY MPFHSAVRF

> RXA02151 (1-1188, translated) 396 residues
MDWPDIAKGI SILGVVLLHV SLAIPGGQDT MMSHLNALLD PLRMPLFFMV SGFFAVKVLN
QSFGELFRGR LWFYLVPYLL WTPVNLYLHR LEGTVFTGRA PGTWEWYSGS MLSATNMYWF

LYFLVIFNLF LWATRKLPAW AIVALVASLW LLMPAYSEIE ILRKSIIYLP TFLIGAYFRP
LISRFAEAAT RPKAIVFAAV LYVSGLALGV ISNGLRDSEN HGASVLWLMN LRDTFAHALG
GNLTGFDMDH LPGMIIRIVS LPAGIVLCVW LGRIKPVGEF LKLIGRHTLP IYIGHATGLS
LIFGFGLRWN FMEIDNFSDS LWHHTNTWMV IAFACAMLGG YLTYLISRVP VLGWTLVPPK
LPEPDKTPAK AQADSHVKAQ SAKPMNASTS SKTYGI

> RXA02152 (1-402, translated) 134 residues
MAIYRKLAAS AAALALSASL VACGDSEDTT EETSTTSSST TSSSSSSSS STAATSEESS
AVEEPAVEAP VEEAPVEAPV EQAPVVEQAP VEQAPAPVQE APAPVEQAPA PVQEAPAADA
PPALPGGGGG HAGY

> RXA02163 (1-753, translated) 251 residues
MAVATFGTIT DMLETKGIVS NVGGTDTIDL GALLNETQAG TRWSELSPNY QSNRVVQIST
TDVRTSNSAA MYLSMMSWVK NGGKTVSSTA EADAIIPELS QLFVGQGYTE STSAGPFDEY
LSQGMGSKPM VMIYEAQFLA EQNKENSRIS GDMELVYPSP TVYSTHTVVS LSDVGAEIGE
LLETDETLQQ LAVKHGFRPK NSAMIADAGM TDRMPNNLNV IDPPDYDFLE RLIDGVGASY
SATPAEEDTD L

> RXA02164 (1-1575, translated) 525 residues
MKNLVKGTAL GLSLVLLAGC STVSDSIDSL GGGLGGSSET LKIVAATELE DLQPAIEQAS
DDLGFDIELS FPGGTLSNSQ ALMDGAFDQD YDATWFATNR YVDLIGASNK LGETTKIATS
PVAFGVKTSM AQELGWDQRQ PTWEELGQAS QTQDFTFGMT DPATSNSGFS ALVAMATAYA
DTGQALTTND IPAIAEPMST SLSGQTITSG SSGWLKDTFL EQPDRANAII NYESVLHTMI
SEDGADITVV VPADGVVSAD YPLSTITGSD QGEHVAELAG WFAEHPDALT DTYRRPTTAN
ATLPAELSSQ TIIEAPFPGS KTVTDALIDA YTNQFRVPGE TTFVLDVSGS MLGQRITLLK
DTMSDLISGG ATTDLANVSL RDREKVSIIP FSFGPHEVIS ETLGAVGSPS RTDLQQRVEA
LQADGGTGIY DAVLAAYAES AGGDYIPSIV LMTDGELTAG RTYDQFLTEW NALPSNIRSI
PVFVILYGEA NVADMEQLAA TTGGETFDAI NGDLDEAFKE IRAYQ

> RXA02165 (1-612, translated) 204 residues
VPTNNGGSFF FSRKNLAGIA IATLIIALHL VIGLGAFWPV VAIAGYGAAV ALTPKNPPKK
ELPPVQATPE LDSPGLLAAR SQELVRTMYS HGAAAPVIEA IKRLDSSLQL VIGNWTSLTN
FPEHQVTIRS IINQYIPGII DAYLKIPTRN DPRAVEDLIE SFDLLNSETM KIFNAIQEQG
LNNLEDHGRA LRMQFGQLPE EFRE

> RXA02166 (1-177, translated) 59 residues
MSLDPQLLEV LACPKDKGPL RYLESEQLLV NERLNLAYRI DDGIPVLLID EATEWTPNN

> RXA02168 (1-2814, translated) 938 residues
VSISSLTPLH SFKEPAILYA GQASAWQQVI ADSSEDHITA THLRELLSRS RAKTAPFARQ
ITAIVPGSLA RLEELTREDA QIGADIDAQP AVSIPGILLG QIAATRQLRD LGLDVAAASR
LGHSQGILGV EAVDNEEDVL AFAILLGAAA SQFAGKGAHM LSVRGLSREI IQDTIAGVDG
VEVSLRNARA HFVVSGKPEA LKKAAAALQR AADVYNEDIN EKRKGGSLAE PKFDYLDVAI
PFHHSSMQDA ADLAVEWATT CGLNVNARAL AEAILVNPAD WVEQIANLKA DYVLSLDAGV
SRFTAPLLDG RGISLVPAFS AAERDNLARP GFHVPTAEDW SEFAPKLVKL PNGEHKVLTG
FSRLTGYSPI VLAGMTPTTV DPEIVAAAAN AGHWAEMAGG GQYSEEVFTK NKEKLVSLLK
VGRSAQFNSM FFDRYMWNLQ FGAQRIVSKA RATGTSINGV VVSAGIPEVE EATELINDLN
ADGFPYVAFK PGTVDQIRAT LKIADANPET KIIIQIEDGH AGGHHSWVNL DDLLLTTYAE
LRSRKNVVVM IGGGIGTPAK AAYYLTGEWS TDLGFPAMPV DGILVGTAAM ATKEATTSPQ
VKQALVDTPG VDPHDAGGWV GRGDARGGVT SGLSHLHADM YELDNDSAAA SRLISSIDSD
DYADHREELI EAINKTAKPF FGEVEEMTYA EWIQRWVELA YPTQDPTWDD RFLDLVHRIE
ARLNEAEHGA ITTLFPDHAS VENEEEAVEK LLAAYPQARE IQVSARDAAW FIGLCRKHHK
PMPWVPAIDA DLARWWGLDT LWQSQNERYG ANSVRVIPGP VSVAGIDRVD EPVAELLGRF
EAACVDALDG EPEEIFARLN ESKNEREFLL ATPHIVWHGN LIDNPAHVLN EGAFELIEED
GYWVIRILAD SYFDDLPVEQ RPYLVQHVDI PVELGDAG

> RXA02169 (1-846, translated) 282 residues
LDMQINRRGF LKATTGLATI GAASMFMPKA NALGAIKGTV IDYAAGVPSA ASIKNAGHLG
AVRYVSQRRP GTESWMIGKP VTLAETRAFE QNGLKTASVY QYGKAETADW KNGAAGAATH
APQAIALHVA AGGPKNRPIY VAIDDNPSWS EYTNQIRPYL QAFNVALSAA GYQLGVYGNY
NVINWAIADG LGEFFWMHNW GSEGKIHPRT TIHQIRIDKD TLDGVGIDMN NVYADDWGQW

TPGNAVDDAI PTIPGNSNTG TGTGIDADTI NQVIKILGTL SS

> RXA02170 (1-774, translated) 258 residues
VSTVLLAGVV IIGGIFTLPQ KEEVKVSELQ PQASAASIPS SSSTAGKAVE ESPLTQFVEN
STGSQITYMS LKDDFHTGTS TERFARPALS LSKLYIAEYV LEHGTNNEKS LAMEMIKDSS
DVSAEILYEA YPESIEEIAD QYGLLSTRGD AHWGYSVTST YDLVKFVSAL IIDDPDSPIL
EAMRNASAVA ADGYPQDWGT AVLDEAEGSK WGWSDDLMLH SSVTFGEDYV VAAAVTGSKE
DLTQLVENQL GEVVSQHG

> RXA02172 (1-339, translated) 113 residues
VNAEQITQGR RQPTAQEFRD MQASPEFGEL RSKFRSFAFP MTVAFFLWYV VYVLVASFAS
EWMATPVFGA INIGLIFGFL QFVTTFVITY IYVMFANKNL EPRQAAIRQK MEG

> RXA02177 (1-933, translated) 311 residues
MREIFLISGD STESSLVFKT SEEDGAEEFF IAVTDELHAI LAGHSEIKSA PEPEEHKEVP
PPVLEPVAAV EEPREEKEID PRISAPLTMS PREIQIRVRS GATIEELAEE IGVTEARVEP
YAHPVLLERA RIADLAKQSH PIRENGPAKL TLWEILATAF ATRGHDLTTA RWDAYKDATN
QWIVRVDWKA GLSDNYAEWT LNLHNTSNPT ADPRTPVAAD LIDPEFIQPV RTLTSVNSTQ
EQYDDETDVF DTVPSPDDAP DSESDAVAEI TNDNEPEVDA EGPRNRRRKA VTPHWEDVLL
GVRANTKRPK K

> RXA02178 (1-870, translated) 290 residues
MPSQLGENAA IVTLWFVSAS DPQSIIRSEP RADRGYGRKL LAQLNPTWPI TPIGQFALNR
SVPASANEFY IAGFPGITII QTVLEDVTSL SKLNPRLLRS VPATDVYIFA VNEETTLGGF
AHIYNGEIKR SFIAYEERVF EDNGIPGGFE TPYWAGKKGT RKTALSLPFN PIELVHEAQR
AWLGFDATTS PDINVVAYAT DGRPEPRIAA PRIINSEEVT RSAVEKLGLR ESAFYDDYEE
YEAPDRVVSK RITSNAKKAA SSAQKFGKSL WRASREFGSN MAERLRHTDR

> RXA02180 (1-1458, translated) 486 residues
MTSGKSTSTR GALDRYFKIS ERGSSIGTEI RAGVVTFFAM AYIIILNPLI LGTTPDVEGN
TLGIAQVAAA TALAAGVMTI AFGLIARYPF GIAAGLGINT MVAVTLVSGE GLTWPEAMGL
VVLDGVVIVI LAVSGFRVAV FRAIPASMKA AISVGIGLFI AMIGLVDAGF VRRIPDAAGT
TVPVTLGIDG SIASWPTFVF VVGVLLCGIL VVRRVRGGLF IGILGTTILA IIAEAIFDSG
ASFENGEANA EGWSLAVPGL PDSFGGIPDL SIVGAVDLIG AFSRIGVVAA TLLIFTLVLA
NFFDAMGTMT ALGKQGNLVD DEGNLPDIKK ALVVEGAGAI VGGAFSASSN TVFADSSAGV
ADGARTGLAN VVTGSLFLAA MFLTPLYEIV PIEAAAPVLV VVGAMMMGQV TEIDFSKFYI
AFPAFLTIVI MPFTYSIANG IGVGFIMYAI MAAAAGKAKQ VHWLMWLVAG LFVVFFAIDP
IMEAVG

> RXA02181 (1-678, translated) 226 residues
MVDGHIRNLQ GHIDRLEAAA PTASQFHDRI ITQLREAPGS VQAAVTIENN HYNVELRPPR
KLNSLVTLDT HGHRDERLHP KIKGHDIAWQ NTATANSRRQ GADDGLLVDE SGQVIMAINA
SLLAIKGDTV FHSTHPRSLP SVLESTVIAY LQEQGCNAKP REQGFNINDL RSSEVWLVDS
LSGIRRVAAW LEYGSKFPVS ETRPVAAFVP TFSEVNDYLW STAQQV

> RXA02183 (1-525, translated) 175 residues
MASRKTKRKN LIQILSLIVA VLLVVILSVV FQQWWNNRPE PLPQEISISA SSPAGEIEVF
PFSMCEPGVE CEENEVPTLE VGADEELHLT IPEAIHDHDW YLLTIYDDPA ANDEFYHTSY
DATEATVPGS VDPTEEGAER PRLVVVEVSA VMIGEDENGE ESPYTVTWSL STMNE

> RXA02185 (1-579, translated) 193 residues
MGRHSTKTSS AFTKLAASTI AFGAAATIMA PSASAAPDSD WDRLAQCESG GNWAINTGNG
YHGGLQFSAS TWAAYGGQEF ATYAYQATRE QQIAVAERTL AGQGWGAWPA CSASLGLNSA
PTQRDLSATT STPEPAAAAP AVAEYNAPAA NIAVGSTDLN TIKSTYGAVT GTLAQYGITV
PAEVESYYNA FVG

> RXA02186 (1-219, translated) 73 residues
LFPEFERMYD MANVEKKHFV DPAWPEHNPA DGHVVTELIS KVAGASSPWG DDKEFPVSAE
ETGYVHPYTR INR

> RXA02187 (1-2199, translated) 733 residues

MKKDSPIPTL KGWLDTQSDD QLSTILRNRP DTVLPLPPNL ASLAARLQLR ASAIRAVLKL
NALELGVLEA VANLGGELHP VTAPEVVEYL HVALAEDLPA QDTIGAALAT LKNFALVYGD
DQLMIAQETM AALPVHWRLL PEVSDRGQSE EQVRESVDKL SDRHRKLLHT LAASGGFGLT
RDAAPDADPS RPIPQLLASG LLARVDEQTV RLPAMVRRVI EGREQLPAQV RPIPRTAAPG
SNDGGIAAGL EVVRHMRLLI DALSHVPAPT LKVGALGVRV VTRLSKELDL DETELARLLS
LGMASGLIRK GVPDPLPMDD DGGDYVAPTP LADEWMEYDL AHQLGTLMSG WWKQTYAPWL
VGRADDKDKP IHVLSKTSII DSLPDARAKI LSSLSRVLVD NLHADLAFHY PLAASRMNPD
TITQLVQEAQ WIGAYSQGVT AAGQALIDGE NPTEVIKAPA PVENFIVQGD FTIMVPGPLT
PAMQKTMDSI ASLESPGLAS VYRLSEKSIR HALDLGLTTP EILEFLKEHS MTDLPQSVGY
LLSDIARKHG TLRGGPALSY IRSDDPALLH SAVEAGADVA LRQIAPTVAI AQAPLLQVIT
VLRAAGFQPV AEDGEGASLN ISPSPARVPA ASPPPVVPAL DESRVQAAVK AIRRENSASQ
GTVSTQPTLS VLQAAVRGQR TVTLGFVDKQ GVAVHRVVKP LTVNAGQVDA VDEATGAVHR
FMLHRITEVI VDN

> RXA02199 (1-570, translated) 190 residues
MTDSTPQGST PGMSPEAILN GTGKPWEEWL KLLDDVKATS WTHTHIAKHI VDNFDVSGWW
AQGIAIGYEY ERGMRKPGMT SDGFAANASK TLNLPVEKVW KLFGDDDLRA QWLDPALIEK
TSASEPRTFN AKWLADDSRV SVNFTSKGDN KSSFGIQHRR LPDQDSIPVM KAFWKERIAA
LVEVSKQFSL

> RXA02203 (1-378, translated) 126 residues
MTIRATFQPS VDEFISTLEE FATGSYLKED EKEFWDEPFD VKALPDLRFI LENYLDSLDK
LGEAPDLDAV NASAQSTLDE LEKFNTKHHG AVVEPEEKEE ITKLMFDAAK QTGADDLSAE
AFPEFE

> RXA02206 (1-936, translated) 312 residues
MVGSSGLRVS RLGLGTSTWG SGTELAEAGD IFKAFINSGG TLIDVSPNYT TGVAEEMLGT
MLDAEVSRSA VVISSSAGVN PALPLGRRVD CSRRNLIAQL DVTLRALNTD YLDLWSVGYW
DEGTPPHEVA DTLDYAVRTG RVRYAGVRGY SGWQLAVTHA ASNHAAASAR PVVVAQNEYS
LLERRAEQEL LPATQHLGVG FFAGAPLGQG VLTAKYRSEI PHDSRAASTG RDAEVQSYLD
NRGRIIVDAL DTAAKGLGIS PAVTATTWVR DRPGVTAVIV GARTHEQLSH LLKAESVTLP
TPITQALDDV SL

> RXA02207 (1-759, translated) 253 residues
MRRRSRVSRL LPATALLAST ALLLSACTQG VTDSPDMGKA TPAVSPAASN PDGQVIEFGN
ITDMEVTDGD ILGVRTEDAL AIGTVSDFEA GSQVELDVDK QCGDLTATGG TFVLPCADGV
YLIDAKDPDL DELRATDKPV TVAALTSDDQ LLVGNGEDEE LTIYREGEEP ETFTVAGPNT
QLIAVPVIDR HDAVVRTWNE NTTIQDVDYP NDREGATLRV GLGVGQMAGG EDGLLVVSDE
MGGQIAIYNA DDV

> RXA02211 (1-453, translated) 151 residues
MVSVLLIQPR QGEAVAAAER RDFLQATGLK PQELTSRMLD TTTSRIGSLE GFDGVIVGGS
PLNATNFEYS DWQRHVHREL SLLINHPLPT IFVCYGNTFL TFFSGGQIGR THPEDSGATT
VLLTDAGKRD VLTQDLPDSF TSFTGHTENS V

> RXA02212 (1-498, translated) 166 residues
MIPENIDLKQ LASELGDDAV AMGEHTGNQF PTLEKDLINV VTDAKESDFG SLGVVILDET
PVMTSNLRDI AQELLIQTDL DTVVVRAPMS AAVVSDVHSR AALESGQHDL LGTTDYVLGT
ELLVQDVTES TVGNIDWGQL LIWGLVALAI AVVVAGASVR RKAISL

> RXA02216 (1-306, translated) 102 residues
VAPAPGHVVL ATGPTCPIQM LRANKNTWSV QFHADMDAVG MKNRMDFYSN YRFFSPEDYD
RIIAELPSVD SIYANRVLRN FVEVCEGIRV ADGAEHQLPK LN

> RXA02217 (1-663, translated) 221 residues
MTNKTRALLI GGHGKVALLA TPMLIDASVQ VTSMYRNPDH RSEIEALGAT TLERDVTTLS
VEDWADLLKD FDVVVWSAGN GGKNGADATY AIDRDAAIAS IDGAASLGEK APRYIMVSYI
GSSTHTIDPS ASFYPYAESK KAADEHLSST NLDYLILAPA ALTLDEVNGV EVIADTNEAA
AGRTTSRVLV AEVITELVVR DFPQTRVLPF VDGESPVSSI S

> RXA02218 (1-267, translated) 89 residues

MFAIMTVTGQ DHTGIIAAVS TALAELDVNI HNVSQTIMDQ WFTMILHVGF DESVLDIATV
QERMKPVEKE QGLVIRIQSE ALFNAVNEI

> RXA02219 (1-1386, translated) 462 residues
MDDFSASLGF TDRSSRGILD TIEMIEKYRL DIRTVTMGIS LLECARGSME ETATAVYDRV
TSQAARLVEV CEGIERELGI PIVNKRISVT PIALVTAGCS GDPVDVARAL DKAAKDVGVN
FIGGYSALVE KGGTTSDIRL IRSIPEALST TDVVCGSVNV ASSRAGINMN AVNEMGKVVK
QAAELTKDRS AIACAKLVVF ANSVGDNPFM AGAFHGIEEP DCVVSVGVSG PGVVSRALGN
LQGATLDQVA EEIKKAAFKI TRTGQLVGAM ASERLGVPFG IVDLSLAPTA EVGDSVANIL
EVMGLDQVGT HGTTAALALL NDAVKKGGMM ACSRVGGLSG SFIPVSEDKG MIDAVRTGAI
SIDKLEAMTA ICSVGLDMIA IPGDTPAETI SGMIADEAAI GVMNHKTTAV RVIPVPGTVP
GDEVDFGGLL GYAPVIPVNT VGNSEFIHRG GFIPAPVHGF RN

> RXA02221 (1-1362, translated) 454 residues
MFTASIPTYE LGSFSKGSYV EIKGTYFYPD TLNTLFRNSG AKDNEEFFVD VTLVPEPDNP
HSTRGHAISV RWNDLVIGHI ASDMTEKFQQ VRRVAASGYD ARVSARIWTN TNYKNERDFW
VSVKLPDPDF LVPLNDPPHD GFTLLPYGTA IQVTKESDHM DVLSEFVPPS GQGQILVSLH
IINAGVRKEW DGIEVRLDNQ RIGELTKASS EKFAPVVRHF DDLGLSTLCR ALIKGSSLAA
EVTLYGARAH ELSEEDLEPK SSSPLPRLVE YQSNPFNYQV PNRWPGEQNQ RAPKSQKSSS
SPFAAYRGPS QPSKSLTPFV AQTPAPQPSD RFIDWDSLLQ PDGTPRATPF QRGVTRGLIG
KHFSNQKSPR IDFATVGQCD AILRTFGEPT DKLYKDGRTS WPLWWALMAI VTLLVMLLNF
IPGIGPIFPL IGLIVLGHHF WTRRKLNPPF GRSK

> RXA02223 (1-420, translated) 140 residues
MSTYQDDRFP GPDPYAPLGE KPSFTLTSTD LENGAKLAEA QLGGTDISPQ LSWSDLPEGT
KSLAITCLDP DAPTGAGFWH WAVFNIPTTV TEIPTGAGDE TLGGIEGVVS LKGDSGKRGF
YGAQPPAGHA PHRYLFAVHA

> RXA02226 (1-1056, translated) 352 residues
MTENQTPSST SAPKPGPRPG PRPGPRPGAQ VAAKKAAVAT PAPIAKTSND PAKFGRVEAD
GSAYVTTSAG ERLIGSWQAG TPEEGLAHYG ARFDDLATEV ELMEQRLISH PDDATSIRTK
AEELKATLPT IAAIGDLDGV EARLSKIINN SEEANERAKE QKAKNRERAV ARKEELAVEA
ETLAENSSDW KVAGDRIRAI LDEWKSIHGI DRKTDDELWK RYSRARDSFN RRRGAHFAEL
DRTRASARKL KEELVERANA LKESTEWNDT ARAFRDLMTE WKAAGRAPRE IDDKLWAAFK
GAQDYFFDKR NAVAKERDQE FEANATAKQQ LIDEYDAQIN PEQGLDGARS KL

> RXA02227 (1-618, translated) 206 residues
VEDVNATLII MPGSPALVPE LAPADAAGAR LLASLRAVFD AELANDDRPI ELVGSRDEAW
FTKHAGNLRA WGAPSVQVSD GHYLPEILQR VALGGFESRV THVRDRLGSV NDNTVTVLAL
DGPTGLTTRA PSALVPGASN IDAWCRSLLS GKPGEVPSTS TLIDASLREP QLWLDLSAVA
TEASTAQLLD SDDTHGVGRY VARWTF

> RXA02230 (1-537, translated) 179 residues
MGEQLPFANG SRSNKLPLIV IGLCCIMLIL WLKLPGVLLA TIIGVATMSV MRMRTSTPET
ASLVTSIRLS AEDISDVQHE WQQFLTSPEA DALADRTLVR PALADPDCGD KAIEKFHYEI
SNANRFLGRL DARLQQNLVV SELETLLKVT DERALELRET WLDARKAAQK LGPNYNRES

> RXA02231 (1-756, translated) 252 residues
MTSDLKTIGM DFAKWQDAVE AAIASQRLEV TGEVRGGQLI QFSDDSGAQI NILAVEPFAT
FAGFNSATVA YGHVSMINDV LSLVDIIDPF GTPVATITCN LAQGPLLVDE PVQRWQQIRI
TALGIDVEVH DNADAYIRNG GETVGMLVSE GAEKIASGSG AVIPDASAEF SARVLSAEYR
TNTLTGQRFI HATVDGLFAF DVCLPDAPEL PARDSVLSGK VMLTAAVIPT EVTGCGGSGG
GCGSGSCGCG GH

> RXA02238 (1-285, translated) 95 residues
VTNVSNETNA TKAVFDPPVG ITAPPIDELL DKVTSKYALV IFAAKRARQI NSFYHQADEG
VFEFIGPLVT PQPGEKPLSI ALREINAGLL DHEEG

> RXA02244 (1-1533, translated) 511 residues
MSLEKSGGFR SRTPKAQQEP AKQKPQARKS PSKKAPARGQ GQSQGQRQGQ SSGKGGGNRK
PPAQAREVRA LGVDKPREIA FEVLDRVRTG EAYANLVLPR LLSKHNLSGR DAAFATEITY

GTLRNVGLLD EVIKAASGRE LSDIDPEVLD VLRLGAYQVM FTRVEDHAAV DTSVKMVGGL
KKFQATGFAN AILRNITRKE PEQWLKELEP AEELARVAFR TAHPRWIAQS FSQVLPADEL
EAALAADSER PVVHLVARPG EISAEELALI TGGDEGKYSP YAVYLEGGDP GDIEPVKDGL
AAVQDEGSQL IARALVEIPV EGTDAGRWLD MCAGPGGKAA LIGALARMDR ATVDAVEVSD
HRARLIEKSV RGLPVKVHVG DGRTINLTGG YDRALVDAPC SGLGALRRRP EARWRKQESD
IVELNTLQYE LLESAVNKVR SGGVIVYSTC SPDLRETRGI VDKALGALEI EELEAAEFMP
GMTDTGDEKS VQMWPHRHGT DAMFVAVLRK K

> RXA02254 (1-681, translated) 227 residues
VIAALTDILG TSQHALDQIA QLAGAKGRII PVCAEPLDLE AEVSGLDSDA RVMRQVRGQV
AVAATPGQVR RVRIIPDNPE PNPAAIEAIL DADLVTLGPG SWFSSVIPHI LVPGIVDALA
QTKATKTVVL NLTSEPGETA GFSAERHIHV LRQHARNLQV DQVIVDAKTL SSQTERNHVE
RAARTLGAEV SFHDVQAEDG RGRFTSIHDP AKLCAALLAS FAGARKR

> RXA02255 (1-936, translated) 312 residues
VAKNSVRAAE VSAILRFAGE MQAVGGKLVI EANLDSMQVG MRLQEFIQGL YNSRVDVHTV
NPTVSRKTPR YLVRIIDNAD EIARRTGLVT RSGHVVKGLA PSVVSGTISD AEAAWRGAFL
ANGSLSDPGR SSSLEVLCPG QESALALVGC ARRIGIAAKT KDSRGFDRVN VRDAEAIGAL
LTRMGAQKTR MLWEEKRIKR ESRTPQTGLA NFDDANLRRS ARAAVAAAAR VERAMKILGD
DVPEHLAEAG QLRVQHRQAS LEELGRLADP QMTKDAVAGR IRRLLTMADK RAEDLKIPDT
NSVVTEDLLE EI

> RXA02266 (1-513, translated) 171 residues
MTQDEHPRQA DSHFNMLLPD GNENAHQLSV ALNQVAHLLA YDADSSIHRP DGLSLASYRI
LFSLWTDGPM SPLQVTDKTG MKKSAISNLL KPLLAESLIV QVTAENDRRS KVLSLSEKGT
TYIQKTATRQ NALESEWFGT LTDIEQDLLE SLLRKLLDSN RASKVRKNRS N

> RXA02267 (1-873, translated) 291 residues
VQKWGLSFVE RIVIVNNVQQ FHRFFDDSAV YYPCFVPLDR AIGEHFDRQN KPMSRFIGTL
ILPLAKLEEA AQYTGDEVLR VSAVISTDGL ADLRRDFYEL PNIDIASVEI KLVGAALTNT
AWLGDVEKLI QQHRNTFVWV EIPTALVTAD IVRKLRHMGA GLKYRTGGDR EELFPSPQDL
VTVLRTAIDA ALPFKLTAGL HRALRYRDEK TGRLHFGFLN IAAAVATLRA GKGEAEALKI
LEGDDAAPLI HALQSGENWR DSFRSFSTCN VVEPLNTLID LDVLAEGDVH P

> RXA02271 (1-558, translated) 186 residues
MSFLNSAKTK TVALTATFVG AATLATPAIA SADIVDNALA ALPSGEISCS QAEKYWTTEA
DYNSKVAQAN ALAMFDSRGP QIQAALARVD EAANRCGLKG GTVAAQAEAT EAAPAAPAPA
PQDNTGTSQT APAPAAPAAP AATPVVNLAP AGSPTFTIEV PGVGGVQLPD LYQIVQQFLA
QFGIKI

> RXA02279 (1-1404, translated) 468 residues
XARATALVDF LESQTVDQLN NPDVQTYLTE AELIRDDLRS WAVIKSNGIG QHRSCSIRRG
NDEPLAIARK IIEETASHPE LRFENLEAQF SEFTILLAQS PENLDVARYQ ELRTQGNFVQ
ELALDSIFGQ HAVVQDTGNG EAILDETIGY MIGAGMRETT ARTASQFAQL YSFVGRQERS
IEMARLAFEE LQAAGLPHRE EELRLGMQLA QVEPIEAREI LEKLLLPKFE QNLTLDELET
EALLPLGATV AIHDPQAAAA ILRHARENAA GFGNFELAVQ AMTMITDVLY TQNMHEQLLE
ELNHSLPYAQ MLDDQHQAEL KLLDSIAIVQ ADLGSTEALE TLGTAMGLAE TTAQKLYVQE
SLNRAYFTFA RPEDCISGAA DASALAMQND DPSNAAAQLE QCAQYLFQLG HETDGASLLE
SAFRVEGIPT EQALYYANAL SSIYEDFGDS AKSQYWEQQA QEKQQLLE

> RXA02280 (1-753, translated) 251 residues
ADLAETMLGL LTLETSRGRI SIGEITTLSI TEDVSLQLAT TLDDFRQLNT IARPDTLIIN
GGYIHDSDLA RLIPVHYPPL TVSTADLRES MDLMELPPLQ DIEKAKALDA QVTESLKDFQ
IKGATRVFEP ADVPAVVIID SKAQASRDRN ETQSATTDRW ADILATVDNT LSRQTANIPQ
DQGLSALCLN WNNSLVRKLA STDDTAVVSR TVRLLYVQAL LSSKRPLRVK ERALLNDSLA
DLVSLSLSSD I

> RXA02285 (1-729, translated) 243 residues
LVLDERWVGV GLVDKWDEGG VEKRLFAAVL CVVGAGRGHV DERGEVRYGG AEAALLSLEG
RVVGVEVEDG GHEVFARGVF LEAAHEVRNG HVEFLWAHGW YVKQQLTDVN ADGARLIGRH
ALQHFELHTV RYPTLHREQM CECYVEKVVA GNAQAQALHV FFAHRPIEDA LVIGIGGLFG

RFCGNWPAGD LRVDVLHRQI STLDQANLNA RPACVDALAA ELRQVLDCTE GIGKVRLQHN
SGF

> RXA02286 (1-549, translated) 183 residues
MKNAKLFLAL ISAPLILAGC SSTDTGTAES TISSETASAV DATTSTSSST ATSAVIDDDP
VFDIIDIVLA QYPDRIITDI DREDSSDQYE VDVVVGQEVL ELDVTTSGQI HTDDRDNDDD
DDIREAHAAT VTAAQAIGLA LDQYPDGIID SVELDEDDGQ LKWKIDLDDT SGNDLADVEI
AAV

> RXA02287 (1-552, translated) 184 residues
VYSISETIAR TLMPRTDHVF DLMGNGNAWF VDALERLGRG IITVRPTVET VAAADTYHRV
TRRPAVATTT YGAGFTNTMT TLADVALSRI PLLLVVGTAP SAGPRCFDID RQGLARAVGV
ETFTVHADDV AAVTLQAWNN TPENTHVILE IPYDLAAATA TDPTVTTYLL RPGFQKLPMS
PTLS

> RXA02294 (1-375, translated) 125 residues
MAKTKLESIS ERNSDDPLSY PDLTLAPIST TVTVVVAEDT PNDNFSELLL GAAESTRLLG
LDELHIIAPS VHLPALAVAA ADIAHHLPEK FQFCEAETCT HLHPDDDTYL TAESVAQLGT
KLKSA

> RXA02295 (1-780, translated) 260 residues
MGLELAASGW GILIAGAAVA GWIDAVIGGG GLVLIPLILA VMPQLAPVTA LASNKLAAVT
GTASAAFTLV RRVKPDKKLL ALYVLVAAVC SGAGALAASL IDKQIMRPLI IVLMLVVGLI
VVFKPNFGTG ESKALPTGWK RWAAIVAVGL IAAYDGIFGP GTGMFLIMAF TALLSQNFLS
SAAMAKVVNT ATNLGALIVF IIGGHMWWTL GLVLAVANVA GAQLGARTVL GGGTRLIRYA
LLTLVVVMSV YLTWQQIQGM

> RXA02296 (1-489, translated) 163 residues
MRNQTIAAVA ALVLLTAATP AIAATPATAG NGLYSIDMGD EQKLTCVLFD EPSTEAHVVA
SCAATFPVTW KLLDGAHEQA AKLEITQAQD GELSVTASKQ PLITTMIAPT SITKPITVNR
LVVVPGENEV RFYATDPDVL PVLITPDSYE VLTDSAAKVK ATL

> RXA02297 (1-1137, translated) 379 residues
LSDKEPDPHE QIPEKPSRKV IALRWCIVAP LSLAVGWLFT MWGVPAAWIL GAILVAGVCA
LTTGQDLPMA KGVHVFGRSI VAMLAALPLI SSSGSELVRF LIPGLVISFF TIAVGIVGGL
LLARSRPEIL PETGVLSMLA GGASVMPILA RELGADFRYV ALTQYLRLLV VSMTLPLVTH
FFVPGGADLG SPPEKWLDVL SLGEFGTSIS VLSLLVLFGI VLAGEPLGRL LRLPAPAVMG
PLILTVLVSF VIPDDLSLQP PTVFKIIAFM AIGWMCGGPL NMTALKVFSK QLPATFLFIF
ALLAVCAGAA GLLTWWLDIS FFEAYLATSP GALETVLALS SEGSAGPVVV TIQIIRLLAI
LTIAGLIPTL LRRILRRDR

> RXA02298 (1-1659, translated) 553 residues
MTLQSSDKRS PSLLDASSEV FVHDLAALSP TDATAWGISG FEGDLQDFSP DYWNAIAERN
RDMVADVDAF DDGTDDNDDE EDFDDVDRVT ADVLRDRVCL DLALHHQGET LANLNNIDSP
VQTIRDTFLI MPRETDDDVE NLRERLSRVP DALHGYCESL AEAASQGHVA AVRQVEEVVS
QCEDLADEDS VLQHLGLDEN DPVVVEAQEA FARVAGWLAE QLAPHAPHVD AVGRDRYEMF
SHLHVGEFVD LDEAYQWSLE QLRDIDAQQL QVAQQLYGPG TTIREAMKKL NADERYLIRG
TDALQEWMQK TADQAIADLD GVSFNIPEQA RQVECLIDPA GTGGIFYTPP SDDFSRPGRM
WWSVPKTQEV FHTWQELTTV FHEGVPGHHL QISQTLVEKD LNLWRRVACW NSGHGEGWAL
YAESLMKELG YHEDPGNLMG YLDAQRLRAA RVAIDIGIHL NKRNPECTGL WDASYARSFL
RENTSMNEDA LYFELNRYLG WPGQAASYAI GQRLWLNLRD EAISQGQTLA QFHSKALSYG
SIPMGILRDQ VLN

> RXA02300 (1-333, translated) 111 residues
MKTYAVLIAV AGLALAGCSS SAPGIWRATE PADAYLEIAD DGTLSGTDGC NRLFGGWEKD
GSTITFGAIG MTEMYCEGVN DWLSQMHTAT VTDATMTIFN EAGSNIGELK R

> RXA02301 (1-717, translated) 239 residues
MDLALAQVDS TVSGLYDALD LIGVLLNGII GGTIARQRGY DIIGFLFLAL FSALGGGMIR
DMLIQQGTVA AIDNQIYLAL AFSGALIAMA VNFKGRVWEL FKVHGDAIVL GVWAVTGSVK
AMNAGVAPLP SIFMGVLTAV GGGMVRDVAT GQTPTIFGGG TLYAVPATLS ATSMVIFHSF

DQVILGMIIS PFLGIALAVT AYWCGWVIPV NTDFAPVNLT VSQLRAMLSK AERKDKDQK

> RXA02302 (1-765, translated) 255 residues
VATNRTSSAG VITSVLASAL FGAIFFISGA IEAKAETLVA WRVLLTAACY LLALLHPAGR
KVFKEFWDTL RSQPRQILYF IFLVVLITLQ LWLFSWSPKS HALDASLGYL LLPIFLVIVG
RFFFADYITR LQWIAVGIAL IAVTLKFVIS AQLSWVTFAI AAGYALYFAL RKYSGLNNAF
AYGAEVLALS PLAFFMLATV EDPLSNAMLS MVILAGLAGA LAMALYLAAS TLLSMPMFGL
LSYGEPILLF VAALL

> RXA02303 (1-720, translated) 240 residues
DPDPADRYIA HLPDRTTHTA MIMLGSGLDH SMPGVAFIGG VSVDDVPEVG GAIFHPSNPT
GRWAVSFHSG GWWRGSGDAL EFQWRPEVAA AAELSGTTIL DLDYPLAPGH NLHDMNEVVG
KAVGYARHHN PVSITGWGYS SGAALAAINA SLFDALVLTF PDLGSVEKLP AEIRGDAVVP
AAAAWPTTFV QIAAQDEIAE RPGELGDATV KEYVSRHRIS TPKVAREKIT DVAEFLKTVC

> RXA02304 (1-891, translated) 297 residues
MKTPRLLKIL SAMVAVTGLL IPTVVPMAAA DAAELSDNVP DRTQIAIINP DGSVQESDNA
EESRPALSLA KLYLGYYVLA QGAEEDIELV PDMIRYSDDF TADYLESEYP EAIPEVIDAF
DLEDTEWAGF WGNATTSAVD IATFVAALID DPTAQPLLDA MSDTAEYAAD GYAQNFGTFT
LSDVTGTKFG WSDSLDVHSS VSFGPGFVIA ANTYGDAETL TEDVQDSVSS LYPEEVTTAI
EEQVDQLCEC AAETTHLGMH TGAELKAQLE GTIYGKTLSF LPNSAPAPAF IYNLLAH

> RXA02307 (1-390, translated) 130 residues
MSGTAIMYDT TVVPSKKEIA QAWTGYVDLQ GSYRLVDTVD GEVGVEVLIS KDREGRLLQI
PFSYRSAEIN PEQTLSTLEH GVLGKRWVTN ALGDPVAVRE FIRTILTGDD GAARSDGVKG
YLDIKGSGDA

> RXA02308 (1-429, translated) 143 residues
MSETQSNSVS AVMPAQLPPG PAERTVYSYG VRAGDQVHIL RMEAFDSDAN IVGERDIEAH
AEQVFKNLQA VIHEAGGTIN NIVSTTTYLA DVTDAPVVNA ARSRYFTGEV LPTHTVIGVA
ALARPQFLVE ISAVAYLGDL SKD

> RXA02314 (1-441, translated) 147 residues
MEWYQVRRRA RQLLIVLFIA AMLGAASMVI GPFLNDRTIE GNSGRALAQV TNVGSYRTTV
DFQDENGIYH SPATGLLFPT GLGEGQRVWV NYAKSDPDLV KVEGRKWTLS IIPALSVAAV
ATATWSVLWL GVGRFGRRSD DANETTV

> RXA02324 (1-1086, translated) 362 residues
MATTTPVTVL SGFLGSGKTT LLNQILHHRG SRKIAVIVND FSEINIDAAL IASEGHLTRG
EDRFVELTNG CICCTLREDL VDSVGELASS DRFDHIVIES TGISEPMPVA ATFEWQWDDG
TRLADKAPID TMVTLVDATQ FIDLIRKNTS LTEADMGATE DDERTIADLL TDQIEFADRI
YITKSDLVDR TVLEQTRALI ASMSPRARID LLIDGLNDGS PITDDILGAF LYDEATARAY
EGYTEELENP HTPETEEYGI SSVVFRSDRP FNKDRLLQVL RSTTGLVRSK GYCWIADHLN
IVQVWHQAGP NLSIRPAAYW ANSEITPGTE LVLIGIHIDG PTLLALLQGA TLTDAEVAAL
VL

> RXA02325 (1-870, translated) 290 residues
MMDHAHDSCS PTLRRDLEVT GQLQPEKAVD LAAPHEGKVA NITKVTSSNM EHTITQASKA
KEVVVLIGHS LLPTFQDLEK DILHFQAGNK GRFSVAIVDP DRSADVVARF RPKQIPVAYV
VKDGASIAEF NSLNKEPVAQ WLDHFVSRET IPNEKEGDVD KQIDPRLWRA AELVNAGDFR
AALALYEQLP QDATVKRAHA AVSVLARMSV ADRGEDPIEK SRRDPDDVNK ALAAADMYVL
MNQPDTALAH LAALLPKPEA ARRIVELLNL FDPLDLVALE IRAQVGNAMS

> RXA02331 (1-366, translated) 122 residues
MELNGGRFYA RKLTSDNRID DVPALSLILA DAAQFIADAT TAWHEDTEYT WAICEQTSVE
LLALARLDPK QRTLEVVPAG DPATQLPNDP VLAPKTIGDA VAEGRDTITR WAQGYLEISL
TD

> RXA02336 (1-180, translated) 60 residues
MKDTTEINWQ GYADGTAIRE AVIHSIEREV SAGEQPTPND LKFLGLFQHR AGYVGSLITG

> RXA02337 (1-924, translated) 308 residues
MSKLYAGARI NALRRTHQLT QSALADKLDL STSYLNQLEN DGRPLTATVL LQLMKVFDVE
ASYFSPDRGT ATATRLAETL AMNQGPTMSM DDLLDFADRF PQLAQHIIQP AEVDPTHSSA
HDFVRDYFAT HKNYIDSLDR LGEELATAIG QPGLRVTRLA QLLDAEYNIT VRFRAPDITG
RRHFDPQSRQ ILLRQDLSEA QQCFQLAEEL TFLAHAELLD TLTTDQPDLP SEAAIRLAKV
GLSQYFAAAV VMPYTRFLEF AQDKHYDIEL ISEAFGVSFE SACHRLSTLQ RSGASGVPFF
FVRSDRAG

> RXA02338 (1-480, translated) 160 residues
MKKSIVVFEV EGGSDKHFDG HRKDTMPIVN SINDAGWQAE VVYYRPEWTE GLFEYVSENF
DGYISRVNPG NIPGGERGYF DLLTRLSEAG LVGMSTPEEM MAYGAKDALV KLSQTDLVPS
DTEAYYDVET FHKVFPTSLS FGEARAQAKT WLHRLPHLAR

> RXA02339 (1-492, translated) 164 residues
PTDNLFSYPA QRYDLLTLAF EVRIGDMVQI NDMLAPPPVK LPEDPALGAD PTLTSTAIAH
PDSPLVWAYR AENLIKSASN DEEKIQAYAF ARTGYHRSLD RLRANGWKGW GPVPFSHEPN
QGVLRAIASL ALAAKLIGED NEYDRCRQML SDADPESVAV LLDK

> RXA02340 (1-639, translated) 213 residues
ERVLKQNRGS TGSGIWRVQL VDKELAASIE PGTALPLDTE IKCTEAVDNH TEVRKLGEFM
DFCDQYIIGD NGMLVDMRFM PRIVEGEIRI LLVGPHPVFV VHKKPAEGGD NFSATLFSGA
KYTYDKPEQW QELIDLFADA RPVIAEKLGG DNIPLIWTAD FMLGDVVDGK DTYVLGEINC
SCVGFTSELD MGIQQLVASE AIKRIEEFAQ LTV

> RXA02341 (1-411, translated) 137 residues
MGNSLEKHIA EGDRIHVDLT SPLSAMLFPI FELIVITGIC WMGIGFLDQL PGIDGTNPAD
SFPEGTRNLL VGVWAVLAAW RFGLPLIRQR RLRVILSDRK LLVRRAGLRT GFDSIPLSYI
QRVQRRRNTL VLGVGGH

> RXA02347 (1-321, translated) 107 residues
MDELGVGWCQ CEKDSITGKA PHPVNKPLVT KSIIRALGDV PDVMSNQDIS LVVVDLWKFD
TITPPIAESL MRSVKAVNGE MHPQYPTATA MAAIKHFSNT FDGQINA

> RXA02349 (1-390, translated) 130 residues
MSTAYFIAHG NDTYRPTEHS SGAWRDDELH LAPVAGLVIH HMERWRREVV GDALVFSRFS
LEVLGQIARD DVTLRTEIVR PGRTIELIET VAEINGRVTI RARAWLLKTS DLAHISGDTF
EALPSMTELA

> RXA02352 (1-555, translated) 185 residues
IYNTSSTLNG FIADKDNSLQ WLFDVPGSDG ASEDFGNFLS KAGTIVMGST TYEWLLKDLD
FISDPHKWTD VYGDRPTWVF SSRNLETPEG KPVKVVNGDV ADVLPAILEE SPENTDIWIV
GGGDLAGQFF DAGALDRIIL TMAPVFLDEG QPAMPRRIES NRLRTVNVRE VGQFTEITLE
TIKGA

> RXA02356 (1-996, translated) 332 residues
MATVTFDKVT IRYPGAERAT VHELDLDIAD GEFLVLVGPS GCGKSTTLRA LAGLEGVESG
VIKIDGKDVT GQEPADRDIA MVFQNYALYP HMTVAKNMGF ALKLAKLPQA QIDAKVNEAA
EILGLTEFLD RKPKDLSGGQ RQRVAMGRAL VRDPKVFLMD EPLSNLDAKL RVQTRAEVAA
LQRRLGTTTV YVTHDQVEAM TMGDRVAVLK DGLLQQVAPP RELYDAPVNE FVAGFIGSPS
MNLFPANGHK MGVRPEKMLV NETPEGFTSI DAVVDIVEEL GSESYVYATW EGHRLVARWV
EGPVPAPGTP VTFSYDAAQA HHFDLESGER IA

> RXA02358 (1-291, translated) 97 residues
MVSYSVHGAL DIDGSLKKLT LDFLNKLATN PASPGLHIEP IKNSIDSRVR TGRVNDQFRA
VLFELHDEFD HHFVVGGFIP MMMPSPRQEK SALKSTL

> RXA02360 (1-2433, translated) 811 residues
MRGDVQKITK VYDGKHRTLE IPVYQRNYDW TEKQCSRLFD DLSEVVKENH RQHFFGAVVG
KPQGSWTWVV IDGQQRLTTI SLFMLALVHS LRASEVEEGE FNAGYNIDLA TLIEDDYLRS
GNEGNLKFKL KPVKNDNEAY QKLFGPESEF IESSNLTANY RYFRNVLKAT DLTAAQLWEA
IEKLRVMYLD LEEFDDPQRI FESLNSTGLE LSEADKVRNL VLMDQELKTQ EKLYEQRWNP

IEVCVKFDTD NFIRWYLTLK TARTPRKQDV YEEFKKFIRN SKLPVEFILD DMYEYAKLYR
DLLGATTGFI AADRCLKRFV PVMGDVVLPF LLPVLKDAKD GIITESDFLG VLKVLESYLF
RRFAVGVASN ALSKIFSTAY SDIKKFWTPG QSYSSLLAYI LKRRDGSGRF PSDSEFRENF
ATKNFWNIHN ENRRYLFDCL ENADSNDVRD IQTSLDEGSL SIEHIMPRSL NDQWRAELGP
EYARIHETWI NRIGNLTITG YNSAYSNSSY ERKRTMENGF LVSPYRINNF IKKQKHWSEE
QLIERTELLT QAALDYWPLP KETFQPPQAV LPTESLDSDL SFRGREIVAF EYEDYKETVT
SWADMLQSVL KVLNQSFRQE LIALTNEEIC LATSNNSNSS LREIDHGLFV DTGSSTSVKI
GFLRRVFTQL GLEQEALVFT LRPLANDVEP RDDELEVEVE KKYSDLTKFI PQLEEAENLE
GADTEVIPLL SKLKEQLTAF SPENPQAALG GLPVPEFLKQ NVIEQLSAEH ILAVLTQHFN
IASMMGDDYL LEELRSGRLR ELLQRLEELD S

> RXA02361 (1-651, translated) 217 residues
MELLSHLLAL DPASPRLTVY NESTGARLDF SAITLDNWAS KVGNMLLEEL DLEEGSLITI
DLPVSWQAAM IMLGALATSV EVSFDDPEAD AIFTSLDRFS HYKGHSDVLI VSEDPFGRGV
VEGGGELPNG AIDFGPTVRF YGDQFFQPTR TLPEIIQHSD VPVGARVLAT GWSDIESFNH
QVLEPLAVGG SAVIVTGLAD IERLNQIATN EKTTHRI

> RXA02362 (1-3699, translated) 1233 residues
VTISRRLKQE RSFADDLQDL KTLNDQLRFT NAKLQARISG IGNDGKKITR PTPLLALDFQ
LTVEEYETII AILVEAVGGN QSKPAILKDL FIEYPLVFLA ALSGTAMLDA QEGFWPAFWK
RTQVSVPEHV YDAIRKELVN SIRKNGLETF SLADLNRREY VGLIQLHSGL SAKDMLALVK
FIDHTRAENQ GWDSGEDFAS YAKSVFSSGD NLLTTESLKQ LVTHIPARSV DFIARVYELT
NWYRDLKDLN EVEAFVGTHG LPELSFKFLL ECLSGEAEQI AEKTKAAPAS LENLEPPHLY
LDPQSFELSL VFPAISKTAA LQIPAPEWTV IYDGNSIKVR PEQDWSYGGF AEYRLPLDKP
LSSLRVITPT EKSLILIEGF GHKNPIMFFK NNGQPYANQE MLSGNAVTAI VPAAAIIRAR
MRASKTFNYQ DLGPLSGWNK WVIRSIPLKR AESITVSHGG FRKELPVRRK VDVQWITEDL
TIENLQGLDH EPVFHTSPRI EFPTSGSNWV IQYSQILPDG SLIEMEDYPV EPENFGYELD
LFEESDDPWV GQFLVTLLKD EKVYETRKFN LAEGLDLSLT FSGGGPENRF RYPSINQGQT
GLTKTFARFS SNSEKHIRFP DEIIGLDAFT SQKAFNIASG DFPEDYNLDV FITPPQLHYQ
VPVTHSQTKW ESTKTTLDFN DFADGNLQIR FPNEVYDPNL KIIKMVAYKK PESSEPKYLS
KIGSSKVWSI PMDRIKELMD DDAQFLLIAE WFAESKDQHR EKIISEAKRT GKISNAALKS
ARPQPQASSH IATIEKKPLL AAAEIKLSTV ELELGRHTSK RLEGWAWSAL NPLDPPIKVD
FQGTSGSLPD THFVVGPLIV EVREKEFLSQ WQPKVPSVKA VVANDPSFEL DPQFDPFLTH
RWMFAPRSGK VLLPQEIRTV WDARFNMRHV LAQRENLHVK SIQDFDDATS TYLTSDPRVA
LDELDKSSIP SNSHFESFIR SGLAELSFEV DDTAGDIHRV PWIGLIQEMN DLRILQIQGY
ETEERAIERR NSQSYIREIG GSELWNILKG NSEGLSLAQK CAPQATEINV IRNSGLEAMR
NGLGADQFSA EFISADSRLR AQLEWLENRR ELNDLGQLPT LFDFAEKYEY LIDHLGDDRI
KVTARELSTL ASEHRRGNAE NWLYAPYVSF IYSLLNRMIA HEVIRPIAQI NYSRHDWANA
ARLIPRLTGF DLVSAEAKVL SAINNNNIIP TAI

> RXA02367 (1-609, translated) 203 residues
MSNAEINPVE YEINNHAPGT ALNPQCEDGA NVEIITSREV PLGGPRAMTV HRTLPQRQRS
LIGAWCFVDH YGPDDVSLTG GMDMASHPHT GLQTVTWLFE GEVTHHDSGG NHAVVLPGEV
NLMTAGAGIC HTEVSATSTT ILHGLQLWTV LPDKDREGPR RFDHYAPEEI TLEGGSARVF
LGSLFGQTSP VHTFTGSSCF RVH

> RXA02368 (1-675, translated) 225 residues
MIVLAGATRV TYEVEPWLAI PLFILAFASI LIPFPISKTK GLRDIDAWKI HTTQGDKKRA
IRQLIIPATA LAIDIIGLPT LFNAPPLASA ALFGGVYGAS LAWAAYRADQ LPRIRTKERL
AELSQNASLD DVRSDDLDVL EQPESRELVR CLLAHGAMDG TRVMARQVAR VLDTEVDEVH
QVARSLEQHG LVSRSTIMPG GDPGKVFIEV SLKGISAIKA LESGR

> RXA02374 (1-621, translated) 207 residues
MSYDFVLFET DGDPGSARIS KTPLTERIDF ATPSTTPVLE SLSAGLAETV PDTVKLEEDA
IHLSGDRCLY VVTNYNSAEE AAEWLTAIAF DYGLGLADMN ADTILLFGDE DSDAVVQIDD
WFSPAFSAYG LPHLLVEVMR LKDSKTPYLR VTLAADDSKF IQTLYETDNK QWLVETSSST
GTDETHVKTI NDVLERIETW FNQETAV

> RXA02381 (1-1023, translated) 341 residues
MSVTNFRRFL AGIAVIAACV AATPTAQAQS SGSSGSSGSS AGSSGLWDLL FPESHESFIE
RLLDPLDDSH ISIHPDLTPD LYEEVFDPPQ IGECPAVVAV VARGSEQNLQ IRPARYSEES

PWTSNGFEEK NFRSFFGRME KHYRESTGES LMKDVYVMGL NNIEYPASLP LSSEGSSAIE
LGTSISSGRD NVISAIDRFE SATGCTPKYL LAGYSQGVLI VDGYEEELIA RDQYLGTLHI
ANPAQQVDDP TLVGHEVTTG GLASSVEPVE DNPFKVSYCL PGDIVCDRSF EQFSAAGSSI
AAAQLSTGNI RPGRVHVQYF VTTQPWDEQI FDEVASWIEA A

> RXA02383 (1-603, translated) 201 residues
MPVRVIVDSS ACLPTHVAED LDITVINLHV MNNGEERSTS GLSSLELAAS YARQLERGGD
DGVLALHISK ELSSTWSAAV TAAAVFDDDS VRVVDTSSLG MAVGAAAMAA ARMAKDGASL
QECYDIAVDT LKRSETWIYL HRIDEIWKSG RISTATAMVS TALATRPIMR FNGGRMEIAA
KTRTQSKAFA KLVELAQIRA D

> RXA02387 (1-678, translated) 226 residues
VWWCLPTWIK AGQDAVDLAL SAAVDPSPGT YLIVMHSGGG RSKSMVKKLE KVAVVHDAAK
LKDRDRPGWV KQEFKNHKVQ VTPDVIHALL EGVGSDLREL ASAVSQLVED TQGNVTVEKV
RAYYVGVAEV SGFDIADSAC AGQMSKAVAS TRRALQLGTS PVALAAALSM KVGQIARLYS
TRGRINGFEL AKELGMPPFV VEKTAKVARN WSGDAVSEAV ILMADL

> RXA02390 (1-669, translated) 223 residues
VEWTAFGTLI LLNLVGSLSP GPDTFFLLRL ATRSRAHAIA GVAGIVTGLT VWVTLTVVGA
AALLTTYPSI LGIIQLVGGT YLSFIGYKLL RSASRELIDA RQFRFNADAR PIPDAVEALG
TRTQVYRQGL ATNLSNPKVV MYFAAILAPL MPAHPSPVLA FSIIVAILVQ TFVTFSAVCL
IVSTERVRKA MLRAGPWFDL LAGVVFLVVG VTLLYEGLTG LLG

> RXA02393 (1-282, translated) 94 residues
MAESLVIINI DEKSAKLLID AARHHIPTRF TGPNARPLSV IPIEDPRSRP TLHPDHGWMM
PLSPPVVDEL LGGGLKIGET ELESTNIAFI VDAS

> RXA02395 (1-732, translated) 244 residues
LITMAIPSFI LILAFTIFGG TAITMNRENV DGFDGSSSKE QVLFDMFSNL PLYSITPFIL
IFVLAVFFVT SADSASVVMG TMSSQGNPAP NKLIVVFWGL CMMGIAVVML LTGGESALTG
LQNLTILIAI PFALVLIVMA IAFIKDLSTD PAAIRQRYAK AAISNAVVRG LEEHGDDFEL
SIEPAEEGRG AGATFDSTAD HITDWYQRTD EEGNDVDYDF TTGKWADGWT PESTEEGEVD
AKKD

> RXA02396 (1-279, translated) 93 residues
MATTASKIST IRPAQQDALW SVREDLHARF DGLVDPVQVD AILDHVASNR EAKITVFSKI
FIAREATAAL QQIAGNVNAD LLDFIALNRG MAA

> RXA02398 (1-1530, translated) 510 residues
VVEVKKRNLL VAPLTASLVF CNLAVAANAV EVEAESPVVI NEVESNSDPV GDWVELANTD
NNNSIDISGW SLVDDKEDLE NALVLPEGTE IESGGYFVIY TDSADYVPTN NTFGGQEYFG
LGKDDTVTLR NAEGEVVATY SWKDLGEHAE NTYGRIPDMT GDFANTGVPT PGAKNVAAEG
SGEEEGVVAN AQLPFHNVEI TPIHLGGDFT GEDMSGVDFD ANSTAWIANN DIGKIYSLAH
DIANNTYKLT GEWETGYPEG GGEPDAEGIV AATNGDIYLS TERNNADKNV SRPSILRFAT
PTGKTGVQNA VQEWDLSEFV GDIQPNGGLE AIAQLEDNIF VVGVEETGDV IVVDLSADQP
VLVQRYESSF DGVMSLDYNA ATKQLSVVCD EACDGLSEIL EWDGEKLYKS DDKIYERPAN
LGNWANEGFG TYTSELKCEN GNTVSVTSYL WADDAATNEG TSLNSAQVIN GDCGDVNIPG
ESSSDNSSSD FATGSIAGAF ATAVLAVVGI

> RXA02403 (1-765, translated) 255 residues
MTTFITSGGL EISPAGAHIV HAESPEGELL FVSSASQYGE GNAIRGGVPI IAPWFGGLLG
LDPAHGWAKR SAWDVTEHDG QIHAEYGRDG LLLDIRANST KNGFEITLRA YNDTDEARTV
QLAFHPYFKV DDVEKIEVRG LDGVDILNRL NNEVETQDGP VTFDGEFDRI ALGTPVVRIF
DTDRIITIEG DGHDSTVVWN PGESRASTVA DIGEGEWRDF VCVEPALLGA DQKGVRVAPG
QSVTVGMQVS VEKRA

> RXA02406 (1-549, translated) 183 residues
METLAAQART LLEKWGVAPT HASFVESIAK AIPILSILLT LIVTVNGISS GNPVQPPALE
QVRTDVVNKI NYERNLKGLV SISPELELHT AAQTIAQRNA DSDSEEKVPD PEGTLVVLQQ
NLPYANANAD TIVDRFLNSP DHVKLLLAND YEAIGVGVAY KGDHAWIVVE FTVAPADSVE
STE

> RXA02407 (1-306, translated) 102 residues
MNRQNQLHYP QEVKAVESVE SSLNMSSPSA PLATPDVELD VHTLSSENLP WLCIVWDDPV
NLMSYVTYVF QTVLGFSKKR ATELMMQVHT EGKAVVSSGE KD

> RXA02408 (1-828, translated) 276 residues
MLIDVAGFLL GHVTKGDTGC SVVIAPNGAF AGVDVRGGGP GTRETDLLEP HNSVQQAHAV
VLCGGSAFGL AAADGVMTAL ENRGIGFPVR PEGPIVPIVP GAVIFDLLVG DPKNRPTAAD
GEQAVENAFA GTHNGSGSVG AGTGATAGRL RGGFGQSSRR VGKYTIAAGV VANPVGEVVD
LTTGALFGRP EVMGVGVDKL KSAAETLNTT IGVVATDAPV TKAQAKRLAL VAHDGLARAV
RPSHSPMDGD TFFAMSSGDG SGVTPVELGE LSAHAA

> RXA02409 (1-414, translated) 138 residues
RAQSVPKDPL AEMTGMTSGH KEAPTDPALA RLLPDFQHEG DEEYDGDNSF LRSLHEGDIT
RAKLENLRVI NDALGPDGNV AVTASEEEAH AWLAALNDIR LYVASGDVRG GEAAEEDREN
LVQWLAYNQE SLLEAMMN

> RXA02412 (1-480, translated) 160 residues
VAIIVIAFVL LFNSLVAPNN SSSPVASPST SESVEQTISE SPESPSATED QPPSSATETP
RNRPAQPSLP AGASPANDAA ATQTDAGNLN NVYTGSASTS AGFAQAVRDA FVNHYLDTNE
LSGRVTATSP VTGGNYTMNC EDNGEYVTCT GGNNAVVYIS

> RXA02417 (1-2124, translated) 708 residues
MDMNSSDRLA LRTALEKLSA SATAMASASN DIKDLVARLD AQEMSLIDAN PAPTPAPTAP
PEAQLEPQPL VYATASTAPA LADVSGTNRI PRFVRHRALD PASEGWPLGV EKQKVQAPAY
PHPVRPARPA KPPMTSEEKI MRGVAIGGGV ITVAGVILLV SVAIQRGWLG PLGRVIGAYL
LAVLLLGAAH YVRKRGTRVE ALVALTVTSQ IAFLATTSAI IFILEWWPPG LGSLVALIGN
IGFLIVGRLW SLSKTEKSAA EGHTVFVGAI AVSGFSAILF ALSADAWWPI FSIVAALLLS
YRISTNIIRA SMAAFAVILQ FVLSASWQTM EWPATIVGTI TAVLLVALTL WDPFKITATD
SHDIALEEYW RSFETNPVST WVGAVSPVLI VFITTSMFIA VDWPWLALIP ACAVAALGIF
ALRSSDTASI ENQRMSRLIA VVGLALIAET FVQLFYGDLP TNPLLVMVFL IAGAALFMWL
RMLPPQRQLG VVPWVAWLIA AVAMTGVLLR NVVSISPLWL TDTQALIQAL LILVFIAATI
QVRRSFYGHK LWLQILVGLT LLTLSAISIV TITTFIGRLI AGNAGMMLGF LIGHATVSIL
WMVIAAALML NRKLLDAPGA LWTGVGLAVA GTFKLVFFDL VALSGVPRAI AFLLSGIALL
TIAAMRGRRT SENKADVARP QVARHGATSH KNEEPSHESP SSSPTTTL

> RXA02421 (1-810, translated) 270 residues
MTLLLKPILQ AAGINPEDAL AMRHVFISIH EDTNSNGITR ESKDEEILAY TASQSSDPRR
FPLNPPRFWM VFIREGGSQA RLWKVVENHG EVTNDGVRRV FNLTEIELMD DLAGRLVIRW
NSPRKWWIKG TTAALYTVDT IADAEPIPFP GFDNLVLSYP FLQEVMREPA YASWRTALGA
VKGIYLITDT RTGRHYVGKA EGLENIRQRW NSYATNGHGG NVKLKQLKPD TFRFSLLRVF
DPATPTSIIN AAESHFKIAL DTIKHGLNAN

> RXA02423 (1-216, translated) 72 residues
MIRKLARPML ASVYVADGAE TVLNTSAHVE GTQVVLDRIR YVLPRKYAKR ISRDPELVTR
VIGGTKVCAG SC

> RXA02425 (1-630, translated) 210 residues
PGAFDELTSV WGEKGGSWAA VIGFFGGIAL IAIIDRLVPT AINPHEPSTV GGAVEGFERR
NRMMKMGVLT ALAIAIHNFP EGFATFLAGL SDPMIAIPVA VAIAIHNIPE GIAVPVPLRE
ATGSRRKALG WATLSGLAEP AGALIGFLLL MPFIGPEALG LCFAAVAGVM VFISVDELLP
TAISSGKHHT AIYGLIAGMA VMAISLLLFI

> RXA02427 (1-387, translated) 129 residues
VDFELGKRCP CGTGLTYGEC CYRFHSGEWV APTAEALMRS RFTAFAVGNS QYLLDTWDPE
TRPSELGLDM GIDFYRLDIL ETTGGGPFDS TGIVKFQAFY KGLASGVQEE DSTFRKVNGA
WVYSTGDVD

> RXA02428 (1-1134, translated) 378 residues
MAATLDLPDT DPIAYAMFAH CFTGSRFTPA AARVSKTLAE SGVACLRFDF PGLSQSEGDF
SKTTFNSNVD DIVAASQWLT EHYSAPQLLI GHSLGGAASL KAATKISCLK AVATIGAPFD

PAHAVLHFAD RICDVDDQGA VTLQLGGRDV TISREFLEDL AEVNPEDHLR RLRKPLLLLH
SPTDQTVGVD NAQLIFRVTR YPKSLMTLDK ADHLLTKDGT AQRAARIIAN WVEPYLVPEN
VCEDLPEFVA EASTIKASKY GAAIRTGGHN FITDRDKSQG GKNLGFTPTS LLVSALAAAN
SQTIKQAAID NRIKGLDDVK VTISQEQSAD HGQIKLRRKI SLIGNLSDAD SASLRAASNS
CSITQLLAQG IVIDDEVN

> RXA02430 (1-186, translated) 62 residues
MSPVSRRHAE FRINEGEFEV VDVGSLNGTY VNREPRNAQV MQTGDEIQIG KFRLVFLAGP
AE

> RXA02433 (1-600, translated) 200 residues
VKLFKATAVT FTVAAALALS ACSSSDDSSS ESSTSSSTSS AASDAATQYP TAEELNAILA
VATDPEAPIE EKVKTVQGSE NAPELFETMT QAKVESGAEF QVVGSVLPGY DPTSEVLTTV
MFQLPDRAEQ EAEGVEFVNT DGNWQLSQDW ACILITNTVA PEQVPAMCVG TDASSAGIEE
APAEEGAVVE EAPVEEVPVQ

> RXA02437 (1-810, translated) 270 residues
MSTIGNLKLV VDGARKAYGT YADYRDRKVS ETYDALSQAA GEYAPKAEQA VETARESAKE
FYTESRDKAG NVTKAARARL EKALAEADKQ GTSALKDARE SGKKLNRKAR RKADKAAKAA
RKATEKKESH WVRNLSLAAL ATSGIVAVAY AFLNKTKKET PGTQPPRVEV QLKKAVEQDE
PEVVAEAAVE EPELVYSTES PETTEAPAEA TETPAETTEE EAKTEAELEA ELEAEADAEQ
EAAEEAEAEA IQAEFDKKNA PQRTQSEKKK

> RXA02443 (1-954, translated) 318 residues
VILKDIFNNG ELFGASSAKN FRKLLAVPAV AASLAFGITA CSAVDDTPDI VVTTNILGDV
VSHIVGDSAD VQVLMKPNAD PHSFGVSAQD AAAMEHADLI VANGLGLEEG LQSNVDNAKS
QGVPVLEVGE HIDVIDYSPG VPDPHFWTDP ARMIAATEVI EAELIKELDP SLTESITQSA
QHYREELVAL DEEVTELLSG VAPENRKLVT NHNVFGYLAS RFNYTVIDTI IPGGSTLAAP
SASDLNDIST AIEDNNVPAI FTDTSSPQRL AEVLASNAGI DVQVVSIFTE SLTDADGEAP
TYISMQKINA ERIASTLS

> RXA02444 (1-1278, translated) 426 residues
MKNSKLLLIA AVSTASILLA SCGTDSSADT ATASSSATAS SEAHDHDGHE AEGSSTAVEV
SSPQARIVTT YDGGIITLDA NTLEILEDTE LAGFNRLNSA GDGRHVFVST GGGFQLFDTG
AWTEPHGDHT HSYTATPELT DITYSTDKPG HVVNHAGKTV LFGDGDGKIQ IFDTASLLKG
DEVEPEIKNA LKAHHGVAVV LENGDLLHTL GDEDSRNGAV VFNAAGEEIA RNEQCPGVHG
ESAALGDAIA VGCEDGVLIY KDGEFTKVQA PDSYGRIGNQ SGSDVSPVVL GDYKVDKDAD
LERPERVSLT NTETGELTLV DLGTSYSFRS LGRGPAGEAV VLGTDGALHI IDANTGAITN
TYPVIDAWTE PEVWQEARPT LFINKDRAYV SDPSNNELHV VDLANGNILA SATLPGTPNE
LTGVSG

> RXA02452 (1-180, translated) 60 residues
MTPAGPAQLL IVALVVIVLF GSNKLPDVAR SVGRSMRIFK SEIKEMNKDQ IESSDQTLKN

> RXA02454 (1-813, translated) 271 residues
MHLLNFYWGD VSLSNTLFRR DAETYSAYLV DAETGEFQPN LSESRRLYDV DIARVNIIGE
LMDLQAGECL DKSIDVIALG GLVESSYLEL WTELTAEESV DASEYWRLSE RIDRLNQLGF
DVGELKVTKD DSRQVVRIRP VVVDPGHYRA ELLSLTGLSV EEHQAQRLLG SIQAYQAVEC
GPHVGLTQAA HLWMTNEYEP TIAAVPVEML DKLEPAQIFH EIVDHRWFLA QERGGAVTLP
EATASYLESV LPARRDEARL LSTNPSDEDL S

> RXA02457 (1-1110, translated) 370 residues
MFYFTVNNPQ DPLSTEIVET NRRDLAFWHR LRPKDDDDLA TAINKICVRT GLSRKLIAAC
LFSICFLPYL PNFHKLVEKL GHLDMARINA ITKAGEKVPS EKRELFDAYL VDYLTPRAEA
QCLPQASSIS AMMRKFIAQH CPDDKASSAT NDGSIRYRRN NKGGISITVD ATASEVTEIK
AALEQMSKDK DCTPGTSLLH IIRGLPTKVV LNTYGTKDSP EYLEGGTWLS KEQSEFWKTR
TTSSRDMDAA HFSYTTAYAP TREMRVYIKG LRTTCSVPGC SVAVENCQLD HIIPWGEGGP
TTPWNIHPLC VFHHIQKTEG RLQCYPLPDG TVLFLVDGIP VFSIPDGPLS KSNKTWGTKF
GKYMERRIAA

> RXA02459 (1-735, translated) 245 residues

LARRSYDESD VRVRPGKGTR PRTKDRPSHE NALVGMVVTK DRGRWGVVLD GRQDAIVTMR
ARELGRTAIE VGDRVGVVGD TSGRPGSLAR IVRLEERTSV LRRTADDTDP FERIVVANAD
QLLIVSAVAD PPPRAGFVER ALIAAFVGNL QPVLCLTKSD LADPAEFAAE FEALEVPVVV
CGVDDPLDPV LEVVEGHITA LIGQSGVGKS TLVNRLVPEC RSLNWCRVGG WQGSAYVDAV
GRSCH

> RXA02460 (1-504, translated) 168 residues
LRVYIPATFS TLRGLNESRV ITARSGYGFA VTPALLDFYT DGDEEEIAHA AFQDAAEASI
RLLAIGDEET FPYRRVVVSV DVDDSVVTYQ PENGESVVKL SPAHINLDDV AAIHIDVEAS
EADTKKAIEV IDESDLGEED AELTVGDAQD NFMAWYDPEE LPFLVELL

> RXA02461 (1-408, translated) 136 residues
MRGLIVDYAG VLDGTDEDQR RWRNLLAAAK KNGVGTVILS NDPGGLGAAP IRELETNGVV
DKVLLSGELG VEKPEEAAFQ AAADAIDLPM RDCVLVDDSI LNVRGAVEAG LVGVYYQQFD
RAVVEIVGLF GLEGEF

> RXA02464 (1-507, translated) 169 residues
MGTTPDDSRT PEITQDIEIT DGRIVAIGQS VAAVYTNDPS PRIVSYNDDG ELVGEQAVDE
VEFPDPPFQS ATADLPHHMS WFNGDSLVLF SPTQLNVRQS FNDALGTGIA LNGSLLYPTA
EGITVANWDT GEVQRTIPVD RAGYDGEVAL GVVGQVIVEK RGSEIVALG

> RXA02465 (1-399, translated) 133 residues
MPASIRWGGI VALIQSTIGF GYAFFLIYRE ATGETDPSIV YETDNANTWV GYGTAAFFII
VFGTVVAGAI NMMKGHRWGR GAVVMLNIIL LPAAYYMFIE GRFSWAIVTG ISALFVLGAL
FNKRAVLWAN NEI

> RXA02466 (1-87, translated) 29 residues
VGEGQEQTFT YVIEIEDGVN TAAYGGDDA

> RXA02467 (1-225, translated) 75 residues
MDIKIGFADT ARELVISSAL QQDEAAAKVS EALANDSGVL DLSDEKGRRY IIRNSRIAYV
EVGTSAPRTV GFAGA

> RXA02472 (1-291, translated) 97 residues
MSFVNITALT FPAGAEKEIE QRFAARKKAV DTAKGFQEFE LLRPQFGEDR YFVVTRWDSR
EDYQAWSDAR PAGNHADDEQ RGMSVEVLGF DVVPLEG

> RXA02473 (1-741, translated) 247 residues
MVAEYPDGSS EIFPVTLNLI PEDTLVYDAV YKFKSIRTGS EDQITPFVSN QPDVPFPAGT
SFTLTGYYEI DQLRSAGWKF ELNPVTGELS VTVPISVIYP DGSRDNTIAT MESVGPDDSE
LFKPDFDLIP IKSGDYIEIG VLAPGLPAGT EFHLDYYALP DRFFDLGGST SLSGNGKFSL
GVPLTWNDDL QLPISITFPD GSHTVENLHV DVTPANFAGN PIDEPKDDDK DHPQPAPKPS
GSSFGSS

> RXA02475 (1-1155, translated) 385 residues
MLGLSRRKFA MLAALTAGIV GVVATGCSTP AEPETIDNPV FIGISIDPIK NLSPNHAANL
FALSADGSGG IFQELAPTYF PSIHRLGNGF IAPDRDSLVV VDASLKEVYR HEVARLGVGM
QTQSARSPLH KSVAFSFNEG TAEAPYRHRI VSATEKTSAS AMTDQRHFAL TACDDGSTRW
VEYSPDRGME DPMGPGSARI VTLQADGELS EIDVEWNFPD RPSAPIILSC EDPSAYIVSE
EDIIYVKDEV SPAESIGKLP AYEIPDRARF DTVSGEDYFA FTSTGMLTRI NIPQAKIVYA
QSIDLYGKHP VSITFDSDRA YVVTSGDSGE SLLEIDLNDP TCTSDQLSLT GFNKLLTARK
PKPEPSIIIE TILPIDPNYS LGCKS

> RXA02478 (1-1236, translated) 412 residues
MRTSLIARGL YRIPALVWDQ GLLTLFDARL SVDDLPAPID VVSARSSDGI TWTTPEPAIV
ETEHRGVGDV CLVTGDLCFH GLSNLAGFFE DPTDLEPRLA RRDVSGWTSI SMAHYFADVD
AAFASSGTGL VLADGRWIQS FVVRRGREIS LRILRSDGHI TDIAGGNESA MTQLPSGRIV
LHSRGVGHRL SSVSDDFGET FTPLEPVPEL IDPGCNGHVF YWKAAGMLAA THLADPDLRR
HLVVDLSSDE GATWAHRITI EREEAAYSTA AEMPNGDVAV VWEAEGTRAI KCTVISVNDI
SLRIDEPISD AISLRHVVIN DDHDGIEVAL PDASQWGEGV FKIVSNPDAS TQKIRTRGKP
ARQTLEIGDE LVFDIRKGGE VAYGVTVPYD GRSLGKLNRI LEWGCRGRFA VL

> RXA02482 (1-810, translated) 270 residues
VGVAKSKKSA LPKVLLTIVV ILLLLVLVAE FGLRFMIGKQ LKDEFQAQAS SQGISATEEP
SISFGASPLL LGIARGSINE VTIDTPDSVS ITNQDGVPSI SGTPESTIQL QGLDIGDRDN
PVADHLTLTT LATDDFILAT IQQQMAEATG GNSTSQGFAE QLIQELIKVT DITSDAANQT
IEVEFTDGAA RASLHPIVTN GQLGFEIVDS QLFGFGLPDE ISQMLTDALQ SSINEVAGGL
QIQSLEVVDA GINVTLTGDN INIQTLEAAQ

> RXA02483 (1-813, translated) 271 residues
MADHAHNLRA SFRKGANGKQ KPIGVITRGT TGVNRLRRFD RWCFHHPKIR SLLDATSLAL
DVGYGASHTT TVEWGRWLHR LQPDMDVIGL EINPERVLEP QNGVSFELGG FELAGYTPQL
VRAFNVLRQY DVDQVEAAWE TVTSRLAPGG LFFEGTCDEI GKRCTWITLN SDGPQELTLA
WDPWGISTPS DVAERLPKML IHRNIPGEKI HALLAAADLA WDYCAGWEPH GPRVRWEKAR
EMLIDQGWPI AVSRRRVGDS LLTVPWETVA P

> RXA02484 (1-501, translated) 167 residues
MATRTENTIT INQPVGKVHQ ALTTEAYWAY IAENLSPEAG EVNEFTAADG GATATLFEVL
PLEVLPEAVR AMISQALKVK RVLTVPALTN NATTVEYNAD VKGTPVDFKG TIAINGDDAA
TTFDYSNEVS VNIPFMGPAI EPKVADALGE LFANEGALTE KWISENL

> RXA02486 (1-636, translated) 212 residues
MTEFSDVPGT AAPLHRALEN AGYSTLESLD GVPYKTLIAL HGVGKTGLGR IQAALLERGL
SLGEETKGAT ITPGHTGKVA SDIKTHITSV DPVAYVDGLE GRRVAHGHQL LSIFGRVTGA
EPKMWGPSMI GYGSVHYVSH TGREGDWFQC GFSPAKSKIC LYGLKDSPRG EELLQKLGKY
TEGRGCVYIN KPEDIDLDVL EAMISESWAG QG

> RXA02488 (1-369, translated) 123 residues
KLTATGVDVM GTFYPEGEAL APITLNLTNE VVCDEPETPV EPEVPVEPET PVDPETSVDP
ETPVDPETSV DPEKPGDDNK DDGSNSSSNG DILGILGILA ALGGVGALVY NFLVASGFLA
AFK

> RXA02489 (1-624, translated) 208 residues
MNRFPSALLA ASVAGAALAI PATSAHAAES ICTFTGDVGW NVRDSFNSYL LGNIANGSAY
KYKGGLDVRD GVQTDGNGKT PALTWPVDSV TSSKISTSGG AHWTGHNLYP GDDLAEVPNN
FTLDLDFSNI TVELSGSTGR LLVDYTSREY INTHTLGEFQ TGEQAELATI TFAKAPDLTS
NSVNVTGDVA LTADGVEVFG GFYTAGEE

> RXA02495 (1-2568, translated) 856 residues
MALTVLSVVL GTAFLCGSLL LTHSLERTFS SIVDAGVEGV DVGVIAQQNN PDGVPFSVIA
EIEQYPEVRA VNIIGDGPGM PSGTTMTGQS ALILTDSDGN PLQAGSSGTH PLAIYPQGEW
VSPEPTLIDG HFPTKPDEVV VNASAAKRGG LSLGDHLTIV TPTERIDATL SGTFESNTDV
AGWVGVGFTP QRYVELLTNG TDASQITIAV NDGADPMAVR NRIGKNHRDL LPLLPEQIID
QTTGDTDRQL EFMTYVLLAF AAIALIVGSF IIANTFAMIV AQRTGEFALL RSIGVSTFQI
GFSVIMEAVF VGLIGGFIGI AVGFGVVNAL VQVLNQFGDT LSSIDITYNA GSFIFPVLFA
VTATVLSSIS PAHRAGNLPP VQAFESSDAR SDALGRIRFL VAAVMLTLGI SLTIAGAVVS
AINGDEFKTE TRLAFIGAGL LLVFFSLSLS GPALMVATSQ TLGVAIMSPF RAVGKLAQRN
TLRNPRRSAT TALAVTLSVG LVACVGVIGA TTRASVFGSM ESTIKSPYVL DSIGGTMIPG
QPAGGSRSLS MSAAVAQEIA QTRGVGKVGT LMTGSVQVNG WDNENTTIFD GDLSQFLDLA
VRSGDAFDDE TPGVMISTTY ADQSDLEVGD TVTVNPYGSD DGIRVPITGI YAETNLVGHL
MVNAAATNRV LTSADTYHRS QIFVNGDGST TNEELRDILV DAVAPFLIVQ VKSKDEFRGS
LGTQINQLLG IIYGLLALAV IIAVLGIVNT LFLSISERTR EIGILRATGV QRGQIRRMIT
LESVILSIHG AIHGLLLGTF IGWAIVSCLR TRGMAPVEFP WTQIGLMLIS AIIIGGIAAL
IPANRASRIS PLEAIN

> RXA02496 (1-807, translated) 269 residues
VNRSNSSSVF LGFPESSPAA ASIRAGEELP LDFPREWYEF TDPTDIEHVF SIDLTWLESN
WNCTFGTPDC LGIDSENADV GCCGHGAFLA DETDRDQLYD AVAQMPAKYW QLRPASTDSF
LASDDGTDIE PWLTWDELDD EDGNPEPALK TTVVNGACIF ANRAGWETGA GCALHQWGVN
ANEDLTVVKP EVCWQLPLRR LEAWEERPDG QEILRTTITE YNRRGWGNGG EDFDWYCTTS
PRCHTNAEPM WKTQETELRA LMGPNSYEV

> RXA02498 (1-804, translated) 268 residues
MSEEKLTVAE LMARAAKEGR STDAPRRRRR RSIEDGGVSV AELTGSIPAV KEKPAESKHS
SVPIDAPAEP EVVEAPKPEP AEEVEVASVE GDVDKQETPE RPAPSNEETM VLRIVDEKDP
ISLTTGAFPV VPAVAAKPAP VVRAEKDADV ETAVKADFAE VEVDNTDTTQ MAVVEEVDEE
PEQENKMSVF AIIMMAIVGV VLGVVVFLGF EMLWERLNKW IVAVLAVGVT LGMVGIIHAL
RTSRDGFSMV LAGIVGLVMT FGPLAIVM

> RXA02500 (1-99, translated) 33 residues
MGSVIKKRRK RMSKKKHRKM LRRTRVQRRK LGK

> RXA02505 (1-171, translated) 57 residues
VAGTHAYVNE TLSENEFSMC RKNEPGLVIE LENISIDRIV ISTPDAHRYA DELMAAV

> RXA02506 (1-882, translated) 294 residues
MHLNQLEFFI AVAQHGQINR AAEELLISQP ALSRQISALE KSVGAPLFER HSRGVSLTKA
GEILHEEALR TLSRMQSVVD EIQSGEHLIT SINIGVPPGI PIDWLRCQLI DLGPETRISL
IESPTDDQLK LLKQRELDIA LCRRQSEAFA TTLVHEQELG IVVRKNSELH QKVAGKDNAT
LFDLEGLRVL AHSRGEVRIQ EEILKNAMLA AGVNATWIFR KFGQYSSLIA DLVQADVALT
TEESARTNFP SWQWVPIEGE DASGNDLVVR TWITWNPQPT PAVKALIQKF IDGN

> RXA02510 (1-636, translated) 212 residues
MDSSDSHVGQ DVYVDQGLGE PDRLERLWAP YRMSYINTRS GGKQSTTAKR DPFIEVPKMS
DEDGLIVARG ELVYCVLNLY PYNAGHMMVI PFRKEKNLED LSLAESAELM LFTQTAIKAL
KQVSNPDAVN VGLNLGKASG GSVGDHLHVH VVPRWSGDAN FMTVIDGVKV LPQTLRQTRA
MLAQAWGTID GAPGTVDPTL TSAIRTAAPK EH

> RXA02514 (1-837, translated) 279 residues
NSHNPTPVTI TVTGKGEGVT SFGAISIEVE AGADAIVALQ YVGSGTHADN VEFIVGDNAR
LTVITDTHWN ADAVHLSNQL AQLGRDATLR HTVATFGGEV VRIVPRVRFT APGGDAEMLG
VYFADDGQYF EQRLLVDHAV PNCRSNVLYK GALQGDKNSD KPDARTCWVG DVLIRSNAHG
TDTYEANRSL VLTEGARADA IPNLEIETGQ IVGAGHAATV GRFDDEHVFY LQARGIPAEE
ARRLIVRGFF NEVINKVPVE SIRGELDNRV SSELAVLGM

> RXA02518 (1-411, translated) 137 residues
MSEHTENTTE VEDQNASTFE AQSSERPEQS EADLAKASDV EEYMRDVIDP ELGINVVDLG
LVYDIYIING NEAHIDMTLT SPACPLTDVI EDQARTAIVG NGIAEKMSLN WVWMPPWGPH
MITEEGRAQL QALGFAV

> RXA02519 (1-1806, translated) 602 residues
MFSAPLRRMM RVTKDEQIQP NSNAPENRKW FPRAPRPLRQ FLDTLPRIGT AGSRSATLHV
EDEQSPLGAT LFDVATGASS INDRDTDASG LEPEKIRRFA WLRLIGTMGA LMIAFGALGA
GALPVVNNPY VDFPGGNFMS RMLQTSSMIV LIGVGFLVLA WVLMAPLVGI PFKRSGNRTA
SVSLSMLRRT FGAWVAPIML TAPLFTQDIY SYLAQGSVTA QGMDAYAGGP LELLGPDNHL
ARSVPFIWAQ SPSPYGPVAL SIAASISVIT NDSIVGGVLA HRIASLLGVV AAGWAITMLA
RRCRVSEEAS FYLGVLNPLL ILHLIGGIHN ESILLGFLLV GLELGLRGTD RIQTGLWGPA
WTYIALSGVL ISCAGLVKVT GFIGLGFVGM ALARAFHARG HRHVVAIGVA GLVQVAALVI
TVVVLSVITG ISLGWITGQG GAATIRSWMS MTTNIGVISG FIGMNLGLGD HTAAMLVVTR
AAGIAVAAAF MVRMLFATYR GHIHAVGGLG VATFVLVILF PVVHPWYMLW AIVPLASWAN
RLFFQLGVIA YSTAFSFFVL PRGLALPVGT VFSIYFGAAL GFSILLLVGW WSLRRNPTFG
LH

> RXA02520 (1-684, translated) 228 residues
VGDVVKGNDA HTGDGDTRRK ILLILLERAP VIASDIAEQL QLSTVGVRRH LDNLVEENLA
EAANPRQNPY EPKMRGRPAK TYRLTDKGRS IFGHEYDSLA AAALATLREV GGDDAVRQFA
RKRIETIVEG ITPADVTDQS IEDTAKSLVE AFSRHGYAAT VDATRNGLQL CQHHCPISTV
ATEFPELCEA EHQAVSELLG QHTQPLATIA DGHGICTTNI ALTPIKHS

> RXA02521 (1-1443, translated) 481 residues
MTSATTNPGV NEPLTDDQII ESIGPYNYGW HDSDDAGASA QRGLSEDVVR DISAKKSEPE
WMLQQRLKAL SIFDKKPVPT WGADLSGIDF DNIKYFVRST EKQAQSWEDL PEDIKNTYDK
LGIPEAEKQR LVAGVAAQYE SEVVYHQIRE DLEEKGVIFL DTDTALKEHP EIFQEYFGTV

IPAGDNKFSA LNSAVWSGGS FIYVPKGVHV DIPLQAYFRI NTENMGQFER TLIIVDEDAY
VHYVEGCTAP IYKSDSLHSA VVEIIVKKGG RCRYTTIQNW SNNVYNLVTK RTKVEEGGTM
EWVDGNIGSK VTMKYPAVWM TGPHAKGEVL SVAFAGEGQF QDTGAKMTHM APYTSSNIVS
KSVARGGGRA AYRGLVQINA NAHHSTSNVE CDALLVDDIS RSDTYPYNDI RNDHVSLGHE
ATVSQVSEEQ LFYLMSRGLA EEEAMAMIVR GFVEPIAKEL PMEYALELNR LIELQMEGSV
G

> RXA02524 (1-690, translated) 230 residues
MTETTPQPPK PEPELPKFLS NPERADIILF IALIVMGIFS LCMIPLRAWM LTQPLAYTLI
VGGYTSAVVG GANASVENGI WWVYWLCTLI GALKFMPVYW LMGKRWGMEF IDMSLQYMPR
FHRMFKKSVD SESTRLYAWI IGLIPLAYLP GPVPGTILNA VAGLVKIPFW IIMAWNAICV
LSVNGLFMWL GYTFGEQVLD IVNVVNRYML WITLGLLALM FFRARKQFAK

> RXA02525 (1-378, translated) 126 residues
MTTMREVSTD LNILIVPSEW EKVLENLPAT LSESGFVASE IHSQIVDLTC EPDNMLVTQF
SQLEGHPPIV EVLHRLVING SSDLELKDLT KKVVGALPQG TYWYGTSLEG ATEPGVNASC
AWQHRG

> RXA02534 (1-804, translated) 268 residues
MNSPNADIIL VVNKLSKFID IENIMLVGAR CRDIHQQKYR DQTAGRRTKD VDFALALESW
DDFNLLKQQF SPTGNAWQGI TIGNIPVDLV PFGNIENPPG EVLSRKGHLL NVAGFKEVFE
QAELYPLNDA IDIKLSTVPG LTALKLHAWL DRKENNIKDA SDLALILSWY EEDVETLWNR
YFALENQGYI GEPEAMAAEL LGLDTGRILG HKETQALLDR FNEQSPPELN QFAESLEAPP
EHSHPLERRR IQVEALLGGL RDSLGYDE

> RXA02537 (1-462, translated) 154 residues
MLALKSSELE GIATSLTAVA GALHESNTDR LQSWQQLETM TSASSLIQGF IKLVDYNRPT
VNIVEQMHKT ASTLFNTADF LRTLEGYVDV LEKQADKSIT LTVMLRYIAS LSSLLDLMCA
REINALCTAI TPEPLKHLGD FGTLPPQQST SFIW

> RXA02538 (1-672, translated) 224 residues
VNAPPEIRAL AEAHPDMQIL EAGDGSLVAS FGDIDRATTV TTIVAGVGSS NPEGWNTYVD
RARTVSASTG SATVLWLGYQ APASIPAAVS GAAANRAAAD LQRFQAALQS RNPHQRKVVM
GYSYGSTVVG KAASSGELSA DALVLVGSPG AGVSHSSQLG APVYAVTGSA DPIGFAGTQY
DGIHGTDPTA ALFGATVWDS PSTHSGYWND QEFLGNVAEV VRGK

> RXA02540 (1-438, translated) 146 residues
MASTPKKSND EGQFDRVDFQ GEVFVISVAA ELAGMHAQTL RTYDRMGLVT PIRTRGGGRR
YSRADVELLR EIQHLSQEEG VNLAGIKAII ELGEENRNLK ESLRKVTAEN EQLKDQLRSG
RPRGELVHVP RSTAVVMWER RKGRSK

> RXA02544 (1-1428, translated) 476 residues
VSHTCGIVIF VSTESGNTPK RDDAKSTIPP KDLPDTVLDA IEGNFEPPLN TQKSAVPPNA
EATVEADSEG TTDRSVILGR DGRWLSGWAL RFIVLVIAGV IALRMLGFIW VGILPVVLAL
LVCTVLWPPV KWLREHKIPT ALAVVITILG FFALIGGVFA AIAPSVSSQT KQVVDQATVG
IEDLMDWVQG PPFNLDISQF EGALNDLTSM LQSQSSTIAS GVFSGLSTAS SIVVTLAVML
VLTFFFLKDG PRFLPWMRGF TGENAGWHLT EVLTRTWNTL AGFIRAQALV SMVDAIFIGI
GLLLLGVPMA LALAVITFFA GFIPIVGAVS AGALAVIIAL VTNGVTNALL VLVLILAVQQ
IEGNILSPFL QSKAMNLHAA VVLLSVTVGS TMFGIIGAFL AVPVAATLAV WVRYHSEMVA
LRAGEITSDD IEIATTKGSP TSLNGQETLA AIRSRFAILG RKKPTSATAE KADSES

> RXA02545 (1-558, translated) 186 residues
MTETLFVSAT TEEAVYLPDG IDLLVTGIGT TAATMILTKE LATREVLPAR IVNIGTAGAL
VDGLAGVYEI EYVLQHDFSS ELIAEMTGKP CSNGSTLATS GHFPVASLAT GNSFIADSET
RNHLATRASL CDMEGAALVG VAKHFGVPIT LLKQVSDSAD EEASGSWFDA VDAGARQLAE
AVKEFK

> RXA02546 (1-1104, translated) 368 residues
MPLFIDDALH RSKKYFHAHL SELLLGEFAG LSLPLHPPTA AKAAADIDAT REFIRQWEGR
DDVEYAIRNW SPVGLGKTEV PVRLTLNTTE ELVVFAQVED EWSSLHERFS QLSGFTAEVV
AKHVSLWRSL SNDDLSKAVL VVDWFLKHPN SGLLKRAVAV EGVHTKWLEN HRVLIETLVA

DKRGEPGRAD LGLGDAEARV RLRFHSVDAP AGLTDIEVPL SNLCELQEPQ VILMVENLDS
FLALPTWPGV TIAWGAGYRA VDIVRGPYFS NGRLLYWGDL DLDGFKILDG VRSHVPHTES
VLMNSETVSR WRYLGVADRE FKAESFDNLH DFESDALDLL ITDGELRIEQ ERIRLDVAVE
EIEKVIRG

> RXA02549 (1-1326, translated) 442 residues
TLTAISSETW PIMLAPWVCL PLLSRNVDAR AIALSLLPAA CMGAVNATAT MAALIPAALI
LLYRGLFLRL LLWGMGVLAV NSWWIGPLLV LGKYAPPFTE FIESSSVTTS WLNPVEILRG
TTSWTPFVDT ERQAGYLLVN DALFVTLSVL VAALGLIGLT LMKHRGLWAF MLAIGLLILG
SAHLTAVQEF LDGPGAALRN IHKFDLLVRM PLMVGVAALG SHISLPLLGT TALTSGQGKH
HTIPLPLQKR QAAGLLVVII AVGALAPAWS ARLLPQGTWD EVPDYWYEAT EFLNQNATGT
RTLIWPSSPF ARQDWGWTRD EPAQPLLDVP WAVRDAIPLV PPEAIRGLDG LDDLGTLGTG
LNDEALKRLG IGAVLVRHDL EADPDIEVDL PGEKHTFGSQ GQVDVYLTDP DRNMWITSGT
SKQLPTVAGG GEILSLLDTI NG

> RXA02552 (1-795, translated) 265 residues
VGKHAAETSE PKKNSPWRIG LLTFLISSVV VTLVGMVMLW PDSDDVVLAD NFSQTFAGNH
EQVDGTITLV DNSACNSPDT GRVFAESPTI SAEPATLECV RALVDITSGA NEGQKTQLIT
YAQPGDPEFS EGDKIRMVET PDTNGEIIYT FADYQRGPAL IIWGVVLIVA MGAFAAWRGV
RALVGLVVTL GIVGIFLLPG LASGHDAMWL ALVCGAAILL IVVPMVHGIN WKSAAALAGT
LVALLLSAVL SWASIVTTEF ARTGR

> RXA02554 (1-624, translated) 208 residues
MSHTKPSIAI LGAGRVGSSL ARSAVAAGYE VKVAGSGAVD KIALTAEILM PGAVPSTADQ
AVKDADIVFL AVPLHKFRSV NPATLEGKIV IDTMNHWVPV NGELEEIDQD PRSTSEIIAE
FFAGSTMVKS FNHIGYHEIE QDAGTGRAIA YATDDVDAGA QVAQLIKSFG FVPLNIGALE
NGRILEPGQE AFGAHLNKDS RLELVNQR

> RXA02555 (1-603, translated) 201 residues
MGEQFPGDKN IRVSDTERSA ALAALGQFYA EGRLSLEETD DRCEAVADAK TRGDLNAIFY
DLPNQQIAVV DRSEQTYTAT EVAELHRKGA RPRAGILGLT TVLAITGTAA FASTTAFATV
LLALIPIVFI MLYVMKIGPE SWHAPTPRQL QRKRMIELRE KEKLRDMELK AQRKERTHAL
TNRALDAAET AFNTKPWKKN K

> RXA02564 (1-675, translated) 225 residues
MAEVGAEPAG SAQSKTKQFV VGTAAVVITA IAAFFSIQSA SGGEDIRSNM TLIAPAAAGG
GWDTFQREQQ QSMRVNKIVN NIQVVNIPGA GGTIALGKLS TMTAPNTLMV GGTGHIAAQI
QFDTPAKIQD VTPIARVVEE FDIITVPADS PYNTLEELIE GWKADPAGVS WTGGGSFDQL
VMTEIALSAG IDPKQTTFIP SDGGGEAIQA LLNGTAKAST GGFAD

> RXA02568 (1-1359, translated) 453 residues
IPAAPSAPGS AIPTPGTAIP VPGSATPVPA PGVSAPGASV PSIPVPGSVT PPAPGISAPG
GALPTPGSAP PTPGGALPTP GEALPVPGAP GAPGASGIPS PGLPTPGVPT PGASLPVPGA
PDAPGTPSIP AAPGIQAPGI PAAPGAPAQA AAHAKPVFQD AEKRPRTDEA GNAKKELPLR
VRLAQPITRK QWAMTLGVLV LGAIVVAAIA VVLAKWAFTT EWLQDFVEKY PGKYDNPEGA
PVGIPTWLSW QHFFNMFFMV LIIKTGIEIN RTRRPKGYWT PKKGGKKISL TLWIHLVLDL
LWIINGAVFI ILLFATGQWM RIVPTSWDVF PNALSAGLQY VSLDWPTENG WANYNSLQEL
TYFFTVFIAA PLSIVSGFRM SSYWPKNNAT MNKLIPIGFA RALHMPVMVY YIVFICIHVF
LVLATGALRN FNHMYAGQDV VNWVGFGWFV ASL

> RXA02569 (1-750, translated) 250 residues
MSRSSKISVA FGGLLIAATW LYLVLVRPTD WESVGGSTEA LITLVGYVAG TIALLVGVLP
TLPARTIAII PVALVLNILL GQVTGSFVIP LYLDAVGTVL VAALAGPSAG LATGALSSVV
WALFNPLALP FAAGSALTGW LTGVVIKKGA FKNIFATIIS GAVIGLITGA VAAPVAAFVY
GGTAGVGTGA VVSLFREMGN SLLASVTWQS FISDPLDKAI VMLIVFVVVK SLPKRTTRAL
VPQRVPEDVA

> RXA02570 (1-642, translated) 214 residues
MNPLTWIIGA FSMWIVVLGV NKLGLSIAVI IIAQVVAMIR VRNVSVLAST ALLSVPALAS
MALIHMPYSS DGWLIALTLT ARFSALMSIF LLAATAITIP ELVKSLYRWP KLAYIVGSAL
QMIPQGKQTL ALVRDANALR GRSVKGPVRA VKYVGLPLIT HLLSAGAARA IPLEVAGLDR

PGPRTVLVEV VEGRVEKHCR WLLPLLAVGM AWWL

> RXA02573 (1-444, translated) 148 residues
MTNKTMLVAF DGSPESRRAL EYAAKLLQPR TVEILTAWEP LHRQAARSVS LITLGVEPED
PAHSAALKTC QEGVELAQSL GLEARAHMVE SATAVWSAIV DAADELRPDV IVTGTRGISG
WKSLWQSSTS DSVLHHADVP VFVVPPLD

> RXA02575 (1-1158, translated) 386 residues
VKNSGKNSAK NRTKGILIGV LVGLIAIFAG IYAVDVFLNK DNIPRGTTVG GVSISNLSAQ
EARTKLETEL ANDVVQPVTV TAGEQSTTFD PVASGVGIDW DATIEGTGEQ SWNPITRFVA
LFKESESPIV STVDPAAFGP TLDRMVGELY RDPISGNLHI DAGTLVVNDT IDGQAVDRTI
LEQAVTENWL NPEGVKAEPY VVPAAISQDT IDKLAEGAGA KAVSSPFVVR GDDGIEGTIP
VERMGEVVSF PEENGTIRVD INAEAATAML AEGLKETEIE PTNAQISFSS GSRVVTPEVT
GHGINWEETL ADLPNNLTGD GPRTIDAIYE DTPATFTATD AQNATFNEVM GEFTTGGFSA
ASGTNIRLTA QMVDGAVVSP GDTFSL

> RXA02576 (1-1422, translated) 474 residues
MTPTRRILLW AWTTVLLGSL LWPLAAPGEL LLRDMSVVDH PALSLNALGF GDLPSRNAPQ
DGVLALLGFL PVSWIVRTML LVAGFAGAWG AMRLGPSKFL AVTVAIYNPF VVERLLQGHW
SLVMAVWLFP LVVALRRHPR WQVVAIWAAS LTPTGAVVAA VTGVASSKRK RFTTLCSFLS
WLPWLIPALL ATPTSGGALT FAIRSETYAG TLGTALGLGG IWNAGAVPAS RELGFAVAGI
LLFAILLAGF KNCPWVLALL AVVGFMGAIG PWLMPNLFTW TIAYVPGAAL FRDSQKLLML
AIPAYVCLAA GVKSPLSWVA TGLALLQIPD APREVSVIRP SSAHVESVEA LAEIADGRDI
LIIGQGPLVT REDGIPVVDP KTKALSVVES GELRVDGIIT DAPSQRWTEA TQAWAAGDIE
RLEELGVGVV VDGDTITETG APPQHGWKYY LGVGLTVLWM ALPLGLLFRR KTKK

> RXA02577 (1-885, translated) 295 residues
MGAYDWVDII STCEFSGKVW AVFMKRSATV LIIAGVLFLI FAFTVPPYVT GQARTIPKDL
DLTLVSESPQ GFVRTEHIVT APTEKVDEIA THVDQTVTDV QGKTVAEISD DVVLIGHSRY
PVIKPTATIS GSPADSSNVV REGLHYFFPA NTLRNSYPYY DIVLGEDSPV DYVSREGNTY
TFYQHLRYVP LDDSHTYSVE RTLKVDRFSG IIVAKDEAMT FHGPDGDDTV EFTYTADTLK
LLQDHAHDID QRLSWAKGFD FFSKFLGLSL LAIGVFLTGI FKRGQLMSTV NKLRS

> RXA02584 (1-351, translated) 117 residues
MSLLCDSIAI GLFALFARVA HQSADMPLNV QGWFFTWLPF LAGVFIAYLV AILPAKLPSE
RIRPAGLTVW ILAVIVGLVI WGFNNGGVPH WSFMIVATTA SAILVLGWRA LFKVTMR

> RXA02585 (1-981, translated) 327 residues
MGIQQIRHVS PVGVALTMVA LVLSFVAMAR VMQIMLKAGG SPATLKATTA LTFAANSWSA
TLPGGPAFSA ILTYKVQRSW GASAVLCSWF FLLSSALSTV WLVALGVIAV FYMGASLNLW
SLIATFIAMV GLSGAVYWAA NNPDSLARWV RKLTKNREWG FVEKLLGSIE QLRSVSLTGP
QFAASTAWSL GNRLFDAISL WICIWAVTGT APMFEPEPNN TTIAGVLLAY TTAKIAGSIQ
ATPGGIGPIE AAYIAALVAT GMTAVEAAGA VIIYRLCSFI IMAIVGWVIY FIYFTPQGLK
ANESLDVEQD TINSDSNRQS AIERPDT

> RXA02588 (1-684, translated) 228 residues
MSDVHEVIHS YNPTDKEGPE SVLLVWDAPN LDMGLGAILG GRPTAAYRPR FDAIGRWLLA
RAGRRAHELG RHIEPEATVF ANITPGGSDV VRPWVEALRN VGFAVFAKPK IGEDSDVDPD
MIDHIRRRYE EGVLRGVIVA SADGQNFRET LEELVAEGIP ATVIGFHEHA SWAVAHDTIE
FVDLEEIPGV FREPLPRVSL DNLPDGGAWL QPFRPLTALL SNRHNSQE

> RXA02591 (1-1830, translated) 610 residues
MTTAAIRGLQ GEAPTKNKEL LNWIADAVEL FQPEAVVFVD GSQAEWDRMA EDLVEAGTLI
KLNEEKRPNS YLARSNPSDV ARVESRTFIC SEKEEDAGPT NNWAPPQAMK DEMSKHYAGS
MKGRTMYVVP FCMGPISDPD PKLGVQLTDS EYVVMSMRIM TRMGIEALDK IGANGSFVRC
LHSVGAPLEP GQEDVAWPCN DTKYITQFPE TKEIWSYGSG YGGNAILAKK CYALRIASVM
AREEGWMAEH MLILKLINPE GKAYHIAAAF PSACGKTNLA MITPTIPGWT AQVVGDDIAW
LKLREDGLYA VNPENGFFGV APGTNYASNP IAMKTMEPGN TLFTNVALTD DGDIWWEGMD
GDAPAHLIDW MGNDWTPESD ENAAHPNSRY CVAIDQSPAA APEFNDWEGV KIDAILFGGR
RADTVPLVTQ TYDWEHGTMV GALLASGQTA ASAEAKVGTL RHDPMAMLPF IGYNAGEYLQ
NWIDMGNKGG DKMPSIFLVN WFRRGEDGRF LWPGFGDNSR VLKWVIDRIE GHVGADETVV

GHTAKAEDLD LDGLDTPIED VKEALTAPAE QWANDVEDNA EYLTFLGPRV PAEVHSQFDA
LKARISAAHA

> RXA02593 (1-213, translated) 71 residues
LKIAHFDLDN PADESSYIFA RSLAEVDGWT LEFGVAGVKN TTIVSSIDDA ITTILRWMNG
EDIRDLNWTR A

> RXA02594 (1-324, translated) 108 residues
MEAMATTITV FSPTHSPAQI RETILSAAKE DDVDFLGVPF THPRNVTIEV DDELINDCLG
WLDDVALASG LGIQYNDEVL RYGDEDISFT VQTKNDDDAR IGASRLGL

> RXA02598 (1-591, translated) 197 residues
VTTDQNKRSL SELAARIVSE ICAPWVLNIG FFLILGGVTG AWTLGIVAAI GTGIVPMILI
LGLMKLGRVG NHHVTTRNQR GLVFVGIIVC VIILIFILRA LEAPQLIWDG MFSALIFLVL
FAQVTLKIKA SVHVGLWVCL VMFLGLTVSS WWLLGLLFTP VTAWARMRIK HHTMSEIVAG
VVTGAVATGI CYALLLA

> RXA02600 (1-1398, translated) 466 residues
MQPFPLSLTN SSVAGIAAGA LLFLSVPFAS PVHAQTILQD TLEVTVLDNA DELAPEDEDF
LSTETPKIDF PDSVTAVRYI TLTDNTDKIN DDVENYLRAE HPEWIQTNSF APGEVIIAVG
FDPNTMGAYA GNDVAAETGI AEQDRIDGTT DAMRPLLQDG RIALGMLEGA KSVADTSVVR
ESSAPSGGVI AAILGGIAAL VAIIVAWATS YANKKKAEKA REQFDYASRH YGEVAQQLDG
INVRAHSLTS PLADDELRRQ WDDVNSRFLE VNDIFGRLEG LTSTSENKAF RKALPDIEKA
HTAVTQMEIA QKNIDTLYDM EHGHEDTRRR ELTRLRADMQ EARQDINDKD AVVDDILRTL
IQRTETIAPS APDFMDQYAR LIRDYAVALQ GVEKNLEQVK QTTERNAPAI YDDNWRVGTG
YNSWVPYYMI SSWHAADVSA ASSASSSSAN TTFSSGFSGA GGGSSW

> RXA02601 (1-1989, translated) 663 residues
MKGEDTSMSA TNLAVEQLQR VLLPRRGEPA DVRSLYLLEA ESNKERLEWE DRFSVSVPAG
AEVSFQTYFN AFPASYWRRW SQLDSVVLKL KVSGEARVDL YRSKIDGARI GITGSVVKDD
FIEFEVSLAP FEDGGWIWFD LTAETDATVE EAGWYAPHAP KAQIMPDGSE VGPFEARATV
GIPTFNRPAD AVAALEALAS DPAVDAVIDT VIMPDQGNKH PADEPGYKAA VEHFGDRFFE
FRQGNLGGSG GYSRIMFEAL GGVDGKGEAG AAKSPYILYM DDDIAIEPDS VLRALQVARY
AKSPILVGGQ MLNLQERSHL HTMGEVVGGH DFMWTAAPHV HYDHDFSAHP LHDRGKFDDK
PDAPNSRDLH RRIDVDFNGW WMCMIPRVVA EQIGQPLPLF IKWDDAEYGL RARKAGFPTA
TWPGIAIWHM AWSDKDDAID WQAYFHLRNR LVVAAMYHQG SVDGIVRSMQ KATFKHLLCL
EYSTVAIQNE AMKDFLAGPD QLFSILDTSL PRIAAIRKTY PDAVVLPSAT ELPRATGAPG
VPTKDIGGRL APIKKAMWLA KGLKHSLSKE DASHHEVPQA NFAPIEARWF SLSRVDGATV
TTADGRGVVY RKRDRDKAKE LGKEARALQK QVAERFDELS RAYRNAHPEL VSREAWGKVF
DEQ

> RXA02602 (1-504, translated) 168 residues
MSNKEVQILV AIQDQLMDAP GVLPTARGLS LLGEHAAGWL ALGAGGAVVD KKRRRSWAGL
FIAALGSHAA SVIIKRVVRR ARPHDPAIRI GVGTPSKLSF PSSHATSTTA TMVYLARITK
SPVPLLGIPI MVLSRMVLGV HYPTDVLAGA LLGAATAEAV HKIERATK

> RXA02604 (1-2076, translated) 692 residues
VLACGLMTFS PQRPEFETGK QPDPETEHAG DFFEETSSSA PRAASNGSSG PNYTLITTFL
AALTAGIFAF WAGWTRKWIS DDGLIVLRTV RNLLAGNGPV FNAGERVEAN TSTLWQYCIY
LVALVTDYRL EDIALWLALL FTTAASIIGV LGTAHLHRKR IAVLLPAGVI GYFSLSPARD
FATSGLEWGL SLMWISIQWL LLVLWATSGK TSGKKASGAK TSNPIVNAGA ITYALAFWSG
LSWLVRPELA MYGGLTGVLL LLTAPRWRVV LGILVAALPL PAAYQIFRMG YYGLMVPHTA
VAKSASDAVW GTGWEYVEDF TGPYNLWLGL ALLLAAGALT VWKTDKHLAI PKGRLGLRTP
GMAIALLVIC ALVHFLYVIR VGGDFMHGRM LLLPLFAILL PVSVIPVNVV DRGWQDLVAL
VLVFSTWVWS TVVFVQGHQW ENTGQHVVDE RDFWIDFTNR DEDHPPLYAE DFLTVDSMND
YAEVMRDQTL VNPTGQQLNI LASSDPTTYS WITTPRVEGV EAGDLANLSP TVFHVNLGMT
SMNAPLNVRV TDLIGLATPL AARQPRIEGG RIGHDKLMDL EWQVAESATP LAYTPGWLDT
QKTYEARQAL RHPELVHLFQ TYREPMSYHR FVDNIKYALT TGRTLEISDN PEDLLKEFNP
TPAEIQDGLE TIAWPGEIKL DEPRGEPLYS SQ

> RXA02606 (1-1371, translated) 457 residues

MQEIHTIMKH MDALIADPSA AAFKATLPFA ELLEKLHNKK ALFDAALAKS AERADAGRII
GKTSHIDALA YLLDISKSEA FRRTKRAEEH YGNPSPEPSS EELAKETPEE KLAREEKEKQ
DLAEQAEANR IAREHGISAE KQDTIRYELE KLNDNTSLSR ASLRKLAMQE ATSRTPEDLR
NWTRNKVIRI NPTAKDPLAA VKKRSLSIGR QDHDGGAKAS LYLDAKGLAL LKSLMSKAKP
GHLLEDSLAE DKRTKPQRQY DAFADILHRA HSDLLPARSG VGTILVSLSA KDVTNLKASG
PDHRYPTSTG IKLTPLEILR LGAAKYDFVT VLDSESGRPL HLARTQRTAS LYQRLALFAS
ELVCTREGCD SPFEDNEIHH IRSWLDGGPT DIENITNICP HDHGNNNDQR DGKDNMGHMN
IDPTTGRVGY QPADRRKPMR FNNTAAAAES GGAQART

> RXA02609 (1-249, translated) 83 residues
VERSAEAQAF LDALKDEKID ISGVEDQLIA TARNYCSSEN KDQNVTVDAV AGQLIVQGRT
SVKEDQAAEI STLLKESADR TYC

> RXA02610 (1-927, translated) 309 residues
MRKTITVIAV LIVLALIGVG IVQYVNTSDD SDFIGQPGEP TGTETTEPPV QPDWCPAVEV
IAAPGTWESA ANDDPINPTA NPLSFMLSIT QPLQERYSAD DVKVWTLPYT AQFRNINSQN
EMSYDDSRNE GTAKMNEELI NTHNECPATE FIIVGFSQGA VIAGDVAAQI GSEQGVIPAD
SVRGVALIAD GRREPGVGQF PGTFVDGIGA EVTLQPLNLL VQPIVPGATM RGGRAGGFGV
LNDRVQDICA PNDAICDAPV NVGNALDRAL AMVSANGVHA LYATNPDVFP GTTTNAWVVD
WATNLIDNG

> RXA02617 (1-507, translated) 169 residues
MSIKHALLVL MLDEPTSASQ LQTKFEETMG IWQLNIGQVT QTIQRLQRDG LAETAGTTVS
SNGRTVDTFQ PTDLGRELVA QWFESPVTVT LSERDELVTK IAIAESRGLN LIPLLDIQRN
TVMAELRALN KSSRDLAETR NTQRLLVEKR IFELEAQARW LDRIEALEQ

> RXA02619 (1-900, translated) 300 residues
MRSVVLELLE NWKESLVLHP SLTELADAAP LAQDFATVRG VLKESLDLLG NALNHGEEPA
ELAGWLSQVI TDVLHSPGLD AHVVLTGPVG RGDALPTSPV RWLAVVDSQE DPNEKISALL
TEVGFIAEPI GAATREEWEQ RARAGEDPEV YLDAGTWVAA IAEVDDKALL QDALSSRPPA
VETYEGLPSL DMVVNIRENL MIPTVKIARW AAHKAGSLAP TTAQRLVDAR GVLTNDEVDA
LTQVWTSALS LQSKRWMDHI HDQETTAWEL PALQRATFGA SARLLSEVLR SVEAREIDTK

> RXA02620 (1-654, translated) 218 residues
VGRPRRSAPR RAGKNPREEI LDASAELFTR QGFATTSTHQ IADAVGIRQA SLYYHFPSKT
EIFLTLLKST VEPSTVLAED LSTLDAGPEM RLWAIVASEV RLLLSTKWNV GRLYQLPIVG
SEEFAEYHSQ REALTNVFRD LATEIVGDDP RAELPFHITM SVIEMRRNDG KIPSPLSADS
LPETAIMLAD ASLAVLGAPL PADRVEKTLE LIKQADAK

> RXA02624 (1-714, translated) 238 residues
QGYDDSASVV ALIVLSILYL PNMMIFAMGN LIGSPLYFGD ASISVFSVHS VPLPPLPILA
ALPSEALSWA VALLVIPAII ATWVCVRNPM RLAVNTTAAV ISALCFLVLA VFAGGTLGVY
NYVGLNLLAS VGLVFVYFAL VGLLIAGIDK LRNPVEVKSV KAVAVVEPEP EEVEEDEEEH
VEEEVDEEEE EVEEGVEEVE EDDAEDPEEN PEEEESDEEI ETETEAEETN DGSEAEDR

> RXA02639 (1-834, translated) 278 residues
MIALGSAPKL VASDVDGTLI NSSERVPQRL RDVITRMTNQ GVTLALSTGR PPRWIHYVLD
QLSVKPICVC ANGAVLYDSA ADEILAAQTL SPEVMASAVM AARAALEEHG GVSIAVERAG
KSAYDPADEL FLVTPEYSHA WPSNDHGTFE EAEVLSEPAT KLLMRSDYLD SKQLFDIVRA
SVPEDQVHVT FSMSGGLIEI AAPGVTKALG VSMLAERLKI AQKDVITFGD MPNDIEMLQW
AGRGVAMGNA RPEVKAVSDH ITRTNDDAGV ADVLEWWF

> RXA02647 (1-462, translated) 154 residues
VALSVFTPVA QAQSSDALTQ LSDNITSSQI LDDDGNPVDG NETWPGSSEG SSMLSNGDIP
AAPSLSSSGK DTSDDDDEIS EEQQALIDRL SEMPVIGSIV SPPEWLAIPF AVLQGLLAIT
TLASTAASFM VTVDPSFKQT LRDMLTQFGI NVDA

> RXA02649 (1-1002, translated) 334 residues
VLKRFSHHSS PQVLSRKVVA SALALTTALA LAACSSSAEP DSPEVEQAVG LAVDTPRVVV
VDPGTGDLQR LQYKDIAPDA TQEQTINIAE GFAQSVVNAD SVDPQAPAGG DVTTFHLPVK
ATTEEAEFSD QEMVSATRDI SLLFGKPTYT DLSQVEDVNS TEGFTLGIRA TDSGQHTTLS

FAAPVDSTET GRMLMEQYLL TFTSLPIVFP SDDIGVGAKW TVDSRVTGES TLLQTVTYTI
TGIDGDKVNL DVEVSQRPSM GALEITDEES DETTGQLTVL NSNTTSVGTL EVDLTQPLPT
SGQVSWTTRV IYGGSNEQVR VVQDSTSSVS FGDQ

> RXA02652 (1-579, translated) 193 residues
MDGVDKGRRI VALLAILALV VVVAILSFSD RTAKPMQLNG DMLGQDNTET SVEYRQRASE
SLENAAVGEE AYSLVTFTQP LSPSEASNLL KGVGRVNAMV MLSAPAMDLP EPIAGETRED
VFNRQIKLVD AQLSGIGNVR APGELNGVVV WDIPQKVRVL SESSLVYSVE TLPPDAAWGS
FGIRPVDTSG TNF

> RXA02655 (1-984, translated) 328 residues
MSPEAKEAQD SRRNEMPEKK RAVLRKAIKL EWATIAWVLF SIVLVGVVAG QSQAMRSAWI
EDMLSLVPPI AFLLASRISK AVATRKHPYG KHRSIAIGHQ AAALALLIMG SLLIYEAVSA
LIKGERPPIG LAILFGHDVW SGWLMIGVMI SVSIPMVIVG RVKINLAKDL HDKLLYADAD
MAKADWGTAV ASTVGVLGIG LGFWWADAVA ALVISASILR DGVINMKAAI SDLGDGRAMT
YDNSAPHPLN DDVEKAALEM HWVKHARARI RDQGRCFHTE LFVEPVEGYT PAPEEITSLV
KRIQNLDWKL QDVVASVVEK IDRFQAPS

> RXA02662 (1-264, translated) 88 residues
MRRKLTTTLE NKPGARLGGF RALAPTSKIA LVFLLLIFLL AIFAPLIAKY DPLASGTPVQ
PPSGEHWFGT DAIGRDIFSR VATAPEPP

> RXA02665 (1-480, translated) 160 residues
VTNPIIPRVG IATDAHQIEA GKPCWIACLL FEGVDGCEGH SDGDVVAHAI VDALLSASGL
GDLGSFVGVG RPEYDGVSGT QLLKEVRELL SAHGYVIGNV AAQLVGQTPK FGPRREEAQQ
VISEIIGAPC SLSATTTDHM GFTGRSEGRA SVATAVVWKA

> RXA02670 (1-582, translated) 194 residues
MEDESVKSLN LAARRGALVT VAAASALALA SCSAGQITQT SSQVAAVDGN QAGSANDPVL
VRDVTVHLTT DGEAGVKFTA INQDTSHTSH TLESVTVDGE EVELDDAEPI ERNCSLVADI
QSELDLIEEP EVGCIQHVAT SLENPGFAYG GVVPVEFVFD TGAITIDATV SAPVLESGVE
NREVGGDTAE ASHH

> RXA02672 (1-1098, translated) 366 residues
MTPTTTPVSN PDALSTGTQD VHTLKGTLQR LAPGTPLRDG LDRIVRGHTG ALIVIGDDEN
VSSICDGGFE FDVSFAATRL RELCKMDGAV ILSSDLERIK RANVQLLPSP TWPTQESGTR
HRSAERTALH TGVPVIAVSE SQNTITLYVE GKSHMLEQPA ALLNRANQAL GTMERYRDRL
DQVNNRLHLA ELHSYVTVID VVSVIQREEM LRRVGEIIDG DVLELGKDAK EIQIQLSELR
GDNDRERESI IADYLVTDGI PADEEIHAAL EAISHLDDKA LLNPANIARV LGLPPTEEAL
DEPVTPRGYR TLNRIPRVQK FLMDKLIVEF GNLDALLNAS VEDLSAVDGV GSLWARHITD
GLGRLS

> RXA02673 (1-633, translated) 211 residues
MAALLVLLVV IALIIWAVVA LRGGSSEPEE EQPNNAVVTS SMESSATSSS SSKESTTEAT
TEEETSSAEP TATSSVAADA KKTCELSDLV ISASTNQPTF SGSAQPELFM AVHNPTAVDC
EIDLEENKLR FEVYNLATNA RIWSDVDCNP AVEDGTSVFP AGEDRYFQAT WSRTTSAPNQ
CNNRTDVPAG GYYLHTVVGN NPSPAVTFNL T

> RXA02678 (1-918, translated) 306 residues
MRMAKKTKKN EQLPEGMSRR QAKLAARAAE RAALEREPRP FEGLAMESQL VALQEFIPSA
TAPITVAGTD RKITLCTVLP GAAAALVREE AFGGEAFVAM QQAIRSNNPS KDLAFALNWV
INAKAGESLA TATADGTQPE LKSLLNDADT LEITTHQDFN WWLAENDNLS PEVAQHMQAA
NDSILPSHEV EADVPGAVWW VNPGGKAHIR WVRTENETAL FNALARIAAR GELNLGEETK
FAGAFRTHGI VVPVWDLDPE RPSTDYADVL VALNEKIVAE LDNDAQLNAD ERRQLENIKS
RQVTIR

> RXA02679 (1-426, translated) 142 residues
VAPSSGDDTV DVGTCRTLLV SELNVDLWAT DLEVDAVAGG GVVLGGAGPV DVGVIQGFAD
GIEFSFGGFL IGEANPVCDD IDEQFFLLIG EVRAFQAGAG WVVARAARCA HHGIQLFTLV
ELCLLLFGEA VVEGEGGFVH VA

> RXA02680 (1-1284, translated) 428 residues
MRLNKRLPAA LSGLLLSAAL LAGCSTSGTA ETTTTTVSSA AASTTTSTSS ASSSSSSSSS
SSSSDSSTTA ETISNTAEAA QAFLSTLSTE EQDAVLYDYD AEEKSTGWSN FPVTFVQRSG
VNLTDLTEEQ QAAALNVLKN LLNDDAYQMI EDIMASDQYL NDESNTTEDS LGQYYIAFFG
DPSSDSDWSI QFGGHHIGIN TTFSDGAITF APTHLGTQPS EWTNEDGETV AALSNMYETA
FAFYDSLAEE QQAQLYQGEE LDSMVCAPGS TCDYPTGTGL KGSDLTDEQK ELLIDVIANW
VGLADEETTE TELDAIRETL DDTYINWSGA TEYDTSTGDG IYFQISGPKV YIEFANQQGS
AGADIDGVIT AGWGHIHTIY RDPTNDYANS VTQEAASGMM GGGPGGNGGE MPSGDMPTGE
MPSGAPSN

> RXA02681 (1-444, translated) 148 residues
VGWGEGDGTV GEGGVDADVV SAELDGPVGV AAWIAEECDV VLAEGILGGV AFVVEVLIAS
HDVFDHLVGV VVEQVLQHVE GSCLLFLSEV GEVHAGTLHE GDWEVRPAGG LFFGVVVVEY
GVLFFGGQGG QESLGSFRGV GDGFGGGA

> RXA02683 (1-678, translated) 226 residues
MTLLENSSGD PGSDSGGARY SLNSLKVSEQ AAANAVLKAV LNDVSYQEFA DSSYLEITGT
PSADGTWGIS FGGPSESASV EFSDGSISFS PVDMTVPATR LPQMGAFYET LTEEQLGMLE
TGLAVSTVDS SQQEMLLDLV SNSIGLADTE TTATAISKIR ATLSETYLFG TPDGLTLALS
GPHVDFEVSH QGSTAKITYR DPSTDTLTAE DRVDTASVAA APPEVV

> RXA02685 (1-657, translated) 219 residues
MSGLRSILRL IDDLLAPVAL NDQQVALNAS MANSAWLDLT LQLCSAGVLF SWGALAIYLL
GERFQWIKPK DWAWGAGLAA LIGIPGLIFY ASAVHLGLSK QVVPTTLETW WEIPVLLIWS
AANAFGEEIV VVMWFFTRLR QLKWSVPAVI VTSSVLRGSY HLYQGISAGL GNIIMGVAFA
YFYHRTGKIW PLVIAHFLID AVAFVGYSAI GGNLSWLGL

> RXA02688 (1-669, translated) 223 residues
MAGRIILLRH GQTHNNVKHL LDTRPPGAEL TDLGRKQALE VGHELATYSG ERLAHVYSSI
VLRAQQTAVL ATSTFEKARD MQSGAIPLDV VEGIQEINVG DFEMRGDEEA HMNYSRALNG
WLHGDPAAGL PGGETYKDVL NRYQPTLDRI MDSHDLDDDR DVAVVSHGAV IRIVATHATG
VDPNFAFNTY LGNCRFVVLE PNGKKFSQWD VVRWTDSPLP WQE

> RXA02689 (1-342, translated) 114 residues
MIEVSDERFE ELVELAFDQV PQQFLDHMRN VVLLIEDFNP DSPYILGLYH GVALTERTFN
HGGLPDSITI YKGALQNYCN SEEQLVEQVR VTVLHEIGHY FGLGEEDLHR LGYA

> RXA02690 (1-1098, translated) 366 residues
MSTNFDTSTS PEGETKKNSS FRTAASVQTM LVAALAATAA VGVYSYNTDN SANGGESPTG
PEQSTVSTTA TIASFTTADV GQCATWDVNN EGLVSGFEQT SCDQEHRFEI SARENLATYP
SSEFGPDAAP PNLTRQAQLR EELCQSPTLA YLNNRFDPSG RYTIAPILPP AEAWAAGDRT
MLCGLQATDA SGTPQLTVGP IAANDQARVF ETGACVKVES SAEFRQVDCT EDHHLESILT
VNLGVPFPQG APSTDEQNNF LGNTCTQASI DYLGSEENVY QSTLQTFWPT ITSNSWLGGS
HSVNCFLMSP STEGAATFNT LNGSATGTFT INGEVPPPQP ERDPLRDTAG TTASAEVGVP
VEENAP

> RXA02693 (1-1647, translated) 549 residues
MVSLPRLASL LTTRLATLKP ALKPATHLAS LGAQVIAELV PGIRMSPNRR RILPANMGAG
FIGAEIAMWW ALSPSLLPKP WWVTAANLAV LQAVGHAAAT GIHSILPRTN RRVSRKIYNA
THIATGAITL TTTVVGLIRH RTQIRLIGQK NFGPKETIAG ISVGTLGYGA LLITGELTQH
SINEVKLLIE RFLPPWISFI AAVSVITLTT LTLADRVLLR RILHNSAIQA AHLNRMVFPG
TEQPWEPERS GSPWSYEKWG AVGSQGRAVL SGGPRKDDII TVTRLSDTET HEPIRIFIGM
VPGRSLSDQV DLVIHEMRRT GALRRDHIVI NNSTGTGWIT DWSAHTFEFL TGGNCVTISM
QYSYLPSALS WYKDNDGPIN AARMLIDAVL HELDQLPTGS RPKLFLAGES LGAYGLAEVW
GDVEKLLGTA DGVLLSGAPR FSDAMNALRT RRDASSSERL PVIDSGRHIR FAGEPEHLDM
PATWQFPRMI VAQHASDPIV WWNAELFIRR PEWLKTPKQD HQDVFNRLRW MPFVAGWQVA
LDLFTSTSV

> RXA02696 (1-456, translated) 152 residues
MSMLKKTKEF FGLAPYEAEH EDAYYADEPR YEGTAAYAPE YRERDYGYAP EAPAPVAPSP
APRSYQSTIV PVELHSFEDA QVIGGAFRDG DAVVFDMSLL SREEARRIVD FAAGLCFALR

GKMQKIDSVT FAVVPELSNI STSELERAAR IR

> RXA02697 (1-699, translated) 233 residues
PFVVWIGMHH FAGFLATKKG KDSPTLKQQV PAFFATGAAG VAVTGVVVSA ITWASGASWG
WISEISGNSK VINPLAFPSL VASVITMVAE VFVDDFDYNA VVNVVRSISM LIMLGGLVVC
WWLFRQNERR AVTGTAAAYA VAFVFNSVTL PWYYASLISL LGTFKPPMWL IRFAAGASVF
IALMFTGSGN HQLYNIVTVI IAAIIAWLAT VVIFDDTDPA TTATEKPSPH TVS

> RXA02700 (1-1236, translated) 412 residues
VVPSLQQWRK PALILAILTV LGVLLTHWFA WPLTWPLGLR LPVDVEVYWQ GAREFWLADD
LYDIRYDTTF DNLPFTYPPF GALVFTPLWW IHDLFGLLVT ERVFALITLL TTYAVAVFLL
RLAGVRDRVW EFVAFAALLV SAPVYFTLNI GQINVMLMAL TLFDVALPRS TRHSGVLKYV
PLGVLTGIAA AIKLTPLVFG LYFLILWVVT KSPRGLFGMI GGFLGASGLA IIFRPSISIQ
YFTDVLFTAE RIGDLHFARN VSIRAVLERL PELGSAASIM WLVAVALVII AVAVAAYRIL
RTDLSAHNRL LAVSLVSLVA LLCSPVSWYH HWVWLGPLIV ALWLTQHRWL ALWGAFAVTF
GSFHNFLPSE NNMELTWPWW MHVLAAHYLI FSAVVTAVFS CGKMPQKTEL SH

> RXA02701 (1-1308, translated) 436 residues
LTNPQTAHAA ASDSASQKEA PNPSLSITVG IKDLLGLLSV LGIAAGLIAN KILIERYNWR
IDAAVYREGA LALVNGESLY AQPFDMGDIS LPFIYPPIGA ILFAPWGYFD FITVELAGNL
VVIGSSLLLL LCLYLVTNAV LSGRDKLLAF TIAAISWPIA LFAEPVFLNA DLGQINILIM
ALVVMDLLPI KRRIPRGVLI GLAAAIKITP LAMLLYFLVK KDFRGIINAV ISLLAFTAIG
AVLAWENTKE FFSSTLLNLS AEGDSGVDTT FQSNSSIQAM LYRWWTSKAD AEASSLPTIL
WIVLSLIAVA AVAYLMHQLF SRGLHVEAVM VNAMLMLLIS PISWSHHWVW LPLWAVVFFV
RYRQHRSHPK FLLWSGVILS VMLLMLPPKW WFGRDGVNVF ELNFWEKLLI SDWTWLSIGL
MITLGLGLKA FPKISK

> RXA02712 (1-795, translated) 265 residues
MTMTNGSRTE SGKIRDRRVA DADPRYGRRV SVSRDFSTAE ASGRGASIST QPRRDMAPER
RHTTRALVNP GVQPTRKRLM QHKLGSQQVM SVRGRRVEAK RADPKVIQLS VLVVILLCVG
VGATMGLSGT STQQTFQLQE LQATETDLSN RIESLNRDVE DARSAATLAA NATEMGLVSP
VEPGVLAVQE NGDVVEEREA NPETRPIVDI NGQQTRPNRA SSNPDETNAV TENLQAIPQE
AAAPPYQTNT VPYAATTGQA GGAGQ

> RXA02714 (1-429, translated) 143 residues
MFLGTYTPKL DDKGRLTLPA KFREDLAGGL MVTKGQDHSL AVYPKEEFAA RARKAAAVSR
TNPEARAFIR NLAASADEQR PDGQGRITLS AAHRTYAGLT KECVVIGSVD FLEIWDAQAW
AAYQEETEAA FSAAEDDVLG GLL

> RXA02715 (1-390, translated) 130 residues
VSLSEQEQRA LREIEQALMA DDPKFGKAVA SNNGLAGGGF TLRGIALFVL GLVLLVAGVA
LSQQTLWFVA LGIIGFLVMF GSGVWMLRGG GSNKISVTSR TSNAKNRQQG NSTIGDKMEE
NFRRRFEGNK

> RXA02719 (1-648, translated) 216 residues
MTLFQRLTNP VVLGGLAGVL LLLGSFGGGA IRYRGGVLDA LGLNFLAFGH AQGISNTVLW
VGQLLLLIGAW VHLGRRLFKK KVADDTADAA DLGLVKRTLY AMVVPLIFAA PMMSRDVYSY
LMQGAMLRDG FDPYTEGAAV NPGPMLLEVS HDWRNTTTPY GPLHLWIGDM ITTVVGDNVT
LGVVAYKILS IIGLAVTGWS IVRIAQHFGA NPAIAL

> RXA02720 (1-627, translated) 209 residues
LERREELQVR LQQVQARIDA TLNEHNRPEG SVRLLPVTKF HPVEDIKILQ EFGVTAVGEN
REQEARAKAL ELPDMDFHMI GQIQSKKANS IARWAAAVHS VDSEKIAEAL GRGVALALDR
GDRTSDELPC FIQLSLDGDP SRGGTPLSQV TQLADCISDT THLRFEGLMC VPPLGWGPEK
AFSQARDVLS GLEEHFDRSL EFSAGMSGD

> RXA02721 (1-738, translated) 246 residues
MDSLDPRNRP VRKVFTTRAG GVSQSPYASF NLGDHVGDDP QAVASNRNRL ADIIGLSPDK
VVYMEQIHSN TVTVIDEAPA DGQAVEATDA LVTTQRGLAL AVLVADCVPV LLSDTDAGVI
AAVHAGRMGA RNGIVAKTIA KMEELGAKPS RIHALMGAAA SGANYEVPEA MARDVEAKLP
GSIARTTKGT TGLDIRAGLL RQMLSLGVQM IDSDPRCTIE DEDLFSYRRE GTTGRQAGVV

WLPKEA

> RXA02725 (1-612, translated) 204 residues
MDNFEHSNAS IRLQAALAAG TAEDTTAIDI LLYRSGVEED FFVRDMITWA LTRMPVDDVF
TSLVADLDSE VPDRPFGASQ ALHTLSKLRV AQSWQELQAR PWLLHREDTA QTAWRTFVGL
VPDDQTAWLA HQLLQELDKG TPEIQRSLSR AMAELEGREA SISVLLGALT SAHAVATAKL
IADPDSDFMA DLEEARRVDN MGAC

> RXA02727 (1-912, translated) 304 residues
VVLLPLLVPQ LQVQPQLQLP SLLTRQRCAR KSKRSCAPNT ASKLDDASKA AQKAQNDAKS
AQDQLQRAQA DAKAARDEAE KAKAEAKSAA SSSTTKAAAV GAVGAGTGAA VATGAANVDT
HMQAAKVLGL AQEMADRLTS EARSESKSML DEAREAAEKQ IEEANSTSNR TLEDARANAE
KQIAEAQNRA DTLVNEADAK AKNLVSEAEK KSAATLAAST SRAEAQIRQA EDKANALQAD
AERKHTETMA AVKEQQNALE TRIAELQTFE REYRTRLKSL LEGQLEELHA RGSSAPTNNK
PSGE

> RXA02734 (1-384, translated) 128 residues
MRIAVTGATG SLGGHVVDSL LNKGVAASDI VAIVRNEEKA ADLKARGIAL GVATFEDETA
LTAALEGVDR LVFISGSEVG QRVAQHTNVI NAAKATGVTF IAYTSLLNLG PQSLHLLQST
LQPEKLLA

> RXA02735 (1-705, translated) 235 residues
MVDVVRARDT EDLVAQAASK FIEVVEAATA NNGTAQVVLT GGGAGIKLLE KLSVDAADLA
WDRIHVFFGD ERNVPVSDSE SNEGQAREAL LSKVSIPEAN IHGYGLGDVD LAEAARAYEA
VLDEFAPNGF DLHLLGMGGE GHINSLFPHT DAVKESSAKV IAVFDSPKPP SERATLTLPA
VHSAKRVWLL VSGAEKAEAA AAIVNGEPAV EWPAAGATGS EETVLFLADD AAGNL

> RXA02736 (1-957, translated) 319 residues
MIFELPDTTT QQISKTLTRL RESGTQVTTG RVLTLIVVTD SESDVAAVTE STNEASREHP
SRVIILVVGD KTAENKVDAE VRIGGDAGAS EMIIMHLNGP VADKLQYVVT PLLLPDTPIV
AWWPGESPKN PSQDPIGRIA QRRITDALYD RDDALEDRVE NYHPGDTDMT WARLTQWRGL
VASSLDHPPH SEITSVRLTG ASGSTSVDLA AGWLARRLKV PVIREVTDAP TVPTDEFGTP
LLAIQRLEIV RTTGSIIITI YDAHTLQVEM PESGNAPSLV AIGRRSESDC LSEELRHMDP
DLGYQHALSG LSSVKLETV

> RXA02744 (1-804, translated) 268 residues
MSKPFENSAL RGSSRFPAGT FTPAPKRATP AKMLAAQGKM ESLLFLRHGE QQLLSIIIPL
VALIALANFD FIPGENSLDK TFPFALATAA MSAGFTGQAI SLAFDRRYGA LKRTGASGVP
AWTIIFGKVI AVIAVTIVQI IFLGVTALLL GWSAPVGGVL FGIVTLFVGV SSFTALGMLM
GGTLSSELVL ALANLIWIVL SGLAAWAVFS PSVNAEGVLS IIPSVALSQG MVDAFNGELP
WLQLGILVGW LIITGVAANK LFNFSASR

> RXA02751 (1-474, translated) 158 residues
VLPIASGNDD RNLIRYVDGG RFDEIMLTGD LTGLSSFLTN AGPNARDDFD LTVLMRAAEA
GNLMVVARLL DLGANPRLTN PRGVTALHIA AIAGDDGIVE CLIDAGAEVD AVDDQGRTPL
WNAAAHHLPD SAVVDVLLRA GANVNLRDCN GVSPEDML

> RXA02753 (1-2493, translated) 831 residues
MLDSLKNRFT KAKGSHGVGE GAVSGDAAVK PLRKEERLAS VIQETEPGAA VEVMRRNDAF
ALPGETGWVV MLLPTHDSQF GGLNAKEKNR EDKGTIINLV VNDDIHSVVT PELLDSDVLG
VIPDADSFDR MDEFDLLRNK ARWHYGVAAI EPDTGELVVF KVPAKNSASA RGDIFSEVGD
VLSGAADLED VVDFEVIATF LEVLNETSEV DIDDEDGDVP YGLEGVNAAG VITDDLIREK
LDVDSYPSSA EIIDNIVHVF TKLQGKHHVA PQPVLHSADV VDVDAQESHD TVVIESPDDV
ALAEQVDVPD FSDGFGIDDA EVTEPEDEEV VEATADADPF GDVAEDDPFG SDDEPDFGAS
DVVAAPAPVA GMSDEQIQAL IRGVSESVQA KTGSELNALR EELAQALAYN PVQDSQAALA
QVHAADARSF DADQVGDAVT KRYVNDDLGL YVDEANFNNA LTRAPFQVAM PQFQETTPWL
GDQLRTLVAV FNGQLLDQHQ RDYEEVRAMY IALNDRSNLE IARDLGLDNK DSEFYEVYRA
IERDRDVMAG DQQRVESERR QQLQQEYEAN REEYVMAKIA EQRVEYDRRH MPRHTASLEA
VGRELTSLRD RTIEDYTARM NTLRRARAGE RANAAESRII DELRPIVERQ AELQRAAFDG
FIVDLDKFIA DHREDDLRLA SVNEQKLAAD NRVAQLTKEA EERIEGIRVE TDKMIASQRK
ALERQEAEFA AELKRRDTIV AASEERAERE ITTARLDAEA ALKRMEEQIR VNNEAHEAEI

VIERDRATQA EANSMTFVES VKQQDRSNNI ILIAVLIVGL IAGMVAGAAF F

> RXA02756 (1-891, translated) 297 residues
MTSPYGSQYP GDDNNNWNSQ FGNPSGEQNY GQPYGAPYGQ PYGQPFDQGF NAYSSPIPPE
VPQPSMQEAQ WRSFDLGTVF GQAWKGFTAT WQAWVLSALI YFAVLLVLMF AWILPMVSVL
AATSSGSDSA AIAATGGTSF FGFMLMIVLA FISFVYSLNC YRNAARVVRG EQITIQSFFK
MKGLGKALGI YILINIVIFI GMILLLIPGI IAAVVLIFAV PVAFQLRDAS IGDAFSASWK
AVSKNVGQVI LLELAIFALS FLGSAVIIGM LVTTPLTFLL YAYAFQTASG GPIMQRQ

> RXA02757 (1-546, translated) 182 residues
VVKLCLDERV STDPDFRAAL ERWYGHLIRK VSRRARNAAW DRVQDLPGVT VEDDAAKVRA
FLPSAVVDVP ADIKKLQISG TELPLDEPNP INDEYPVIYI DESLKMTLGK AAAQVGHASM
LLAAHQPFEW VEQWEAADFA LHVREIPSEE FLRLIESPGA VPVRDGGFTE VAPNTVTVVA
IP

> RXA02765 (1-759, translated) 253 residues
MSNQLPDHVR DAFQVGAGPA EQLGQAWDFG FRVGNTVFAK VTAPEVSGWS SKTRETLKPE
GVRVVRPIRS TDGRFVVAGW RASVFSTGTI SKRVDETVVA GLRLADALVD THAPEPVDNV
FNRADVQAWE EQPGRIGELL EPINRVNQVG HADMLATTLY AGTQPPAVTD LVPVLRPHGF
TAALVIVDGL LLGAVDEGIL RRFSHLPEIE QLVLRAFLFR RNLQEFSENN DPNVISNLNR
VESTLVSYVS DKI

> RXA02766 (1-393, translated) 131 residues
MTTSENFYDS VGGEETFSLI VHRFYEQVPN DDILGPMYPP DDFEGAEQRL KMFLSQYWGG
PKDYQEQRGH PRLRMRHVNY PIGVTAAERW LQLMSNALDG VDLTAEQREA IWEHMVRAAD
MLINSNPDPH A

> RXA02770 (1-1320, translated) 440 residues
GINRQVIYTI NEDATYSDGQ PVVCDDFLLS ATAGQMPELF QSHVPLTSQI ERVDCVSGSK
VATVVFKEDL GERWRYLFEQ GDLLPAHAVA SKAGMTLEEL NQALKDKDPE ALTEPARVWS
EGFQLSQFDP ELQTAFGPYK VDSVGEFGEV KLVRNEFYSG DQAVEAEITM WPKGSDLSAI
ADNGNLQIAH VVAWESEPWV NRDDPLNPYD IKEEVGVLTE QLTLASAGVF YAAEARQAFA
ACVDQEAVAA ASSSISGIDV PAVGVHSVRH QNPVVHQIGD LPAQHMAVDI NAASALAGQS
IRIGYDGPDE RKAAMVEAIR QSCEPAGITV IDASQEAVSL NDLSRTEVSE WGYEQYFEGT
LDAVLRTVDP HREYENANTI GTDAESTRRT EEQLWAEVPS IPLAAQPRVF VIDRTVGNVV
VNTDLAGIGW NMDRWSRSEE

> RXA02774 (1-471, translated) 157 residues
PCPPTQKLLY AQMREIAAEL TACDATRGLH AEVAAEWLSD AITGEPTSIE IDPHRNLFYA
LNVEHPRLHE LFAGYATRLD ELDRAPQQCE SRQYFLDYVC ADNPFGSDKP EGIIVLLADH
VLAADPVTNK PALKSEAFPT VTDYCRTHSA KPTDILI

> RXA02775 (1-225, translated) 75 residues
MTTVQVSTRT VREHRFTVPV DYAVGATISE IYAACAMAEK KANNLGLNTT KDDWARVTVT
DNAVVFIVEN VIGNT

> RXA02776 (1-342, translated) 114 residues
VLYPVEAGTV SLVDVKKAAS RAFEQWEKHN ESAGDVGDDL SLQSIVDLIE RDTFPTDDEQ
ELNNVALLIG ELLVREAGGE WTSYISKKND EDESLEIFGV FGTGGTEGLS VVGN

> RXA02777 (1-1107, translated) 369 residues
MNRPLQSQNF SITSEWANAT FNDIEDSLEG SFDIEPGQYI GRGEYFVATS GTGSKKFIKV
VLGDGIDSEL NRRIEGEILA SSLHLPSTDL ISPVVIQYVK ESSNFPGDFY IVSDFKDDTE
TLELSKASLP LTDLAKIGAF LFRLESVTVP PQNPARRAMD VLDGLSLLAN KGNIETGAQL
TKGTIQALEI INQEATNIEN ALEKVTKVGS RKFFSHGDLK FSQFLINGET GKIFLCDWEE
CGSAHFANDL CFLAGDLFYS TIRELVDTNI KNIKGSSIIQ EAYDNATLEA VSKVNAILTG
YSSERGYSLT SDEKRIISIR IGLAGLFRLY TVSAKSNELR PRELALASIG MQITLGQAPN
LVFTDSKVV

> RXA02778 (1-225, translated) 75 residues
MQVIETLDPD QRAAVLAAAI PREAKILGRK VTLRPGWGNM RVHVVIAVIF IKFLQPDLRQ

ALLTTGDAVL VEDDT

> RXA02779 (1-279, translated) 93 residues
MGEYFQVVQN IAMTLGAGES VDLVVREYIN DVEGNPTIYH GMPLRTEYRA FIDLDHCDPS
AGEPEPRLLG VTPYWHPSVM EKALRLCFKR CWC

> RXA02780 (1-327, translated) 109 residues
MSKFHTHRDD VISRITALLP QLRAQELQGQ WSVDIMKNGE DFYLIDMALM CESALSELLT
VTDEYATVEP SVINDFANQL VIDYDEHDMG FDRDFPAGVY NTRQASAIN

> RXA02781 (1-1191, translated) 397 residues
VVAALVFGFL LPTWERGLSD AALKFVFEGG PDAAREVLGT IAASTISVTG LIFSITLVVL
QLVSSQFSPR MLNGFLRNRI VQATLAMFLG TFVFSLTVIR YVWSEDEDIT GFVPRASVSV
AFLLVLGCLG LFLAFIRLIT FSMRVANAIS EIGEETMALA ARIYPVQSDD AGPVQGPGWS
PRPGDPREEI RVGNHGSLVW IDYRKLVSWS TEHQAVITVD RPVGDFLVEG QPLLRVWWDG
ELSDRDRRVL HSAIEVRTER ELHQDVAFGL RQLVDIADRA LSPGINDPAT AAQCVQEIHR
IFRYLVTVIE PSPYIADDDG RVRVVHQPQR IADMLYEVIR EIHLYGADSA MIPRLLRTMV
EDLVTAAADH SLPAVERARG ILDDETDEDR DSDTANV

> RXA02782 (1-672, translated) 224 residues
VAPALNDLAT THPKLAEQIA DPQPSGVSAA AIIPTISRGS HTQLTWQCSK NHDHQWVATV
KDRVRGTDCP TCANTGTSRK EAELIEVIRA LFPNTDVQQG ALINGRTGNQ GASPSTDVLI
PSKNLAIEFN GLYWHSELFI KDKHYHANKS ALAEQAGVQL IHVWEDDWNL RRDIVIRMIA
HKLHATHNLS AVLPTETTDS RVATTAFAVH SHCRWSLVHA LLHS

> RXA02783 (1-549, translated) 183 residues
VVSGSRAAAF LNSNHIQGAV SATKHFALCD NNDDIRALLS VRSPKNNARM YRKKGTWEIQ
RYATLGNVPG GFTRLLKFAE HTLNEHSTVL KQWISFSAAD VSDGSLYRTA GFTAEQQLAP
DYRYVGGATG WRRTPKESFQ RKRFRDDPAL LWNESWTEHE AALNNELYRI YDAGKTRWVK
NVA

> RXA02784 (1-186, translated) 62 residues
VAFAEGYYQE MAEVVCEARE EGITHEDTLH MLNDMMAMKR SGEVLNTLAD VLYANECPEY
RI

> RXA02786 (1-807, translated) 269 residues
ILRNLGQSLG SLHAATADRE EDFNILLNRM LAKYPATAEM QKNRDRLLPA AIEVGKKILV
DAGVTVPEVV EEFARVARRR LISGRHRAFT PFDLSPDNII VAERTHFLDY EVAGFRDATF
DVACVIAGFP QFVFSRPISD DEVDELIESW VQEVRGIWPN VNNEERLQAR IVTALIGWAL
SSVAFMKLGS ISGMLNLLHV TEDGNTTLDV SNLDELLIPR SAEDDELVQQ DLHDTFSALQ
RFAARGLDSR FPEVARFADD VVRLFLKND

> RXA02789 (1-546, translated) 182 residues
MKVSADTPGH DDPGPGRRLG LDVGTVRIGV AASDRDAKLA MPVETVPRET GFKGPDLADI
DRLVAIVEEY NAVEVIVGLP TDLQGNGSAS VKHAKEIAFR VRRRLTNAGK NIPVRLGDER
LTTVVATQAL RASGVSEKAG RKVIDQAAAV EILQTWLDAR TRALEPQSTD TQDFDEKGNF
PG

> RXA02793 (1-702, translated) 234 residues
MKSAAVPTLD ALGVLDRVVT KAGAFPAGYY DADLSERVTD IPTLSNKIDA SGHVLISKEV
VVAANPDIVF GETDTINRAS MASSNIPVVE EPAFCGSIDG DVSFDDVWSQ ISTYGTIFDR
STEADAYIAT LKERVSEVSS RVTDSGKTVA VLYPTIGGGV TYAYGRGSMA NPLVAEAGLT
NVFADQSERV FEVTAEELIS ETPTHHRFTQ RRFPFRHRRR GGQSPRVQRT HCSE

> RXA02796 (1-549, translated) 183 residues
MRLFASITPP IEVTEHLINA LRPYKDDLRW SDPDNWHITL AFYGELPDGA VEDLIEHLTS
AARINEEFTI RIKGAGSFNR KNLWMGVGGD TKDLRRLMAD CLIDPEERRR QRAHLTVAKP
TQRQRSRDWD PVIPDLVHAL SIYEGPEWPV DEIELVSSEP GKGRSGGPLY TTVATIALSS
ALV

> RXA02798 (1-1425, translated) 475 residues

MRSVLDYWIM TLAPSTNAVS QQTRRNPSQA PRLLHRLHFF AGIICAPLIF IAALTGLVYA
FSPTIESISN QEMLTVSKSA SDTALPVREQ VSIAQELHPD LDLSGVRLGD DSSTTRVLFA
DETLAESTVR AVFVDPYTGE ITGDTTQYGS SAALPFRQWV SQGHRMLWLG EPGRIYSELA
ASWLGVLAVG GFALLWLRNK KPGRLRKMVR TGGRGRVKTY RRHAALGTVA GLGFVFLTFT
GLTWSTYAGS NITDLRTQLN WTQPSVNASL TAAPQVDMHD EHAGHHMHME SATSGSGSID
LVAATAISEL RTPLTITPPA QDGLAWTATE NRDAYRFTTD TIAVDGDTGM LTNRLNSTDW
PLAAQASAWL IQLHMGTLFG LPNQVVLGLL AASIIVMIGL GYWMLWQHRP REGWPSAPKR
AGFEKPTWGT IALGVVVIAY GLLAPLFAVS LLVFIGLSLG VRFISRMSGR ADTSN

> RXA02799 (1-273, translated) 91 residues
VARNIEDIQR DIERTRRQLA STLDELADRS KPSNLVDDAK NQATAKLQES NVQKVLLGVA
AVVVGAVVFS VVRGRKKAND LKEIQRLLSE R

> RXA02812 (1-567, translated) 189 residues
ASGTDASTIT LDQVALPVAT NSGASAAVAL ALAETPEAAA AALNRDADVT ATGAADSPAF
ATVEGAELPE GYTFEAVDSA EVPVWAVAIN AGNGISEDQA RAASDFSSFS FDTGNADNSA
LESVLTQASS ESAAETTEAQ PSETPVEPAA ASPSDTIINL DTSSNMDRVV DGSQETYHTV
TSRTLANLA

> RXA02815 (1-552, translated) 184 residues
WLRSTKEFED QPVIPAFEVI ATVASEFAGD DGNYSNEFPV EDLVGYVDAI TEAGGYAVLD
LQPGRANFLD QAKMYEELLK RPNVGLALDP EWKIGPDEQP MTRVGSADAA EINEVSQWLA
DLTAENDLPQ KAFVLHQFQL EMLTNRDQIN TDHLELAVVL HADGHGNAGD KYATWNMLRE
GLSP

> RXA02817 (1-399, translated) 133 residues
MILGVPIQYL LYSLWNWIVD TGFDVAIILV LAFLIPRIGR LAMRIIKRRV ESAADADTTK
NQLAFAGVGV YIAQIVAFFM LAVSAMQAFG FSLAGAAIPA TIASAAIGLG AQSIVADFLA
GFFILTEKQF GVG

> RXA02818 (1-606, translated) 202 residues
SYSRKFLTQV WIRDNVGDYK GLTDTAFRKK LQRDLAYLRR VGVPIEQFTV TSGIAEGQQA
YRLAQDSYKL PEVEFTPDEA AVLGMAGEMG HNQELGAFAR SGWTKLAAGG AQRDLSTSTA
LTNAGDLGSL SAKTLDAIIK ARQLGKQISF EYRRAPKDAP SLRHMDPWGL VPERDRIYLV
GFDLDRQEAR TFRITRVRNI KL

> RXA02823 (1-270, translated) 90 residues
MTVRNPDREA IRHGKITTEA LRERPAYPTW AMKLTMAITG LMFGGFVLVH MIGNLKIFMP
DYAADSAHPG EAQVDVYGEF LREIGSPILP

> RXA02824 (1-528, translated) 176 residues
FYETGEALDP TGDSLTISST TTAPSTSTTS TSASTSGGTA DCSSGALGVV TTGTNDGMLG
TIQEVNNTFA IWNNLIVNTE RMFCNIDTLK ARFDTDDSSD SATSATSGTT ASTGTTAATT
AGTTGTTGTA STASGTSGTS GTSGTAATVA GTTPTDNGVC TASGSLGVTQ ASAQWG

> RXA02825 (1-384, translated) 128 residues
NVSATEASGS ASVSLSQSGS QAFADFYTPG TQLDPISFSA TLGGDASCAT GSTSTTGAAA
TANTDNTEGV AGEESTTPAN QNSQFQIRQA AADSTGLDTT TTMLLILAAF VVAGGSMTRF
TVGNPTGK

> RXA02827 (1-423, translated) 141 residues
MYEQQKILNE VSEKRLQAIK DFTELGSGFK IAMRDLSIRG AGNLLGAQQH GFIDAVGFDM
YSQMLSEAVX RKQGKNSQVE KXXVEIDXGV DAYLPETYVA DXRQKIEIYK RIRELDSQEM
LDELEDDLLD RFGEXPEEVA H

> RXA02838 (1-462, translated) 154 residues
TVPLGDGQGR YIAKIPSTAF VGVSENKFAN LALAEAIGME VPARELVGRA QFEGVPPEFE
AMTDGLVLLV RRFDRAGDGV RVHMEDFAQV FGLYPARKYD GAASHDIAAV LGSAVSIAAG
LEFVRRLALS VVMGNGDMHL KNWSLIYHGR GDVP

> RXA02840 (1-150, translated) 50 residues

MTVISGALNV LLPDATDWQV YEAGSVFNVP GHSEFHLQVA EPTSYLCRYL

> RXA02841 (1-279, translated) 93 residues
MFAAFKSNLP TIKKLVYEVI NGVDAALNEL ERHVTNESVR ARELPNVQYK ATAGRNFAIS
KLVQNLRRIN KAQNNPRGVP THATVILLKG DGS

> RXA02842 (1-342, translated) 114 residues
DAGFVYFGEI DDAGHIFGLA GDEYRGGIRR VDTHVKKVLS EVSRRSDELG EDWLVVITTD
HGHLDEGGHG GTTDRERESW IITWSPHREL PQWPEEIAPX ELAELMLVER RTLR

> RXA02845 (1-615, translated) 205 residues
EDHTSMLTHF SAAVGMHDRD PARFPGQGDG SYPDLFWLYK NALNLVISSV LFTREQMDNM
LDQMDEHFTR AGIPRIAINI ERRDDALMNG SLERALELQE LIDASQHDDP FDDCPTCQIA
GKAALAMAAD DYDETQNLVS QIISYGSIGC VMEPETTLAA FMLRVLKSGD ADYARYLQDV
SAKANPEFQS LDSVGRHLEF LGITG

> RXA02846 (1-573, translated) 191 residues
VNGLSIINAV NNAWSVRKRT DWAKFRILAG ALVLGSVPAV AVVYFLNGPW LLIFVGAMVL
LALGVSLFPT EKFALKQEAK LPMVIFGMIG GFMSTVAGIA GPSLTVYARL SRWDYRDFVA
TLHPVLLVAN TVSFLLKVIL IGGLDFGGAP AWLWIGAVAM IFVGAWLGEI VNAKVSTPMA
KRIATLLAAA G

> RXA02847 (1-594, translated) 198 residues
MAVQGQFYLF AILLSMAIIL IRRYRPEYSA VRLATPVLAV LTSVSFFSAI LWHFIDQSVN
YYSTFTRFWE LGLGALLVLH APRILISAKT KSILAAVGLF MVLSTGFFMD GAETFPGFPA
LYPILGACLV ILGDGKISVF LSRKWMLWLG DIAYPLYLWH WPLLIIFTAL FNQEEPSIWL
GIAVIMLSLG LAQLTNKY

> RXA02848 (1-399, translated) 133 residues
MQIVLASQSP SRRRILNSAG VEPLIHPADV DEDALLHSLN GSAPEEIVRQ LALAKAQVVA
PSYPGDVVIG GDSMLLIDAT LQGKPHTREA TIERWKQQRG NKATLITGHA IIFGDEVIVE
SSSTNIHFAE ASD

> RXA02849 (1-282, translated) 94 residues
SPYPVMISTS ADASNVTVRI MGVDTTSVES INNGRWSTTQ PNTVRVSGSD CVPSTGAPGF
TTSDTRIISD LSGNEITREP VTTVYDPSPN VVCS

> RXA02856 (1-249, translated) 83 residues
LPHAKELAHE LCLLPTPAVP ALPTDSGAQF DIHQALSASL ATYARNLTLL SHTAENLGNR
ALTGLAEIED TDDQLAHALE RLT

> RXA02858 (1-1026, translated) 342 residues
PEWKKFNSGD AARVVPDANA ELDIIGAPAL LADRPSYANV KTLSRIFAVM RSLGHVTAAS
PVTVFFSSHS VLSNVDRGSE HYSGPNGLGE WTSVGRAVAT NWNGVVDALD EAITVKEVNS
LFTEDAATRI QEAQAAVQAA REAEEQIAKE EAEKVDPYDN SPWAAAGIDP IKVSIDGRTI
YTLRTYLGGQ PVFLGKFGEI FTFNSQKSLL RWLVEHDDHD LARASTWSDL MLGINAGETE
LLVHSDNVYS FNGLVKDINT SVDAVDTQQM ARAYELMADT ADWADDDSMN SYFLANPRMQ
DYISYMLGGS DTSGYVPHAP FNDHSESWRE LEEMLIKRFS KF

> RXA02862 (1-636, translated) 212 residues
MNTNLPNLYT AFDLDRSESS EALGVSLSAR DLRLEQMGIA QDDPRRAQTV QAFAVLADPA
KRATYDAQLE AGVPLTWAQI QHLGNFGTLP STPTAQPFAA PQPEPSPEPQ QQWNSGQNYA
YGNPTMDYQT QQSYNPMQDQ TQASMYAQPF ANTPAPMYNS NQVFNRPTAG TRLWMAILDS
IFAGIAGGIV SGIFGFGSEF LTSVIMILVL IV

> RXA02867 (1-606, translated) 202 residues
MSATNPDALD VQHVYPIKTK KTPLAVIFNI ISGGLIGMAE LVPGISGGTV ALVLGIYERA
LHNGDLLIDL IKVLIKDRSK VKEAAAKIDW WFLGAIGVGM VVMVFSMSSI LHTVVEDYPE
ITRGLFLGMV AVSILVPLGM MDMRDAKKRL AIVIPLFIIC AMLGFFGTSF TSAPRTDPSL
IFVFICAAIA VCALVLPGVQ DH

> RXA02874 (1-480, translated) 160 residues
TELNRDTHHL WVVLTTDSDD FDADSFTTEV IRITGYSRHE VNNGLNAMAA MTNLPHLRAI
QERYYFLSIR YLASIMIAVA KADPTLWEEL DLRITDALTP VTAGEVMIQS STLSKXHRXP
GSKNSTPNPH QSPHRKRTMF TSTPLMRRPM SASKSAAPTA

> RXA02876 (1-663, translated) 221 residues
MTSDKDTEQL EAAGTEILMP RRRPAQQRSR ERFNRILTAA RSVLVDLGFE SFTFDEVAKR
AEVPIGTLYQ FFANKYVLIC ELDRVDTAEA VAELKKFSDQ VPALQWPDIL DEFIEHLARL
WRDDPSRRAV WHAIQSTPAT RATAAATEKE MLEIIAEVMR PLARGAGYEE RMSLAGLLVH
TVSSLLNYAV RDVNSSEEDF DSIVEEIKRM LISYLFSVAT G

> RXA02881 (1-666, translated) 222 residues
VKKKLMLPLI VAALGLSACS SEPAAAPLEA EPLHNLLIDG SESGLDNATE GNDTSLSGQP
INLTVVNGAL DIDGSCGKAL QAVEDVNLDS VASASRALAS GDKQVGIAMY STAEDNDISP
MDLYADIANA CEDPVVDSSD TTYTFGKLDD APDGAVGFTL DIEVTPDNQG STVMMIQELG
NHHIIVAGLE TTPEETATVF EAQRTKLEEG LQLKQNWQLG WV

> RXA02884 (1-462, translated) 154 residues
MLLTILWAIG ITAEGMTGAL AAGRQKMDLF GVSVIACVTA IGGGSIRDML LGHYPLVWVE
KPLYLLLIIG AAILTVSISF LMEHFRVLFL VLDAVGLSAF AVIGTQIALE MGYGFIIAVV
ASVLTGVFGG VMRDLLCDRI PLVFQKELYA SIAF

> RXA02885 (1-1536, translated) 512 residues
RGKGFHFTST EFAGSYSLVT NGLNDVAGEY VGVMRGDVNN SAVLFDVDRW SGHVVCADSS
INTSPLLKRP RVVDMWGSKI SQAALLNNRR VVHLVLNGAK LDEMGPKLES MTAHVDMTSG
DLNMFELFGK QEDELSLYST HMDKIVFMTE QALGDKTSEL ALLRGKLKEI ITAFYVDMKM
WALNAGENRD KLRLVGVPHE QIPLLSVFVS YLDQEYERQK YEGTKDPEMF RAISVLRLTY
KDLLDTHGDL FNQHTADGID SVNSARRVIY DFSGVLRRGA GVAMAQLVNV IGFAVETLGQ
GDVVIIHGAD GIVDVDVQDY LANQFAYMAE RGGRVAYLYS SMDAMLGTVG FNQFQRAAYT
ILGPMNVDSV DTYQSLINSQ IPMDLARLVT TQNSGASYLR RGSTNVVFET NLALGVNPYM
EQRRKIEAQR GQRRSKRDKH YGGGTTMVGT ADLDVVAIQA KAEHREERFD EKSARKMKEL
DDVEAKELAL KTGPKNLDDA LAQVEKKRLA KR

> RXA02888 (1-429, translated) 143 residues
MYSDKLILLF LSEQDSSYEC CVGLLDGSDG RDYIEKLLKG RKLKNHFLEW EDINKADVAR
EEIYKGQLVH LVFVTALSTP GEISFVFPGQ SLMSATLEED FAALVLEEER TSFRPELSHL
WSLPVGWVAP GLEGFVERNS EAA

> RXA02892 (1-504, translated) 168 residues
MEGPEAFTVA AIAAAAGVSP RTFHNYFPSR EDALVQFVVI RVQELTDQLY EFPTSVPPRD
AIEQLVINQL RDGDDAMDSF SAMFRIGEIL ENLDPIKCVI DKERLIAPLL EFMVERDKDL
DKFDAATLIH LHAAAIATSL HTFYQASEPR DIEDGVALIR RACAWIKK

> RXA02898 (1-1626, translated) 542 residues
LVVDSSGRYN VTITGLTTTE TDSATALNLQ MSEAGYLERY TDGATVPSVM LSAADGTTPQ
ELVDALAAEL GSNFDVETGE ALVEQATGMI TQALSFVQYF LVAFGLIALL VGTFIIANTF
SMIVAQRMRE FALLRALGAA PGQITRSVVL EATIVGLFGS ALGVLGGMGL VAIISAVLNN
LGMPMGSSVG LTPSAVVTAL VLGTVVTIVS AWAPARRAGE VKPVEAMRNM ETTTMRSMMG
RTITGGIVLA LGIIFAIAGA MMTDSSTATR SILVGIGALF VIVGTFLFSP ALSMPVVGGL
GKVIGAPFGS VGSLAATNSK RNPRRTATTA FALTLGIALV TAIGMLSATM KDAVSDMMAE
QYTADYILQG PTNGSITMPK ESVNDVRDAE GVADVVLVSM NSASVNGQAS YSQLGQSVTF
VADGDLSKVI STESIDGSLD LSNPGVVTNQ TFADENGWAV GDTLQLESMG QTIGDIELIG
TFTGNDAIGN MIISESSLAD TPAADTAVPQ MMLVVGEEGF DKEQLRTNLE DAVADYIVIS
VK

> RXA02899 (1-480, translated) 160 residues
MNSGSTMRRI SLRNIGAHKV RLFLTVLAVV LGTSFVSGAM MFTNALSSTF DEAIASSFDG
VDVVVSPNGA SEVQGVPVET VESLREDSRI NHLNINGSQT VVLADADSKA IQTTGGSSLS
IYYSADDAVA QAPELAEGEA PTGTEEVLAS KAGAEANGLE

> RXA02905 (1-474, translated) 158 residues

MDSVNVLLIG IIVAIAALLP RKGKYGPIAT LLVAGDWLGV FLLSILVMLV FDGLEDLVQG
FLDSIWFGVI LLVTGIVSFV ATLVSKTDST RKLDGFLAPV KTPSWKTVGA GLILGIVQSA
TSVPFYAGLG YLSVGNFSPE IRYGGLVVYA TLALSLPI

>RXN00022 TRANSLATE of: rxn00022.seq check: 7277 from: 1 to: 1701
MSAPTIYPGTKTSIDPITMDDARIIFFDIESLHNIFTVATYDSLSHHVDVFYLLDHTTSP
QITVLPHSMDYFDQTRSDAVMAAIIEQNPAFAEIKGSPITTADVALHNLGDTNANRRWQS
NVLLARLLGGISVRGEVPEHQSHNHLAKQFAEATLVTRDFDVNYDPTSAHPFTAGFNSIN
YDTTLLSLYFAMLTSNIGSTPTYFPVITAQELRAHNDKLFSPEFIKNMPKYLWDRDSGAG
LRAASGFRNAMLKSGRHIDIQRLNEKQLFVGLKRLLGLLGHQILESDRLSGDDAHVDTNE
DVLDLIAYNVSDVVGTRLLAEDPVYSGSFDLRAGLLSTYPETVFDHDGTFRQPSTQMRKD
RLTINTSSAQFAARILAPYRPLRDVPDAIGDMPVVSYLYPDAAVAEATGQKQVNVLDESK
KFFYDNITDPEARAAFDEVFAFYADIEGRNFNSHNEAIDTQINQLRAYLNQVVAFDAAGY
ALYDVRTRFEQIFPKDRSYINDATDMTPRAVSSFDDLVALCDDIRGVLDRGLEISSPNHH
EMVDAMRKQLHYIQAFYRAWDPSTPLQ

>RXN00027 TRANSLATE of: rxn00027.seq check: 3923 from: 1 to: 366
VDERSRFARSVFPDGEEPDPRFTLANERTFLAWTRTSLAFLAGGIAFEAFQISGLSDTVR
TTIAVFIIAVGMIIAAGAAVRWMNVERAMRKQKPLPVPAIIPFLSIAALVASAAVLVLII
VQ

>RXN00028 TRANSLATE of: rxn00028.seq check: 5847 from: 1 to: 1947
MTLTASSLEAGKMSFSGGYIVGETMIFLVDPDEVEIRRSPNSLHVLRNGSDILRRNEHHC
WVFENFNKPIDPPVRLGPRDIICPSALAWVLQQHSISRSLSHHLHADKITAGEIAGRPTW
ILREEPTSGGQDPSRLVSLEIDQEHGVILAVETGQERLEATEISFPDTLPNPSWDGAWEP
FHYPDSTPHTAPDVAEIPGYIQSLPPQSEDPRRLRVFVNEIALEGDFPDYRQGQSVRLTL
GISSSPVPLEGMTTRRRGRVRNLGEEASPGDDGMPQWPILLTGDGWTALAYTPIPKRGDA
EIQGWFYYSAYGIVDVPTDLRVERIFAGIGTSGTNERLWQEIDNTSSAYHSEDWWIRDVV
LDVTLDGAVPPPLRRDVFTAVDPIVAGDKLWLCDVHFPVARCWETTTGRYLGQTLVPAPL
RDRSYVLELHSDQQLGAVAASGKSGWILTPGQAVATKAPDWTPPTRATDLPQVPSPWEIV
AVRGQGLFELQVETSRRTALGRVNATGGVDIGELPPNGYTISSVVQIGDEYIVGRWVEEY
RLNSKLEVISTKELDISASGWKSKGTVAYLSEDTHICFFDQVSGAELPSLGIAEGHQGEV
MSATSSESIVLIYRRNPNNSMSIVPTSVATYDNGTWTTMPLQEAPAELS

>RXN00033 TRANSLATE of: rxn00033.seq check: 3319 from: 1 to: 1335
MSVQQSGLLERLGIPRPLIFGFIGLTIFMIGDGVETNILEPFLSSEHGFSVSLAGTLVTV
YGVAVAIAAFFAAALSDLWGPRKVMILGASIWIVFELIFLTVALTTDHTWLIFLAYGLRG
FGYPFFAYGFLVWITATASPKQLGTGVGWFYVAFSAGLPTLGALVATISMQYVNLTFYET
LWVSLVLVVIGSLIALLGVKERRGRHPLVANPDDVKQTLGQGFKLLRNDRRARFVTYIRT
INSIPTYAMAVFFPSFFTDDLKWQLSWFLILTTVIYAVNLPFNPFFGSFGDRHGWARTVF
WGGSIGGAVTLALVYFIPMFGVQAGMSNGVVFGITIAAGALFGVSLAGFVPLSAIAVSLD
PKHPGAAMATYNLGVGGAVAVGPLLVAVFHPLIGPTGLILVMIALYLLSGWMTLQLRGTQ
PGFDGVPALAEDAHIEDLADVNANA

>RXN00056 TRANSLATE of: rxn00056.seq check: 471 from: 1 to: 750
LLNRVSRIAGASAITLCIGLTTILSPTSTAQSLEQITPLPESAIDLNAEIHVNTSDISAE
QILGAQDEITTMYDSHDPYEYFDTLTDIEQRSIIAALKRDPSSLQQRQETRLAAQSDPYK
IYISGLEMLSCINLVDVVSCGIANQAATKANNEAVARYPGDSLRNGKGDAFRHCSWNALM
TIRIGSNGAERIATNHETIGDGPADENAMDLFNNAQGRQIGAGFINSKDETSALAICALW
TNLGRLKTLK

>RXN00067 TRANSLATE of: rxn00067.seq check: 5053 from: 1 to: 486
MVDAQRPKAGIFGSHTEETWVWLGNELFDESGEVIADVRSDVLYVDRERLLIESTPGTMR
FRCRATLSGGEVYTMTQNSFTVGDLTAVCGRRTYSLKRVSPWRKERLITNNGVEVARLRP
MTSGKVEFIVGTAGSEALPFVDAVFLSWACVLVDSAVRRPKI

>RXN00077 TRANSLATE of: rxn00077.seq check: 3953 from: 1 to: 1362
MNDENIQSSNYQPFPSFDDWKQIEVSLLDVIESSRHFSDLKDSTDRSALDAALERAKRAA
AVDTNAIEGIFQTDRGFTHTVATQVGAWEQQMAMKGKHVKPAFDDTLEGFEYVLDAVTGR
TPISQQWIRNLHAVILRSQESHEVFTAVGVQNQALQKGEYKTQPNSPQRSDGSVHAYAPV

EDTPAEMARFISELESKEFLAAEKVIQAAYAHYAFVCIHPFADGNGRVARALASVFLYKD
PGVPLVIYQDQRRDYIHALEAADKNNPLLLIRFFAERVTDTINSIIVDLTTPIAGKSGSA
KLSDALRPTRVLPELHDAAHRLQESLFTEIRSRLDEEGKRNGLEFLLQRIFIGSPFNLPE
GYNAFPDSYCLTLAFNSNSPKQIFHPLSIVIAARDGKRASSDLVAATSIGYNFHAYGREV
EPVVTESFRERVKIYADGIVDHFLTELAKKFQQN

>RXN00080 TRANSLATE of: rxn00080.seq check: 4040 from: 1 to: 1530
MDILSLLMEGFAGALTPMNLLWVIVGCLLGTAVGVMPGLGSSMAVALLLPMTFALDPTAA
FIMFSGVYFGGLFGDSTMAILMNTPGQASAIASTFEGHRMALNGRAPQALATAAIGAFIG
GIVSSFIVVFLAPTLAELSTAFGPAEYFALALFAFVATSSVVSDSVFKGLASLIFGLGIA
TIGIDSVTGIERFTLGAPQLFDGISLVTVTVAILALGEVFYIAARARRDKANLETRSAGR
PWLTGTEFKEAAPAWARGTIIGLPFGVIPVGGSEVPTFLAYSTERALDKRRKDPQFGDKG
AIRGLAAPEAAGNATTGMAMGALLALGLPVSATAAIMLAAFRQYGIQPGPLLFDRNPELV
WALLASFFIAMIVLLFINLPFAQLWAKLLLIPNHYLYSGIALFCGLGIYATSGAVFDLLM
LLGIGVVALIMRRYGYPLAPLMIGMVLGPLAETSLRDALLSSVGDFSILVSSPITWSLYA
VLAIFIAVSVITAIRGRRKHLTSQLETIDA

>RXN00087 TRANSLATE of: rxn00087.seq check: 6949 from: 1 to: 528
MIGGIIGLILSVIIMAEKLAILEDPGHITSCDFNAVLACGDVMRSGQANAFGIPNPLIGI
AGFAAVAIIGAGILAGGGFRGWFWFGAQAGLTFAMMFCHWLAYQSMSVIRALCPYCMGVW
TVSIIMFVLVTAWNVKTFSGSDSTFVNALYKYKWVIAIVWLLLIAAAAVWSFRYMF

>RXN00096 TRANSLATE of: rxn00096.seq check: 1688 from: 1 to: 303
MTNAGDNFEIRMPSGTDDPLSDAEIQKYREEINRLDREILDAVKRRTKISQTIGKTRMSS
GGTRLVHTREVAIINQFREEIGEEGPALAGILLRMGRGKLG

>RXN00097 TRANSLATE of: rxn00097.seq check: 3726 from: 1 to: 1176
MEVPSLFTNFFAVNNPDSPPARQKTKLRELEHRFWQEHLPGDDDDHSTAISSLAIVTGLT
KAQVSRISIAFATLADLPELKALQQKLYHLDLSRLITISNELAGINPDNLAGADAILTEY
LTATSPNQILPSPASIGRKIKEIRDLLDDARATGSRGTQDDSSFGVTFSPDGTAEIGASV
DAVDGHIINDAVTQHAKKNDLTYGEAFSDILRNNIQVKVVLNLYTAKDLANAPVWASGIG
WLDAKTGTFWSEKANKEQDMDAAAKISTDKHDPPPALRDALIGRDGTCRFPGCSVPALKT
QADHRIPYEEGGETCLGGIGCLCQHHHNMKTDGRVTYLLDPFSGIIVWLMGDGTWAVSEP
NGPLNPKNARWAQTVAQHRARHHKRWVKEDAK

>RXN00114 TRANSLATE of: rxn00114.seq check: 4118 from: 1 to: 489
MKLLKFAAAGTFALALAGCTQTESLVATIESATSAAQASGNDVEGDQTSAFELSVGECFN
DTYEEEISEVPIVDCAEPHDNEIYYLYDIEGDDFPTDITTTGYEGCLPTFEGFVGAPYET
SIYEVYPMTPTFGSWTNGDREVVCSVYLATGEQMTGTAAGTAQ

>RXN00120 TRANSLATE of: rxn00120.seq check: 1348 from: 1 to: 840
MLIGMSNQTVNQAVSSGVKASPHRFNRFEIKYLITEQDVPALREQLATRMSTDPLSPPGG
YRVESLYFDSADLRCYTEKIEGLKFRRKLRIRTYGDGVLTPESTVSVEIKQRVNKVTQKR
RLDLPFIYALALGDSTGAAVGEQVDVEKLLEISPENQHALIHEMASFAKNYRLRPIATTK
YHREAFVGADAEESSRVTIDHGVSGRDRDFLLGQDLEDRPTVAQGLAVVEIKCDERVPFW
LTDMTAQLEMSVIRMSKYCETIEAFHNRPASAFGAVDPIF

>RXN00128 TRANSLATE of: rxn00128.seq check: 1749 from: 1 to: 1704
VSKISTKLKALTAVLSVTTLVAGCSTLPQNTDPQVLRSFSGSQSTQEIAGPTPNQDPDLL
IRGFFSAGAYPTQQYEAAKAYLTEGTRSTWNPAASTRILDRIDLNTLPGSTNAERTIAIR
GTQVGTLLSGGVYQPENAEFEAEITMRREDGEWRIDALPDGILLERNDLRNHYTPHDVYF
FDPSGQVLVGDRRWLFNESQSMSTVLMALLVNGPSPAISPGVVNQLSTDASFVGFNDGEY
QFTGLGNLDDDARLRFAAQAVWTLAHADVAGPYTLVADGAPLLSEFPTLTTDDLAEYNPE
AYTNTVSTLFALQDGSLSRVSSGNVSPLQGIWSGGDIDSAAISSSANVVAAVRHENNEAV
LTVGSMEGVTSDALRSETITRPTFEYASSGLWAVVDGETPVRVARSATTGELVQTEAEIV
LPRDVTGPISEFQLSRTGVRAAMIIEGKVYVGVVTRPGPGERRVTNITEVAPSLGEAALS
INWRPDGILLVGTSIPETPLWRVEQDGSAISSMPSGNLSAPVVAVASSATTVYVTDSHAM
LQLPTADNDIWREVPGLLGTRAAPVVAY

>RXN00154 TRANSLATE of: rxn00154.seq check: 3981 from: 1 to: 843
MSFSDPYAGNIFGGHSRNKQPEYPDVPAKPGLVVEVRGDGFVGAVTGFERTYDGDFVRLE

DRRGRDALYKLRKGAFMIDGQIVNLTRFVEKQAPRKSNSGSRRVENAQAKVAAPSRIWVE
GIHDAAIVEKVWGHDLRVEGVVVEYLEGLDNLEERLAEFQPGPGRRIGVLADHLVEGSKE
TRMTKSLPADVAVTGHPYIDIWAAVKPERLGLKAWPEVPYGEDWKTGICKRVGWSDPKEG
WHRVYNAVNSFRDLDYTLIGAVERLVDFVTNLDLSKEDVLA

>RXN00162 TRANSLATE of: rxn00162.seq check: 4822 from: 1 to: 354
VSTTTPIHPERKKRVRQALTMFSIAAWVTGVFLLALVAEMIMKYIIGMDLPEWARFVPIA
HGWVYIVFLMTTLNLGLKARWNPTRWVTTAIAGVVPLLSFFVEHNRRKEVTQTFQLNS

>RXN00167 TRANSLATE of: rxn00167.seq check: 5803 from: 1 to: 498
MYLLNPPVTEPEILTVNEIPTVVAVFDNHPMNDMPAAFDQTYQVLFPTLGAKGIAPIGPG
FALYTSEPTDTVSFEVGIPVSQPLEGDVSAASGIVLKNSVVPAGKIARISHIGSFDGLSQ
AWGSFVEALESAGHEIDMPCWEVYVTEPSPDMDPATLQTDLYVLLK

>RXN00171 TRANSLATE of: rxn00171.seq check: 2615 from: 1 to: 258
KDQQKQIHNLAAEVKRLRERDDARDQQLGVLNEAMFSLLGDGLDRFRESGDEASFNAALN
YQAVVAPEMFKTVYGVDPSTGEPIPT

>RXN00194 TRANSLATE of: rxn00194.seq check: 2468 from: 1 to: 441
VAGSSHTIEPEIYRGVSTLDEPSAAWGWHGLKRNTIQLAGWISVLFMLGYNFGNHKGHVE
TIWLLVITALLVIGLLIHLFEPKLFQVRTITSRNKPVGHVEPDWTYDQATLTGTWGNLTD
SQLRSVNIEPSRVAHLRAADSAKELDN

>RXN00197 TRANSLATE of: rxn00197.seq check: 7429 from: 1 to: 1212
VAAYLLGVVLFFLGIAVTIALHEWGHFITARIFGMKVRRFFIGFGPTVFAKRRGETVYGL
KAIPVGGFCDIAGMTAQDELDPEDLPRAMYLKPWWQRIIVLSGGVIMNLIVGFLVLYGVA
VSSGIPNPDVDTTATVDTVQCVPETQISATELSSCVGSGPAGDAGIEHGDKILAVNGQEM
ASFTAIRDAILELPGETATLTIEREGTLFDVDLQVASVTRLASDGSEITVGAVGMSSLPP
TDVYKKYGPIEGVGATARFTGDMISATWDGLKAFPAKIPGVVASIFGAERDVESPMSVVG
AVRIGGEFVERSMWDMFMMMLASLNFFLALFNLVPLPPLDGGHIAVVIYEKIRDFFRKLR
GKPAGGPADYTKLMPVTVAVAALLMTVGGLVIVADVVNPIRLFG

>RXN00216 TRANSLATE of: rxn00216.seq check: 8301 from: 1 to: 990
LGAYGLGELPGKSAAEAADIIQGETGDLLHIPQLPARGLGADLIGRTVGLLDMINVDRGA
RSWVMSTRPSRLTHLTGDFLDMDLDACEETWGTGVDKLKIQVAGPWTLGARIELANGHRV
LSDRGAMRDLTQALIAGIDAHARKVAGRFRAEVQVQIDEPELKSLIDGSLPGTSTFDIIP
AVNVADASERLQQVFSSIEGPTYLNLTGQIPTWDVARGAGADTVQISMDQVRGNEHLDGF
GETITSGIRLGLGITTGKDVVDELLERPRQKAVEVARFFDRLGVGRNYLVDAVDIHPGED
LVQGTITEAAQAYRMARVMSEMLSKDSCDL

>RXN00222 TRANSLATE of: rxn00222.seq check: 4411 from: 1 to: 1146
MTPTADIWFKDTLAAHFTRDGDQTTFSYTADYAGPPIATSLPINSEPVITRSGAIPPFFA
GLLPEGRRLSSLRRNIKASADDELSLLLAVGADPVGAVAIFPHGENTQPAPPTVDFDDEL
DFSAALTESGIADPVALAGVQDKASARTIAVPVASDAILKLSPPEYPYLVENEAACYQLL
TKNKLRIELSKVEVLHDKHGRSGLLVHRFDRTPKGKIPVEDAGQVLGIWPADKYLVSYED
IAQALTKVCASPILAMRNLAFQIAVAWLSGNGDLHAKNISIINKGRGFEISPIYDIPATA
VYGDTTMALEIQGSKKDLSQKKFLKFCTSIGLPEKTAMSVANAALLATENAAETILASGN
FDTRMNRDLARVLKHRRSAWGA

>RXN00232 TRANSLATE of: rxn00232.seq check: 1106 from: 1 to: 510
MNDRAHQRIGDIERSQALDRLGSYFADGYLDIDEFDTRTGAAAIARTAGEIDVLFTDLPE
QQASTAVTPVQDDTEKELDLVLQRGKKLKQIDSAIWAVVMVSFFLGLFVFNVPYFWVVFI
LGGAASAGARFLLKVDDADEKLFEELHSKEQSEREARLRIAAQRRRELEQ

>RXN00236 TRANSLATE of: rxn00236.seq check: 116 from: 1 to: 726
MVISFVGWALSFMDGTAPIRQLQQIPEDVPPARGVEVPQIDTEADGRTSNHLRFWAEPIA
QDTGVSAQAIAAYGNAELIASTAWPGCNLGWNTLAGIGQVETRHGTYNGKMFGGSSLDEN
GVATPPIIGVPLDGSPGFAEIPDTDGGELDGDTEYDRAVGPMQFIPETWRLMGLDANGDG
VADPNQIDDAALSAANLLCSNDRDLSTPEGWTAAVHSYNMSNQYLMDVRDAAASYALRQP
AI

>RXN00242 TRANSLATE of: rxn00242.seq check: 7148 from: 1 to: 1278
VNEWRTVSLVDSTALTVIISVAVFTSAVALLGVVKKRSRWRVLGALISSAVLTSGAWVVI
EKLWKPFPDPNPWTIYLSAGLAVFPLLSILFRTGRTRILMATLTVIALVNTAAVINVIYQ
PYPTLGSFNPVPTAVSMSYADFESQTTAPTMDDREVGALVQVPLAGTTDDSTSGFDARDA
YAYIPPAYWDNPSLQLPVLVLMPGNPGQPDQWFSSGNADQTADNFQATHDGISPIVISVD
GTGSFSGNPACVDSDAQSVMTYLSHDVPMLIKQKFRVNQDQRTWTIGGLSYGGTCALQIM
TNHPEAYGSFLDFSGQEEPTLGTRQQTVDQLFGGDEDAFKAVNPEDLLNQAISSGAHTYS
GISGRFIAGSNDKSAVSALSHLDNLSNQAGMSTTFDTVAGGHSFQVWRVALANTFDWVAK
RGGLQV

>RXN00247 TRANSLATE of: rxn00247.seq check: 2491 from: 1 to: 927
MQTLIFIAIAGVAAQLVDGGLGMGFGVTSTTILIMLAGLGPAQASAVVHTAEVGTTLVSG
LSHWKFGNVDWKVVVRLGIPGAIGAFAGATFLSNISTEAAAPITSLILALIGMNLVWRFS
KGRIRRDYSDRPHSRGFLGGLGIVGGFVDASGGGGWGPVTTSTLLSLGRTEPRKVVGTVN
TAEFLVSLAATLGFVVGLWDDLVANLSAVLALLIGGAIAAPIGAWMISRVNATVLGGFVG
TLIVTLNLPKVLNVVGLDFIPTGLIQVTVLLIGLPLTYLGFRRYRKNLLNETISSEVVSE
PKGQKIKST

>RXN00256 TRANSLATE of: rxn00256.seq check: 519 from: 1 to: 771
MFMSLKTRRIFGALAVSLSISFSAIATPAASAQELVVSTSAVNEFGVVTSDITAEQILQA
QDLIAEMKQSEDIYEYFGALSDVEQRSIIAAVKENPYLIENESPRMRVQSETPDEETPDK
KKPSKTYKLYMSILEMMSCINLVDVPSCAQALKAANIAEREAKARYPDSVTNGKGDALRH
CAWSALMTIRIGKDAAERIGNAHETVVRGEPEEREMDLINNALGRDIGERFIINGDETGA
LSTCVSMANIGLLHTLL

>RXN00264 TRANSLATE of: rxn00264.seq check: 1681 from: 1 to: 378
LLVDSGDVQLEGVTVEPTQLAYTGINETQLRIRNIGTTPARTVLLGGEPFTEDIVMWWNF
IGRSHEEIAEYRKQWQAEADRFGITHGYISHHKDGLTRLPAPELPNAAIKARKNPAPTAR
PETRID

>RXN00267 TRANSLATE of: rxn00267.seq check: 9930 from: 1 to: 318
MRNSKSGLAFSAAALFCVVAVITRIASSPSFIAIVAIIVAAIALFVGLNSRVGTKLVDQP
VVFTQEQIDQLKELKSRDQEAAAIRQAQLWSRGSSSEAVAEAVRKL

>RXN00271 TRANSLATE of: rxn00271.seq check: 7582 from: 1 to: 990
MFSSRSKVLASIFTVGALALASCSSDSSDSSTSTDAAGGDSYRVGINQLVQHPALDAATT
GFKEAFEEAGVDVTFDEQNANGEQGTALTISQQFASDNLDLVLAVATPAAQATAQNITDI
PVLFTAVTDAVSAELVDSNEAPGGNVTGTSDIAPIEQQLELLQQLVPDAKSIGIVYASGE
VNSQVQVDEVTKAAEPLGLSVNTQTVTTVNEIQQAVEALGDVDVIYVPTDNMVVSGISSL
VQVAEQKQIPVIGAESGTVEGGALATLGIDYTELGRQTGEMALRILQDGEDPATMPVETA
TEFTYVINEDAAERQGVEIPQEILDKAERV

>RXN00272 TRANSLATE of: rxn00272.seq check: 8098 from: 1 to: 372
MPEPETSTMGSIQKSGEWLVPAYSAYKLNGADLFLDIRHATAAAPVITFDVNMTMGSMTL
IVPPGVYVEVQMASKNWSDFKVQTTNPLPGAPRVFITGVARASGLKVFTKHPHEPFGFWQ
KMFE

>RXN00283 TRANSLATE of: rxn00283.seq check: 5995 from: 1 to: 1032
VASATASDSHLSTCCSSSGRSASPSSPGLAPSWLTTGELFAQFTSTDGNAAIIAASGGGA
IGPQALFDASVRTFLISPALLLVAVVAVFFAYRRRDPEPIIPLALIGSVVFFQIITYSLG
STFGLLRFFLTALPLTIILLFQIIPPRHRFPSLRPGACYRDRVTGKYVPKTITGVLVLAI
FGGTGITLYGMSSANWAPQEYAIQELVFNMGSPSQDAVHTLNTFSTEMDVADFVDSLNLG
DGEVLLSTTYGFAVLTASNNQKQFIIPSDEDFITTLNEPAEHGVKYILALPREGRGATDP
INLRYPDMYETGSHIATMEIEFINQGQGQPNWRLYRVLTTPEQS

>RXN00334 TRANSLATE of: rxn00334.seq check: 4035 from: 1 to: 336
MAKLDDNVQIETVNVSFEAGGRTNWHTHPVGQNIIVLSGLGIYEAEGEPARLLEPGDVVF
AAAGVRHWHGAVSGAPMFHVVVNLKGIDGETVDWEEPVDEEHYRSVSAELQR

>RXN00338 TRANSLATE of: rxn00338.seq check: 9343 from: 1 to: 1140
VSDVTVGDIRRILDEAYPPALAESWDKVGLICGDPTESVKRVGLALDCTQAVADKAVDMG

LDMLIIHHPLLLRGVTSVAADEPKGKVIHTLIRGGVALFSAHTNADSARPGVNDKLAELV
GITAGRPIATRLLGGMDKWGVHVLPKDAAYLKKMLFDAGAGAIGDYRECAFEIEGTGQFR
PVEGANPAEGDVDKLFKSLELRIEFVAPRNLRARLTSVLREAHPYEEPAFDIVEMHSAES
LENATGLGRVGELPEPMRLADFVQQVANNLPVTEWGVRATGDPEQMVSRVAVSSGSGDSF
LNDVIKLGVDVYVTSDLRHHPVDEYLREGGPAVIDTAHWASEFPWTSQAQEILQDKAPQV
EVDVISIRTDPWTMSARAVN

>RXN00342 TRANSLATE of: rxn00342.seq check: 3222 from: 1 to: 429
VADAPGAVKQGAQDYAQLLGIQSGHIVQEIGWDEDSDTLISESIEDAIGEELLDEETDEL
CDVVLLWWREDDGDLVDGLVDSIRSLAENGRIWVLTPGIGKEGALAPGVISESAQLAGLV
QTKAERLGNWQGSCLVQRGNKKP

>RXN00344 TRANSLATE of: rxn00344.seq check: 1354 from: 1 to: 879
VDLSTWLSDTQYLISVDFVQHALIASALLGLLSGVIAPLIVVRQQSFAVHGTAELALMGA
AAALLFGLNVGGGAVIGSVVAAILLALLGMKQQDSAVGAVMSFGLGLSVLFIHLYPGRSS
TAFSLLTGQIVGVSSSSLWILVAVTVIVVSAVVIFWRPLLFASADPIMAQASGVNVRFIA
VAFAVLVGLTTSQSVQIVGALLVMALLITPGAAAVAVTANPVKAVVLAVIFAEVSAVGGL
LLSLAPGLPVSVFVTTISFVIYLVCRLIGWLRGRGAQRDEDAYRRRQHDHHPH

>RXN00353 TRANSLATE of: rxn00353.seq check: 5475 from: 1 to: 693
VGRSFTNRTFDPLPFMVVYPDGVDQHWNDARLGLDENTRHLGIDDVGFFVKLATHLGNTY
GIKRIFIVGYSNGGQMVLRLMHEVPKMLSGAATIASNMPVAENTLPQVKTFKTHPVPYLA
MAGTADTFSPYEGGDAGIGREHRRGVGMSAFDSAAYIAARNGLTEHRHDVIDDVVSIDTW
DGENPVEFWTLNGIGHLVPSGKTYPEFLGPSTTSVIAAEEIGKFFDGVRRR

>RXN00354 TRANSLATE of: rxn00354.seq check: 80 from: 1 to: 813
MGKLLFVDIGGTLLDYSNEVPRSAVDAIRKARAKGHRVYLSSGRSSAEVTSQLWDIGVDG
LIGANGGYVESAQESVFHRRLSGEETRHIVEWLYNRGLEFYLESNNGLYASRGFREASKP
VLSRLSEKTDVTVDSMYPDMFWGASLDRDDVNKISYIFNSQEDLDAAREAFPNLEHTTWG
GQTGALFGTIGVSVNKKIGVDRLLKYLNADRANTIAFGDSDEDLSLFEASAYGVAMGEAT
ESLKAAADLVTDAVGQDGLRNAFLKLELIDA

>RXN00362 TRANSLATE of: rxn00362.seq check: 1707 from: 1 to: 1347
MGIIALLVFIAIAVILNVFLKRDISEALLVGLVGTALVGGVNAPTLLIDAVVDAAQSEVT
FAGMAFVFMGIVVQSTGLIDRLIAILNSIFGRLRGGAGYVSTLGSALIGLIAGSTAGNSA
TVGSVTIPWMKKTGWTAERSATLVAGNSGLGVALPPNSTMFIILALPAAAASSASQVYIA
LACGGAYAVLYRLAVVFYWTRKDKIPATPDDQRVSFGEAMKTGWRSPLIFLGILIPVILT
IGPLSEWLKTHGVGESGVKSMSIIVWVPILITAIALIEGRKRIANNMAHFRVQISKDLPQ
FATVGISLFSALAAANIMEELGVGPQLSNWLDSMDLPKSVMVIIVCIMCIVVATPLSSTA
TAAAIGAPAVAALAAVGIDPTVAIVVILLCTSTEGASPPVGAPIYLSAAIADANPTKMFV
PLITYFVVPMILLAWLVGMGFLPVIVPTG

>RXN00373 TRANSLATE of: rxn00373.seq check: 1756 from: 1 to: 339
MDIQQLDAETTAWKDSLLRAAQEAGFHFEPPKLFEDFETMVEQYKQAAASDPDIDVTDIQ
QMWGIVVGEYLREKMGMEWVVITDDYGTDLAILATAPNGDHVYSCPIIVVGKR

>RXN00390 TRANSLATE of: rxn00390.seq check: 7582 from: 1 to: 405
MSTTREIAFLIARILLGVILIAHGWDKFAITGLEGVTGFFDSLGIPAAGIAAIAAAVVEL
LGGILIILGVFTRIVAAFVAIDMLFAALFAHVSSGIFVTNNGWELTGAIGAGALLLIAVG
ASAWSIDGVLAKRKA

>RXN00399 TRANSLATE of: rxn00399.seq check: 2271 from: 1 to: 315
MSHNDSPNFARRALNWLRQGYPTGVPRHDTFALFYVLERELTEEDLNELAELLIAEGENN
GLHDNPITREKIGKLITHVHSQPPEDEDIDRIQKKLQAEGFPTRN

>RXN00416 TRANSLATE of: rxn00416.seq check: 8529 from: 1 to: 1650
LASYLSPTALVVAVLAIPLSATRLYLDGISVDQGFRTQFLTRMADDIGLSDMNYIDMPTF
YPAGWFWLGGRLANLLGLPGWEAFQPWAIVSMAVAASVLVPVWQRITGSLPVATGIALVT
TCIILAMNSEEPYAAIVAMGIPAMLVLASRIAKGDKFALAGGIIYLGVSATFYTLFTGAI
ALSAVAVCIVVAAIVQRSIKPLLWLAVLGGGSIVIALISWGPYLLASINGAERSGDSATH
YLPLEGTQFPVPFLASSVVGLLCLVGLIYLVVRFHNNEVRAMWVGIAVFYAWMGMSMAIT

LLGNTLLGFRLDTVLVLIFATAGVLGIADFRLASVYQLYPTQITERTATHLTNLIVVLVL
LGGLYYAQDLPQKNARAIDLAYTDTDGYGERADLYPAGAARYYKDINDHLLDQGFEPSET
VVLTDELDFMSYYPYRGYQAFTSHYANPLGEFGNRNAFIEDLAIRSWDELADPQQFSDAL
NTSPWTIPEVFIFRGSIDDPDAGWKYDVAEDLYPNNPNVRFRGVYFNPESFDQMWQTKQV
GPFVVVTHNE

>RXN00422 TRANSLATE of: rxn00422.seq check: 3762 from: 1 to: 894
MPTNYARDNVISLASAREQRSGKPEPKPELTLIVRATNVQADGEVHRQIGLNSAMSLDEL
HNVLNIVFGVGGEQSPWRFEDQFHQPSAPDTNLGELLPEPGDFLFYFWGLWQFNLQCVEM
YPRDNGTPRALCIGGSGGLGDDFDQATINAELTGTDTIRDVLSGVRPEVIDLVDRTGVFD
FIPLLQALDLKREPLIDATRYHTCRTLPVENSAEASDAFWSCVLALSCLGNDELFIEVIE
STMSTLGWVADDGSPLRAPEITSACEASLKILAELGGYGPERLAPVDRLDIYRELLCF

>RXN00447 TRANSLATE of: rxn00447.seq check: 3535 from: 1 to: 420
MLGSLWRFAVRTAAGAVALWVVIKLIDGISLSFPTTPLYQDGQHDNLLTFLAVAAIIVVL
NATVKPVLKLLGLPLTIITLGLFSLVINAVIMLLAEYVSDLIGFGLRIETFGAAFWGAIV
LALVNWVLGPITGLLGAKKD

>RXN00455 TRANSLATE of: rxn00455.seq check: 9756 from: 1 to: 750
MVVDVQNQSHTPETQPQPGQGAAKKTPVASGNSTFIHIQPSLYPILLALFVAVFLISNIT
ATKGVEIGPLVTDGAFFLFPISYVLGDVLAECYGFKSTRRAILTGFGITMLAALSFYISI
WLPGASFWEGQEAFEATLGLVPQIIVASLAGYIVGQLLNAKVLVAIKKRTGEKSLWARLI
GSTVVGEFVDTLLFCAIAAPVIGIATAPDFINYVVVGFVWKTLLEVILMPITYAVIRWVK
RREGYETFDA

>RXN00473 TRANSLATE of: rxn00473.seq check: 5144 from: 1 to: 789
MSGTGVRKLWGDGTPVSLPDLSGLSRAERIDALRSRMSTMGAAVPKFEPSVEESAEQKQD
SLAEKQDIVAVPSAFSDLFPGDGLPRRAVTQLVEQPLVVVDFLAHITAQGGHAAVIGWKD
LAYAGVIDSGGVCENIIAIPNPGTEPLNVAAVLCEGLDVVVYKGPEISLSPTRARPLLGK
LRQGTAALVMVGTKVSSPALSVDAEITDYVGIGAGSGRIRGVEMQVRAVSKTHGVRSGKV
LISRPQDAALLEPEQPTTLRAVP

>RXN00485 TRANSLATE of: rxn00485.seq check: 6436 from: 1 to: 2295
VSSVNDLFAKPYENADLVVTVSAKNEDSFAAFEQQLATTPGVEALAFDQNFAASVKQSDG
IYASTSVQSISEGPLQWRPILEGRLPQGPGEIAVTTAPGAPEVGEHVSIRLSQNTEDTEV
LVVGVVEPAAQETLGGAPFVVASPDALMEWNSSGVRGEFRVATSDPASLEAASFSDATVV
VASAEGHVDKLADSYLGQRDRYFLLLAAFVAVAAAVAFLVVFSAYSVLTGERVREFGLIR
SVGASTPQILGSVIFEAGILGVVAAGFGAPAGLMAARLLADNAARFGIRVPIDVIDLPSS
TMWLIAGVGVVMSVIAALPAVFSVCRKSAVESLSTPAISRTSPWFGALWLLLAGIVGAGG
MWAYEATSDYRGMRSVALSIAGSGALVCALLIATAVLVPWLLHVFSRIVGGTVPTLQLGL
AFAAKQKSRSAALIAVILAGSALSSAVLHGQAHIGTHLVAVAKGMGGTDMMVTALDGEIP
AGMLEEISSIDGVKTAIAPATTAVELEDSGNFSVLMLAEEDGASVMRAGDTGAPAGGLVL
GRNSPDQDAYPAGQAANIIVADTPTQAEIFHSDNYFSMIDPALATGPSTTRNVLILLDGD
SNQAPDNATAQAVRKTISLFDGRYSITEGFSARQNTFELVSRITTMSTLLAIVALAIAAV
GLINTVALTISERARDRYLLRTIGLTSTGQILVMAIEMIALSLPAAIVGAVSGGFLGRFV
ASSATNTAATAPLQVDILGGTVLAMVAGSVLCALIVLANKRRRVV

>RXN00496 TRANSLATE of: rxn00496.seq check: 7171 from: 1 to: 1026
MTRRLHGGEQDGQEHVKGQLKQLFDDDAFLTDLSRGVDPSEGDDALAGLLLDLTKEAQEP
PATMPDWSTLLPGILDQDQDLPVESTSDTTVMQASNPATQEFAPVSISDTPNTATNSADA
DESATVVPLAARREKRAKSGSSGVHSLDASATQRKSHPFLSGLVGAAAATLVIAGGGAAV
YNADENSPLYGMNQQLFGNQDSPSVVELASTLEEVDSRTASGDVEGARALLEQARAMLDG
MAPPRKAPSEATRTVESEPGTQTLTATVTESASPEPPVTETQTVTSTEVQTVTTTAVAPP
VWTPNPEPTTTAAPTSTPSTGGGEGTGNDGDSGLVPPQTPGN

>RXN00503 TRANSLATE of: rxn00503.seq check: 5802 from: 1 to: 1722
MKPVFSVDQIRRAENTLFELQADPDELMISAASAVADVALAMVDGPAPAVSSEESILLLV
GPGGNGGDALYAGAFLAEEGHHVDALLLGNGKVHQSALAYYESLGGQIISDFPPHYLYRL
VIDGLFGIGGRGGLTPELASLVESFSASGIPILAIDVPSGVHADSGELPPGVMVTVEGFD
NDAPMARQKIPAHIDADVTITFGGLRRAHAVSPACGEVLCADINIAGGGGKSLSAELSQV
QAEDATPQMFASKAYQRKDSLFERANLKATAPHIHRIGQHFTVLNMEPGPDHDKYSGGIV

GIVAGSGTYPGAAVLSVKAAVRATSAMVRYVGPALNFVIQSLPEVVATQSLATAGRVQAW
VHGPGRGLEAEQSAELAELLSRPEPVLIDADSLSLLQLSAELRQALRERKAPTVLTPHKG
EFERIAAELRSEGVEIPQADKDPIGAAQALAKEFDCCVLLKGKYTVIAAHDFVHAINAGH
SWLATPGSGDVLSGLVGAHLAQSYAELNRLPEFFPDVTLSDSAIYTQIAPAATIHAVAAG
LAARTEFGFAPTSASLIADAIPAATAKVDLKRIV

>RXN00504 TRANSLATE of: rxn00504.seq check: 4338 from: 1 to: 420
MTYGFLVNTDLTHRAIDFDLENAAKFLGGADDGRVAVAFQEDGTLYAALYSASAKDEGAA
ANPVASLGRNAAATGDGSFFSDPTTAICGPVIFVGAEGEDITLDEIERIKDGIRAARNYR
DDYPEEFNLWRNAVYNLRTA

>RXN00505 TRANSLATE of: rxn00505.seq check: 7863 from: 1 to: 495
MKSEFPVSGTRRFEHAADTQNFGEELGRHLEAGDVVILDGPLGAGKTTFTQGIARGLQVK
GRVTSPTFVIAREHRSEIGGPDLIHMDAYRLLGEDSEDADPIGALDSLDLDTDLDLAVVV
AEWGGGLVEQIADSYLLITIDRETAVQEDPESEARIFHWEWREGR

>RXN00507 TRANSLATE of: rxn00507.seq check: 8687 from: 1 to: 855
VAENLNKHLSKLSKRGPHRVLVGDMNYAGIPGKIYTPAEGDGIPGVAFGHDWMKSIKYYH
QTLRHLASWGIAVAAPDTENGFMPDHKGFASDLESSIQILGGVKLGSGNVTVNPACLGVV
GHGMGAGAAVLSAANRDLVRAVGAIYPAKTSPSAIDAAFAVKAPGLVIGSSSLGLFESGE
PAKLAANWAGDVCYRESEKGNQQGFSEDTMFKLVAGIGSPQTGAQETVRGLLTGFLLHQL
AGEKKYKAFSEPDAEAKKVVSYFGQELQEHAFPKDTSPFAFLNEK

>RXN00510 TRANSLATE of: rxn00510.seq check: 4920 from: 1 to: 1509
VNDPLAGYGAVISALQGASGGMYRGPAKSEGQLREMYQTIEGLDTSSLREAAEAAVGGTN
EARIQGWVGPLLKFFGTVGGGMIATEIAERAVDWFKNRNDVEEVSEAADKAADAIDSTVT
ESDQGMMHIIQQLLDIVSTLTQILGSMDRGKFPQEFRDCVQTGADLIDQAGDMLEGLCAD
RDDAISQCFSALTDHGKQVCETEPKPLCSAASGGSSGGATSSAAASSGGSSSSTASSGSS
GGSSSAADSSTSTNAESSVEKEKTTPAAVEKPDEKPVEKPVEKTPEKPVEKPVEKQECEE
KPDPDPEKCKTEPVECEPTPKPETEPEPKPTPTPTPGTPTPIPELETEDCEPGKETGTDS
ESESEECAPELNDVPEESDLIGQLIKGAIGIGIVVVGVGLLVNFLEQCVPVIEEVPVPEP
EPIPEPAPQPEPTSVKPPESELDKVAEPAPKPIPQANYTAAAATNYSAPAHAPVVPITPA
APEVPAAPEVPAPAVNLHKAGGW

>RXN00515 TRANSLATE of: rxn00515.seq check: 5675 from: 1 to: 702
MRFSRVLPALLITTAVSIPTASAATLTADTDKELCIASNTDDSAVVTFWNSIEDSVREQR
LDELDAQDPGIKAAIESYIAQDDNAPTAAELQVRLDAIESGEGLAMLLPDDPTLADPNAE
ESFKTEYTYDEAKDIISGFSSDPASDVLSQLQQAATTGTRTAEIRAEVFADRTDDYNESQ
TALKEDFQNCIDAIDDARPIPLQYILIGGAIALAVIVLGIRAWTNSRKQSKHSQ

>RXN00527 TRANSLATE of: rxn00527.seq check: 7113 from: 1 to: 1764
VIATSDVREISSEGIVARVSVNGNIEAARTTTIYTSLTVPVANLPVAVGDRVAADQVLAE
LDASALQRQLDETDANNARAAMANRNSIAQSQQAYEQSRELLDSGLSPEINSARSSLRAS
SQAYQDAIRSFEAKQRDVDGGLDSTMVAQSDALKAAREQADAAEIERLRADFGLLNNDRS
NLNDVIGLLDERESLASAESELAQARAAGDLEAVAAAEAKVAGLEQSIASKTSTWPSQDQ
TYLQSYTALEEAERRVASTTEALEIAERIYIDSLGKVDSELAAAQRAVAEAHSAQQDAAL
GLETAQLSTQHQLEAQSSAIDAALGLASVDNEAATRSTSQLRMDINNTTVRSPYSGIVSS
VQAAQGQPAAGALLSVADDSELKITANVKEAEISNVTIGSRVTFTTPSTGTKEFAGRVSK
VSPIAAAASAPATGEGAAAGATTTNTDVTFPIEISVTGDREGLNLGGSARVRIVHEIAPH
VLTVPLEAVYKNDDGKDAVLIISDDNKVEEVEVKTAESDDFDIAVSGAGISEDARVLTQP
GNYRGLIGETVKLHADTVEQAAAPFSPAAPFDPAAPAVSAKQTVGQVI

>RXN00547 TRANSLATE of: rxn00547.seq check: 6032 from: 1 to: 1398
VARDFINAIGGRFGRFAQVGTQRFWTPLRVLITTSLVFLAMGFLTKANCIQGSRGTDGVV
SLNWSGSRQYTSACYNDIVPLYGGRGIDAPGFPYAFSWQEGDLTRYMEYPVLGGIFQWIC
GIITRFLYPVVDVIPFHTLPESGLYFIVTALALAFFWVLVIRMMVELTGNRVWDTVLVAA
SPLVAVHAFTNWDTPAIAAVIGAMLAVKRGNPLVAGVLIGAGTAFKLWPLYLLGAYLVLA
VKNKNLKPFITMAAAAAVTWLVVNVPVMIAYPKAWNEFLRLNRERGAEWTTIYQVIDRNL
PINLNDPVLLNVLSFGLFGASCVAILILGLKVQRTPRVAELAFLIVAAFLLFNKVWSPQY
SLWLVPLAVLAFPQWKVLFPWMVTDAMVWPILMWHMLGTDNKGLPHEMLDLIVISRDAFI
VVMIVGVIRQMLGRRADPVMDAHAGRDLLAGPFGAGERRKALKEVS

>RXN00552 TRANSLATE of: rxn00552.seq check: 471 from: 1 to: 936
VATSKILLYYAFTPLSDPKAVQLWQRELCESLNLRGRILISTHGINGTVGGDIDDCKAYI
KKTREYPGFNRMQFKWSEGGAEDFPKLSVKVRDEIVAFGAPDELKVDENGVVGGGVHLKP
QQVNELVEARGDEVVFFDGRNAMEAQIGKFKDAVVPDVETTHDFIAEIESGKYDDLKDKP
VVTYCTGGIRCEILSSLMINRGFKEVYQIDGGIVRYGEQFGNKGLWEGSLYVFDKRMHME
FGEDYKEVGHCIHCDTPTNKFEHCLNEDDCRELVLMCPDCFANVETRHCKRERCAAIAAD
FAEQGIDPLVTS

>RXN00555 TRANSLATE of: rxn00555.seq check: 6336 from: 1 to: 939
MKQPLRVLISCRPEENSGGKRSEQNDAVFEFAAWLARTSDINVRGITTFIRPWPSSSISK
LGGKYHKWYKNLDSYYRSRTIKGLKEAGVEKSQWDDDVSVFVDGPSESTLLTHAAEEFEA
DLILLGSDATAPKGRFLASSTADALLHSSPVPLGLVPRGVKLSKKGVTRVNYAFTNESDD
FEQGLRSSAELATNWNVPLRILAFSPTGITSAPTSRSLDISTELSSEWRELTLAMLDRAR
DGVLTDHPNLSVSSETGSGWGWSGAIDALRWKKGDLLCMGSHRTDTLSRVFVGSETMEII
RNSPVPTIIYPGL

>RXN00560 TRANSLATE of: rxn00560.seq check: 5757 from: 1 to: 375
MRIDPLETRQAVLAVKDWIEGEGDVKKPGRAALAAATRLSVRLLAQHAPGNSVEVRVPPF
VAVQCIEGPKHTRGTPPNVVETDAKTWLRLAPGQTTFDAEFESGKISASGTRAKEIADWL
PVVKL

>RXN00574 TRANSLATE of: rxn00574.seq check: 6894 from: 1 to: 879
MSFKVISTGPQAIFQDRGRFGFASAGVGTSGSFDRLSAARANHALGNDPNATVVEILLGG
FEVEALHTTSIVFTGTEAEVMVRTAGGQSKNATTNTIIDVAAGERIRVEPATYGMRAYFA
ARGGFAVKKTLGSASTDLISHMGPCPIEPGDVIDVATDIADSQWWPKLRQLPTLWKRMPT
ETLTVIRGPRDKWFTQESLNNFFTQVFTVSNDSNRIGLRMHSSEPIQHRVEGELKSEGMV
RGSIQIPPGGNPVVFGPDHPVTGGYPVIAVLTSRSCDRSAQLLPGDKVRFKLL

>RXN00589 TRANSLATE of: rxn00589.seq check: 4154 from: 1 to: 450
MTTLSRKFFVSATTALAAVALVACSPNEIDSELKVPTATGVSLPSKNVSATSTATTDEDA
PGYIDCVAAPTQQPAEISLNCAMDIDRLTDISWSEWDTDSATGTGTRIVTAANGQETETE
DIEVKLSFPTESSQGLVFTQVTVDGQVLFL

>RXN00616 TRANSLATE of: rxn00616.seq check: 2419 from: 1 to: 345
MKSLPRFAPLITILALLVLVAIGGSALANNRATPNVESEPATVNQRSTPTTSAYEPPATE
SPEEPTTQIQESPVQPPVPAPAQIPQAPQVPLNYQYYDDDWDDDDDDFDDDWDDD

>RXN00647 TRANSLATE of: rxn00647.seq check: 2211 from: 1 to: 633
MGIFEAIRAARAKTKAEIKAAEAKVKTEAKNKAKLDLKREKLLVQQEKNLLKVEEKGLKK
RNKHELKMAKNILEQKRQGRLNKDKVKRWAGTARVLTPLLLPIIYRLSTEARDQVVKGRA
RRAGVTAEQLSQFAGHAAALKARIQGVRETAKNSSLPAGFVRDVEERLNELEAAANNSEF
MSPQQRNRAHQSISRDLNQVSDQIQDRLLDK

>RXN00653 TRANSLATE of: rxn00653.seq check: 8269 from: 1 to: 765
VSVSQVVGEILLTVGILALLFAYYEAYWTNVESGKLQESAGQKLDEDWNEARVNPRQKLT
PELGEAFARMYVPAFGSDFNFAVIEGTDEEDLLAGPGRYVDSQMPGEAGNFAVAGHRVGK
GAPFNDLGNLEVCDAIVVETYNSWDVYRVMPMSTNGADRAAEAADCFNENQVSRMAEGDY
VNVSGRSITTPDRIDATYPTPGVFDTAVREGSEALLTLTTCHPQFSNAERMIVHAMLVEE
IDKSSGERPAALEEN

>RXN00662 TRANSLATE of: rxn00662.seq check: 7679 from: 1 to: 1269
VSTIPLNRLAVIAAIIGVGTGLFVAALNWSAIGVERLVYGADHLHNYNPVANVSPLRLSI
TVIVLSVVASWAWFFVHRTGPKEVSIVGAIRGEKMPILETIASAFLQVTTVAAGAPVGAE
NAPRIAGALVGERFSRWLQLDIDAKRILVASAAGAGLGASFHLPLAGVLFALEVLLVEAS
TRTVVIAIITTTAAVATTGFFVQTPDVFSTVPLTESPWMLLAAMVTGVVAGMCGHWFSAA
AHKMAQASPKGVKILWQMPLGFVVIAAVIYFFPETLANPRWLADSMLGDGLILSTILLVL
VLRTAMFLLAFRVGMVGGNLIPAFALGSMVGGVVGAVLEPITNVPIAAFALLGAAAFLST
TMAAPLFGLIAAVEFTDMEAQGYLPIFLAVASAVLAVRVWSVIAKHELRAIPITYASWTG
ELK

>RXN00666 TRANSLATE of: rxn00666.seq check: 5076 from: 1 to: 915
MTAGEAIAHSVRAAQIAEEHNYARFWVAEHHNSEGLASSATTLLMGHIAGHTSRIRVGSG
GIMMPNHSALHVAEELGTLEAIYPGRIEAGLGRAPGTDPMTARELGRASSLVDDVLSTIV
SLQNYLDTPEERPNIIAHPGINSRVPLFMLGSSLNGAAMAAKLDLPFAFASHFAPFQMGP
AIASYRELAANPYVMAAANVLVCDTEEEAEFQISTLHQMFAGIVTNSRGKLAPPVRNLKD
KLDPMIWKHIEDSLEMTFIGTAESVVLQLQEFADRYKLDEIITVTYSYDPEVRFRSIAAL
GTAWN

>RXN00704 TRANSLATE of: rxn00704.seq check: 5954 from: 1 to: 627
LTITFSRVALTTLAVTATTLSLSTAANAQSSLLDKTLDARQCIDADNVWVSVDYGADSEK
EPEGACATEFTDGVVALESAGFKLTFDESEMGKYMTGINGVVPDWVETGTYWSYYSGEVA
DDYSVDYTYYEVGASNSEPEGGTVEAWVVGTGEETPALETLPETPAATGSSEDGGWIAVI
AGLLALIGGGVAALYQGLITIPGLVLPKF

>RXN00712 TRANSLATE of: rxn00712.seq check: 8070 from: 1 to: 696
MSLRKNLALGSSTVLLTAVLSGCVSLDERSTDTSTENVTTVTATLTSTAAAEPTTRTTVQ
SATEASTTAPVQCNLDPRTSDFGPYLAQSRTPVGELAGSADSVVQVPDWFYHFQMGDNGY
DSCSKLSYVVLNGSNGDAERSTGTGAAIADVVVLFIDGHMVARPAPFEMKTVESVTRVSD
SEIQVVYGHAGRSTAEGVTDYFTFNFFVDNGVLSGRGDLPEHIDTHMRLYLL

>RXN00720 TRANSLATE of: rxn00720.seq check: 5001 from: 1 to: 666
MASPRRPQVAAPRIKELRLTGLDNADPQDIESNEQIESCRFNEAELSERDLSGAGFIECE
FLGLEAHETELRRAQFVETRIERANAPSFKAARSIWRNATISDSRFGAVEMYEATVQALK
ISDSKLSFVNLRGASLRDVLFENCVIDELDLGQARAERIAFKDCTVHSLTFDHAVLSNVD
LRGLDIERISGVESMSGTVISSLQAADLSGAFARHLGITVND

>RXN00722 TRANSLATE of: rxn00722.seq check: 460 from: 1 to: 1065
AVLREAGVVDAGGQGLVILLESLAEQINGNPPHHPSHHSEPAEEPSFHGKTGDLEVMFYI
ACDSAQTLDALHNELETLGDSLLIARETNTRGTVHIHSRRAGEVIQKAFAAGDVSELRLE
ILPDTSGSFTEEPRRVLMAVAPDGLVAELYRSAGVKVVARNIAQSKSDDVVAKIVSIARK
SGADEVILLPNGLLTKRELVSIERSSHAFEQSVVILPTATLVAGLAAVSVHEPAQPLAVD
SYAMAEAAGSMRTATIRAATSAALTQAGACSKGDLLSFIGPEIALVSEELNDALSRTALR
LLDGSSEQITLLIAQDRQSAFDEDVFRRGLGTHTDVEITVYPATGMENLVEIGVE

>RXN00729 TRANSLATE of: rxn00729.seq check: 9733 from: 1 to: 978
MSATNPDALDVQHVYPIKTKKTPLAVIFNIISGGLIGMAELVPGISGGTVALVLGIYERA
LHNGDLLIDLIKVLIKDRSKVKEAAAKIDWWFLGAIGVGMVVMVFSMSSILHTVVEDYPE
ITRGLFLGMVAVSILVPLGMMDMRDAKKRLAIVIPLFIICAMLGFFGTSFTSAPRTDPSL
IFVFICAAIAVCALVLPGVSGSFFLLAVGMYAPIMESLSNRDLSVIGVFLLGALTGVILF
VKVLSYVLEHHRTITLTIMAGLMLGSLRALWPWQDGDANLLAPGDNAVMIFSIIILGGAI
VAALMFAERVSSKNIDSETVAEEHPR

>RXN00730 TRANSLATE of: rxn00730.seq check: 2858 from: 1 to: 807
MSSQQTIFIILLFAAVILISIVMITAAFKTRKKRFAARAEGMANPTIPAPTVPWQRFAGA
LAALYARPEWHKTRGAKRVYSAEQTYFGFVSAMPLGMVQNMLQTDWGVKKSEHAVDQLSK
GVEVIVGVAAGNWRKNGVSPAQVEEAGQRLAAEGLAHPHFVVFQKQLQQADPNAEYDLDV
LAFDIARVANLLRWAAYTDLLLPAEARWFQDQLGIAAAVSFGSWEEYGERYVRGLQKNFK
GGNKPYIEGERWLNTEAESPWKTQKWISA

>RXN00731 TRANSLATE of: rxn00731.seq check: 8578 from: 1 to: 2496
MKDASQSYLLFGLRWLGRSLRFAPLSLLMIVVMRGLREVFGAEDPANSSLVDNLGLTLPW
SLNDPHFLTAGFSASTTTAALMSTLWIIVFAVPSERILGSLKFAITAALIHITSIPLGIG
IAHLIEEADLNRWGNNMLADVLLTPDFWVFGVAAFASASMPLLWRRRTRLFLFTITLTLL
LYTGTLADVTMLTATIIGTVAGELNRHRKTPGGRWLPGSLTVREARIMTAILVTAVAAGP
VLAALNPLTHGPFSSATKLIWQPLVTEEHMHHLCHTDSTSDACQGALDQLQQHGVGPSVA
NLIPLILTVVLAMGLSRGRRLAWILAVLAQLISIAVLMFQLTKLSADSTDLLWSVNAFSV
IVPWLVALAVLVFSRRAFQVKIDTTRISKSLGALMVTWLATAALWILATLFLPHAFHPHP
TLGLAFKELPFRYLPPTIETVLSHQLFPRSPAGWAVFEWTGTLFWLVVAATLYHLLMGVP
SNKAHEDQENAATLLRSGSGDHLSWMTIWGGNTYWWAPENAGYVAYRVKRGIAITLGEPI
LGPDSSVSKAELAAQFEEFASNQGWIVAWYSVCEEFSKERINAGHHTLRVAEEAVLSSAN
ADFKGKHFQNVRTARNRAAKEGVSSIWTTWADLSAEMQHKIITLSEEWVSDKALPEMGFT

LGTVNELSDPDTYLLLAIDEEEHLHGVTSWLPVYEKGRIVGYTLDVMRRDPQGFKSVIEF
LISEAVVIARDHDLEWMSMSGAPLSTPPGVADDGTIGQILELLGRAMEPFYGFRSLAASK
NKFHPEHHGWYLCYRDELSLPSIGLAVAACYLNEFPLPNWLKKTATSAPSHS

>RXN00738 TRANSLATE of: rxn00738.seq check: 6764 from: 1 to: 363
CQEETDGFFDFGRDMRPGERRSYGTLLNDATTQVSHILGNAFTRSGLNAEYANLYGQALV
GMVSMTAQWWLDERTPPKEEVAAHIVNLCWNGLTGMEADPKLTPISSAEGAIFGQEKESE
A

>RXN00750 TRANSLATE of: rxn00750.seq check: 8593 from: 1 to: 438
MDWSIIINVLAVATVVILTLIIAAALYRGFTRNKIKKLEAIREAQQHERDNPTIRIADLR
GIMDTHHYIYTDVMVTRAHELMITAPAFFDVTLPEAVLYEDTKRAAHDALNGYKDTTVAS
AEKIMLVDAVTAAWTLYSTKANTGST

>RXN00762 TRANSLATE of: rxn00762.seq check: 9427 from: 1 to: 876
MNTSDRIKSTQIALDRDLREQALLLLKEVRAVDGVDALSEQFVRGLAEPGLVHSHLIVTL
NSELVGLAAADEETTELAVHPAHRRQGIGKALIDAAPTSSIWAHGNTAGAQALASTLRMK
KTRELLVMEISDRALDDSAAYKDPDGITHSSLANAPVEKSVAEAKWLQSNNEAFDWHPEQ
GGWTTHRLAQAQKADWYKDSDVLFLWDGEEIVGFHWVKQHSPELQEIYVVGLSSAYRGRG
LGDPLVRLGLHHMRAHGARKVILYVEAGNTPAVAAYEKLGFTVAESHVVYEK

>RXN00768 TRANSLATE of: rxn00768.seq check: 4486 from: 1 to: 1119
VGTIEDVANEQIEVANNTDQIPAGYKSPLLSRSGAAEAQGAAAQAGTEGVAWHYGSPLVE
QRIFETGTGLVDRSNRKVIKVEGPDAPTFLNNILSQKVDSVENGFTAGALDLDAQGRIQH
TMQVTVVDGVFYLDTSAAEFDTLIGFLTKMIFWSEVTVQEADLAIITLLGQEIALPDAVF
ARRVDWNGPSRIDVAIRRENLEEGVDKLLEAGAKLTGLMAYTAERVKALEPAAGVDLDDK
TIPHEIPHWIGRGEHLGAVHLTKGCYRGQETVARVDNLGRSPRVLVLLHLDGSAPLDPVT
GAEIKAGARTVGRLGTVVHDADYGPIALGLVKRSALDKELHIDDVSVNVDRDLLPAEESE
QRGRAAINKLKGL

>RXN00769 TRANSLATE of: rxn00769.seq check: 3734 from: 1 to: 213
MGRGRAKAKQTKVARQLKYSSPDMDLDSLQRELANQSPRRSYSDTPDDEDQYAEYADWDE
DDTDNRAYGTN

>RXN00771 TRANSLATE of: rxn00771.seq check: 865 from: 1 to: 819
MTNPYEAFIPLKHRTGIEPEHTFWEWENKRVHIARRRREAPVRVIVVHGLGTHSGALWPL
VAAIEGADLAAIDLPKTPLYDDWLRLLESFISSEDDGRPLILIGAGTGGLLCAEAAHRTG
LVAHVIATCLLNPSDQPTRRALFRFSPLTRLIQGRLRNREIPVTRVLNFSKISRSPALSK
LCAADEFSGASKITWGFLASYVQHKAKLGAVPVTLMHPDHDLLTPVELSLRTLSRLKAPT
DVVMLKDCGHFPIEEPGFTTMLETVTSVIARNS

>RXN00785 TRANSLATE of: rxn00785.seq check: 7074 from: 1 to: 657
IIATLGVTLLVEARGLFLTVASIPILFGIFTPLTSWFVSQQGVAANVSPGVSVTEILTAV
YPLAQLFPTLIMVTLVAALIAVVRIILLRRNQESRQVSGELTRRAQREAEEANQNAARRA
RAQSTRVQSSKTRNRRAQPTGDTGSQVTVDELIRRSQERRQTVAQRQTERGVPFTPTPGP
VVAPKPRPSAPEAPAPTDVGERRQAAPKRRTSLDDDLYS

>RXN00795 TRANSLATE of: rxn00795.seq check: 1530 from: 1 to: 528
MIISLVVSAIIMLVAVGFTGMCSFNTGSPENGQVPEVDASTFMSMEARAMTDHATRLPET
PEGWTTNSARRTMVDDTPASVVGYVTADEGYIQLTQTGETVEDAVAGYDTRWRDLSESYD
LDGHDVGIYTSQESDVRDLRVMDLGDARVMVSGAATDEEFNDLLRAVANSEPLPTN

>RXN00831 TRANSLATE of: rxn00831.seq check: 2669 from: 1 to: 702
MSALETLQWQDWSSVLIVVAHPDDPEYGLSAAVKEWTDAGVEVSYLLLTHGEAGIQGLDP
KETGSLRAAEQRAACDVVGVRNLTILNHPDSMLVYNLVLRKDIAREIRIRKPNAVVVSNF
DVEAYGGLNQADHRVAGLAAIDATRDAANPWAQPELLQEDLQPWGAEVIIIAGHPEPTHT
MDLAKDSVDAGVASLQAHKEYLAALPDPPKPEEFIPAFLEVEGGYAAAFRVFGR

>RXN00835 TRANSLATE of: rxn00835.seq check: 6529 from: 1 to: 954
MAGGLAALLDDVAAITRAAAASLDDVTAMAGKTSVKAAGVVVDDTAVTPQYVQGVKPARE
LPMIWRIAKGSLVNKIIIILPIALLLSAFAPWALTPILMLGGSYLCFEGAEKIWHSLHRR

IKGEQHSTEPKSQESPKSEDQLVKSAITTDLILSAEIMVISLNQIADQTIWMQAAVLFVV
GIGITALVYGVVGVLVKMDDVGLTLSKRDSAGIQKFGRGLVKAMPIVLQVISVVGVFAML
WVGGHIMVVGTEELGWELPYHLVHGLESWANGIGGSALGWVGNTFGSLVFGLIWGAIITV
VVSVIKKFIPQRAQNSSH

>RXN00836 TRANSLATE of: rxn00836.seq check: 6589 from: 1 to: 1716
MYTHSTGTPQLDFDGDIYPLHLFFSAQTAQHFALERVNWHVLRAIVKPEQGELIVEALLA
PIESATKIGVWVQDEFLGVIAESQFLLNSQLSRIFASGHLISSQLLLTPSKGSLASVLLP
NLKFGLISNDPPRADSHLLPLGRMWRVEPTVHALFEDFSLGSTILFGLRLDLEALIVSYN
GIECGILNFDDASALSSAVKFSNANGLTPTVLGHVVRENGETSFEIDVLPLELWSKKQHR
LEVLKIPRLIPKEADSQNYVKATALLSDEILRPQTLSKKALSLSDTAVKYSPHVACGVGM
FSLFAVIPFDKLSDHSAMLLAVISLMLFVLALVILFKRIQSTNTQRWNLASSVGLLATLP
IIIFLVADTLIPQGSLENHAQPDVQVTTLANRRPSSPTSLDSLGALNSPSSPNSPSSSML
QNSEMFASPPIASGQSPVSTFRSWLDRSILPLTRENSASESAVTALGPSIVQPASESITT
PAQTSQSRHAIDDGDDSKTSTGRPAPTTNSPIIALPPTWIIGPEDPESTDPTAPTEPTEP
SEPVATDEPSETSEQTSPLLARDTPELNRKQL

>RXN00840 TRANSLATE of: rxn00840.seq check: 2272 from: 1 to: 714
VTKTLPRLLTVAAALAIALPATPVASAVTPVEQAFNASSNLSSGLPVDQWGRPNEQFRQQ
IEQAVNQPWVPQEIKNIVSQAMGFITGDGSEGGDIEIPDNAPRIAQFFWPTRSENCINGN
SAAVGSAFAVPGPADLPLPGAGVGQTSFVFTALGTGPLAEQQSTAMTVQWANLSNFTHGT
TTLSNTGINPDGPSTISGVADTGRGIIVASMSGGLTTSTENGSANCNFIPTAVVFDVR

>RXN00841 TRANSLATE of: rxn00841.seq check: 5409 from: 1 to: 537
MTDLHPVKQEIFNTAESINTDPKGFLREVDTFKVTDFGLYMARGANHPKFGYLESWLLPE
LGLRANIFHFRKGVDERQDYYIDVAEIRVEDNIWTTRDLYVDLISVCGEPVTVMDIDELA
AATSAGLITADDAERAIDATLNAVEGITRHGDDPMQWLRSKGIELTWADASQVELVPAE

>RXN00846 TRANSLATE of: rxn00846.seq check: 1812 from: 1 to: 870
MLKNDLSGARVVAVHAHPDDEAITTGGVLADLAARGADVTVITCTLGEQGEVIGETFAQL
VNGDADQLGGFRIHELYASLEILGVRGIHLGGAGCWRDSGMVGDPANEHPRAFIHSGDRA
VEQLKELLAELKPHLLITYGPDGGYGHPDHIRAHEITHAAAGEQRILWAVSDREELEDGL
KAITGLPEGWGRGELSAVDSVDLSVELNDEVYATKVESMRAHATQLWIADGSVSRTNPVA
AHAVTQQDNVKVWALSNLIAQPIMRHEHYQLGAGTPLPEGATGVLDGLEF

>RXN00850 TRANSLATE of: rxn00850.seq check: 9820 from: 1 to: 828
MANPFSKAWKYLMALFDSKIEENADPKVQIQQAIEDAQRQHQELSQQAAAVIGNQRQLEM
QLNRRLAEIEKLQGNTRQAIQLADKARADGDVKKATEYENAAEAFAAQLVTAEQSVEDTK
QLHDQALQQADQAKKAVERNSMALQQKVAERTKLLSQLEQAKMQEKVSESLKSMDSLTSG
STPNLDQVREKIERRYANALGQAELASNSVEGRMAEVEQAGVQMAGHSRLEQIRAEMAGG
SLTAGNKQESIEAPAAGNNVTDDAVAQRMRELRGEA

>RXN00854 TRANSLATE of: rxn00854.seq check: 1696 from: 1 to: 213
MRLSEFRQLIEDEFGEAKGEWIAHSHVIGALGVTADVAVDTGVDLRDVWEQLCIDFSVPE
ERRLGKDEPGF

>RXN00855 TRANSLATE of: rxn00855.seq check: 9166 from: 1 to: 285
MTYFAVLYTYNPDSEKVAEVRTVHREFIANLHAEGKIVGSGPFVDGDGGALIVIKLEEGS
NLVDAETLMNNDPFHVENVLDNRVIRSWNPVTKDF

>RXN00869 TRANSLATE of: rxn00869.seq check: 9381 from: 1 to: 921
MTPPIISPESFEALRRMRAAEPTMVAERFKQRRKRELLGEDGKLFIVAADHPARGALAVG
DNETAMANRYELLERMAIALSRPGVDGVLGTPDIIDDLAALGLLDDKIVVGSMNRGGLRG
ASFEMDDRYTGYNVSSMVDRGVDFAKTLVRINLSDAGTAPTLEATAHAVNEAAAAQLPIM
LEPFMSNWVNGKVVNDLSTDAVIQSVAIAAGLGNDSSYTWMKLPVVEEMERVMESTTMPT
LLLGGEGGNDPDATFASWEHALTLPGVRGLTVGRTLLYPQDGDVAAAVDTAARLVHTDIQ
QFTSQSI

>RXN00915 TRANSLATE of: rxn00915.seq check: 6638 from: 1 to: 630
MSAAYSQDTILTVFLGRGLTAEGIRQTLEDFAETGLVRNLVWIDADSFHESSSEVTHLAT
NQDGLPELQRRPFNELVSRSRTTKLHIGVINVIDGSEGMLHAEELNPLVGIIDSVCSHHQ

IHRSNVMIGAVAATLDEELPILRGYVNLMLAPEDSHSPGTATVTYRHGFSDHRLPCTAWL
ISPACTDCGKAAHPHQSNSSYLRKVPAFVW

>RXN00917 TRANSLATE of: rxn00917.seq check: 3769 from: 1 to: 2679
MVNTLNSKTVNVPRFARGVVAAATALFFGALVSLAPSALAQEPPAVEAGASGSLSNLGAC
IADKGTLDVIIMIDETESLIHEARDGVVNANEPGADAQHHRVPAAQSFVDELLAKQSDGD
LNTRIRVAGFGQTYKSGATDPDNYGAWTQLDASTVGGVQDEISRFADRTQEQYTNYASAI
EGAYQDFTRSGSEDACRMLVTFTDGALTAQEGADVAEAALCAPGGVTDRLRSAGITHIGI
GLSAPTNPSDFSLLRGTTAGGGTCGVEPANGAFFPADNVGGLFAAFREALAIGGETIGET
RAGDPFSFTLDNSVNSVRFTAIAKDDLGPNAHLVLTAPNGETVELKDSGSSVANSTDVSW
EAESSPVKMADGSLNLQQGGDWKGVWQIQFQGIDPAAVDGRVFNSVEIQPDLQLVFSGGD
STSGALNLRDDQQLNMQLVGRDGQPRILEGSALVDLGFTRADTGEFAPLAQGIDISGGEL
SFPLDTISQLPAIGTVEARTTITTAGVDDLPGTTLSPILNTTRITITQRDMPQLPASVRF
TADEDVVTVDIPITGPGKVWIAPGTQLSGVLPDGVDGIAASSTFDSPDNALVLGLDEQGT
IPVELTVSDLRDGLVNGSIPLQISNAEGANETSVDLPTEGTLSVPINASTFALAFILALV
LSLLIPLLILYIVRFLSAKVPSSAMSGVRIPVEFSGEALRYAGSTMPDLASQTTATKQVV
VHGDTFNVEGHKLKVQRFQLNPIASPAVIVQTDPSISFDGKQKGTQAKLPLAVQGSWFLT
ASGADPSKMELIALTNLPLEQGQIDRMIAGITSKAPDRARELQKLLDDAATSQPAKVPPR
APAAQGHVEKQAPSFGTGSGGGFGSSNGGGFGSGSGSNDTNGGFGSSGGFGAR

>RXN00921 TRANSLATE of: rxn00921.seq check: 1572 from: 1 to: 513
PAAILLDHIVPNFSRDRSLPDIEDWTRSDEAQQIFAGIIAGASVQTGRSHFMWDLLRAYF
GVALIGDEDTYRAFTTLTVDSVLSFVQLTLQEGRTEDIRRFEKYGEQIAREDLPSILTNA
RAVQQYLGYIDQDIINKKVSRSRDVNQIFTEMARAIIRAISRNNIGKDMRS

>RXN00943 TRANSLATE of: rxn00943.seq check: 2288 from: 1 to: 912
MIRKLARPMLASVYVADGAETVLNTSAHVEGTQVVLDRIRYVLPRKYAKRISRDPELVTR
VIGGTKVGAGSLLAIGRAPRTSAATLAILTIPNILARNAFWETQDADEKRNRRNGFLTNI
ALLGGLFITSVDTEGKPGVKWRATNATKRGKKQLQQALPTKSETEKFGEKASDWFNDTSD
KVTEYAYTAQDFVGENKDDWIKSATETAHKVADTVSDYAHKATSYLEENSGDWLEAAQAN
AKTARKSAVKAAGKAQEKANFALQVAEETSGRANKKATKSYDKLQKQADKAIDRAQKKLK
GIEL

>RXN00945 TRANSLATE of: rxn00945.seq check: 2895 from: 1 to: 972
MLERLKRLDPLIVLIVLAVIVAIIIPVRGVAADWFDVAVKIAIALLFFLYGARLSTQEAL
NGLKHWRLHLTILAITFGIFPLIGIGLEPMTAFVSEDIYRGILFLTLVPSTVQSSVAFTS
IAKGNVAGAIVSASLSNLAGVFLTPLLVMLIMSAGGGVHVDSQVFLDIAIQLLLPFILGQ
VCRRWVKNFAANKATKIVDRGSIAMVVYSAFSAGMVAGIWSTVSVLEIIYLIVFAILLVM
AMLWFTLFMATRLGFNRADSIAIQFCGTKKSLATGLPMAAVIFGGANIGLLILPLMIFHQ
VQLMICAWLAARYGRDAQEQKANA

>RXN00946 TRANSLATE of: rxn00946.seq check: 9850 from: 1 to: 774
MTHTLQATNPLDQTAWHAWHFSRNKEAISRTGATSLSATEWISATTLKDAHTFPSLPGRW
YKRGGGVVGAHLPPAFATTGTVQLRPGELLIAEDFTLTVIERLGQFALQVFDARNPKRFE
FHSIAAFPPSEEWRIEARFFPEPDTVNTAAADGVIVATPTAGWVHFLKGRLDYRLRVTVQ
KNNLRALFSDNSSTLGVYQHRFVDIPRPDAEGNTIIDFNRAYLPPKALNRKFLCPSPSLN
NHLNLTVEAGEKWVVAGG

>RXN00953 TRANSLATE of: rxn00953.seq check: 8687 from: 1 to: 753
MAPPTVGNYIMQSFTQGLQFGVAVAVILFGVRTILGELVPAFQGIAAKVVPGAIPALDAP
IVFPYAQNAVLIGFLSSFVGGLVGLTVLASWLNPAFGVALILPGLVPHFFTGGAAGVYGN
ATGGRRGAVFGAFANGLLITFLPAFLLGVLGSFGSENTTFGDADFGWFGIVVGSAAKVEG
AGGLILLLIIAAVLLGGAMVFQKRVVNGHWDPAPNRERVEKAEADATPTAGARTYPKIAP
PAGAPTPPARS

>RXN00959 TRANSLATE of: rxn00959.seq check: 3462 from: 1 to: 456
MTVIGIILGSLFGVLAVLLIVVGALGWAAKLPGNPVVGIRVPEVRKSQELWDMAHRVAGP
LWVLSGVSFVIASLVAFVASGWMWLVVALGVEAAIAFIGMGAGMAAHTVAMVDAKRIRET
PQAPVSAEIEEAGGVTITSADYQQDSAECPQD

>RXN00963 TRANSLATE of: rxn00963.seq check: 4671 from: 1 to: 837

MRLATIRTNGTTIAARVESENTATTIEGFANVGELLQESNWRELAENAAGEAVTFENKEL
DAVVPAPKKIVCVGLNYANHIKEMGRDLPDTPTLFVKFPDALIGPFDDVVVPEWANKALD
WEGEMAVIIGKRARRVKQADAAEYIAGYAVMNDYTTRDFQYAAPAKTPQWHQGKSLEKSA
GFGPWMTTPDSFEFGGELATYLEGEKVQSTPTNDLVFSPEKLIEYITHIYPLDAGDVIVT
GTPGGVGHARNPQRYIGDGETVKVEIAGLGFIENKTVFE

>RXN00971 TRANSLATE of: rxn00971.seq check: 9758 from: 1 to: 318
KALSIGTQWAQVMGINHAEAEELDEALSPLINRLREMGFDPTETEEANSLALHSCPFVVN
DKRPSAFVCAIHAGFIQESLGENNRIQLELKPLNAPGTCKVHVFSE

>RXN00991 TRANSLATE of: rxn00991.seq check: 2362 from: 1 to: 1380
MDILISILSLLGFVLLTASTGLFVAIEFALTGLEKSTVETHVKQKGDSSARAVQRDHQNL
SFVLSGAQLGITITTLATGFLAEPVLAKFFTPALELVGLNESASSAVALIIALLVATTLS
MVFGELVPKNWAITNPLGVARFVVHPVNWFNMVLKPFINGMNKSANFIVRKLGIEPAEEL
ASARSSQELTALVRSSAESGGLDQNTAAVINRSLQFGDATADEFMTPRSTIESLRATDTV
NDLIELALETGHSRFPVTEGDLDETIGMVHIKDAFSVVQAERATTMVRDLARKIPVVPAS
LDGDSVLNAVRSAGSQVILVADEYGGTAGMVTIEDVVEEILGEIHDEHDDSDAERDFQQF
GASWEVSGLVRIDELEKRVGYVSPDGPYETLGGLIMYTVGAIPRVGDVALLPLTDTPTMD
EFESGFSGRWIARVTVMEDRRIDKAVLTPITHEEAKEYEK

>RXN01004 TRANSLATE of: rxn01004.seq check: 9066 from: 1 to: 1062
VSIWATVLLIIVLLSANAFFVAAEFALISSRRDRLDSLVSQGKKGAEKVLYATEHLSIML
AGAQFGITVCSLILGKVAEPAIAHFIEVPFTSWGVPNDLIHPISFVIALAIITWLHILFG
EMVPKNIAIAGPETLGMWLAPVLIAFVKITRPLIEFMNWIARLTLRAFGVEQKNELDSTV
DPEQLASMISESRSEGLLDAEEHARLSKALRSEQRSIKELVIKDEDVRTLAFGKSGPTLH
QLEEAVRETGFSRFPVTGRDGSYLGYIHIKDILPRLADPEMDPSETIPRSALRPLSNVDA
DGLMDDVLDFMHYRSAHMAQVRLKGELLGVITLEDLIEEYVGTVNDWTHESSDD

>RXN01016 TRANSLATE of: rxn01016.seq check: 586 from: 1 to: 648
LLPYAIVGLVILLPSSWLPRWAVAVLGEVSLVPAVVFGGGFLLIPSMFLIGSALVRYGVV
DRAENAPRAMGVFFAVSAAIAIPTLIIQARDITSSGFSIVSTVAGLALGGVYISLVLLAL
HTPIRGALAAVFAPLGRMALTNYIGATILMLIGGLIVDLPHSTSWTATVLLAAGILIIQE
LLSALWLRHYTQGPLGYLWRWVTWGSRSPFLTRSAS

>RXN01023 TRANSLATE of: rxn01023.seq check: 9173 from: 1 to: 978
MSAVNSAGRPANGGINKTPMIIALVLSIVLVLAVLFGARVLLGPAGQQQIAMSGLPAPDA
ESAECAALLEDLPGEAFGHTRAEIMDPVPPGAAAWSTSDLERVTLRCGVDMPFQYTALAN
TVDVDGTTWLPVSDMTPGSSLETWYSVNRFPVVAITADDISTDSADNPVAPFSSAVDKLE
KRDGQPFDAPLTGLSSAGTTCTSLFDALPRQLEVGGDDGTTYERIEEDRMQAAGYSDDAV
AWDTPGLEPIVIRCGVEPSENYAAGAMLQQIDDIPWFEDTILASGTTSSTWYALGREIDI
AVSLPQAASSSLITISGFIEDTVPAE

>RXN01028 TRANSLATE of: rxn01028.seq check: 7950 from: 1 to: 2049
VIYPPLTPASEEKFNKITSVAAVSKRPTTLPYFRADGSPTRGFANFSTGGIHGAEYNEDR
FDHDQDLHTVATREFFAILDATLAALYAAHQAEPESADYQIAQDALAWAKNVLSDQKLIA
KSPQLYNPETGVTYEWEFVAQAAWWIRNKPVEVILPTGESMTVKHKSVLASASYPLRDNV
AYWRSEPKTPQLFPVAKSGGSSLEKKYNYTSVGTAIHEDFSSYYPLLLTNMAAFTNADLG
IDEKTGRPRDRYREIYEQKEIYGAQRKDPSIDEETKQRLGILREGTKLILNSATGAADAG
HDTPILMNNRVIAMRIIGQLFSWRIGQAQSLAGATIISTNTDGLYSVLDMGTNQRVLDEH
ATAIGVQIEPEELDIVSKDSNSRAEFLGNGYINAAGDLACWDGPNSRNSLDHPAFVDHVL
VKYFQLVVNNTVPEIPETPELEGVPLALDQPMNRHEVSKIVATMHKEFEPKKLLSFYQNI
LASSRGSNTFLFSVPYIPATEGEETHPATDTSTIATPTLSFDAYGNKAEVMPTQSTVDKR
VPSLLQYYTRTFHVRQDTQQAVFDVIGANPVLIAAAKAASISPASADSRRKKGLASTNAD
PVAKHVLEIAGADVESLRHEKDLKVTKHTGQDPALPVVVFNQTIWHNPNDDVINALLGAI
DQDAYIDMAISSYNKSWHNIIPA

>RXN01069 TRANSLATE of: rxn01069.seq check: 984 from: 1 to: 714
VNDLPNLPKLPFNWTWVLATVATTVVLAGIGLYVYYPSLPDPMPVHWNGSGEADNWTPKS
VGSFLSLILIGPGIILLTLSGMQALLTMQSGVITQRGGAKSANEAHRQWETYKATSMHMG
WYMFVLNALILVMILNEFRPNPLPGGFIIGLIGIIAATIVLLVLIGKTTTSLAKKYPMPD
QDGKTWGIFYNDPDDNRILVDTGMGMNYTFNIAHTWGKIFAVLIFAVPVLIVLLTVLL

>RXN01071 TRANSLATE of: rxn01071.seq check: 172 from: 1 to: 2064
LVVDSSGRYNVTITGLTTTETDSATALNLQMSEAGYLERYTDGATVPSVMLSAADGTTPQ
ELVDALAAELGSNFDVETGEALVEQATGMITQALSFVQYFLVAFGLIALLVGTFIIANTF
SMIVAQRMREFALLRALGAAPGQITRSVVLEATIVGLFGSALGVLGGMGLVAIISAVLNN
LGMPMGSSVGLTPSAVVTALVLGTVVTIVSAWAPARRAGEVKPVEAMRNMETTTMRSMMG
RTITGGIVLALGIIFAIAGAMMTDSSTATRSILVGIGALFVIVGTFLFSPALSMPVVGGL
GKVIGAPFGSVGSLAATNSKRNPRRTATTAFALTLGIALVTAIGMLSATMKDAVSDMMAE
QYTADYILQGPTNGSITMPKESVNDVRDAEGVADVVLVSMNSASVNGQASYSQLGQSVTF
VADGDLSKVISTESIDGSLDLSNPGVVTNQTFADENGWAVGDTLQLESMGQTIGDIELIG
TFTGNDAIGNMIISESSLADTPAADTAVPQMMLVVGEEGFDKEQLRTNLEDAVADYIVIS
VKSATEFAGETVAMIDTMMNILYALLALSVIVAIIGIINTLALNVIERRQEIGMLRAVGV
KRGQVRTMITLESVQIAIYGAVIGIAIGLGLGWAFVTVMSGEGLDAAVSIPWGQVGLMLV
GSAVVGVIAALWPAVKASRTPPLDAITD

>RXN01075 TRANSLATE of: rxn01075.seq check: 2212 from: 1 to: 411
MDNPVNILNEQEALERLQSVSLGRVVVRRSDEMDIFPVNFIVDKGAIYIRTAEGNKLFSM
NLNHDVLFEADEVKDGKAWSVVVRATAEIVRKLDEIATADTLELKPWIPTLKSNFARIVP
NEITGREFTLGEEPERY

>RXN01085 TRANSLATE of: rxn01085.seq check: 551 from: 1 to: 879
RKRGEGLDPNSPEAIEQAKKKGERKARNERCRKNFKGGGTKDLKQTDRTFDQLRKQRVTD
KARNRDVHNEQQLARGEIGEMRSPMWVEVGAAILGVFVLVVMWLAWGGIGLLIQTMMNTG
SPNDKELFDELGVRPYYVAVEQQIGTSSAHTTCYQPLDEFGNNFGDCTRSVPKEPVWYAD
YVASVFAEHGFDAPEPIDNSVGSWLLFGHVGIIRVTFVIAVAAGVYAMSRAAMMRQLETQ
NVAVDTTDINQHTNDARLAIPQEIVRDLSLFPDVGAHFTSPALKHDFPCDAVE

>RXN01121 TRANSLATE of: rxn01121.seq check: 3374 from: 1 to: 1086
MNPEFIHGATEIETTNRGLRPHRLSKEIVERYCDPQFSAMERQPSGVRVVCRTTATSVTL
TTYSTRVVYLDSGRPGGKIDVLIDGAPTSSTPTSGGETTEVNFITGATERRLKDPQVLTV
DGLSEQEKVVEFWLPHNEEIEVISLKANAALNTVEDTRPVWINYGSSISHGSVATAPTKI
WPAIVAQSKNYNLRNFGFGGSAMLDPFMARLIRDTPADLITLEIGINIVNGDVMRRRGLE
AAVDGFINTIRDGHPTTPIKIVSPFYCPIHEKTPGPGAFDTSSFGSGQIRFIATGEPDEH
GRLTLEMVREVLEGFVEKQKDPHLTYVDGASLYQASDAPLLDNLHPDEASHALIAQRLLK
QL

>RXN01128 TRANSLATE of: rxn01128.seq check: 7667 from: 1 to: 1014
MSFTFIRTFFVLFGITLLVSCVPEPPDSYTKESTVLRYQVSDFNLNFVELAVALGYLNNI
ELQVVGSVQGGVESIESLKKDDIDFAAVPFIGLVAGEIATGAPIKAVAASYGISHDSSSA
LLVLKDSEIHEVHDLIGKTVGINTLGALGSAMVERHLFDAGLTEPEIVSVTQRALPGEYL
EQRLYQGQVDAIWVTDSAKHQALETGDFRILAEDSDLVQELNTGCMVVSQKLIDEHPAVV
GELVDGVAQAIEFERSHSPEEVREVYFNYLEAHGQSDRISSFRYWEHSGIATRGGVLSDR
EFSMWSHWIDRQYDVPDINPASIYTNQFNPYRKVNPSP

>RXN01134 TRANSLATE of: rxn01134.seq check: 3892 from: 1 to: 771
LSLDQVPYTAQIVPLAVILTLLDAEEMATARSWDRLNQWFWSGVLGELYGSPAVIARSGR
DTDQVAAWIREGAGETAVVPKTIRDTVFHESRLLSATQDTGVWKGIFALLMGRGARDWRT
GQQFDRWTFDELGCNFHQIFPTKWCKERGIDPVLTESVLNRTPMGRRTEVVIGDTPPSRY
LSRVQSKSLMGDEEFDQMLDTHLLSAEDLHSSNTTHFFASRRTNFIDMVEDAIGKAVIRD
VNESDLTGGHDGPSVHG

>RXN01140 TRANSLATE of: rxn01140.seq check: 3026 from: 1 to: 933
MALDTRGEEMRFRPRALSGAPDTGKDPGLLLLDGQQRLTTLYHCFSGDGYVNTVDFRSKK
VTRKFYIDVAKAVESPVMSDEAIFSVDETGKIISHFGPVIDGGITDLETALAHGCLPVSV
LLDDNGTDFLFDLADMAGEGAREHAKRFQSQIVKTLVSYDIPMIRLDRETAKGGIGSIFA
QANSSGLQMDVFDLLTAVFAADESVETEFSLRDDWVRVERNLRQHSALDGIGSTEFLTAV
ALLVSARKGHASGYREDILNLTLAEYIPAADEMIKGFDEAAEFLRQRCIFESRPGSIHRA
DCSTGRDPHPA

>RXN01148 TRANSLATE of: rxn01148.seq check: 3053 from: 1 to: 600
MTSPVENVKKKPRPLALSPSRAGDYQQCPLLYRFRAIDRLPEPKTVAQVKGTLVHAVLEY

MHKLPREEREYPAMVKQLKPTWAQMCEEDAELKELVPEDELYDFLVDSRTLLRGYFEMEN
PQGFDATECEMYVDTVLPNGVPVRGFIDRVDTAPPAKSELSTTRLARNQSRSGASKRSSR
CCSMHWSTGACSMKSQLSFV

>RXN01153 TRANSLATE of: rxn01153.seq check: 8673 from: 1 to: 543
PFLSPIVTSTHAVVAYSTARGFGEHRVRWDYAQESPLRDTRGFDLRRYHQAPVVDPHAIG
VANVFVPNGARFYVDHAHPEYSSPEVTNAWDAMVYDAAGDHILMQAVSDVASFTSQNRSV
LDGHDPCPALKIYKNNVDGKGASYGFHENYLYSRETDFDVLAQALIPFFVCRQVIIGAGR
V

>RXN01154 TRANSLATE of: rxn01154.seq check: 4612 from: 1 to: 639
LSKKISLETTLNRGIINTRDEPHTDADHWGRLHVIIGDANMSQTANFLKFGMTSLVLDAI
EAGVDFSELKLKNAVSEVAKVSHDLSLTHQLRLADGSELTAIDILRRYLDKVQPFAETPV
EQRVTALWGEVLGLLENDLLSTSHLLDWTAKLALIKSFEARGLSINDPKMYLIDLQYSDI
DPQKSLYHALVSKGRMKTLCSAQDIADAAATSP

>RXN01155 TRANSLATE of: rxn01155.seq check: 3917 from: 1 to: 1470
VESALTRRIMGIETEYGLTFVDGDSKKLRPDEIARRMFRPIVEKYSSSNIFIPNGSRLYL
DVGSHPEYATAECDNLTQLINFEKAGDVIADRMAVDAEESLAKEDIAGQVYLFKNNVDSV
GNSYGCHENYLVGRSMPLKALGKRLMPFLITRQLICGAGRIHHPNPLDKGESFPLGYCIS
QRSDHVWEGVSSATTRSRPIINTRDEPHADSHSYRRLHVIVGDANMAEPSIALKVGSTLL
VLEMIEADFGLPSLELANDIASIREISRDATGSTLLSLKDGTTMTALQIQQVVFEHASKW
LEQRPEPEFSGTSNTEMARVLDLWGRMLKAIESGDFSEVDTEIDWVIKKKLIDRFIQRGN
LGLDDPKLAQVDLTYHDIRPGRGLFSVLQSRGMIKRWTTDEAILAAVDTAPDTTRAHLRG
RILKAADTLGVPVTVDWMRHKVNRPEPQSVELGDPFSLLNPQQPAQETALSILLLGGTSY
IAGEIATLTF

>RXN01167 TRANSLATE of: rxn01167.seq check: 6639 from: 1 to: 396
MADRVLRGSRMGAVSYETDRDHDLAPRQLVKYKTADGEIYEVPFADDAEIPEEWMCKNGK
LGILMEGEGVESKPVKPPRTHWDMLRERRSIEELDVLLEERIEALRKRRRNAAKLLKAQQ
EAEEAEKAAEEV

>RXN01169 TRANSLATE of: rxn01169.seq check: 2636 from: 1 to: 996
LKRVVEAWDRFQIPLYITALIAGALVGLQWPGSTGGFESAINPALMALLYATFLGIPITR
IGAALKDLRFLIVLMSVNFVAVPLVAFALSRFIAGDEALLIGFLLVILAPCIDYVIVFAG
LARAAQDKLLAATPILMLVQILLIPVFLAVFVGSDALGSISFGPFVEAFFLLILIPLVAA
AGTQQVARKWQVGRTIMAAAEAIMVPLMMLTLFAVIASQVEAVSGQFTDIATVVPLYVAF
LMVMIPIGGGISKLGGLGFKEQRAIVFSGATRNSLVVLPLALALPAGLEIAAVVVVTQTL
VELIGMVVYVRIIPLIFHEKQTYRKLSGIGES

>RXN01173 TRANSLATE of: rxn01173.seq check: 4063 from: 1 to: 615
MHVSTLPNKKLRTRIFAGTAAVALSLGVASCSNAEDAVDSATDAANSATSAAGSAINDAT
GTSSASTTEPSGTSGSDSGSDSAGGDTTEVESADGSTISIPTAVVTAANAAGFSTPESVE
EGPNGESLVTFPEGYIVNSAEGGAQALVGMIGETWIGEGGLSAAVGLPTGPEEATTNGWT
QQFTSGVISWLDDGSGQFAASVEPA

>RXN01174 TRANSLATE of: rxn01174.seq check: 9196 from: 1 to: 750
MSNMQGNDSKKSSGASRAESPLIKFRTLIIVIFVILIVGLASIAVGPVVYQLIMGPGVKT
EGIQADGAAPASTDMNGTWDVAPGSIPNTTSAGFTFAEILPGEEKITSGSTTGVTGEVVI
EDNSLISGLITVNMTHITTDQEKRDINVRTKLFHTDQYPEATFEVTDSVDLSALPDTGSI
AQVVIPGELTIHGETKAVEPTFDVLRTGDQVIVASDIEINRLDFGVETPEFIAAKINETG
EINVRIVLEK

>RXN01206 TRANSLATE of: rxn01206.seq check: 3690 from: 1 to: 300
VSAENTENTDSPFEISEFDDHRRPLQRALKFGSIALIVFTLISLAIWGATRGVPGVSAVV
IGAAVGAGFVLLTALSVLFTTNSNVTTTGAVVLGGWLLKI

>RXN01210 TRANSLATE of: rxn01210.seq check: 8240 from: 1 to: 831
MTTSHTARGLQHATPERRKTSFFKTSLFKAEWLQFRRNKTLLFMATVFPVGIPLLLFLIG
NGGAAESANSFDYFVMYTLLFVQFYTVLSMATTRRDERVLKRLRTGEARDIDIIGAICFP
GALLTLIFTVVIIPLLMVLGAPAPINLVPIVFAVLIGLLLCSALALMTSGFTRNAEAAQM

TSMPVFMLAMGGLGSIRFVFGDSIVADILAYTPFAAISDLVQIGWAGATFADSVGGVEAA
NFAGIFQDMLIPLGILAAWTAAAVWAANRYMRWDSYR

>RXN01229 TRANSLATE of: rxn01229.seq check: 2418 from: 1 to: 1278
MIISTNTAHPLHEPHVPSHHNRMNTLRAGVLGANDGIVSIAALLLGVIATGASDTVVFGA
GLASTIAGAVSMALGEYVSVSSQRDTERVLIAKEAKELAEDPTAEHVELSEILHSYGIXX
XXXXXAXXXXGXGDALGAHLQLELGIDNEQLTSPLAAAFSSAVAFLLGALLPMVXVFXAP
XGWDAGVXFVVTXLVLAXTGFISXXXXGTXPMRXCXXXXXGGXLXXALTXPSWXXXXXAX
XXXXXXXXXXXXXXVXXXXXRRXXXXXXXXXLXXXXXXXXXXAXXGXXXXXXXXXXXXX
XXXXXXXXXFXXXXXXXXPPLSGEILLAGLGGEIGMGEPRIPVTTGDLETRGLQCLGKL
GQWPPVGGGHGMIHRFQRRPGEKGHQQATTILHRHPQCDQGVGQLARAHVDQGVPGQQAC
PALRRV

>RXN01231 TRANSLATE of: rxn01231.seq check: 7153 from: 1 to: 243
MLGYTFVIFILAPFLILTGIAMAPAIRSRFPWYVKLFGGHQGARSLHFIAMVLMTGFVIM
HVGLVFWSMATTTWSTWSSAI

>RXN01246 TRANSLATE of: rxn01246.seq check: 4104 from: 1 to: 507
MKRTITIAALALTSTLVLSACADNTEGENTDTTTIATTSAPDTTETTGATTDPETETGAA
GEVSAEHNDADIMFAQMMIPHHQQAVEMSEILLAKDDIPAEVIEFTQGVIDAQGPEIDRM
NTMLETWEEDPVTGDMGEMDHGGMSGMMSEEDMTALEDAQGTRGCPALP

>RXN01249 TRANSLATE of: rxn01249.seq check: 8446 from: 1 to: 471
SQIVAVSSHGLTTIQEIDVKRAAIAAAALTLALTGCSAADPEPTADGTVSQDTFLTTHGL
AAMDAVEIIDHLDRQKVTERPTDLIASVRADELLLSSDDQEVVVDLPDNQTYVSIAPYLN
STHDCFYHSLTTCLGDLDNEDIHVMITDEATGEVLFD

>RXN01251 TRANSLATE of: rxn01251.seq check: 4314 from: 1 to: 309
MTQPDMSQILAQAQQMQAQLQAAQQEILATTVVGNAGNGLVTVTMAGNGEVSAVTVDPKV
VDPEDVETLQDLLLGAFKDAHNKVANVAEEKMGPLSQGMGGLF

>RXN01263 TRANSLATE of: rxn01263.seq check: 84 from: 1 to: 912
LTPYDPTAVNKESEKEAAKNLFGAEALTVDPDAGEVVDRVDNFYPTTAKAKRDYPSNYAA
GCHQEVNETSPESCVYGDKNSDFSVALVGDSHAGHWLPALEPIAEAQGWRLEVYTKSQCP
LISTAIKLGETFYAECYEWNEKLLAKLTGPSAPNHVIVSSQRYASANPLIDSVATGTVSE
GYEMAWNSLKDAGVSISVLLDTPRPQIDIPECVASNRDNLSECSVHRSVALGTEAHPQQK
TAAQNIDVPVLDLSNWICPEEYCSAVIGNVLVYRDSHHLTATYARSLSSALWNELVASNG
EPFK

>RXN01266 TRANSLATE of: rxn01266.seq check: 6088 from: 1 to: 1035
MPKVSVVTGFYNRCEHLERTIESILNQTYSDFELIVFDDASTDGTASRLLELKEKYDDPR
FRFIIHEENKGFVKGLSEAISGAKGQYIAVQGSGDVSLPRRLELQVEFLDANPSVGAVGG
AIYNIQEDTGTRNPQRFEKPIATFDDLLTSNPFTHGEVMYRLDLYKSIGGYRSGFTFAQD
RDLWLRMAKKADLGIIPDFLYHRYTLLDGVSFVPDKTIRQRCFSEAAVRLALMPEEEGAL
AYSRLEAEGPTAVVPIADRAVQKFVPKAAIRLCLYGAPETGLHMARDYIQNPLRRTIVVV
LISIYSSRLIKPLQDILYKSIFKGVSISKPIKSSLVKFTRRIQGK

>RXN01275 TRANSLATE of: rxn01275.seq check: 5209 from: 1 to: 918
MEKIRSPAVQSDALQVFKSALAATVTWWISVNLLNSQLPFLAPWVALMTMQFTVYHTFIS
GIQTAIASVIGVGLSFVIGTYLDVSVWTFGLAMVIGLIGARVPKLRAEGIGIATTSIFLL
ASGFDDQQPLLYDRILEILLGVAVAIAINLIIFPPLRDQEANMVVGNLDRRMGEVLQKMA
DELAEKWNIDNADEWLEEINSINNDLEKAWHSVRFVRESRRVNPRKIRIQEGRPQPTETS
YESNLTSIDEGIAHLRHLARTLRDTPIIDSDWGSSIPATVGIPYARCRSFARRSESGNRS
YPRPAL

>RXN01276 TRANSLATE of: rxn01276.seq check: 3553 from: 1 to: 444
VSSELSSGTSSGSSEDSEDSDISNRDIIFGIAAIAAVGGLIASGVHWAVQQRMIPNPLPG
IIPNPPALAPQAPAPAPAPAPAPQAVAPQVVAPQVVAPAPAPVQTNRTYKNCTEVWNVLG
RSIRQSDPGYGTHLDRDRDGIGCESRPR

>RXN01281 TRANSLATE of: rxn01281.seq check: 193 from: 1 to: 762

VGLSRSHYQLAAENTKSLVRMVPMTVPQGNEPAKKLATDLNRNQVVDELSAAVSRGQLTL
EEFEDRSSKAWNARHLDTLVELISDVNDNPYTLLGQQFPGASYAPAAYETTPPAMPNVSD
PVNIVRNRITGNPNGSKMSVSFMGGTVRKGGWHVPNVHTSFAMMGGNQIDLRDAFLESDR
IQINAYTFMGGIEIIVPEGVFVICDGMGIFGGFEQSVDKAGALNPARLPSNAPTVHIKGL
AFMGGVSVVTKKNI

>RXN01296 TRANSLATE of: rxn01296.seq check: 1595 from: 1 to: 1083
MSIEQAITSLSARVRELKPIIETEEATKTALIIPFISNVLGYDVTDPREVIPEYTADVGV
KKGEKVDFAIKTGDDFHFLIECKKVGSPLSLDHANQLVRYFNVTDTEFAILTNGEIYQFY
GQLDAANRMDAKPFMTLDLNNIDARQFPHLEMCTRKHFNPQALAANAEELKYIAELKKVI
ANQFQEPDVEIVKMLAATVTTKRMTAQNLEFFTRLVNTASSQFLKDEVNRRLRSAQVFED
PVQTQGADAETPAEDEAVIEEVVSEIVTTEEEIHGHSIVRAICCSEVSAQEITMRDAKSY
CAILFQDNNRKPIARFYFDRKIPRIGIFNAEGEQEHFDLESIEDIYNHADLLHSRVVALN
A

>RXN01301 TRANSLATE of: rxn01301.seq check: 6647 from: 1 to: 525
LIVDTQFEKIPAHDVVGIRVILSSEDLPELFKRGYAEVKKFLRLEGIEPKGPARAYYFGD
VSDTVDILIGFPVSPAQAESLRRGALSQSGGDIDDVVLHHFRDMKTMHSRHSGPFDGVER
VWDEILDEVEDLGCTLPSSSIGWEEYIEGPATADTCDQLASEVYVQVCQAPVKSA

>RXN01306 TRANSLATE of: rxn01306.seq check: 7259 from: 1 to: 1008
MTEWYVVLPATILLIALSAFFVIIEFALLAARRNRLEETVETSRSSRAALRSLNELTLML
AGAQLGITMVTFALGAITKPWVHYALMPLFEWARIPLVMADVIAFILSLFIVTFLHLVIG
EMAPKSWAIAHPETALRTIAIPARGFINLFRPLLQWINKMANDLVRKVGETPVDRAAAGG
YDTDTLHALIEHSRETGALDQQSAAQISGIIKLDKITVGQTLTASPFTHSASATVAEVQA
AAQRSGSLRVLIDAPSHLFPHVIHVRDTLGASPDEKASKWSRPILTVAETDTLHQALEYM
REHNEQISAVLSADGKTVLGVITWDHILKYLWPASV

>RXN01324 TRANSLATE of: rxn01324.seq check: 6882 from: 1 to: 300
MSNSECHTHGYIEEKQRYLARLKRIEGQTRGIHRMIDEEQYCIDILTQISAVNSALKNVA
FGLLDDHLAHCVKEAADLGGDELDAKLKEVSDAIARFSKA

>RXN01326 TRANSLATE of: rxn01326.seq check: 1197 from: 1 to: 366
MAFPVTEDKILAAEETLGRRLPETLRERLLQNNGGEVIDNENNDWILHPVRDDSDRKRLV
RTANDIIRETESAREWDNFPENAIAIANDGTGDLIILLPDDDAFYIWSHEDEPLIETELE
DA

>RXN01331 TRANSLATE of: rxn01331.seq check: 1587 from: 1 to: 2397
MLTTLWIAVLVFTVPGLVVSWVSGLKVPWAIAASIPATFGIYGLSAWLLGLWEMRFDLHS
VVISTLVFAAVALVWRLFFVGGWLVRRRKARIRRQTLADEERAENAEVSAGEPAESSTNE
AAESESETSERRGIWRVIFDYMRDGGILDHRWLLPAAGAITGAWLIIDRAVDLLLSTEHG
LGDIVQGWDVHWHASTVRFIDETGIASSTMMGQLRNIETQQDLFYPSAWHAGAWVLSDVG
NLTIVEATNLTGIVLSGLLLPLAVALIAWRMINNRGLTAQIGAGFAGLITIASPVLFWVG
NYVGAWPYVAAIGASGVVLALFMSTPSVPVRIFAAALAFMGMFQLHPAPSTIVIMVLLLW
WLLKLVVVPSQKVKGWKAGIGIRLKDVGILAITGIIGVLFMLPQVISGSEQTEDVLSYSA
EEQVTRSESWLVSIFMETRHVDFFGNIDIVPVLVFAAIGGVVALVWRGNLWAPVFYFASV
ALTANSLKPFEEPWGDWLNIVGGLHYSTGHRLIMPVAMFTFAAAGIGAAAVIRLICLGPI
KKFTTVSGVVSVVMALVVAVPLQTWAKDFVEEGSETTILAPHNDERMVSNNDLAAWDWLI
QQPGGADMNIMGDPADGNGWMYAYNGLHSVARHYAWPAAGEGSATAMLFWWPQLLGVGTD
ENPDQVNDVDQAARDLNVGYFMISPWTFWDFQIPNFRQIDLLWQTPGVTPVCKKGDSVIF
AVNDMFTDAELDQMRAPGNSPEPLPELPTLGELGLAETEDEVDQTYYHRPTVPAGVNSEM
PSAETLYAPDPTKPHTVPN

>RXN01337 TRANSLATE of: rxn01337.seq check: 282 from: 1 to: 1413
VTFRGGNTGAKHAVVVGSGPNGLTTAAVLAKAGWQVDVYEAAPTPGGAARSESVLGEGTI
SDLGAAGHPFGVASPAFHYLGLEDHGLEWAYSPFAMAHPLDYGRAGLLETSLPETAKKLG
PDARRWKNLHQGLTKNIDKHLANLLGPVLKWPAHPIRMAKFGPFALLPAKRLASAAFETE
EARSLFIGSAMHSVTPPHKPMTASLGLLFGALGMSRGWPVAVGGSGRIVDALVNVINHHG
GTIHCDSQIDSLSQFRDTDAIILNQTPSQVLKLKGTDLNAGLPQRMSTWKHGPSSYKVDY
LLDEPIPWSNPQVGQATTVHVGGSSEEIAFAEAEVAAGRMPERPFIILCQQQVADPSRAR
EGRHVVWAYAHVPRGFVDKRAALLITAQIERFAPGFRDRIVHSVDTNAEDLEAWNPNLVG

GDITAGSALLRRMPTKIGEKTYMASASNAPGGGVHGMPGWWAAQAVLADHR

>RXN01351 TRANSLATE of: rxn01351.seq check: 2597 from: 1 to: 585
MTSLFDAPTLQRVTVFTGSALGSSSLYTQAAQTLAKTAVDRGIDLVYGGGKVGLMGIVAD
AFLESGGEAFGVITESLMKGELGHEKLTELEIVPDMHIRKRRMAELGDGFIAMPGGAGTL
EELFEVWTWQQLGIHQKPVALYDVDGFWQPLLEMLEQMTQRGFIKRDFFECLIVESDPHA
LLKAMQTWTPPAPKW

>RXN01362 TRANSLATE of: rxn01362.seq check: 8917 from: 1 to: 3654
KWLGTPAQSLFLIPPVTQHARTGTHLYDSLQLLFTLVDKGHHPTDAKAVAFDAEAGEEGL
HFRNLSADLFLPAATELIDRVGLSNEALNKVLENLLLSRVQSGKDRGFISYATLGVTELG
QVYEGLMSYTGFIAQEDLFEVAPHGKADKGSWMLPVSKADEVPADSFIEVDQEAPGGGVI
KVRKRHPRGSFVFRQSSRDRERSASFYTPQVLTSFTVTQAIEELQASKRITTANDVLSLT
ICEPAMGSGAFAVEAVRQLAELYLELRQEELEQQIPAEDRAKELQKVKAHIALHQVYGVD
LNSTAVELAEISLWLDTMNAEMDAPWYGLHLRNGNSLVGATRSLYAPSLLNKKAWLTATP
TRYRLDDIAQAIDENKAEPLFNHGIHHFLLPSTGWGATADAKDLKDLMATEIKELKSWRT
SIRASLSKTQIKQLNNLALRVETLWRFVLMRIRIAESQISRSTTLWGQEPAEVSEVVTRE
QIEQDLFGNIDGAYNRLRLVMDAWCALWFWPLDAVATAEHPERPALPDLDEWLATLTEIL
GIDLPLKSKNENQIVLGPDTNWLAINDAEATDLGFSGALSFERVSANHPWINVARQVAKQ
QSFFHWDLDFAHVFAKGGFDLQVGNPPWVRPDVNFEDLLAEHDPWWAVMSKPTQASKKER
QKNFHNNPKSLEHVVSGAGEPVATSAILGSVTLYPHLKDQRPDLYRGFMEKTWSNASPAG
AISLIHPESHFTEKKAAPLRRGAYERLRRHWQFINELILFDVHDLVKYGVHVYGAPQESI
NFLSAASLYHPQTVLDSFDHDGSGNLPGLKDDNGNWDRRPHKDRIQLVNADTLTVWKSIL
EDEQTPYLDTRMVYTVNTEAAAALEKLASAPRIKELGLQFSSGWNETTDKKKGYFDVGWG
YPASWSDAILQGPHLGVATPMIKQPNPTMKHNQDWSEIDFEAIPANFIPATAYQPDRQTK
PTYDADYGTWTFGDKQVPVADTFRIAWREMAATTGFRTVYPSVIPPGANHVHTVNSAASR
SNLKTILVGAQLGAILSDYFARSSGSSHIFNDIVRKIPLPNFTSLEKQFARTYLRLNCLT
SAYAPLWEEITGEPWDVQVPLRNAEQRRAAQNDIDAMVALSLGISADELCMIYRTQFPVM
RRYDQEDHFDANGRKVPKEIIKLQQKLKDGQELSVEKRTWVHPQSEVSYTFEYPFRVLDR
EADLRAAYAKFENQLKEP

>RXN01379 TRANSLATE of: rxn01379.seq check: 3028 from: 1 to: 942
MSAFDSILNVEEWISDHYLTNDDAKGASFSKRVRERIKEWKTTEDATQQSGPLTRFSSNR
LQLQHALSELDDATTAASLVASALGYGVPSARHAQRGSDTISYSSWVGNAGSVEFLAATP
AESFEENFRSLPLEPVAVNDKPQDITAAKLVGQIFLSDTPPAFVVITAGKWVVLAERETW
PLGRHLAIDISLVVERNDTKAQGEMQQTVVALARENTERAADGTTWWEETIEQSREHAVK
VSGELRSAVRESIEILGNDVLTRYEAKELSTAEIDGGELAKQSLRYLYRILFLLFAEASP
ELEILPTGTPEYDE

>RXN01390 TRANSLATE of: rxn01390.seq check: 97 from: 1 to: 657
MFRRSLPSNKTSSASSASSADTSYSVRLGRPEEPGYQPEPSYSEPYTDSDFAPAGAAAAA
AAVAPPMIAEQPQIVEDARRGTLDFGLLIIRAVIGVYLIVRGVFTFFTLGGSAGLAGLEA
EFAGYQWPEILAILLPSIELAAGVFLLLGLMTPVAAAVATVATSFTTLHQVNTHEGGWGE
LSEPLMLALILTIVVVGLQFTGPGKISLDSGRGWQSVHW

>RXN01391 TRANSLATE of: rxn01391.seq check: 3163 from: 1 to: 690
VAAVAFAAYVIDGGVEEASGTPTSSESSVAATAPAASSETAAEYRAMLASLDVKGRAPGT
GYDRELFGPAWTDTVSVEYGHNGCDTRNDILQRDLDDIQLREGTKDCIVTSGLLSDPFSG
ELIDFVRGERSGDVQIDHLVPLHDAWVKGAQQWDEQTRKNFANDPDNLLAVKGTLNQQKG
AGDAATWLPPNTAFRCDYAKKIITVKDRYNVWVTEAEASALERQLDTCAA

>RXN01400 TRANSLATE of: rxn01400.seq check: 8655 from: 1 to: 1500
MAISVSMPKAISREELERAWLEVIERHGTLRTVFSTGMGGEVQQHRIDVGPGKWIDHAVA
PGESINEALRAVLNRQCSPYSRPSHSLCIIDAHPRPTVIIGSDHSHVDMWSMLVIVRDLL
AALDMELPVEPPLAFESHTAELLAAPPAPERIHQRWREILEAGGGKMPQFPLPLGDAISM
PERVEVRDIFGVNGLAIYSARARAQQVSSLALTISVMADVTAALADLPLRAVFPVHSRFD
QRWHDSVGWFISNSVIEVPDSDPHTAAQAVREAVSLGSYPLAELLEPWGGMPETPGMFAI
SWLDLRRLPVSIDDIGLQAQYVSASLRTDGVMLWFILDRSGAHLRCRYPDSLVARENVGR
WIDAIVAQMRAEAGTVNLQAGGEQLTLRHGTRADISEIAPLLARNAADPCELVDLEHALD
LLTHESSHFLAVVRNARGKIIAAMQLTIVPEFSRGGALHLHIEGPFIIPEYRTTDLDKKL
RAWAVEHGRARGVKVEEVVG

>RXN01403 TRANSLATE of: rxn01403.seq check: 3765 from: 1 to: 648
LVRGRGYFNAVDIYETSTQPDQEFPFDFDTFSADPTPFQLSAVRADTGETVFWGREDTPD
LSALMKRVRASSTMPGFMPITYIDGHPYVDGAVGETGGLMLQPAIDAGFTRFFVIASRPR
DYWRKEIGRPGFIKAALRRFPTIADLTIARPALYNSVKQQILDLEKQGSAYVFFADNMNI
QNTEINLKKLRASFDAGMQQTRKDWPEIMSFLNQTR

>RXN01409 TRANSLATE of: rxn01409.seq check: 6984 from: 1 to: 822
WVDFPDVTARLGYEYMQLTPHVDFGPFFRHPKADDDLVAALKKRAKDAGVTIPALLPVQR
ISWPEETQRVAAVRNIKRIIQLAVDLEVDTLNTEFSGRPERSEDSEDAFYRSMEELLPIL
EKEGIKFNIDPHPDDFVENGIEAWRVIRGLNSKQVGFVYVAPHSFHMGDQAEAILPAVGD
RLGAVYLSDTFDHHKSHGLRYITNPPGNAVRVHQHLKIGDGDVNFEEIFSLLRSTGYLDR
EDALLVSNVFAEDEAADEVSRYQLEKIRSLIENA

>RXN01422 TRANSLATE of: rxn01422.seq check: 4360 from: 1 to: 972
MAQRKLASVIGAALAASAVLVGLMTPATAQSSGSSSTDITRALTSSGGVADSRAPEGGAK
VVVFGDSHTSGTNAPFRTDERGCLKGANNWADQLQSQLGLGAGDLIDVSCSGASINSDGF
HFSDEVRHAEARGAIGPNTTDIFVQLGKNDQWGLSNVNLLQSVQTCLTDVFAGCGDAAVA
AGKMQDPNAVTAENYAERMKPVIDYLKYYAPNAEITLVGYQEYTARSGSQVCVRLGGTPL
VKNDAPALVSFMNKLDMAIDGAAGILGVSHVDLRSATEGHDSCSNDPWVNGVFDARAEIV
GGPWHPSVKGDSVTAGILRDRVNA

>RXN01434 TRANSLATE of: rxn01434.seq check: 1389 from: 1 to: 2952
VLGAVLTSLVIPVLTRAEKEDADGGSGFFRRLLTLSVTLLGGVTILSIIGAPLLTRMMLS
SEGQVNVVMSTAFAYWLLPQIFFYGLFALFMAVLNTREVFKPGAWAPVVNNVITLTVLGV
YMVLPARLHPHEQVGIFDPQIIFLGVGTTLGVVAQCLIMIPYLRRAGIDMRPLWGIDARL
KQFGGMAMAIIVYVAISQFGYIITTRIASIADDAAPFIYQQHWMLLQVPYGIIGVTLLTA
IMPRLSRNAADGDDRAVVSDLQLGSKLTFIALIPIVVFFTAFGVPIANGLFAYGQFDANA
ANILGWTLSFSAFTLIPYALVLLHLRVFYAREEVWTPTFIIAGITATKVVLSLLAPLLSS
SPERVVVLLGAANGFSFITGAVIGAYLLRNKLGLLGMRSLAKTSLWALGSAAVGAAAAWA
LGWLIQAVVGDFLLGTLSSVGYLLNLAVLGVFFIFVTGIVLSRSGLPEVQNLGQALTRIP
GLSRFIRPNTKISLDVGEVSEQDFSTQLVAPSEFAATPVPPPMSAGIVRGPRLVPGAPVG
DGRFRLLADHGGVQGARFWQAREIATGKEVALIFVDTSGNAPFAPLSSAAAAGIAYEVQR
RTKKLASLGSLAVAPNIHSEAYRNGCLIVADWVPGSSLSAVAESGADPRAAAAFALAELTE
TIGEAHEMGIPAGLDNKCRIRINTDGHAVLALPAILPDASELRDAKSLASAAEMLIDATL
APSDVKAMVTEAQGLATEDNPDYASLAMAMRTCGLFTEEPTHLVVKKEKTPKPATRDGFG
ASDYTVKGMAAIAAVVIILVSLVAAGTAFLTSFFGSSTNEQSPLASVEATTSATPEPVGP
PVYLDLDQARTWDDGAGTDVTDVTDGNTSTAWTSTGGDGLLVDLSTPARLDRVILTTGTG
SDSNVTSTVKIYAFNDASPHSLSEGIEIGTVDYSGRSLSHSIRDSSKLPGQVESVVILVD
EVRSSQTSDTNPQMQIAEVQLVGW

>RXN01448 TRANSLATE of: rxn01448.seq check: 5425 from: 1 to: 1167
MAKKKLGTVARLSELDKSLRNRLLRVRSRLLFIVHSAIGAGVAYWIAVEVIKHGQPFFAP
MSAVIILGLSGGDRIKRATELTLGCALGVGLGDLLIMQIGTGYWQIFVVVGLALLVASFV
SPAPLVSNQMAIGGILIATMFPPGDGGSIDRMIDAFIGGGVGILVIALLPSSPLDAGRHQ
VANVLGIAASVLEDVAASLKAKDAAKLNNALEALRRSQASVNKLETAASSGKEATTVSPF
LWGDRARVRSLYRILAPVDNVIRNARVLARRAVVLTEDNDTVSDEQIHVIEEIADIALRL
SDLYEHHKEISEALEIPELVNRLRQLGSEVGEDIAEDRVLSAQVILAQSRSIIVDLLQIC
GMSRESAVAVLVPTSESPAYPPELWDDED

>RXN01459 TRANSLATE of: rxn01459.seq check: 4910 from: 1 to: 810
MNSNGFGFSFGNNDDDDDKNRNNDPFGLFGGNFGFGGQGGAGGPGGLGDILNQFGQMLSG
MGDSMNSPEAAGPVNYDLAARIARQQIGRVAPVKDSEKEAVEESLRLAELWLDNATQLPT
SGHRVEAWNPENWLENTLPVWKRLVSPVAEQMNKAQLENLPEEAREMMGPMSSLMNSMSS
MNFGVQLGNALGDLAKQTLTGSDFGLPISPVGVSAVLPGNIAEASKGLNVAPQEMLVYIC
AREAAANASSSTCRGLSSASFPPLRNTPSA

>RXN01460 TRANSLATE of: rxn01460.seq check: 5642 from: 1 to: 294
VPWLVERLVSSVEEYAVGLEIDTSHIQEAMGNFQMDNPDPERLQEMMNELQGMDLSPRIG
SRNANAVSRLETLLALVEGWVDIVVTQALSERIPSPTP

>RXN01471 TRANSLATE of: rxn01471.seq check: 6310 from: 1 to: 807
MQSFKTLESWPVDNVSASVISDGAVHFYGDVDRVFELMSVTKLLATYGFLVAIEEGVFEL
DSPMGPEGSTVRHLLSHASGVAFDKPVAEKGVGERRIYSSAGMDILADAVAAEAEMPFAE
YLREAVFEPLGMENSELWGSAGHEARSTVADLTKFGQELTAPTLISPETLAEAFQVQFPE
LIGTVPGYGMQKPCPWGLGFEIKGQKSPHWTGDLMPENTAGHFGQSGTFFWTVPGSGQVG
VVLTDRNFGPWAKPLWTAFNDEVWAELNS

>RXN01479 TRANSLATE of: rxn01479.seq check: 8990 from: 1 to: 240
MIQLVIGAAAGYVLGTKAGRKRYHQIKKGYEAAINSPATKSAVNAARKAIANKLDPQPRM
KEVKNLRTADGHEVLEQDQD

>RXN01484 TRANSLATE of: rxn01484.seq check: 1102 from: 1 to: 546
VLGTAQYDGVPSRQFAARLRHAAKLWRLHEIQHVYTVGGKLPGDRFTEAEVAREYLIKEG
VDPDLIFVSAVGNDTVSSYEALDPEKLGRVLIVTDPNHSYRAVRIARRMGFDAKPSPTTY
SPAKFPSIVYFLTLSHEWGGVVVQDVSRLLGERVPDKVKHLCAQSKVCCALRGVHAMSNF
GG

>RXN01485 TRANSLATE of: rxn01485.seq check: 9216 from: 1 to: 2052
MNFSLVHLRENVRRVSVTVAIGAGALLISGPFFTAHTAEATETYVLAESPEFYQDNVTDY
TGQISSSDITNIQAAIDDVKASEQKVIFVVFLSSFDGVDPETWTQQALQANGGGNVLIYA
LAPEERQYGIQGGTQWTDAELDAANNAAFQALSQEDWAGSALALAESVGSSSSSSSGSSS
SSDFSGAWLAAAGVGTVAAGGGIWAYSRSRKKKTSAATLEDAREIDPRDTNRLMQLPMET
LEHLAQEELTSTDDSIRRGKEELAIATSEFGPERTRSFNRAMNHSTGTLQKAFEIQQRLN
DSIPESEAERQSMLVEIISSCGQADDALDAEAQNFADMRNLLINAGSKLDALTQKSVDLR
TRLPKAQETLAGLRTRYSAEVLESIDDNVDLASASLDEAEEVLPQAYEIESMPAGEQGGL
IDAIRHIEHAITTADKLLAGVEHADENISTAKANVADLIQEISDEINEAGQLKQSAGADG
ARADWASLDDAVRAASAALITASADAEKDPLGTYTELVDVDSALDTQLDTLRATAADQAR
QLRVFDQQLQSARSQIQKAEDLISTRGRIVKSEARTHLANAQKLYAMAQQNRTRDTRAGI
DYGRQAAVAAQRASKSAQNDITTYNNRHNSGGGTTGAIVTGMVINSILNSGRGGGFCGGG
GFGGGGGGFSGGGGGGGGFRGGRF

>RXN01492 TRANSLATE of: rxn01492.seq check: 9162 from: 1 to: 804
VTTTLWAVSDLHAAVKANADPIENIQPKDPSDWLIVAGDVAERTELVLEILARLRRRFAK
VIWVPGNHELFSRSADRYQGRDKYSELVEGCRKIDVLTPEDPYLTFGGVTIVPLFTLYDY
SFRRPGFTVEQAVQAARDRQVMMTDEFSIAPFVDIRAWCWDRLAYSIKRLSKINGPTILI
NHWPLVVEPTYQMRWQELALWCGTRHTRGWAERYNAEAVIYGHLHMPGITNVNGVKHIEV
SLGYPREWEHWSGQHVWPYPVMEVDNAG

>RXN01518 TRANSLATE of: rxn01518.seq check: 9224 from: 1 to: 474
VAFMQKTSAGWLIATGGFLAAVSAILTWRFYGSMTSISITVSITFWLLAVVCGFAGVKVQ
GRLDEGLIGQDKSQMNPVTIAYLAMLGRACAWGGAIFGGVYVGIGSYVIPRAGELSAASN
DLPGVIACALGGIALSAAGLYLERSCEAPPPQSGEAIS

>RXN01539 TRANSLATE of: rxn01539.seq check: 9014 from: 1 to: 2166
VVTVAGNEKNKIREERVARRAQAVVEAEISLAAQASEQVREQAEAPDVNEQVEEVSVEVS
SVQSLTQPKTLGQLHDPRKNVMSSSDLASIIGVEQQPVAYGESEEPETLRDVLPRRKLHP
SEITPSYEVADGEQRSIFGESAPSDFDDLSDVEEFDTSHWVRAGQDDRSDDDRLADEAGV
PRSGAQDVADNEANLSGVDEQLHMREVHAQSFDPIDVAKKERKAAEKKYAKPPKSDNPYL
ARDAKDAAARKRKINAAHDNFAQEMAQAAMGPLRKGVNTQTVMAACTTAAVMWCMSPRMT
GVNVDMKRKFNKDLEQAKDTKLSKYVSKDFWKSKLTRDKTEKEAKSLSDAFMQQKTAIIS
NRERIPMSVASAAQTVVRLSDQAYEAMREVDTDGQAIVDAKDVSAQVAEDIDMVVKQGEE
HGLKSKDIYGAARDIVGRRMERDPGYAARFNETAFGTVRLGEQRRGMVISKTPTWQFPDG
AGLSKNAGWFSVREPMGNAQNFADNLAATLATEMRVAGEQYGSDGVRDVVAGFMTATDVS
ESGLASAKKLLPDFDTRGRSASRVRQIAMAQRTQAAIKVLQDDGNQTAMTTEQVKEVQVW
AMDQAEKVMQRDHPAILDKFVRKHGQTFGQDADAFVKSITMEKDTSSEYTDAMVRPQENR
GSGRELAARRRVQAAQINQAAQLDMNVHDFRESNLPEERPANPYEAYVRETEAKTNDPQY
GY

>RXN01549 TRANSLATE of: rxn01549.seq check: 789 from: 1 to: 1659
VANDFIEPNDAPDAPDNGDSGSSGFVDEAKDKTRSAAQGLGYGALRVGFGTAALAANGAR
SMGNLAKNLWTRMMGLALSAGTGISAATGGMITARVGAMLAGTGSVLSSVTTIALIVSMI

VVPAGRKDGIIELCEPPVTANPFTIDAGDMTENAKLVYGALSYLGMNDQNIAGVLGNFET
ESGIDPTAVEGIFDEPNTIGPRKRAAWDKNFEPQPMGIGLGQWTAGRTQMLLDFAADRNR
DWHYIDVQLAFAISGDNESDRKVFLEMVDNKNSSSNSPTAASEYFLREWERPADVAGNAP
IRAEQASKWYAQMGGWQKNSTLGESVIAMADGAAAKSTARDEQDALNDCPEEDRTSGGNT
SAAEAMVTISHPYLADSRGNDGTDIYRYIHDEVLTGDPYYASCDRGVATAIRWSGTDDTF
PAGPTAAQYEYVVGTGSGRWEEIGNLATMSENDLLPGDVLLGAPNHVAMYVSNEVVVDML
GPGNAEPNAAIGHASLNDRSPGLDTLSLDGWGVNFKVFRNTQAETNSVFSGVQIPAGKEI
GEMTNPTRTTPAG

>RXN01557 TRANSLATE of: rxn01557.seq check: 9051 from: 1 to: 816
VRSSNPVFSSLKETQRPQGQNPYGGYDNFGGVYQQNVAPQKAERPMTVDDVITKTGITLA
VIIVFALVTFGVWLVSPGLGMILTLVGAIGGFITVLVSTFGKKYGSAAVTLIYAVFEGLF
VGGISLLLSGFTVGNANAGGLIGQAVLGTIGVFIGMLFVYKTGAIKVTPKFNRILTGMMV
GVLVLVLGNVVWALFTGGASPLRDGGIIAIIFSLFCIGLAAFSFLSDFDAADRLVREGAP
SKMAWGVALGLAVTLVWLYTEILRLLSYFQNR

>RXN01574 TRANSLATE of: rxn01574.seq check: 7504 from: 1 to: 1035
MSNKRIGVVIVSYGHEQDVANLVDTFADQLKTGDRVVVVDNRKPWVLKDAVGERLEKHGA
EIINHDNGGFAAGCNVGAAHIVDDVDLLFFLNPDTVIDDPTLFNSLRRVDEQWAAFMPYL
LLPDSTINSAGNALHISGLSWVTGLDEKPVEGSSEVTDISIASGACLAVRVDWWKRLGGM
EELYFMYHEDTDFSARLLLAGGRIGLLHSAYVTHHYDYAKGDYKWIYIERNRHVLLLSVL
PLPLLFVLIPQILGVNLGLWAIAAKEKRVGLKVKSLRLLIRDLPAIFKLRRSTQELAELT
PSQYLAKMEWRLDNPNLGNIGSNKIVATGYKTYYKLCMSILKLLA

>RXN01589 TRANSLATE of: rxn01589.seq check: 4956 from: 1 to: 1020
MVEQIKDKLGRPIRDLRLSVTDRCNFRCDYCMPKEVFGDDFVFLPKNELLTFDEMARIAK
VYAELGVKKIRITGGEPLMRRDLDVLIAKLNQIDGIEDIGLTTNGLLLKKHGQKLYDAGL
RRINVSLDAIDDTLFQSINNRNIKATTILEQIDYATSIGLNVKVNVVIQKGINDDQIIPM
LEYFKDKHIEIRFIEFMDVGNDNGWDFSKVVTKDEMLTMIEQHFEIDPVEPKYFGEVAKY
YRHKDNGVQFGLITSVSQSFCSTCTRARLSSDGKFYGCLFATVDGFNVKAFIRSGVTDEE
LKEQFKALWQIRDDRYSDERTAQTVANRQRKKINMNYIGG

>RXN01590 TRANSLATE of: rxn01590.seq check: 4837 from: 1 to: 6447
WGQKDHWGKAPLGDHDAVRIYRQAEALMKQRAANNKGLDLNDEATYGAIMFASFDDAFAA
DAEAHGCVHRPQFAKVTRRNILNSPQYTAIKSSYDALVQQDLVAQQQQAQALQQAAYEQE
QAAIFQARDQATFQAEQTLAQESVRQSEGVGLPVIDPMESYFREYAFYEGVEMFGTWGTH
VDAGVSQFSTSDGRAIRALVDEHLATYEPVEQRGSTQAFFASVNAAFAEVAPHAAPMFSA
IAREGEGSKGYQALRHRFDKMVGTAIGPNGLPEGPDLGGRRLPISPYDPRWSDREVVRVH
GTKLLSLSEESVGMIRDLDLATIHLQDNDVYEGTHREDDTKGGVRPLTQWVNGEAIAWRT
ITENDQMRLPNIGQFMTAKEYRAAASWLRAGLIDTADVASQKIDPNKVMSDEGIARSEAI
LTYLSDEGVDFRIEPDREPGQLKVRIEGTRIDIRLTDTRANEQWVGRVYDSGTVIKYSAE
QTAEERLRARERMENGDGTWTPATDYEPSPTEVVDLVKFALGREVERQDGKGLVGVPNAR
HPRALEQAQDAYFTKNRSAFMVREGLSIVQDARDRSAGPGKWFDNEAKASEWLGNNIALT
RARVAEELGVEELIALSAQYADDPDFMPAFAGEDELMAIKQDYWAMLRGEETDLLNPGVN
RDDYMAAIRDGDHEQIAAMTSAMNAVTVEDRVRQHAALVLDDYVGTVEPDPVTGLRFNPV
TVAQHMPSAKSLWSNHDDIIAALRATSITGDELRGDEFYNDVINQQLLKFNPETAQKMVN
NPDLDPQLARFGTVIAETISRNGADVVDIAVDDNGVVRWTAQRRVGAKDSRAVDSKGQVR
GERTRHVQGEIGQIFTRGEHGEIVTKFNGGENYMFAPGYTASVVPQKPGETKSLEERTKL
KGYEQVMSEALVYRVREDLMFTERSRVGATTSINSAYKRLYDNRFPVDFFERSAEEGLSD
EWRAALLETASLRVRYDNSIRDGANVMEDIRAQQRGFDARNDNSRDALVLTGGRNISVLD
VDAGKGFFDPMMTGMAANQGSVRYLLPSAKVGADGMITPGDPADRVPVAAHPESWAMGFD
PHDRQNMTFSNIMQASAVTGGARTAMIQLGGWNFEDGIIVSADFANTHVIRDTEDEMRPL
VAGDKLSDFHGNKGVTALVVDPAMSDADARAAGLESEVAFFRDNPDLEVVMSPFSAISRF
NGGTARELMTNPQDVVFRNNDGSTRVQPGASGDLNFIVTHMAVDAKTNVYDEEAVREGQG
RKASSQLAWVLQAQECHEIMEHFYGNNVSALANFQEYLRVTGLDVTPYGELREGFSESNE
QRNIIEMPSIYDENGELNNRVNRAQVREAFVEQISRAGGVMEIPFQLQLRNGAQLEESPN
NPDMYQLPLLSPHLRSDEDLADGSTSRHEYTTRYMAIFDTCYKLAEEQAKIDALRQEEAQ
HGTLPRAAEKRLSESQKFVDQAQKKVQASFDGIANDIVASRIETKNNVFKDGFMSARQSH
SATAVWTGDPRLSVDEVAMNSSMARELGVLDNGYAMVWRDPVIRDGGVRYLRVVINDDLH
GVAVNPVSVKSFDGDFDGDSVGLVGNLPKKAHEEALSRLTVEANMLDLGDGKRMEDGTMF
YGLTLHDSLDVQVAQHHDPAMAENMKVIVSELNRYQREYEAGEISREELLEVNRAHMDDL

NEHYAQAFANRDGLVTLRFDGMENHMASVAQCFETGAKGSPGKLKEYATYIGADPAQGFK
DVGQPTPEALRSHYEGSQKATAIKVLFTGVAGKKEQEMVALCRNLGLTKEAMAASAPAQQ
SILQAKHDPIDALYRAETLMGPVGDLYQGRKMRRGENEQGRYEWEVVRDENHQPIQATKD
EWVQQYMEMYADDKGMGVSVGVDQVEKIAEEFSDEQGYMRVLSHDELPTEIKPLALDQLA
YGDKKNRFDLLCEMAKQQVNIYDGDAYDFAPRVVRANMKAMEDAARFGIPDVEIQSISAQ
QSLASFERVPQRSGFRIERRVPAEVGTGIAAPAPLPDAGVQGNYVQQQVPATPPVMPVTP
PAQQPVSPAQTDFRGVGQPLDQGGKIGNYGHQGPAMGAQQPVVPQQQNIPPVHNPVPQNS
VPPTPVVPKPGTGNPFTHGGANNQFMGRFDTSRYNQQEPPQRQDGGFEL

>RXN01592 TRANSLATE of: rxn01592.seq check: 5848 from: 1 to: 1302
MADNFDRSRDNDRSSDRTPRGDRGDRGGYRNSRGNDDRGNYRQNRDGESRDRGGYLGDRR
DNRSGEYRQRDDRRDDRRDNRSDDRRGGYRSDRNFDDRNSNMRDDRRGGDRSYSRNDRSD
RGYRSNDRYDRNDRRDDNRDTRGGDRGDRRYDRRDDRRDDRRDDRRGGQGQGRPGGDRRH
ANRAGAGRDQQRDSLHPQRAGFREERLNTRLNEPDLPGDIDIKDLDPLVLQDLKVLSKDN
ADAVAKHMIMAATWLADDPQLALRHARAAKDRAGRVSVVRETNGIAAYHAGEWKEALSEL
RAARRMSGGPGLIAVMADCERGLGRPEKAIELAREEDLSSLDQDNLIELAIVVAGARHDL
GQHDSAIVELQKVNPSLKSTGFTHSRLSYAYADALVLAGRGDEAREWFQHAATLDEDGYL
DAEERIEQLDNGNN

>RXN01597 TRANSLATE of: rxn01597.seq check: 4048 from: 1 to: 1182
MSLFNRKADLPGLQGATRICTPQGKGLKRLSEGDLAIIDAPDLSRTFAQRLLAAKPAAVL
NVSRFTTGSVPNFGPQMLIDGGIQLVEGFGQELLDGTKDGKKGRLTEDGQLFYGERLISN
GSVLSGPAAENAFADAQQSLLDRMEAYFGNTIQFIHSEAPLLIDGLGIPDTGNAIEGRKV
LIASPGDNHRSRLKELRSFIREYDPVLIGVDGAADTLVELGYKPALIVGNPTGIGADALR
SGANVILPADPDGHAVGLERIQDLGIGAMTFPSSVNSSTDLALLLADFHNPQMIVNVGGP
VTLDGVFENREDSDPAALLTRAKLGTKLVDGSVIASLYTVRSSSNLGWMWALLAILVVLA
VVIVIAGTAGSGSFTDNLIDTWNSFALTVQGWFK

>RXN01598 TRANSLATE of: rxn01598.seq check: 5340 from: 1 to: 963
MAKRRGRGAATFAALGFGAAAGIAFGTYVLAPNLPENIDPNAPTSAELVEAETLAEVNAV
QADQADSIIDHIVEDVVAGTLTDRPVLVMRTADAEESDVADVSWLLQQAGAINAGSITLE
ENFFSQDGADQLKSIVANTLPAGAQLSETQLDPGTHAGEALGAALLLNPETGEPLASTAE
RGLLLNVLRDNGYISYEDGTILPGQVIVMITGDSDGSGDGAFAAETQSLFARALDAQGSG
VVVAGRIHTAADTGVIGRLRANPDAAENVSTIDSVNRTWGKMATVLSVREELAGRSGAFG
SAASADAASPSLDGTAAAPAQ

>RXN01618 TRANSLATE of: rxn01618.seq check: 189 from: 1 to: 384
MIIIGAVFAILAVLLHVFIFYMESFAWTSEKARGVFGTTEIDAENTKEMAYNQGFYNFFL
AVIAGVGVAFLFAGSTGIGAALALAGTGSMLAAAAVLALSSPDKRGAAFKQGTFPLLAVV
FLVIGLLV

>RXN01634 TRANSLATE of: rxn01634.seq check: 2339 from: 1 to: 552
MAVGQETDLLNAMETLAGVPSDLVVTEILPDTTSYDNFEFFEVHNTGSAPVTIGEGEYTF
AYSFDDSADTSRDKALDLGGEVTVDAGETIVVWIEYSSSTVDTAAFSEQDFRDFYGMDSS
ARIFRATGQAGLANGGDRGIRVLYNGEVSGWSHYPSDSAAVQKGIDFALPKVGEQASIAS
AHQN

>RXN01635 TRANSLATE of: rxn01635.seq check: 47 from: 1 to: 741
LIPGGLDTPEEPEAPEDSLFEGRTPPRDASTRLILTELMVNSTNMGSSDGFEYVEITNTT
AEPIDFSDYTLNYLYPQDEFTNTNEAVWAAEPGDVIIQPGKSLVFWIKNGPNDEATAADF
NAEYGTNLEAGKDLVEISSGGMANGTARGMQIQTNTGHIVNRGFYNMAGASDVKANEGLH
FAVDESDLLKQTLVGSGAPTPGTVYTSQIPNPLSAVIADSSVPLITDNTATSINPAEPFT
FAFKYHR

>RXN01638 TRANSLATE of: rxn01638.seq check: 2292 from: 1 to: 900
MSTQTITITVLETATIFDGPETIYRYDLAAEGILDGWAHSAVLDQVKQIAGENWPTVEIV
VDGTDNVVNALTSMFASKGVTCGGVGVEAPPVAEEPPKIKRPTSGKQVRQFYGIKPLHLL
LVSILVGSIAGIWVISGFTGPVDSRPVDKVAEISTQGETSISNQPQPQPTVLVTEDLLIE
APFGFEMRSDEQSRYLEGPDPNLRIHVGVDPLHGADAALVAEELRRLITEDPSLEEIPAG
EWGEKTTIDYRETPGDGSHVLWVTWFDTDRQLNVGCHSKAAETLVHKAQCRNVIEHLTLK

>RXN01647 TRANSLATE of: rxn01647.seq check: 6883 from: 1 to: 1170
MGDVRMIHDPLGRRRRALVFGVVACVMLAVGSLALAIFRPAKDPADAPLIRSESGALFVQ
LDGSVHPVANVASARLIVGEPVDPVNASDAIIAGMPRGVPVGVPDAPGLFSSTEEPEQDW
FVCQDVGTGDLHITVPRGGLGPTLIAEGNGWLGASKSETGEVTWNLITADGRRELPAWGS
EHGRIMRRHLGISEDTPRVYLTTELLNAIPEHDAVRFPAPLPELVDASTRNWLRLDGALA
EITPLQRGLLIDAGSGVFPDPTALLGVHEETANTLTLPEQTVSWQDLDGGFACADGEGQI
GFLETLESGVALSGDSRAKSFSTNAGGAVGVDSGFGYYVVSDFGLMHPVSTGESMVALGI
TDVQVVPWSVLRLLPQGSELAKETALAPTY

>RXN01658 TRANSLATE of: rxn01658.seq check: 7999 from: 1 to: 1833
DPQILSPTFTQQQQLRNFYGFPDQLAMDRFEVDGKLRDFVVAARELDPNALQQNQQDWIN
RHTVYTHGNGFIAAQANQVDEVARDVGSTRGGYPVYTVSDLQSNARAAESEDAEELGIKV
DEPRVYYGPLIASATDGADYAIVGDTGDGPVEYDTDTSSYTYEGAGGVDIGNMVNRAMFA
LRYQEMNMLLSDRVGSESKILFERDPRSRVEKVAPWLTTDSKTYPTVIDGRIKWIVDGYT
TLDSLPYSTRTSLTEATQDAVMPDGTPQPLITDRVGYIRNSVKAVVDAYDGTVELYEFDT
EDPVLKAWRGVFPDTVKDGSEISDELRAHLRYPEDLFKVQRDMLAKYNVDDSGTFFTNDA
FWSVPGDPTAAEGRQELKQPPYYVVAADPETGESSFQLITPFRGLQREYLSAHMSASSDP
VTYGEITVRVLPTDSVTQGPKQAQDAMMSSDQVAQDQTLWRGSNDLHNGNLLTLPVGGGE
ILYVEPIYSQRKDQASAFPKLLRVLVFYKGQVGYAPTIAEALSQVGIDPKEAQDIEEVDG
TATTPSTDETDTDTDQPATETPTAPVSEAEGIAAINDALSNLEAARDSSFEEYGRALDAL
DRAVDSYQSAQ

>RXN01659 TRANSLATE of: rxn01659.seq check: 8569 from: 1 to: 546
VAGVAQRFVDERIHVGLDSMPEAVTAVWMESDWVLAETIKGSTPSDWEEILRPLALLTDA
SFTLPPRSTRAQTLDLKHLEPSRLKPEQPEKPAFTPNASEEDLSQPLVIRPEEPLQMPVR
GVQESRGVVEPRSLGADDVESIAEGDPERPSDLYGTRVLRDLNGQSSIFQDSTDADEPPK
KW

>RXN01663 TRANSLATE of: rxn01663.seq check: 7844 from: 1 to: 858
MEISVLIIAALILVAGIVLWRADSSKQAAKKAESPVGSVAPAPVLVEEEPDPEFEPELDP
EPEAQPEPELEVAPRFAPEPVQDLEPDQAEDIYFDDSPELDADVENALAELTEVEDYPEE
PVQSEQPQAPATAEVAADEEQRGVDKHSFLSSLPGSQRRERRNWAAKHHFDFIKEDAFLT
DEWSRGAASTGAVARDVVSGMAEGYETHLVDLAGVPVMAMRRGITSDVVIDARRGEQPAD
PEREESDDLVEIDTVSGFRLLSTWRGLRSVLSTSAFTSVWIPCQKL

>RXN01669 TRANSLATE of: rxn01669.seq check: 9448 from: 1 to: 915
LYEIFVPHSHDTADSIDDAMEANSEGIRALKFSLVLMLLTTVLQAIIVSFSGSVALLADT
VHNLSDALTAIPLWIAFILSRRAATQKYTYGFNRAEDLAGLFIVAMIALSAIVAAWQAID
RMINPRPMENIEWVIAAGVIGFLGNEAVAMYRIRVGKRIGSAALVADGVHARTDGFTSLA
VVAGGVGVFLGFPLADPIIGLIISAMIATLLVGTIRSVGRRLMDGIEPELVEKATHAIWH
VKEIESIDRLRLRWVGHRLHGDATVSTSTSSLSEATAIALEAELSVKQHLPNVDEMTVTI
TPSKP

>RXN01672 TRANSLATE of: rxn01672.seq check: 2451 from: 1 to: 342
MASREVSITRISPLATFRVALAMSIIGLVAWIICVTVLYFGLNVAGVWQNFNDVIGGVGA
EQTITFGLVLSISALLGAIGAITVAVLAPLCAIIYNSIVDLFGGLQIQLQEEVD

>RXN01694 TRANSLATE of: rxn01694.seq check: 8929 from: 1 to: 900
MQKITPNIWCQGTADEAAEFYVNAFSEFPGGAEVLTTVKYPEAGLLDFQEPFAGKTLTVE
LAISGFKIILINAGEEFTPNPSISFMVNFDAVRDENAKEHLDAVWEKLHEGGSTLMPVDT
YPFSEYYGWVQDKYGVSWQLMLSRPEEKPGPAVIPTLLFGGAAQNQAGPAQENYVEVFPN
SQLGDRAPYGQQTGPATPEALMFSQFQLDGQWIFAMDSGVEQDFTFSEGVSLMYEAHGQE
ELDAIWNALSAVPEAEACGWLKDKFGVSWQIVPDNMEELMAKPGAYEKLLAMKKINIAEF

>RXN01696 TRANSLATE of: rxn01696.seq check: 7405 from: 1 to: 1179
LSTPIGLGLPPTPPPVLAPRRKTRQLMVGKVGVGSDHPISVQSMTTTKTHDINGTLQQIA
QLTATGCDIVRVACPKTVDAEALPIIAKKSPIPVIADIHFQPKYIFAAIDAGCAAVRVNP
GNIKEFDGRVKEVAKAAGDAGIPIRIGVNGGSLDKRILDKYHGKATPEALVESAMWEAGL
FEEHGFGDIAISVKHSDPVLMVEAYRQLAEQSDYPLHLGVTEAGPKFMGTIKSSVAFGAL
LSQGIGDTIRVSLSADPVEEIKVGDQILQSLNLRPRKLEIVSCPSCGRAQVDVYSLAEEV
TEALDGMEVPLRVAVMGCVVNGPGEARDADLGVASGNGKGQIFVKGEVIKTVPESQIVET

LIEEAMRIAEEMDPEVLAAASASGMKAEVKVTK

>RXN01697 TRANSLATE of: rxn01697.seq check: 2521 from: 1 to: 957
MFQGLKELTAAKGRTLLITVTVGLIAVLVTFLSALTAGLGHQSVSALKYLAGDNELILAD
SGSTTLSASTLSDQAVAQLEDEGAQMLWQVRDRVADTPTMLLNSPDLAPGEVSLPAELAD
SELATAHDVVDSSNDLYLDHLPVVLMNTSDLASLAQVRGVTGPAGAFASDVALPSDTVAL
SGSERWNASASYQGEQMSLNLMIVMLYVISALVLGAFFTVWTIQRLRGIAISSALGAARR
VLIADALGQAIIVLGIGITAGTLITVISAFGMGDAMPVVISSSTTLFPALILAAAGLIGA
AISLGPILRVEPRSALMNA

>RXN01701 TRANSLATE of: rxn01701.seq check: 3619 from: 1 to: 372
MLSHEEIVAIAEDLLSKRYGGVQTLSDVEQLNGSGTSAVLRARVANSPFLQQRSVVLKYV
PSTGDVFDDSALVREIVSYQFTTSLSEDVRPGPVILAYDIDKRILVISDSGNGDTFADLI
DQRP

>RXN01703 TRANSLATE of: rxn01703.seq check: 3504 from: 1 to: 1113
VAWPSNAKEKLFIHWHYWWQAHYLDCLVDAARRRTTKARRDRIRDTIRGISVRNVGKLTS
NRYYDDKAWLALALGRAGKVRKVRTPKSLPSLEQNIVDGIDSLTGVLPWRSGETFYNVPS
NGPAAIMMARTDRLDEAMKITDWIFDNLIDGDGLVMDGLRMRMHGPELVRSIHPYCQGVA
IGACLEIALKLRERAGLTTTVVDHWSDADKAEDSLKYFAHIHAVVQAVSRKMTNFHGVID
WDTGDGDGGLFKGILVRYLADVAIRLPDDSPTNRETKKIAARLVLESAESVWNHRLEVDG
LPVFATDWTTDARLPQNFGLSSSSLSDLVSVVRVDERDLSVQLSGWMLMEAAAKVAEELE
NNGNSYTGRSR

>RXN01709 TRANSLATE of: rxn01709.seq check: 6991 from: 1 to: 432
VFEQALGLTTLAQTAGAGAAGGLGFMAMALLSAGMRSGVDMILNETGGEKMLAQADLVIT
GEGRIDAQTLSGKAPTGIAKRARAKGIPVLAVCGQSLLGPAISNELFEDIYSFTDFESDI
NECIRNPLPILEGIGFNIAKHHLS

>RXN01711 TRANSLATE of: rxn01711.seq check: 1589 from: 1 to: 1158
MLLMAHRFFVLAINGAVTDDFTTVYSALRRFVEGIPVYNEVYHFVDPHYLYNPGATLLLA
PLGYITHFTLARWMFIAVNLLAIVLAFGLLTRLSGWALRSMVWPIAIALAMLTETVQNTL
IFSNINGILLLMLAIFLWCVVHKKSWLGGLVIGLAILIKPMFLPLLFLPLVKKQWGSLIL
GILTPVIFNAVAWFLVPGASEYVTRTMPYLGETRDFANSSLPGLAIYFGMPTWMEITWFL
IFGAMVGLAVLALLRFRNTEPYFWAATTTGVLLTGVFFLSSLGQMYYSMMIFPMIFTLLG
SRSVFHNWVAWVAAYFLLSPDTFTSQRLPDVARWMEFFSATVGWGLLIVVTFVSALIWFI
GDIRAKGTPSSPITTDPTHDHLERTA

>RXN01721 TRANSLATE of: rxn01721.seq check: 7358 from: 1 to: 1023
VLVDRFGRIARDLRVSLTDRCNLRCTYCMPAEGLEWLPTEQTLNDAEVLRLIRIAVVKLG
IRQIRFTGGEPLLRKNLEDIIAGTAALRTDEGEKVHIALTTNGLGLDKRIAGLKEAGLDR
VNISLDTIDAERYVSLTKRDRLSGVLASIDAAVAAGLHPVKINAVVMPGVNEVDIVPLAE
YCISKGSQLRFIEQMPLGPREQWKRGDMVTAEEILARLEEKFTLSPAKEPRGAAPAALWN
VVDKSNPDITGQIGIIASVTHPFCGDCDRSRLTTDGTIRNCLFSRTETPLRDALRDGASD
DELAQLWAGAMWEKKPGHGIDDEGFLQPDRPMSAIGASPYQ

>RXN01734 TRANSLATE of: rxn01734.seq check: 3461 from: 1 to: 534
MTDPIEQAFERIRAEAMRRNGSVPDLNKNDAFRRPPAPKGGVEKRKKGRASGLDGRQKRY
VRGAESLGSVLNKEIQRRGWGKDIAGGWVTSNWEELVGAKIAQHTRVEMIKDKKLFITCD
STAWATNLRMMQRQILQVIAEKVGPNIITELRIFGPQAPSWRKGPLHVKGRGPRDTYG

>RXN01742 TRANSLATE of: rxn01742.seq check: 7621 from: 1 to: 504
MQEKPEMPAIEVIRSAKRTKTVQARIVDGQIQVRIPARMSKAEEEKAVGEIVAKLKRRTQ
SAVSSDADLIERAHKLNKTVLEGRARVESIRWVSNQKGRWGSCTVATAEIRISDRLKHVP
DYVLDAVLVHELTHTFIAGHSAEFWEWADKTPLAERAKGYLEAYQRWG

>RXN01754 TRANSLATE of: rxn01754.seq check: 1605 from: 1 to: 1941
VKIKSVFLSTALSASLLLGITPPVLGATINPSLPLSALSSSDDIAVPNFAKELPLAFDVP
AGTVPQSLSGTLQIPAEFSGGVVEFYDGDRLFHTLRLEVNDSRAHIEVPLQSVPVEDGRA
TFWLRAMLDPVNNQWCYEEQEVRFLDGNVTFEGATINPAVVADYFPSVLRALTIYVPENP
SEAVQEATLEVATSLDSVYRRSGLDVNVETLPTGTDAPPTRPQDFERQIVLVDEATESNT

QKTELVNPGQDNAFLRLNGNADELYDQARLLTDATLPLAVDTEVTASGFGDVPNLSTDVA
TLQELGITQLTSESVARTSVTLGIERSRLRTYSQSMDLHITGTYTPLPPQNAGQITFSIG
DTVLDSLTTDDTGIIDREFNVPGDLVNRYTAIVVEFTSTGDVNCGVTQPVGLNIDSDSLV
TSQHSDVPVLNGFRSLPQSFQPRVDVAFADPSVQELSRAVSVVLGIQSMSSQRIRPHLVN
WDEAVASERPTIFIDAAGAKTDQVPSYLAQQGQTLEITSKNDQNADGEQLTRSLQTNAAL
VVGSIQAVWDADKKRTVIVASSQDNPPDLDALISWMGEDRERWSDLNGDLIVKVRDREPV
QLTTVEAPDQPGRSATAFIAIGVSLVVIALIVAAVVSVSRRSQKGYK

>RXN01761 TRANSLATE of: rxn01761.seq check: 9482 from: 1 to: 4464
VTATVLEPQPVQLSEQDVDAEIARMELKHNRHKTWRRRTMAVVMTLLISVGLSFGAFGNK
EREANAFASAIIAQVVGAMGEVAFEAICPSDGDTEMLLKCITENLGEMHIIEKCLEAEDV
LKCFYDAKNEEQRKEQNLDKAPDYSMYRMASAMASFYGNGRAATAGVEEGGPNEFLDSED
AGLKVWEGILSKAANGGNVLGYADAKHNEDSGWFFGNGVANNEKTYSYDSLADHAFQGPY
HFALFGATLSGLGFDSSKAEDSQTDFAQRKGMGYAMMIAYIISGGIDLVFNTVLNILSTI
NPFRLLVGPVSQNTNKTFTENMAGGQTTEGTPFEGMTDFFGLIYNWSVTVGWLIGIPVSI
GLFMMGALMFRRMDKGSAFKKVVIRVVYGVVGLPLLGVSYTGALDSFLDSGSSTSAGSNA
TKIVLSTYVDFQSWAENTRMRVPDKVTLAWSLEDQAPTGQSMRMVRNSALEINAQSNESF
TTFKNPGSMDLGYSMDWMEKMADPANSGTDGTSSSSATTIFQGTIALLSRYIDNDSISSG
SFETSIRSAMESLTSKEGSGEAVAGGDVMAWVTGYNTASGLNEITAAELADANNPLLEVS
DSAGLQGRPIDRNAVSFKSGDATASCNNSVVTGSRAVVGDYRSDCNMSPLTMYNFLNTSF
HPADASVFSTSTSASSYTRASHSAVSLIGSGAMNFVYWFSAMSLMGSFIVIGIGYAGAML
FNTIRRTLSLIGAVPFAAMGFIAGVAKVIVYTIAMLVEVIGTIILYQLITRFLMAVPALF
EQPLADSLSSNESAELVAGAGMGLVGMALATSGNWAIAGMVITVASSMGVIIFTIIAMKV
RGSLVSGVDETVTSVINRFLDTQVSSAGATSGDGMMRRAAATGLGIGATHMVLNRDGDGG
GSDSGSGGSGGGSDSGLGEKAAGLAKVVTTVAGAGLVGKYATDALDNYADGVINGDGDGA
FAAGGDATVDGDYVADGDAIASADANADFVDGVVDGAGRASFSNAAYSSDGTTLDGEGAS
VDAQGNPLHADGTPMSAAEAEMKMAGLSSSGTMMEKSGVKSSGITTAADVMDDQSLASSV
TESGLSKIPDTYGADVSGAAGTVGTTGADYSATDSSAGLNMSEAALQSGTPMGALAGGSV
SSSDQAMNDAALQIAASQGLAPAGSIAGMEQLSAQATEAPAGKAGKQLGDLSGSALNTQL
ASMGQQVGDSVNSAYAAGGMGGVDVAGKVTEAAQHLSQVPGQIQNAVTNADAGSSGASFG
QMAQGAAGIAGVAGVIGAAGAASSAAQGAGTVQGAMGNAAAGAGMINNAVSGGATGSTGA
AHVVNASHGPVAPGQAHYQESGHAQAFVQNNQANTAHTANTRAPSSAQIMGANVAGSLAS
QAVRGIGQPGQMGANVRDAMGGSGRSGGRGGATQGGRGAQRSGVSAKNGIRAQRGQKPSV
TGQAMNAAMRSAAVSGRMANMDGNSVGGTEADPQQGSGVTEKGDKGVK

>RXN01765 TRANSLATE of: rxn01765.seq check: 8067 from: 1 to: 942
MSNNVVKYECAVDADNIVAVDMHVHLEVDSCGHKSMPADIMAASSKYFKTAERTPSADAI
ADIYREHKMAAVVFTIDARTQMGHLPNSIDDLVASCARNNDVLIPFGSVDPRTGEDALVE
ARRQVEELGVRGFKFHPSVQGFDPSAPEFYPLWELLESFGLPCVFHTGQNGMGAGLPGGR
GIKLRFSNPMLLDDVAADFPNLTIIMAHPSVPWQDEANSIATHKANVFIDLSGWSPKYFP
ESLVRQSNNVLSKKVLFGTDFPLITPEKWLAAFANLPLKDEVRPGILKDNAVKVLGLAAS
TERGSQAEKVVQHA

>RXN01767 TRANSLATE of: rxn01767.seq check: 5940 from: 1 to: 465
MIDHKLWFNTVTNNASVREAAGKCDIPIRTLNEQLNRRILPEKTVIALARAYDLSPVDAL
VRTGHLTEEEAGSREEDASPDSADDYPTWALNSHLDYGILGAFGDIAEEVNSERVNRDNA
IEQIRAWLDELPGSLFNNLRSTKTGYIELFETYLD

>RXN01769 TRANSLATE of: rxn01769.seq check: 4062 from: 1 to: 441
VTGLLGRAPHSLFFPIGFYYTPMTSITTTDTPLYTALPHTRISDAELLTPTTTVHEILVY
GPAECPGCTATLDFFARKNMPATKVTVAAGDVAHTYITQDLGYLQAPIVTVRISSSASNH
DNEHNTQILHWSGVNRYLMQALSRTHF

>RXN01771 TRANSLATE of: rxn01771.seq check: 4536 from: 1 to: 702
MHQAGQLINDPSQGLWRTSALRSPVARVGHAVLRQRAGEISRMQGREFSRPGDQFRQVDL
RRRLIQVHPQSIPTADAMAVTITMALTAATIDPVKFVADSQNPDEEIYLAAQIALREMVI
AMPLEDFIGVRIDLEPVLVAAQAAAKNVGVEVSSILLKDLNLPQEYSGALQESIVAKIQA
ETDLERARNEVKTTRARLASAKVLEQNPILAKIRMIEALPPGSTIEVREGDSKA

>RXN01774 TRANSLATE of: rxn01774.seq check: 7116 from: 1 to: 726
MSPNFQARGTTAPTVALSMRQIAHIREEIKKSPLAASVFITPTTKQMVVRDLESLFQQLY

HTDLPEPSIKDSGLISAIGSSAGNTNNPALALETQMAYHLVLAMHHTDVATWHKVVTKNI
TESAAAQDAAVEHSAKYDAVYDAAQLMGITVEEGNVGSIAIAFSTARADGKSDWCVSGIS
RYIEVTEALDAARAVTKNTDALNKTALPDVQPAPVVHSAQFMNKSAHDHGVNTAEKDQPT
LF

>RXN01787 TRANSLATE of: rxn01787.seq check: 474 from: 1 to: 693
MSNNALLVANEADIGLYLHWNGGRDSIEAFLAYAAYAQLPPINENNDWLPPFITVLKNFF
GNDGSGVYLEPVNQDYLDGIDYDNGVYMLDDYEITERINPPAVEQDSHDLHDMLIKIDKA
QPPVDQLGSFLHGLETSVADLGVGDRVFLPRFSTFDKKLGRYRIHTVLGFAENDPFNPMT
SSERFKGKPYVDMFDNQDNAFNPNSYITTDTVRIVVDPVPETNPDDEKAGR

>RXN01796 TRANSLATE of: rxn01796.seq check: 303 from: 1 to: 774
LLLGGNPAEIDQVLGGDQTQIESGESTGAGDFDHCQTGADANASDDCRLYYTSFSVNEMW
QTLLPAQAGIEYTEPTLTLFKNSTQTGCGFASASTGPFYCPSDQDAYFDLTFFDQMRQFG
AENAPLAQMYIVAHEYGHHVQNLEGTLGLSNYNDPGADSNAVKIELQADCYAGIWANHSS
EGPDPLLQPITESELDSALLAASAVGDDNIQQRSGGDVNPESWTHGSSQQRKDAFLAGYN
TGQMSACDFLGRGVYNDA

>RXN01803 TRANSLATE of: rxn01803.seq check: 8304 from: 1 to: 960
MRKKKDGQNLPDFRKNPPKLDKKAYEKELKRLQAELVDLQQWVVETGARVVIVMEGRDAA
GKGSAIKRITQYLNPRSARIEALPTPNSREKGQWYFQRYIEKLPTAGEIVIFDRSWYNRA
GVERVMGFCTSQEYRRFLHQAPIFERLLVEDGIHLRKYWFSVSDEEQIERFEDRLSDPLR
RWKLSPMDLQSITRWEDYSRAKDEMFIHTDIPSAPWYTVESEDKKRSRINVISHLLSTIP
YEKIDRPLPEIPHRPDSESDYVRPPRDEFRYVPDVAAHLEEERIKKEEKAKKAKKPAKAA
GKNSDKQKSSGGKGKKKSKK

>RXN01809 TRANSLATE of: rxn01809.seq check: 4529 from: 1 to: 1176
MNEQEREALEDAALEEAALADELAALEAEAGVQGSVEPYDYAADLDDEDEFDEDPFAQDE
PRDAGPLGELSSDNHVSEAVAEDTGTSTEESAQEGSHEESVDNPRDFTGTATAVRSFRPR
LPVPNALRPGPPIRTQPAVNTDIDDGGQENTAGATAADVGAGVFFGTHFELAFGQVDVHR
HIRHEQAMRDGHQDLSVFVGADGAIMLEELKNRYQRPPENEPHDDDVTEMIKTTEETEKE
NVEMDQDIAVVDNVDEQVVVTPAHDADSVAVVAEQVVASEPTPEPVPKVEHVEMSVDLAG
ETITPIDQAIRSFMQLNGIEHSVVLRRLGLMTQVAHNKELDEVYAKALAEGESHAQQQHE
LEAENERLKKEVDALAAELSAALMGEGGGDHD

>RXN01811 TRANSLATE of: rxn01811.seq check: 3834 from: 1 to: 681
VFEFDDTLAKDIQVDRTSMQVFEASETVKEAIKASIEQGHTRYPVILESKDNVLGYVTLP
DLIKQSYKDDQLTVEQLIEEPIVTTETIPIKKLLTIMRKKGKHIAILKDEYGGTSGLVTI
EDILEEIVGEIRDETDLDEALIAEQSDGSYIISGKLTLDDFQRYFHVEIPEFEETNFTTL
AGFASSRYKEIKAGTIIEIASFRFTVLEYQHAHIDYFKVESTERKTE

>RXN01813 TRANSLATE of: rxn01813.seq check: 1579 from: 1 to: 666
MVAIVVVAIVVVGFIVIQGQGSKAAKLGDRDYEDTSLAMEVGSDSITLTSANTSADAKSV
QLFEDFSCSHCSELSLATDADMKTQIEDGNLVVEIKPLNFLDRENIDGHSTHALAAALAV
ADSNDATLYWNFRAFLMEDQSEIYNQWSDDDFADGVEALGADSSVVDAIRNGDNIQRAYD
LATANGEELTEETGSLSSPRVLQDGKDVEGNISDWITTVLAS

>RXN01815 TRANSLATE of: rxn01815.seq check: 2232 from: 1 to: 792
MNRSTISPVEARQQFRAGLIQPTSGWSAGFAQANLISMPQDLAYDFLLFAQRNPKPCPIL
EVLNAGETFGGIFGSNATEADIRTDAPQYRIYAHGELIDSPASAVDYWRDDLVSFIIGCS
FTFEHPMVQAGVPVRHLEAGRNVPMYETSLACRPAGSLSGNLVVSLRMIPASQVADAVRI
TSRYPAVHGAPVHIGDPSLIGIDDINNPDFGDAPLSEPSDVPVFWACGVTPQAMVMSSKP
PLAITHAPGHMLITDAPDLGFQVP

>RXN01825 TRANSLATE of: rxn01825.seq check: 7373 from: 1 to: 270
MPKARVTKNETAPVSSNPSANRTPVKINSAGTPMWYKVIMFAFMIVGLAWLIINYLVGPQ
IPFMADLGAWNYGIGFGLMIIGLLMTMGWR

>RXN01831 TRANSLATE of: rxn01831.seq check: 8077 from: 1 to: 462
MDSLVLLGLRIALLVVLWFFVLMALRAMRADLKVTGQASTSSSSVAAPQGLARAFNRSSP
PRLLTVVEGPLAGSSIEVSEDMTMGRSPECTFVVGDDYASGMHARVFKRGSEWFVEDLDS

RNGTFVGGTRIDQPEQIAVGTDIRIGRTAVRLVP

>RXN01834 TRANSLATE of: rxn01834.seq check: 6044 from: 1 to: 702
MLGGGGAILAIPLLIYGFSFSATQATAASLIIIGLGALIGLISQYAAGHVRLKEGLSFGL
LGLVGSFVGSHLASNIPDSLLLSGFAILTLVVALTMISKLRSTREYITRRPSILAIALSA
TGVGFLTGFFGVGGGFAIVPALIFALGFSMRQASATSLVVIAVNSAIAMGFRYSDLASID
WSVISPIIITTVLGAFSGVKLAKKVKASSLQLGFAGFLIFISIYMGFQNFPDLF

>RXN01846 TRANSLATE of: rxn01846.seq check: 4543 from: 1 to: 282
MSIPGNVSYVAQGGTGWDGADQYTTGESWDLQSFLENSTDYLMIIGGSLLALVGGAAVIW
GFVNVMRKLFGGQSGQQIQWFTTILLIIVGGALP

>RXN01847 TRANSLATE of: rxn01847.seq check: 7155 from: 1 to: 735
MLIVLPPSETKTHGGSGKPLDFHHLSFPSLTKARQTILADLQALEVDEALKVLGISEKLR
PEAESNRALETSPTMPAIFRYSGVLYDALDAATLPEKALERLAIGSALFGVIHATDPIPH
YRLSGGTKLPTKSGELPTMKARWGTSISEALIDVNQLVIDLRSGTYQQLGRVKDAVTVRV
ESVMEDGSRKVVSHFNKHYKGELARVLALSEKEAHTAEDVMSIAQAAGLVVEENPNHKET
LTLVV

>RXN01874 TRANSLATE of: rxn01874.seq check: 6539 from: 1 to: 348
VIAYVASACCLPFGAFAGALLSKELSGHLQERVLLTHTVINFLGFVGFAALGSLSVLFAA
IWRTKIRHNFTPWSVGIMAVSLPIIVTGILLNNGYVAATGLAAYVAAWLLAMVGWG

>RXN01875 TRANSLATE of: rxn01875.seq check: 5040 from: 1 to: 846
MRIAVTGATGSLGGHVVDSLLNKGVAASDIVAIVRNEEKAADLKARGIALGVATFEDEAA
LTAALEGVDRLVFISGSEVGQRVAQHTNVINAAKAAGVTFIAYTSLLNLGTSKLALAPEH
IATEKLLAESGIDHALLRNGWYWENYESSIGAAKATGKVFGAAEGARVSAAARKDYAEAA
AVVITSDNQAGKVYELAGAPALTYPEIAAGIGEVIGSEAEYVNLSVEEYQNALEQAGVPA
EFAALLAGMDPIIAEGALYSDSTDLQDLIGRPSTSIVEALSS

>RXN01877 TRANSLATE of: rxn01877.seq check: 5596 from: 1 to: 1071
VPLRLATGGVLATLLIGGVTAAATKKDIIVDVNGEQMSLVTMSGTVEGVLAQAGVELGDQ
DIVSPSLDSSISDEDTVTVRTAKQVALVVEGQIQNVTTTAVSVEDLLQEVGGITGADAVD
ADLSETIPESGLKVSVTKPKIISINDGGKVTYVSLAAQNVQEALELRDIELGAQDRINVP
LDQQLKNNAAIQIDRVDNTEITETVSFDAEPTYVDDPEAPAGDETVVEEGAPGTKEVTRT
VTTVNGQEESSTVINEVEITAAKPATISRGTKTVAANSVWDQLAQCESGGNWAINTGNGF
SGGLQFHPQTWLAYGGGAFSGDASGASREQQISIAEKVQAAQGWGAWPACTASLGIR

>RXN01879 TRANSLATE of: rxn01879.seq check: 6847 from: 1 to: 933
VKITAKAWAKTNLHLGVGPAHDDGFHELMTVFQTIDLFDTVTLTTLDEELVEEGSVVKQL
SVTGARGVPEDASNLAWRAVDALVKRRAEKTPLSAVSLHISKGIPVAGGMAGGSADAAAT
LRAVDAWIGPFGEDTLLEVAAELGSDVPFCLLGGTMRGTGRGEQLVDMLTRGKLHWVVAA
MAHGLSTPEVFKKHDELNPESHMDISDLSAALLTGNTAEVGQWLHNDLTSAALSLRPELR
SVLQEGIRSGAHAGIVSGSGPTTVFLCESEHKAQDVKEALIDAGQVYAAYTATGPAASTA
DQRGAHILTVS

>RXN01896 TRANSLATE of: rxn01896.seq check: 5243 from: 1 to: 636
MTHAILFDLDGTLVDHASAARAALHAWSPTVGVDTDVERWIELDKWGFARFERGETTHLG
QRRDRIRAYLNRELDDATCDDIYSGYLKAYEQNWTAYPDAKGVLDRAVATGAPVGILTNG
AAPMQQDKLDRTGLGLPELVMLAASTLDSAKPRPEMYARALTHLGARTATIIGDDWTNDV
AAPRELGWNALYLDRSGTDPRADIHSLDELFH

>RXN01899 TRANSLATE of: rxn01899.seq check: 7424 from: 1 to: 786
MSRTLWAVSDLHVTFAQNQNTVDALMPQDPGDWLIVAGDVAEKIPDVVRTLSALVKRFDT
VIWVPGNHELFNRKTDRVNGKARYRALVGQLRAIGVITPEDPYPIFGGVTICPLFTLYDY
SFRPLGLTAKQALAQAKIKLDDELAIAPYVDIPAWCAERVTYTEDRLKATKGPKVLVNHW
PLVIEPTHRLFQKDIALWCGTTATRDWAVRFNALMAIHGHLHIPAETRVDGVSHVEVSLG
YPFEKHPPHMKRPWPFPVMQIN

>RXN01902 TRANSLATE of: rxn01902.seq check: 3503 from: 1 to: 1059
VQKKSRTGQTTWNGGPPIENPGTSFILSAGDQANHSSWDEHSAYISPETLRNYRLAVNNG

NHDQYNYDAYNAMYPRPNQVDENYFFEYNNALFLSLDSNDYLDIDDDIAFLRDTVAAHGD
DKDWIVLTYHHSTFSQAYHMDDARIKYQRERLTPVISELNVDLVLGGHDHIYTRSHLMNG
FTPVDAGREAVVGETLNPKAGEVVYLATNSSSGSKFYDFYDFQLGQRYDTGLDFQETVDQ
KKIRTYTAVWNQDQVQDYTNVELTPEGLTVTTKDAVSGELVDQFTLSKQDRDEESEVPVE
DDKDGDNATGSSNLGLAAILAPVLAIFGFVGGLFVGGGSLAEFFANLGVKMPF

>RXN01908 TRANSLATE of: rxn01908.seq check: 3792 from: 1 to: 846
MHSDRFEHPDNGYGYTIRQDTDAENPMTHHDTKDAALWVHNRPRRGDTVADKPEGNEILD
IFAKFICGQHDNDDNPFEVWSDGDSDASLIRTKAYVAEHHPELIFDISAKTITGYSQGDW
LDVVCVTTAATCDELIPADSLIDIYRQWAFGDVWTVIPDSQPGLAGIYADDPADALAYYQ
ENFEDEPIWDLLSRHDADKDAAALAAASAAENHALARGTTPVVIRTQDIITNARYLMSDS
ADDNPEYDRALVELSAYLLSIDLDDRVAAEMTILGRPVPKEG

>RXN01909 TRANSLATE of: rxn01909.seq check: 5615 from: 1 to: 879
MANFRSKDKDGNVINPNASTKGVDLVVNVYDSAKHVTEKGNTVHFVDVQVAQIPIDADGT
RANANLAPQTMPHLHLDTKDGQRNTGVAYSDAQIQAMQTVAAQGRNHMTPLLSKDGETVG
YSMLVKADVMFPKTKDGKSLPAVMNTKSLQPSGVPISDAMNIQQQQFMAVAMNRQAAEAQ
KAAQAQATQAQAPQVAPQPVMQNQQFQAPVPQGQQPAYAGAPVYADAVAHATAQQQAAAA
QAPQAPAGNPFNQPPAVAAALAPQTQPPAVAAALAPQTQQPAAQPQMDNEPPF

>RXN01910 TRANSLATE of: rxn01910.seq check: 445 from: 1 to: 846
MAFPLLAVAGTVAPVAAGWAKDKFLSNSQNNQQAQNQQMSFGQVNNSAQNSGSENSGFMG
QYGNLGAGLAGAATGAGLAYSDFEDGQSLSSKARNMVGKGLAGAGAGVFTKLANDAIQAE
GGSMKASAYSAIAGGLGSYLKDGGPGVIKSAMASGAAGFGADKVHDKLAESGHEGLADSL
SGAIQGGGLGYSTLGGVTGAGIGGATGGLAGLAQNYFGGGDDYSNAGASASGFSANQVNS
EISTEIPQFANLGQPQRSELEQLALPQESRSVDKSYDQGYEA

>RXN01911 TRANSLATE of: rxn01911.seq check: 9256 from: 1 to: 939
VFIIGAGLPLLYVPIFVTVIVMVVYALLRYEQRMSGTVYEEADPVEMDSVIWEGIKCDIA
SDIAARAEAKKAKKPVASDAVAVGNYIASLRQHMLVETQRRYHHKLGRELHNDPAQLEDY
GSGLRDCECRACVVAQKLGVTVHAHGVVQASARKKDRVIIGRADGIDVAGWWNHRQEARR
KTSAAKQLERDAQRKRTQAERDKEIERKRKAQEFVAEQSGKAAAAQRRAEKKAAKQARVD
ELVAQKQAAQEQKTHCKRDKQRAKKAQGRKVGAVDNSAVDDVLAYAEKTRSIAGCRDDDS
VVHVDMAAGVRDV

>RXN01930 TRANSLATE of: rxn01930.seq check: 8516 from: 1 to: 951
VISTNEIENIHSTRRDIEIALDESSTSEPKRFSEISHLYLALAEGKISFPESPSELRELY
DHLMHGELGKENELDGEIFRQGPVEIRDSRQKVIHSGFSPESQIIEGINAIIKLAHSEEE
SNLVGIMMSHFMFESIHPFYDGNGRTGRYLLGIQLSKILSPATALTMSSAINQFRNKYYK
AFHAVEHRLNRGDGTPFVISMLELLIAAQEGLIENIKQRIDFLASLEDAIKTLRGTNSFK
NHQINLLYILGQIQLFGKDETLSLESAAKFLKVSKATATRYFRTLREMELVHEVSKRPLR
FALTDKGREIVGLEVKI

>RXN01944 TRANSLATE of: rxn01944.seq check: 9781 from: 1 to: 972
VRTATLHVTSSAGEAATTINLTEDDGSFNWALPAADLTGKSWFEYTVTATDGFNSVTTEP
VRVTVDGANTDPLRLNLEENQWVSGTTDVIGASDVFGDKLELLIDDAPAVTNSSLSAAPT
FAMEVTQTDVFFRNGILAGGEELRIFDQGTYANTETISTPVPLYHINEDGTLTVSVYAGT
KAAPEIDLNENNDDFQIRNLRLILPDGRTLTPAGISDSNAWLNMGDSAGKLDFFDATFAL
PEDAFTGVAHAWDTTQSTDGEHHITISREDGGEISRTIRVDNTAPELTVSGVEEGQELRG
TVEIDAQATDAGAGVKSVETLLDG

>RXN01945 TRANSLATE of: rxn01945.seq check: 3307 from: 1 to: 1992
VQLPLTTGSIALDKGEHTLVIRAEDEVGNRTEKTITFSTPDENPISGDYAPSNGATVGVG
DVKLSARASDPSGDTVKMTFLEADSPKLDSGRVRMSSGTVEDAGSVSRAEAKMLERGDVE
KLSSLDGLGMEVTSDAALPYQLFEVDAADALAADTEVRLNWAGSADGRAQVIMYVFDGEA
WVEVDRHLTGDELEEFTLQGVVNAEKFAIGGTVTVLIQHSEGFAGADHSTRNSDVTAAHP
DDVARSEYDFTLAWESDTQYYNEEFHEHQTNIHDYVLAERENKNIQFMFHTGDVVDDWDQ
PAQWATANPEYQRLDDAGLPYSVLAGNHDVGHTSNDYTEFSRHFGEQRYVDNPWYGESYQ
DNRGHYDLFSAGGIDFINVAMGWGPDDEEIAWMNEVLAKHPERVAILNLHEFMLTTGGLG
PIPQRILDEVAATNPNVSMIMSGHYHDAFQRTDSFDDDGDGVDDRTVTSMLFDYQGLPEG
GQGYLRLLHFDNQGQKMMVRTYSPSLKDYNSDEPSLLGPAEDPNMYQEFEVSYEQLGIKP

EGRTLIGDSFSADFLTSNEIGIVDEVPSGTIAFTNWKDVTEGRHSWYVRSEDPFGGVEIS
PVQSFIAGEEAGGNAPGTGSSNGGSSHGLWGALAEFFAGAAALAGAAIAFVPGIWDYVTN
AFKR

>RXN01960 TRANSLATE of: rxn01960.seq check: 2689 from: 1 to: 318
MPQHFSQENYRKAPVIMSAPLTIHDLLSTNSKLNLKWLTCTVLNSPNLTEPCITVSVNHT
EGMSLVSFEGGHGLTEIANTQLVPVLELPKFNPFEALAIHLEAANN

>RXN01985 TRANSLATE of: rxn01985.seq check: 6664 from: 1 to: 1050
MRTSRVLAGILAATLTVSLAACSQDSSETSSNSSSAASQSSDVSNEAFPVTIEHAFGETT
IESKPERIATVGWSNHEVPLALGVTPVGFEKVTWGDDDNNGILPWVEETLSKLGSDEPVL
FDATDSIPFEEIANTAPDVILASYSGITQEDYDQLSQIAPVVAYPEIAWGTSLDEMIEMN
SKAIGLEQEGKDLIADLDAEVASAIDANPELKDAKPVFAFFDESDFSQIGVYTSIDPRMS
FLLDAGVQEASVLKEHSSPDSFYEQVSAENPETFDDVDVIITYGTEDDAANAELLSKMQA
DPLLSRIPAIAEGKVVFLGANPLAASANESPLSIPWGINDYFAKLAEPLK

>RXN01987 TRANSLATE of: rxn01987.seq check: 9043 from: 1 to: 213
MTFPAQSRRLARSTTDKWIGGVAGGLAETYGWNPAYVRLAFVASVLFPLPGSQILFYALA
WLIIPSRENRF

>RXN01988 TRANSLATE of: rxn01988.seq check: 4185 from: 1 to: 426
MNMKTHPASAKQTTELRLLTATVYFKALNEVHNVMQMIDPLTPVVPITTGTSVAELYADA
REHLDNGATQVMIPVISPSNLTLSVVALGNEEVDALGHSEGQAVHSLLEIHTPKRSWPLS
ELYIDDNEGLAQVSRCFARLVG

>RXN01991 TRANSLATE of: rxn01991.seq check: 5467 from: 1 to: 873
MTNLLPHFPSTDVAAWEPTVVYSADKTTATATFKNIPSDISFSWTGIEALEPFSPGKTFE
HKVQGSVGEPAGAFTRDNYFTEGELYKHRHADDLLSGDGLFGPNITDGDGNLPSVDDGKD
GDDGSDGSDGRDGVVAIDVVDNADGTVTVTLSDGTTFTLDAGQDGKDGLDGLDGTGLTLE
SATPDEDGNITYVLSDGTEFTVRNGVDGSDGKDGKDGVNGTDGVDGSDGKGLVEVSRVTN
DNGSVTITYEDGSQITTKPTPTNWLSKLLDLLLPLFNLFGLGGGSVISSSK

>RXN01996 TRANSLATE of: rxn01996.seq check: 8265 from: 1 to: 537
MSKLTGTWTLDPAHTEIKFVARHAMVTKVRGEFTEYTDSIVVDAENPENSSAKVVIKTAS
VTTGNADRDAHVKGDDFFAVDKFPEMTFEATSFVIKNENEGTVTGDLTIRDTTKSVTLDV
EVGGVAEDPFGNTRLGFEASTEINRKDFGVDFQAPLSTGGVLVSEKIKIEIDGSAIKAA

>RXN02007 TRANSLATE of: rxn02007.seq check: 3631 from: 1 to: 633
MSSDAEKASVELSEKFHPERTHILGAVVFGLISLLVIGAAPQYLFWLLALPVIFGYWVLK
SSTIVDEQGITANYAFKGKKVVAWEDLAGIGFKGARTFARTTSDAEVTLPGVTFNSLPRL
EAASHGRIPDAITASKEAADGKVVVVQEDGYSVMMSKEEYLERQKALGKPVQLNFDDDTD
GNTTQTESVESQETGQAASETSHRDNPASQH

>RXN02014 TRANSLATE of: rxn02014.seq check: 217 from: 1 to: 507
MENIAEQAGVGVATLYRNFPDRFTLDMACAQYLFNVVISLQLQAISTFPTDPEGVWTSFN
QLLFDRGLGSLVPALAPESLDDLPDEVSALRRTTEKNTTTLINLAKQHGLVHHDIAPGTY
IVGLITISRPPITALATISENSHKALLGLYLSGLKHGMMANIGEHDGKS

>RXN02019 TRANSLATE of: rxn02019.seq check: 8826 from: 1 to: 501
EIPAGTKVEASDLGLQAIPTSLLPSTSYDSIDDVVGLVAASTLSSGEIATKPRFVGTELI
NSIATNVTDSSLVEEINMVPLSLAEPSVIPLLQHGDTISVVSQDPDTGLPENIAAGGTVI
LAGGTDPSTILIALPQSIAEKVAAQSLNTPLAVVLTGDRADNYTTEE

>RXN02023 TRANSLATE of: rxn02023.seq check: 8728 from: 1 to: 768
MAPKQTPSPEKNRNLVGPVLQRRQTEGTFDQRLLEMRADHNWKHADPWRVLRIQSEFVAG
FDALHEMPKAVTVFGSARIKEDHPYYKAGVELGEKLVAADYAVVTGGGPGLMEAPNKGAS
EANGLSVGLGIELPHEQHLNPYVDLGLNFRYFFARKTMFLKYSQAFVCLPGGFGTLDELF
EVLCMVQTGKVPNFPIVLIGTEFWAGLVDWIRHRLVEEGMIDEKDVDRMLVTDDLDQAVK
FIVDAHAGLDVARLHN

>RXN02032 TRANSLATE of: rxn02032.seq check: 9048 from: 1 to: 570

MPFLQISLLSIGVAADAFACSVVRGTAIQVNLFKRALVLAGIFGVFQAAMPLIGWFIGRF
FAGITFIAEIDHWIAFALLGIVGTKMIWDAFQPEDDETIVDDGRVQFRPAIILGLATSID
ALAVGMGLAFVEVSILKVALSMGSITFALSLAGAWIGHHGGGKFGKWATILGGIILIGIG
ANIVYEHLSA

>RXN02039 TRANSLATE of: rxn02039.seq check: 6804 from: 1 to: 840
KASISNLSFWTSTSTTAPLWLVGTLVWLAVQAVMHDGELYHVEVPTIALVIGFGAQLLIG
VMSYLLPSTMGGGASAVRTGTHILNTAGLFRWTLINGGLAIWLLTDNSWLRVVVSLLSIG
ALAVFVILLPKAVRAQRGVITKKREPITPPEEPRLNQITAGISVLALILAAFGGLNPGVA
PVASSNEDVYAVTITAGDMVFIPDVIEVPAGKSLEVTMLNEDDMVHDLKFANGVQTGRVA
PGDEITVTVGDISEDMDGWCTIAGHRAQGMDLEVKVAAPN

>RXN02044 TRANSLATE of: rxn02044.seq check: 4936 from: 1 to: 1383
MVTPIMGNSNSILGIYRQKIQNRHLVSTLFRAYFPIVTELIILLIVIVTALAFDFTNGFH
DTGNAMATSIATGALKPKVAVALSASLNLVGAFLSVEVATTVAKGVVDLDQFDLSNAWDS
HQLLLVVFAGLIGAIVWNLLTWLLGIPSSSSHALFGGLIGAAIASLGFGGVVWEGVLSKM
IIPALAAPVVAGLVAAIGTFAVYSITKAVGDNEKNRYFRWGQIGSASLVSLAHGTNDAQK
TMGVIFLSLVATGHLGTDADIPFWVKATCALAIAIGTYLGGWRVIRTLGKGLVEIDSPQG
MAAETSSAAIILTSSHFGMALSTTHVATGSIMGTGIGRKGAKVRWSVAGRMAMAWVITLP
ASAIVGVFCWWVAHGIGLISSDLLGVLVAFAILVILSGYIYARSRRVPVDPSNVNADWNE
ESNSVEPATPSAPAASEITEAPAAPAAQAVQDLNNENEVTK

>RXN02045 TRANSLATE of: rxn02045.seq check: 8713 from: 1 to: 261
MNFATIFGSIFEVTLVGILLGAGLPALFALGIRFAHSPSSNGTNALGKIASTICFAIIAV
AIIAGILWVTKATIYQYSGFDIFGTEG

>RXN02049 TRANSLATE of: rxn02049.seq check: 6577 from: 1 to: 609
VRYLTLATIIAGLSGFVVIIIAAWALGDSSQLSEEFTAYWGLFFAGTGVLTGLTQETTRA
VTAGSRGGSRGGRAGSVVGFRPFLFSFVVAAIVLVVLGASAPLWIGQLLSNLQGVGVGLL
AVGLASYAIQATISGIFVRLPIVERVCLADFFGHRRAHGFNCCRLVAGLSIAGVLDHHRC
GINILAGHRAVLRFGAFRFGIGC

>RXN02050 TRANSLATE of: rxn02050.seq check: 1487 from: 1 to: 795
LDTGVRMVLTVAAWLLGYQLLAFLIITVVGSISWLVIVLCFGSVRSVLGSVADVSRGVFI
RQALLAMAASGATAVLITGFPTLLKFTNPSAVAGGVSMAAVSYAVILTRAPLLVPLQQFQ
SAIIVRFVKGTSGPLKTLAGPLAIVWAVGLVGAGLAWLVGPWILDVVLQKELFAVPGWLL
AMLTLGATTTASLMVSGCAAIAFERHGIYLTGWVVATVVAVGFLLGPFDLGVAAGLALIV
GPLCGLLVHMGAFVGGDRNRVLTAG

>RXN02059 TRANSLATE of: rxn02059.seq check: 3288 from: 1 to: 495
MTQPRPDAASVSLEKKRPEGWPVGSFETYPEAQAAVDLLSDNAFPVTELTIVGVDLIEVE
RVTGRLTWGRVIAGGMASGAWLGLFFGIVMALMSGFWFSSIAAGIGMGLVFGIVGAAVPY
AASKGKRDFTSSTQIVAGRYDVICSPERAREARDMIALKTRDLRQ

>RXN02066 TRANSLATE of: rxn02066.seq check: 2735 from: 1 to: 492
MFNSDTTANLQAKSRDRAGSKAKRSRPSFDSVARDVLDVRTKTAQVKNKAKEFSSVDHLS
ADAAAMFVDNELSRGAMHRARLHIVHCAECREEINRQRETVDYLRSECKNEEVSAPMDLK
ARLASLATECMPGPGAENLAMQRPESFVAKVESVVRAVRKNQGR

>RXN02067 TRANSLATE of: rxn02067.seq check: 4916 from: 1 to: 456
VGWGEIFLLVVVGLVVIGPERLPRLIQDARAALLAARTAIDNAKQSLDSDFGSEFDEIRK
PLTQVAQYSRMSPKTAITKALFDNDSSFLDDFDPKKIMAEGTEGEAQRNKQAADNNANVV
ERPADGSTARPTQNDPKDGPNYSGGVSWTDII

>RXN02075 TRANSLATE of: rxn02075.seq check: 2111 from: 1 to: 789
MYKVFEALDDLVQAVQRAYGVPMTGNCVVPRQEVLALLDDLRDALPVELDDAQDVLDHRD
GVIREAEEKAIALVDDAENEARNLLARATEESDAMVEDATKHAHSVVAKANDTADRIVSD
ARREANSVTERAQAESERLVNSGNDAYRRAVAEGQAEQDRLVSEAEVVRRSTEEAHRIVD
AAHADSNKLRNECDDYVDTKLAEFETSLSTTLRSVTADRSALRRGAGATGRELRDEQPAA
RGEYERDYERDYERGYERDDRDY

>RXN02076 TRANSLATE of: rxn02076.seq check: 9502 from: 1 to: 534
MKSPFIFDVAALLRGSALPEHLTQSGPSPTRIGPEMIAIPEGGKVIVEAQIIPLGGGLAV
EADIEAQLLGQCSRCLRELTPTKTLHVSEVFAADPDFVTGEDAADDEDELPMVNQDQIDL
LQSVIDEAGLTLPFNPVCEELGYGACQDDETPAPDGVSEEVEDEEKVDPRWAGLEKFL

>RXN02094 TRANSLATE of: rxn02094.seq check: 8559 from: 1 to: 717
MAEHNAIITDAVHSDPAVLEDNAGFSGKYLIRALDKAAHMQTGAIEGYISWLRKHNPEKT
PAQLQVLVDKHFMRLATGSGAGVGMAAAVPGIGFVTGALAVGAESLVFLDAAAFYTMASA
HLRGIDIRHPERRRGLILVVLLGTAGKAIVDAGVGDLSKKNHAPGIAISRFNIGGLMEVN
GRLMRYAVKEVSKRFRSALIGKILPFGIGAVLGTMANRKIAKRTVGNAYDSLGPLPTHF

>RXN02104 TRANSLATE of: rxn02104.seq check: 737 from: 1 to: 1122
MSNSPTDVSTSAPRIMIAPDSYKGTATASEAAQYLGEGVLEILPNASITLAPMADGGEGT
SSVFGGQVITLPTTNAAGRLTEASYTLDSETNTAYIDIAAASGLPAVADDLVPTTGDTYG
TGVLIADAVTRGATRIALGLGGSATTDAGSGILIALGAVPRNKEGYALRTGGADLINLDY
IDTAELNIPAAAVEWILLTDVDAPATGPQGAATVFGPQKGATEKDISLLDAALHHACAQL
EVDGTKPGMGAAGGIAIGLTWLSTLMHGNDQQIHILPGAPLIARSNGIEDALPETDLLIT
GEGRLDSQSFTGKVVGTLHGLAKAHDVDLAVAAGIVEGGIPDDFLAVEMIKSSDVAAQLR
DAGRRIAQEYVAQN

>RXN02107 TRANSLATE of: rxn02107.seq check: 3646 from: 1 to: 342
MDLHKVAAAHAATLPLSTKEFPFGPEHEVYKVRGKVFLLLTILNDEPIITLKSDPEIGAS
LRSGFPTIQAGYHMNKVHWLSISDGERITKDFIEGLVEESYELVISTLPKYKRP

>RXN02108 TRANSLATE of: rxn02108.seq check: 5369 from: 1 to: 609
MGDMKITRHIHACVEISQGNDRIIIDPGTFGAPDLCGATILVTHNHADHVDPELLKPGMT
IYAPRSVAHSIPVECHIVEHGRNFTVGSLSVEVLGSEHAMLTHSMPIAENVGYLINGRVL
HPGDTFQPIKDVELALVPVNGPWVKMLDVEGYLKKFPPKRFIGIHDGIVNDRGLAINKKF
LTHLGETYGSEYSPLEEGESLEI

>RXN02114 TRANSLATE of: rxn02114.seq check: 7318 from: 1 to: 486
SIGYAWTTAFHALTPGLGGIAIGIWLLGGVLGGLVIRKPGAAIFVEVVAACVSAALASQF
GISTIYSGLAQGIGAEIIFALFLYRRYSLPTTMLAGMGAGGGAIFLEMFFYGNLAKTMSF
NIIYSTTVLISGAILAGLLSWYLVRALARTGALDRFAAGREV

>RXN02121 TRANSLATE of: rxn02121.seq check: 4238 from: 1 to: 705
MITSPFERELKLLNEGELGIVQQLVESSNIGFIVDLELDGDYGWAVYKPELGEQPLWDFP
PGLYKRERAAFVISEFLGWNIVPPTVIMHDAPAGVGSVQWFIENNGEHYFPLFDTRADLH
PQFVRMAVFDLLCNNTDRKAGHVLLDGDHIWGIDHGLCFSVEPKLRTVIWDFAGCTIPDD
LVTDVEQLLEDVPEELHQLLHPAEIDALQRRASRISRLPFLPQAKSHRQFPWPLV

>RXN02138 TRANSLATE of: rxn02138.seq check: 8752 from: 1 to: 342
MTAPSTNTGVILTESAASKAKALIDQEGRDDLSLRIAVQPGGCSGLRYQLYFDDRTLDGD
KEDIVGGVRLVVDKMSTPYLLGAQIDFADTIEQQGFTIDNPNAGSSCACGDSFN

>RXN02151 TRANSLATE of: rxn02151.seq check: 8209 from: 1 to: 1188
MDWPDIAKGISILGVVLLHVSLAIPGGQDTMMSHLNALLDPLRMPLFFMVSGFFAVKVLN
QSFGELFRGRLWFYLVPYLLWTPVNLYLHRLEGTVFTGRAPGTWEWYSGSMLSATNMYWF
LYFLVIFNLFLWATRKLPAWAIVALVASLWLLMPAYSEIEILRKSIIYLPTFLIGAYFRP
LISRFAEAATRPKAIVFAAVLYVSGLALGVISNGLRDSENHGASVLWLMNLRDTFAHALG
GNLTGFDMDHLPGMIIRIVSLPAGIVLCVWLGRIKPVGEFLKLIGRHTLPIYIGHATGLS
LIFGFGLRWNFMEIDNFSDSLWHHTNTWMVIAFACAMLGGYLTYLISRVPVLGWTLVPPK
LPEPDKTPAKAQADSHVKAQSAKPMNASTSSKTYGI

>RXN02169 TRANSLATE of: rxn02169.seq check: 3541 from: 1 to: 846
LDMQINRRGFLKATTGLATIGAASMFMPKANALGAIKGTVIDYAAGVPSAASIKNAGHLG
AVRYVSQRRPGTESWMIGKPVTLAETRAFEQNGLKTASVYQYGKAETADWKNGAAGAATH
APQAIALHVAAGGPKNRPIYVAIDDNPSWSEYTNQIRPYLQAFNVALSAAGYQLGVYGNY
NVINWAIADGLGEFFWMHNWGSEGKIHPRTTIHQIRIDKDTLDGVGIDMNNVYADDWGQW
TPGNAVDDAIPTIPGNSNTGTGTGIDADTINQVIKILGTLSS

>RXN02180 TRANSLATE of: rxn02180.seq check: 4458 from: 1 to: 1458
MTSGKSTSTRGALDRYFKISERGSSIGTEIRAGVVTFFAMAYIIILNPLILGTTPDVEGN
TLGIAQVAAATALAAGVMTIAFGLIARYPFGIAAGLGINTMVAVTLVSGEGLTWPEAMGL
VVLDGVVIVILAVSGFRVAVFRAIPASMKAAISVGIGLFIAMIGLVDAGFVRRIPDAAGT
TVPVTLGIDGSIASWPTFVFVVGVLLCGILVVRRVRGGLFIGILGTTILAIIAEAIFDSG
ASFENGEANAEGWSLAVPGLPDSFGGIPDLSIVGAVDLIGAFSRIGVVAATLLIFTLVLA
NFFDAMGTMTALGKQGNLVDDEGNLPDIKKALVVEGAGAIVGGAFSASSNTVFADSSAGV
ADGARTGLANVVTGSLFLAAMFLTPLYEIVPIEAAAPVLVVVGAMMMGQVTEIDFSKFYI
AFPAFLTIVIMPFTYSIANGIGVGFIMYAIMAAAAGKAKQVHWLMWLVAGLFVVFFAIDP
IMEAVG

>RXN02185 TRANSLATE of: rxn02185.seq check: 8940 from: 1 to: 579
MGRHSTKTSSAFTKLAASTIAFGAAATIMAPSASAAPDSDWDRLAQCESGGNWAINTGNG
YHGGLQFSASTWAAYGGQEFATYAYQATREQQIAVAERTLAGQGWGAWPACSASLGLNSA
PTQRDLSATTSTPEPAAAAPAVAEYNAPAANIAVGSTDLNTIKSTYGAVTGTLAQYGITV
PAEVESYYNAFVG

>RXN02186 TRANSLATE of: rxn02186.seq check: 5727 from: 1 to: 198
MYDMANVEKKHFVDPAWPEHNPADGHVVTELISKVAGASSPWGDDKEFPVSAEETGYVHP
YTRINR

>RXN02207 TRANSLATE of: rxn02207.seq check: 6831 from: 1 to: 798
MRRRSRVSRLLPATALLASTALLLSACTQGVTDSPDMGKATPAVSPAASNPDGQVIEFGN
ITDMEVTDGDILGVRTEDALAIGTVSDFEAGSQVELDVDKQCGDLTATGGTFVLPCADGV
YLIDAKDPDLDELRATDKPVTVAALTSDDQLLVGNGEDEELTIYREGEEPETFTVAGPNT
QLIAVPVIDRHDAVVRTWNENTTIQDVDYPNDREGATLRVGLGVGQMAGGEDGLLVVSDE
MGGQIAIYNADDVIRLQNDRPHRRGT

>RXN02223 TRANSLATE of: rxn02223.seq check: 9117 from: 1 to: 501
MSTYQDDRFPGPDPYAPLGEKPSFTLTSTDLENGAKLAEAQLGGTDISPQLSWSDLPEGT
KSLAITCLDPDAPTGAGFWHWAVFNIPTTVTEIPTGAGDETLGGIEGVVSLKGDSGKRGF
YGAQPPAGHAPHRYLFAVHALDVEKLDIAPDATPTGLGFNLYFHTLG

>RXN02226 TRANSLATE of: rxn02226.seq check: 1898 from: 1 to: 1056
MTENQTPSSTSAPKPGPRPGPRPGPRPGAQVAAKKAAVATPAPIAKTSNDPAKFGRVEAD
GSAYVTTSAGERLIGSWQAGTPEEGLAHYGARFDDLATEVELMEQRLISHPDDATSIRTK
AEELKATLPTIAAIGDLDGVEARLSKIINNSEEANERAKEQKAKNRERAVARKEELAVEA
ETLAENSSDWKVAGDRIRAILDEWKSIHGIDRKTDDELWKRYSRARDSFNRRRGAHFAEL
DRTRASARKLKEELVERANALKESTEWNDTARAFRDLMTEWKAAGRAPREIDDKLWAAFK
GAQDYFFDKRNAVAKERDQEFEANATAKQQLIDEYDAQINPEQGLDGARSKL

>RXN02238 TRANSLATE of: rxn02238.seq check: 4471 from: 1 to: 285
VTNVSNETNATKAVFDPPVGITAPPIDELLDKVTSKYALVIFAAKRARQINSFYHQADEG
VFEFIGPLVTPQPGEKPLSIALREINAGLLDHEEG

>RXN02254 TRANSLATE of: rxn02254.seq check: 1030 from: 1 to: 777
IAVAEEGGLWENLLQHRFGGHGALAGHALGNLVIAALTDILGTSQHALDQIAQLAGAKGR
IIPVCAEPLDLEAEVSGLDSDARVMRQVRGQVAVAATPGQVRRVRIIPDNPEPNPAAIEA
ILDADLVTLGPGSWFSSVIPHILVPGIVDALAQTKATKTVVLNLTSEPGETAGFSAERHI
HVLRQHARNLQVDQVIVDAKTLSSQTERNHVERAARTLGAEVSFHDVQAEDGRGRFTSIH
DPAKLCAALLASFAGARKR

>RXN02271 TRANSLATE of: rxn02271.seq check: 4621 from: 1 to: 558
MSFLNSAKTKTVALTATFVGAATLATPAIASADIVDNALAALPSGEISCSQAEKYWTTEA
DYNSKVAQANALAMFDSRGPQIQAALARVDEAANRCGLKGGTVAAQAEATEAAPAAPAPA
PQDNTGTSQTAPAPAAPAAPAATPVVNLAPAGSPTFTIEVPGVGGVQLPDLYQIVQQFLA
QFGIKI

>RXN02279 TRANSLATE of: rxn02279.seq check: 6646 from: 1 to: 1458
LISLEKKQKDANFFLSELRRQGYRAVDFLESQTVDQLNNPDVQTYLTEAELIRDDLRSWA
VINQMALDNIDLVPYGEENDEPLAIARKIIEETASHPELRFENLEAQFSEFTILLAQSPE

NLDVARYQELRTQGNFVQELALDSIFGQHAVVQDTGNGEAILDETIGYMIGAGMRETTAR
TASQFAQLYSFVGRQERSIEMARLAFEELQAAGLPHREEELRLGMQLAQVEPIEAREILE
KLLLPKFEQNLTLDELETEALLPLGATVAIHDPQAAAAILRHARENAAGFGNFELAVQAM
TMITDVLYTQNMHEQLLEELNHSLPYAQMLDDQHQAELKLLDSIAIVQADLGSTEALETL
GTAMGLAETTAQKLYVQESLNRAYFTFARPEDCISGAADASALAMQNDDPSNAAAQLEQC
AQYLFQLGHETDGASLLESAFRVEGIPTEQALYYANALSSIYEDFGDSAKSQYWEQQAQE
KQQLLE

>RXN02296 TRANSLATE of: rxn02296.seq check: 7700 from: 1 to: 489
MRNQTIAAVAALVLLTAATPAIAATPATAGNGLYSIDMGDEQKLTCVLFDEPSTEAHVVA
SCAATFPVTWKLLDGAHEQAAKLEITQAQDGELSVTASKQPLITTMIAPTSITKPITVNR
LVVVPGENEVRFYATDPDVLPVLITPDSYEVLTDSAAKVKATL

>RXN02300 TRANSLATE of: rxn02300.seq check: 2962 from: 1 to: 333
MKTYAVLIAVAGLALAGCSSSAPGIWRATEPADAYLEIADDGTLSGTDGCNRLFGGWEKD
GSTITFGAIGMTEMYCEGVNDWLSQMHTATVTDATMTIFNEAGSNIGELKR

>RXN02301 TRANSLATE of: rxn02301.seq check: 2104 from: 1 to: 717
MDLALAQVDSTVSGLYDALDLIGVLLNGIIGGTIARQRGYDIIGFLFLALFSALGGGMIR
DMLIQQGTVAAIDNQIYLALAFSGALIAMAVNFKGRVWELFKVHGDAIVLGVWAVTGSVK
AMNAGVAPLPSIFMGVLTAVGGGMVRDVATGQTPTIFGGGTLYAVPATLSATSMVIFHSF
DQVILGMIISPFLGIALAVTAYWCGWVIPVNTDFAPVNLTVSQLRAMLSKAERKDKDQK

>RXN02302 TRANSLATE of: rxn02302.seq check: 9010 from: 1 to: 879
VATNRTSSAGVITSVLASALFGAIFFISGAIEAKAETLVAWRVLLTAACYLLALLHPAGR
KVFKEFWDTLRSQPRQILYFIFLVVLITLQLWLFSWSPKSHALDASLGYLLLPIFLVIVG
RFFFADYITRLQWIAVGIALIAVTLKFVISAQLSWVTFAIAAGYALYFALRKYSGLNNAF
AYGAEVLALSPLAFFMLATVEDPLSNAMLSMVILAGLAGALAMALYLAASTLLSMPMFGL
LSYGEPILLFVAALLLGETLNLSDAIVYSLLACALALLGFDGIRRSRKNLETD

>RXN02303 TRANSLATE of: rxn02303.seq check: 6641 from: 1 to: 906
MAENNTPQETEQDQEARFREEFEVGGKDRQLSEEEQLEQLGSYIDAHYPVPDFTPPWAGG
AGDPDPADRYIAHLPDRTTHTAMIMLGSGLDHSMPGVAFIGGVSVDDVPEVGGAIFHPSN
PTGRWAVSFHSGGWWRGSGDALEFQWRPEVAAAAELSGTTILDLDYPLAPGHNLHDMNEV
VGKAVGYARHHNPVSITGWGYSSGAALAAINASLFDALVLTFPDLGSVEKLPAEIRGDAV
VPAAAAWPTTFVQIAAQDEIAERPGELGDATVKEYVSRHRISTPKVAREKITDVAEFLKT
VC

>RXN02307 TRANSLATE of: rxn02307.seq check: 9052 from: 1 to: 621
MSGTAIMYDTTVVPSKKEIAQAWTGYVDLQGSYRLVDTVDGEVGVEVLISKDREGRLLQI
PFSYRSAEINPEQTLSTLEHGVLGKRWVTNALGDPVAVREFIRTILTGDDGAARSDGVKG
YLDIKGSGDAESVDLQDVKLTEVTRQRAIGSVTINGERKQFSLRLPQLLKNFRETAAGHT
ATTLRIVATHPEKDDVELLVAEFNWME

>RXN02314 TRANSLATE of: rxn02314.seq check: 2536 from: 1 to: 441
MEWYQVRRRARQLLIVLFIAAMLGAASMVIGPFLNDRTIEGNSGRALAQVTNVGSYRTTV
DFQDENGIYHSPATGLLFPTGLGEGQRVWVNYAKSDPDLVKVEGRKWTLSIIPALSVAAV
ATATWSVLWLGVGRFGRRSDDANETTV

>RXN02337 TRANSLATE of: rxn02337.seq check: 408 from: 1 to: 1323
MSKLYAGARINALRRTHQLTQSALADKLDLSTSYLNQLENDGRPLTATVLLQLMKVFDVE
ASYFSPDRGTATATRLAETLAMNQGPTMSMDDLLDFADRFPQLAQHIIQPAEVDPTHSSA
HDFVRDYFATHKNYIDSLDRLGEELATAIGQPGLRVTRLAQLLDAEYNITVRFRAPDITG
RRHFDPQSRQILLRQDLSEAQQCFQLAEELTFLAHAELLDTLTTDQPDLPSEAAIRLAKV
GLSQYFAAAVVMPYTRFLEFAQDKHYDIELISEAFGVSFESACHRLSTLQRSGASGVPFF
FVRSDRAGNISKRQSAATFHFSRTDGTCPLWALHRAFERQGNITRQVARMPDGRTYLWLA
RAVKGRTHGFGYPAAEFAIGLGCDISEAPGLVYSQGLNLDPESAAEIGPGCRICPRENCV
QRAFPPSGQESIRPAPVQLLN

>RXN02339 TRANSLATE of: rxn02339.seq check: 8878 from: 1 to: 492
PTDNLFSYPAQRYDLLTLAFEVRIGDMVQINDMLAPPPVKLPEDPALGADPTLTSTAIAH

PDSPLVWAYRAENLIKSASNDEEKIQAYAFARTGYHRSLDRLRANGWKGWGPVPFSHEPN
QGVLRAIASLALAAKLIGEDNEYDRCRQMLSDADPESVAVLLDK

>RXN02340 TRANSLATE of: rxn02340.seq check: 7304 from: 1 to: 1065
MKKSIVVFEVEGGSDKHFDGHRKDTMPIVNSINDAGWQAEVVYYRPEWTEGLFEYVSENF
DGYISRVNPGNIPGGERGYFDLLTRLSEAGLVGMSTPEEMMAYGAKDALVKLSQTDLVPS
DTEAYYDVETFHKVFPTSLSFGERVLKQNRGSTGSGIWRVQLVDKELAASIEPGTALPLD
TEIKCTEAVDNHTEVRKLGEFMDFCDQYIIGDNGMLVDMRFMPRIVEGEIRILLVGPHPV
FVVHKKPAEGGDNFSATLFSGAKYTYDKPEQWQELIDLFADARPVIAEKLGGDNIPLIWT
ADFMLGDVVDGKDTYVLGEINCSCVGFTSELDMGIQQLVASEAIKRIEEFAQLTV

>RXN02341 TRANSLATE of: rxn02341.seq check: 4129 from: 1 to: 486
MGNSLEKHIAEGDRIHVDLTSPLSAMLFPIFELIVITGICWMGIGFLDQLPGIDGTNPAD
SFPEGTRNLLVGVWAVLAAWRFGLPLIRQRRLRVILSDRKLLVRRAGLRTGFDSIPLSYI
QRVQRRRNTLVLGVGGHHRPYVINQVPKARKVEALLKDLTFW

>RXN02360 TRANSLATE of: rxn02360.seq check: 7403 from: 1 to: 2433
MRGDVQKITKVYDGKHRTLEIPVYQRNYDWTEKQCSRLFDDLSEVVKENHRQHFFGAVVG
KPQGSWTWVVIDGQQRLTTISLFMLALVHSLRASEVEEGEFNAGYNIDLATLIEDDYLRS
GNEGNLKFKLKPVKNDNEAYQKLFGPESEFIESSNLTANYRYFRNVLKATDLTAAQLWEA
IEKLRVMYLDLEEFDDPQRIFESLNSTGLELSEADKVRNLVLMDQELKTQEKLYEQRWNP
IEVCVKFDTDNFIRWYLTLKTARTPRKQDVYEEFKKFIRNSKLPVEFILDDMYEYAKLYR
DLLGATTGFIAADRCLKRFVPVMGDVVLPFLLPVLKDAKDGIITESDFLGVLKVLESYLF
RRFAVGVASNALSKIFSTAYSDIKKFWTPGQSYSSLLAYILKRRDGSGRFPSDSEFRENF
ATKNFWNIHNENRRYLFDCLENADSNDVRDIQTSLDEGSLSIEHIMPRSLNDQWRAELGP
EYARIHETWINRIGNLTITGYNSAYSNSSYERKRTMENGFLVSPYRINNFIKKQKHWSEE
QLIERTELLTQAALDYWPLPKETFQPPQAVLPTESLDSDLSFRGREIVAFEYEDYKETVT
SWADMLQSVLKVLNQSFRQELIALTNEEICLATSNNSNSSLREIDHGLFVDTGSSTSVKI
GFLRRVFTQLGLEQEALVFTLRPLANDVEPRDDELEVEVEKKYSDLTKFIPQLEEAENLE
GADTEVIPLLSKLKEQLTAFSPENPQAALGGLPVPEFLKQNVIEQLSAEHILAVLTQHFN
IASMMGDDYLLEELRSGRLRELLQRLEELDS

>RXN02361 TRANSLATE of: rxn02361.seq check: 1002 from: 1 to: 651
MELLSHLLALDPASPRLTVYNESTGARLDFSAITLDNWASKVGNMLLEELDLEEGSLITI
DLPVSWQAAMIMLGALATSVEVSFDDPEADAIFTSLDRFSHYKGHSDVLIVSEDPFGRGV
VEGGGELPNGAIDFGPTVRFYGDQFFQPTRTLPEIIQHSDVPVGARVLATGWSDIESFNH
QVLEPLAVGGSAVIVTGLADIERLNQIATNEKTTHRI

>RXN02367 TRANSLATE of: rxn02367.seq check: 8247 from: 1 to: 609
MSNAEINPVEYEINNHAPGTALNPQCEDGANVEIITSREVPLGGPRAMTVHRTLPQRQRS
LIGAWCFVDHYGPDDVSLTGGMDMASHPHTGLQTVTWLFEGEVTHHDSGGNHAVVLPGEV
NLMTAGAGICHTEVSATSTTILHGLQLWTVLPDKDREGPRRFDHYAPEEITLEGGSARVF
LGSLFGQTSPVHTFTGSSCFRVH

>RXN02368 TRANSLATE of: rxn02368.seq check: 7600 from: 1 to: 675
MIVLAGATRVTYEVEPWLAIPLFILAFASILIPFPISKTKGLRDIDAWKIHTTQGDKKRA
IRQLIIPATALAIDIIGLPTLFNAPPLASAALFGGVYGASLAWAAYRADQLPRIRTKERL
AELSQNASLDDVRSDDLDVLEQPESRELVRCLLAHGAMDGTRVMARQVARVLDTEVDEVH
QVARSLEQHGLVSRSTIMPGGDPGKVFIEVSLKGISAIKALESGR

>RXN02381 TRANSLATE of: rxn02381.seq check: 8210 from: 1 to: 1023
MSVTNFRRFLAGIAVIAACVAATPTAQAQSSGSSGSSGSSAGSSGLWDLLFPESHESFIE
RLLDPLDDSHISIHPDLTPDLYEEVFDPPQIGECPAVVAVVARGSEQNLQIRPARYSEES
PWTSNGFEEKNFRSFFGRMEKHYRESTGESLMKDVYVMGLNNIEYPASLPLSSEGSSAIE
LGTSISSGRDNVISAIDRFESATGCTPKYLLAGYSQGVLIVDGYEEELIARDQYLGTLHI
ANPAQQVDDPTLVGHEVTTGGLASSVEPVEDNPFKVSYCLPGDIVCDRSFEQFSAAGSSI
AAAQLSTGNIRPGRVHVQYFVTTQPWDEQIFDEVASWIEAA

>RXN02383 TRANSLATE of: rxn02383.seq check: 712 from: 1 to: 636
MPVRVIVDSSACLPTHVAEDLDITVINLHVMNNGEERSTSGLSSLELAASYARQLERGGD
DGVLALHISKELSSTWSAAVTAAAVFDDDSVRVVDTSSLGMAVGAAAMAAARMAKDGASL

QECYDIAVDTLKRSETWIYLHRIDEIWKSGRISTATAMVSTALATRPIMRFNGGRMEIAA
KTRTQSKAFAKLVELAQIRADGEPVFIAIGQN

>RXN02387 TRANSLATE of: rxn02387.seq check: 2544 from: 1 to: 762
VWWCLPTWIKAGQDAVDLALSAAVDPSPGTYLIVMHSGGGRSKSMVKKLEKVAVVHDAAK
LKDRDRPGWVKQEFKNHKVQVTPDVIHALLEGVGSDLRELASAVSQLVEDTQGNVTVEKV
RAYYVGVAEVSGFDIADSACAGQMSKAVASTRRALQLGTSPVALAAALSMKVGQIARLYS
TRGRINGFELAKELGMPPFVVEKTAKVARNWSGDAVSEAVILMADLDAAVKGQSGDPEFA
IESAVRRVAELARR

>RXN02398 TRANSLATE of: rxn02398.seq check: 7197 from: 1 to: 1602
VVEVKKRNLLVAPLTASLVFCNLAVAANAVEVEAESPVVINEVESNSDPVGDWVELANTD
NNNSIDISGWSLVDDKEDLENALVLPEGTEIESGGYFVIYTDSADYVPTNNTFGGQEYFG
LGKDDTVTLRNAEGEVVATYSWKDLGEHAENTYGRIPDMTGDFANTGVPTPGAKNVAAEG
SGEEEGVVANAQLPFHNVEITPIHLGGDFTGEDMSGVDFDANSTAWIANNDIGKIYSLAH
DIANNTYKLTGEWETGYPEGGGEPDAEGIVAATNGDIYLSTERNNADKNVSRPSILRFAT
PTGKTGVQNAVQEWDLSEFVGDIQPNGGLEAIAQLEDNIFVVGVEETGDVIVVDLSADQP
VLVQRYESSFDGVMSLDYNAATKQLSVVCDEACDGLSEILEWDGEKLYKSDDKIYERPAN
LGNWANEGFGTYTSELKCENGNTVSVTSYLWADDAATNEGTSLNSAQVINGDCGDVNIPG
ESSSDNSSSDFATGSIAGAFATAVLAVVGIAGALGGFFQQILAAFPALQQVIRF

>RXN02406 TRANSLATE of: rxn02406.seq check: 9586 from: 1 to: 549
METLAAQARTLLEKWGVAPTHASFVESIAKAIPILSILLTLIVTVNGISSGNPVQPPALE
QVRTDVVNKINYERNLKGLVSISPELELHTAAQTIAQRNADSDSEEKVPDPEGNLVVLQQ
NLPYANANADTIVDRFLNSPDHVKLLLANDYEAIGVGVAYKGDHAWIVVEFTVAPADSVE
STE

>RXN02407 TRANSLATE of: rxn02407.seq check: 3013 from: 1 to: 372
MNRQNQLHYPQEVKAVESVESSLNMSSPSAPLATPDVELDVHTLSSENLPWLCIVWDDPV
NLMSYVTYVFQTVLGFSKKRATELMMQVHTEGKAVVSSGEKDKVEGDVKKLHTAGLWATM
QQAG

>RXN02408 TRANSLATE of: rxn02408.seq check: 1367 from: 1 to: 912
MLIDVAGFLLGHVTKGDTGCSVVIAPNGAFAGVDVRGGGPGTRETDLLEPHNSVQQAHAV
VLCGGSAFGLAAADGVMTALENRGIGFPVRPEGPIVPIVPGAVIFDLLVGDPKNRPTAAD
GEQAVENAFAGTHNGSGSVGAGTGATAGRLRGGFGQSSRRVGKYTIAAGVVANPVGEVVD
LTTGALFGRPEVMGVGVDKLKSAAETLNTTIGVVATDAPVTKAQAKRLALVAHDGLARAV
RPSHSPMDGDTFFAMSSGDGSGVTPVELAELSAHAADCVQDAIIDAILTASPGLGLKSFR
ELLP

>RXN02409 TRANSLATE of: rxn02409.seq check: 5850 from: 1 to: 537
MQQWKKKKGLMRQARYAVVFEPMEREVLGDLSAAVSEALIQRAQSVPKDPLAEMTGMTSG
HKEAPTDPALARLLPDFQHEGDEEYDGDNSFLRSLHEGDITRAKLENLRVINDALGPDGN
VAVTASEEEAHAWLAALNDIRLYVASGDVRGGEAAEEDRENLVQWLAYNQESLLEAMMN

>RXN02428 TRANSLATE of: rxn02428.seq check: 3176 from: 1 to: 1134
MAATLDLPDTDPIAYAMFAHCFTGSRFTPAAARVSKTLAESGVACLRFDFPGLGQSEGDF
SKTTFNSNVDDIVAASQWLTEHYSAPQLLIGHSLGGAASLKAATKISCLKAVATIGAPFD
PAHAVLHFADRICDVDDQGAVTLQLGGRDVTISREFLEDLAEVNPEDHLRRLRKPLLLLH
SPTDQTVGVDNAQLIFRVTRYPKSLMTLDKADHLLTKDGTAQRAARIIANWVEPYLVPEN
VCEDLPEFVAEASTIKASKYGAAIRTGGHNFITDRDKSQGGKNLGFTPTSLLVSALAAAN
SQTIKQAAIDNRIKGLDDVKVTISQEQSADHGQIKLRRKISLIGNLSDADSASLRAASNS
CSITQLLAQGIVIDDEVN

>RXN02454 TRANSLATE of: rxn02454.seq check: 5811 from: 1 to: 1242
MKESMSITSSTYASALLTLPWGTPLEQWPDNLIAALPRGISRHIVRFVGINRGIVAVKEI
GARTAHHEYKMLRELQRLGAPSVRPVAVITGRHPAEEDYGELTAALVTEHLEFSLPYREI
FSRHLTVVESEKLIRALSVLLVRMHLLNFYWGDVSLSNTLFRRDAETYSAYLVDAETGEF
QPNLSESRRLYDVDIARVNIIGELMDLQAGECLDKSIDVIALGGLVESSYLELWTELTAE
ESVDASEYWRLSERIDRLNQLGFDVGELKVTKDDSRQVVRIRPVVVDPGHYRAELLSLTG
LSVEEHQAQRLLGSIQAYQAVECGPHVGLTQAAHLWMTNEYEPTIAAVPVEMLDKLEPAQ

IFHEIVDHRWFLAQERGGAVTLPEATASYLESVLPARRDEARLLSTNPSDEDLS

>RXN02457 TRANSLATE of: rxn02457.seq check: 8018 from: 1 to: 1110
MFYFTVNNPQDPLSTEIVETNRRDLAFWHRLRPKDDDDLATAINKICVRTGLSRKLIAAC
LFSICFLPYLPNFHKLVEKLGHLDMARINAITKAGEKVPSEKRELFDAYLVDYLTPRAEA
QCLPQASSISAMMRKFIAQHCPDDKASSATNDGSIRYRRNNKGGISITVDATASEVTEIK
AALEQMSKDKDCTPGTSLLHIIRGLPTKVVLNTYGTKDSPEYLEGGTWLSKEQSEFWKTR
TTSSRDMDAAHFSYTTAYAPTREMRVYIKGLRTTCSVPGCSVAVENCQLDHIIPWGEGGP
TTPWNIHPLCVFHHIQKTEGRLQCYPLPDGTVLFLVDGIPVFSIPDGPLSKSNKTWGTKF
GKYMERRIAA

>RXN02460 TRANSLATE of: rxn02460.seq check: 7527 from: 1 to: 504
LRVYIPATFSTLRGLNESRVITARSGYGFAVTPALLDFYTDGDEEEIAHAAFQDAAEASI
RLLAIGDEETFPYRRVVVSVDVDDSVVTYQPENGESVVKLSPAHINLDDVAAIHIDVEAS
EADTKKAIEVIDESDLGEEDAELTVGDAQDNFMAWYDPEELPFLVELL

>RXN02464 TRANSLATE of: rxn02464.seq check: 6833 from: 1 to: 1200
MAAKLQPLKRTKKDLIATGVITALAVIGVGTVWATAPIRGSELTPADEPFIGSTTLDAIP
ETLSEHWRATDTLTNHKPLITGGVIFTADGNTIKTYTPDGALLWSYERDKELCSLSVGFD
AAVATYKTGIGCGDVTAINANDGQYQATRSAISSDHVAPISSNDRIGVLGTERLELWRSD
LVRTIEYGDVEAPQESGQQPHPECSITSAMTRKDLLAITEDCPDGSSYLRFMGTTPDDSR
TPEITQDIEITDGRIVAIGQSVAAVYTNDPSPRIVSYNDDGELVGEQAVDEVEFPDPPFQ
SATADLPHHMSWFNGDSLVLFSPTQLNVRQSFNDALGTGIALNGSLLYPTAEGITVANWD
TGEVQRTIPVDRAGYDGEVALGVVGQVIVEKRGSEIVALG

>RXN02465 TRANSLATE of: rxn02465.seq check: 154 from: 1 to: 399
MPASIRWGGIVALIQSTIGFGYAFFLIYREATGETDPSIVYETDNANTWVGYGTAAFFII
VFGTVVAGAINMMKGHRWGRGAVVMLNIILLPAAYYMFIEGRFSWAIVTGISALFVLGAL
FNKRAVLWANNEI

>RXN02466 TRANSLATE of: rxn02466.seq check: 2914 from: 1 to: 87
VGEGQEQTFTYVIEIEDGVNTAAYGGDDA

>RXN02505 TRANSLATE of: rxn02505.seq check: 6513 from: 1 to: 171
VAGTHAYVNETLSENEFSMCRKNEPGLVIELENISIDRIVISTPDAHRYADELMAAV

>RXN02510 TRANSLATE of: rxn02510.seq check: 1304 from: 1 to: 636
MDSSDSHVGQDVYVDQGLGEPDRLERLWAPYRMSYINTRSGGKQSTTAKRDPFIEVPKMS
DEDGLIVARGELVYCVLNLYPYNAGHMMVIPFRKEKNLEDLSLAESAELMLFTQTAIKAL
KQVSNPDAVNVGLNLGKASGGSVGDHLHVHVVPRWSGDANFMTVIDGVKVLPQTLRQTRA
MLAQAWGTIDGAPGTVDPTLTSAIRTAAPKEH

>RXN02519 TRANSLATE of: rxn02519.seq check: 317 from: 1 to: 1629
VEDEQSPLGATLFDVATGASSINDRDTDASGLEPEKIRRFAWLRLIGTMGALMIAFGALG
AGALPVVNNPYVDFPGGNFMSRMLQTSSMIVLIGVGFLVLAWVLMAPLVGIPFKRSGNRT
ASVSLSMLRRTFGAWVAPIMLTAPLFTQDIYSYLAQGSVTAQGMDAYAGGPLELLGPDNH
LARSVPFIWAQSPSPYGPVALSIAASISVITNDSIVGGVLAHRIASLLGVVAAGWAITML
ARRCRVSEEASFYLGVLNPLLILHLIGGIHNESILLGFLLVGLELGLRGTDRIQTGLWGP
AWTYIALSGVLISCAGLVKVTGFIGLGFVGMALARAFHARGHRHVVAIGVAGLVQVAALV
ITVVVLSVITGISLGWITGQGGAATIRSWMSMTTNIGVISGFIGMNLGLGDHTAAMLVVT
RAAGIAVAAAFMVRMLFATYRGHIHAVGGLGVATFVLVILFPVVHPWYMLWAIVPLASWA
NRLFFQLGVIAYSTAFSFFVLPRGLALPVGTVFSIYFGAALGFSILLLVGWWSLRRNPTF
GLH

>RXN02520 TRANSLATE of: rxn02520.seq check: 9529 from: 1 to: 684
VGDVVKGNDAHTGDGDTRRKILLILLERAPVIASDIAEQLQLSTVGVRRHLDNLVEENLA
EAANPRQNPYEPKMRGRPAKTYRLTDKGRSIFGHEYDSLAAAALATLREVGGDDAVRQFA
RKRIETIVEGITPADVTDQSIEDTAKSLVEAFSRHGYAATVDATRNGLQLCQHHCPISTV
ATEFPELCEAEHQAVSELLGQHTQPLATIADGHGICTTNIALTPIKHS

>RXN02534 TRANSLATE of: rxn02534.seq check: 3127 from: 1 to: 804

MNSPNADIILVVNKLSKFIDIENIMLVGARCRDIHQQKYRDQTAGRRTKDVDFALALESW
DDFNLLKQQFSPTGNAWQGITIGNIPVDLVPFGNIENPPGEVLSRKGHLLNVAGFKEVFE
QAELYPLNDAIDIKLSTVPGLTALKLHAWLDRKENNIKDASDLALILSWYEEDVETLWNR
YFALENQGYIGEPEAMAAELLGLDTGRILGHKETQALLDRFNEQSPPELNQFAESLEAPP
EHSHPLERRRIQVEALLGGLRDSLGYDE

>RXN02537 TRANSLATE of: rxn02537.seq check: 3878 from: 1 to: 462
MLALKSSELEGIATSLTAVAGALHESNTDRLQSWQQLETMTSASSLIQGFIKLVDYNRPT
VNIVEQMHKTASTLFNTADFLRTLEGYVDVLEKQADKSITLTVMLRYIASLSSLLDLMCA
REINALCTAITPEPLKHLGDFGTLPPQQSTSFIW

>RXN02538 TRANSLATE of: rxn02538.seq check: 5301 from: 1 to: 672
VNAPPEIRALAEAHPDMQILEAGDGSLVASFGDIDRATTVTTIVAGVGSSNPEGWNTYVD
RARTVSASTGSATVLWLGYQAPASIPAAVSGAAANRAAADLQRFQAALQSRNPHQRKVVM
GYSYGSTVVGKAASSGELSADALVLVGSPGAGVSHSSQLGAPVYAVTGSADPIGFAGTQY
DGIHGTDPTAALFGATVWDSPSTHSGYWNDQEFLGNVAEVVRGK

>RXN02555 TRANSLATE of: rxn02555.seq check: 3981 from: 1 to: 603
MGEQFPGDKNIRVSDTERSAALAALGQFYAEGRLSLEETDDRCEAVADAKTRGDLNAIFY
DLPNQQIAVVDRSEQTYTATEVAELHRKGARPRAGILGLTTVLAITGTAAFASTTAFATV
LLALIPIVFIMLYVMKIGPESWHAPTPRQLQRKRMIELREKEKLRDMELKAQRKERTHAL
TNRALDAAETAFNTKPWKKNK

>RXN02564 TRANSLATE of: rxn02564.seq check: 3452 from: 1 to: 1002
MAEVGAEPAGSAQSKTKQFVVGTAAVVITAIAAFFSIQSASGGEDIRSNMTLIAPAAAGG
GWDTFQREQQQSMRVNKIVNNIQVVNIPGAGGTIALGKLSTMTAPNTLMVGGTGHIAAQI
QFDTPAKIQDVTPIARVVEEFDIITVPADSPYNTLEELIEGWKADPAGVSWTGGGSFDQL
VMTEIALSAGIDPKQTTFIPSDGGGEAIQALLNGTAKASTGGFADMYPQVEAGRLKVLGI
AAEERLPGSDIPTLVEQGYDVTLTNWRAMFAPPGLSDDQIAELRAIVAESVETAEWQSAV
ERNYWMNASLEGEELDQFVEDEIDRIDQLFKEMG

>RXN02568 TRANSLATE of: rxn02568.seq check: 2134 from: 1 to: 1653
MDGTSPQNKISTTPPAPGNAIPAPGGAIPTPAKTEQDAVPPTVAAKLPVPGSSIPAPGRA
LPTPVAPGGSVPAPRASAPAVPNVPAAPGAAVPAPGISIPAAPSAPGSAIPTPGTAIPVP
GSATPVPAPGVSAPGASVPSIPVPGSVTPPAPGISAPGGALPTPGSAPPTPGGALPTPGE
ALPVPGAPGAPGASGIPSPGLPTPGVPTPGASLPVPGAPDAPGTPSIPAAPGIQAPGIPA
APGAPAQAAAHAKPVFQDAEKRPRTDEAGNAKKELPLRVRLAQPITRKQWAMTLGVLVLG
AIVVAAIAVVLAKWAFTTEWLQDFVEKYPGKYDNPEGAPVGIPTWLSWQHFFNMFFMVLI
IKTGIEINRTRRPKGYWTPKKGGKKISLTLWIHLVLDLLWIINGAVFIILLFATGQWMRI
VPTSWDVFPNALSAGLQYVSLDWPTENGWANYNSLQELTYFFTVFIAAPLSIVSGFRMSS
YWPKNNATMNKLIPIGFARALHMPVMVYYIVFICIHVFLVLATGALRNFNHMYAGQDVVN
WVGFGWFVASL

>RXN02593 TRANSLATE of: rxn02593.seq check: 9101 from: 1 to: 597
MEAMATTITVFSPTHSPAQIRETILSAAKEDDVDFLGVPFTHPRNVTIEVDDELINDCLG
WLDDVALASGLGIQYNDEVLRYGDEDISFTVQTKNDDDARIGASRLGLEHQLNVIAGGSG
DSGDSGDYLKIAHFDLDNPADESSYIFARSLAEVDGWTLEFGVAGVKNTTIVSSIDDAIT
TILRWMNGEDIRDLNWTRA

>RXN02606 TRANSLATE of: rxn02606.seq check: 7692 from: 1 to: 1371
MQEIHTIMKHMDALIADPSAAAFKATLPFAELLEKLHNKKALFDAALAKSAERADAGRII
GKTSHIDALAYLLDISKSEAFRRTKRAEEHYGNPSPEPSSEELAKETPEEKLAREEKEKQ
DLAEQAEANRIAREHGISAEKQDTIRYELEKLNDNTSLSRASLRKLAMQEATSRTPEDLR
NWTRNKVIRINPTAKDPLAAVKKRSLSIGRQDHDGGAKASLYLDAKGLALLKSLMSKAKP
GHLLEDSLAEDKRTKPQRQYDAFADILHRAHSDLLPARSGVGTILVSLSAKDVTNLKASG
PDHRYPTSTGIKLTPLEILRLGAAKYDFVTVLDSESGRPLHLARTQRTASLYQRLALFAS
ELVCTREGCDSPFEDNEIHHIRSWLDGGPTDIENITNICPHDHGNNNDQRDGKDNMGHMN
IDPTTGRVGYQPADRRKPMRFNNTAAAAESGGAQART

>RXN02610 TRANSLATE of: rxn02610.seq check: 4081 from: 1 to: 927
MRKTITVIAVLIVLALIGVGIVQYVNTSDDSDFIGQPGEPTGTETTEPPVQPDWCPAVEV

IAAPGTWESAANDDPINPTANPLSFMLSITQPLQERYSADDVKVWTLPYTAQFRNINSQN
EMSYDDSRNEGTAKMNEELINTHNECPATEFIIVGFSQGAVIAGDVAAQIGSEQGVIPAD
SVRGVALIADGRREPGVGQFPGTFVDGIGAEVTLQPLNLLVQPIVPGATMRGGRAGGFGV
LNDRVQDICAPNDAICDAPVNVGNALDRALAMVSANGVHALYATNPDVFPGTTTNAWVVD
WATNLIDNG

>RXN02624 TRANSLATE of: rxn02624.seq check: 3015 from: 1 to: 1296
VLIPHGVAVLLVIILAVASLMFTNSSMVNLSATIAQLWLSLNLGAVDGSGEVISVLPTLP
GFIFLWAIAARIHRAVKDRVSIADLGVLAALVLGIPLALTAIAAFMLFDASSVLNVEVPP
ITRLLRVMLFHLSALFLGMGPRLWQALARRYGAPEWLIDAITQAFRFLIAFGTVSLVSVL
VMTAINHSAFTATMQGYDDSASVVALIVLSILYLPNMMIFAMGNLIGSPLYFGDASISVF
SVHSVPLPPLPILAALPSEALSWAVALLVIPAIIATWVCVRNPMRLAVNTTAAVISALCF
LVLAVFAGGTLGVYNYVGLNLLASVGLVFVYFALVGLLIAGIDKLRNPVEVKSVKAVAVV
EPEPEEVEEDEEEHVEEEVDEEEEEVEEGVEEVEEDDAEDPEENPEEEESDEEIETETEA
EETNDGSEAEDR

>RXN02626 TRANSLATE of: rxn02626.seq check: 9067 from: 1 to: 1005
MSTQVELKTPKSEDRAAYIAALGFPVLVIIGGIIGFTASDVVLNISSWVNPLLGIIMFSM
GLTLKPVDFALVAKRPLPVLIGVIAQFVIMPLIALLVVWVLQLPAEIAAGVILVGCAPGG
TSSNVVSYLSRGDVALSVTMTSISTLLAPIFTPLLTLWLAGQYMPLNAADMAVSIVQVVL
IPVVGGLVVRLIFPTLIGKVLPLLPWISVIAISLIVAIVVAGSRDKILEAGLLVLAAVII
HNTLGYSLGYLAAKFTGQPAAARRTTAIEVGMQNSGLADGLASQYMSPMSALPGAIFSVW
HNLSGALLAALCRASDKRAAEKVASEKAASEKAAS

>RXN02656 TRANSLATE of: rxn02656.seq check: 1781 from: 1 to: 840
MIFGVLAYLGWGMFPAFFPLLLPAGPFEILAHRILWTAVLMMIIISFTSGWKELKSADRG
TWLRIILSSLFIAGNWLIYVIAVNSGQVTEAALGYFINPLLSVVLGIVFFKEQLRKLQIS
AVVIAAAGVLVLTFLGDKPPYLAITLAFTFGIYGALKKQVKMSAASSLCAETLVLLPIAV
IYLIGLEASGHSTFFNNGSGHMALLICSGLVTAVPLLMFALAAKAIPLSTVGMLQYLTPT
MQMLWALFVVNESVEPMRWFGFVFIWIAVTIYITDSLLKK

>RXN02673 TRANSLATE of: rxn02673.seq check: 5852 from: 1 to: 633
MAALLVLLVVIALIIWAVVALRGGSSEPEEEQPNNAVVTSSMESSATSSSSSKESTTEAT
TEEETSSAEPTATSSVAADAKKTCELSDLVISASTNQPTFSGSAQPELFMAVHNPTAVDC
EIDLEENKLRFEVYNLATNARIWSDVDCNPAVEDGTSVFPAGEDRYFQATWSRTTSAPNQ
CNNRTDVPAGGYYLHTVVGNNPSPAVTFNLT

>RXN02680 TRANSLATE of: rxn02680.seq check: 5186 from: 1 to: 1284
MRLNKRLPAALSGLLLSAALLAGCSTSGTAETTTTTVSSAAASTTTSTSSASSSSSSSSS
SSSSDSSTTAETISNTAEAAQAFLSTLSTEEQDAVLYDYDAEEKSTGWSNFPVTFVQRSG
VNLTDLTEEQQAAALNVLKNLLNDDAYQMIEDIMASDQYLNDESNTTEDSLGQYYIAFFG
DPSSDSDWSIQFGGHHIGINTTFSDGAITFAPTHLGTQPSEWTNEDGETVAALSNMYETA
FAFYDSLAEEQQAQLYQGEELDSMVCAPGSTCDYPTGTGLKGSDLTDEQKELLIDVIANW
VGLADEETTETELDAIRETLDDTYINWSGATEYDTSTGDGIYFQISGPKVYIEFANQQGS
AGADIDGVITAGWGHIHTIYRDPTNDYANSVTQEAASGMMGGGPGGNGGEMPSGDMPTGE
MPSGAPSN

>RXN02693 TRANSLATE of: rxn02693.seq check: 9728 from: 1 to: 1776
MVSLPRLASLLTTRLATLKPALKPATHLASLGAQVIAELVPGIRMSPNRRRILPANMGAG
FIGAEIAMWWALSPSLLPKPWWVTAANLAVLQAVGHAAATGIHSILPRTNRRVSRKIYNA
THIATGAITLTTTVVGLIRHRTQIRLIGQKNFGPKETIAGISVGTLGYGALLITGELTQH
SINEVKLLIERFLPPWISFIAAVSVITLTTLTLADRVLLRRILHNSAIQAAHLNRMVFPG
TEQPWEPERSGSPWSYEKWGAVGSQGRAVLSGGPRKDDIITVTRLSDTETHEPIRIFIGM
VPGRSLSDQVDLVIHEMRRTGALRRDHIVINNSTGTGWITDWSAHTFEFLTGGNCVTISM
QYSYLPSALSWYKDNDGPINAARMLIDAVLHELDQLPTGSRPKLFLAGESLGAYGLAEVW
GDVEKLLGTADGVLLSGAPRFSDAMNALRTRRDASSSERLPVIDSGRHIRFAGEPEHLDM
PATWQFPRMIVAQHASDPIVWWNAELFIRRPEWLKTPKQDHQDVFPRLRWMPFVTGWQVA
LDLFTSTSVPGGHGHNYHEEFIDYWAALLDREVTPELRHSIAYWIRANHIKR

>RXN02696 TRANSLATE of: rxn02696.seq check: 3394 from: 1 to: 456
MSMLKKTKEFFGLAPYEAEHEDAYYADEPRYEGTAAYAPEYRERDYGYAPEAPAPVAPSP

APRSYQSTIVPVELHSFEDAQVIGGAFRDGDAVVFDMSLLSREEARRIVDFAAGLCFALR
GKMQKIDSVTFAVVPELSNISTSELERAARIR

>RXN02697 TRANSLATE of: rxn02697.seq check: 1664 from: 1 to: 1527
MTLFQRLTNPVVLGGLAGVLLLLGSFGGGAIRYRGGVLDALGLNFLAFGHAQGISNTVLW
VGQLLLIGAWVHLGRRLFKKKVADDTADAADLGLVKRTLYAMVVPLIFAAPMMSRDVYSY
LMQGAMLRDGFDPYTEGAAVNPGPMLLEVSHDWRNTTTPYGPLHLWIGDMITTVVGDNVT
LGVVAYKILSIIGLAVTGWSIVRIAQHFGANPAIALWIGVANPVMIIHMIGGMHNESLMV
GLVSVGLLLALKKRFVAGVALIAVAVSLKATAAIALPFVVWIGMHHFAGFLATKKGKDSP
TLKQQVPAFFATGAAGVAVTGVVVSAITWASGASWGWISEISGNSKVINPLAFPSLVASV
ITMVAEVFVDDFDYNAVVNVVRSISMLIMLGGLVVCWWLFRQNERRAVTGTAAAYAVAFV
FNSVTLPWYYASLISLLGTFKPPMWLIRFAAGASVFIALMFTGSGNHQLYNIVTVIIAAI
IAWLATVVIFDDTDPATTATEKPSPHTVS

>RXN02720 TRANSLATE of: rxn02720.seq check: 5443 from: 1 to: 702
LERREELQVRLQQVQARIDATLNEHNRPEGSVRLLPVTKFHPVEDIKILQEFGVTAVGEN
REQEARAKALELPDMDFHMIGQIQSKKANSIARWAAAVHSVDSEKIAEALGRGVALALDR
GDRTSDELPCFIQLSLDGDPSRGGTPLSQVTQLADCISDTTHLRFEGLMCVPPLGWGPEK
AFSQARDVLSGLEEHFDRSLEFSAGMSGDLVAAIKHGSTIVRVGTEILGNRPLA

>RXN02744 TRANSLATE of: rxn02744.seq check: 343 from: 1 to: 804
MSKPFENSALRGSSRFPAGTFTPAPKRATPAKMLAAQGKMESLLFLRHGEQQLLSIIIPL
VALIALANFDFIPGENSLDKTFPFALATAAMSAGFTGQAISLAFDRRYGALKRTGASGVP
AWTIIFGKVIAVIAVTIVQIIFLGVTALLLGWSAPVGGVLFGIVTLFVGVSSFTALGMLM
GGTLSSELVLALANLIWIVLSGLAAWAVFSPSVNAEGVLSIIPSVALSQGMVDAFNGELP
WLQLGILVGWLIITGVAANKLFNFSASR

>RXN02770 TRANSLATE of: rxn02770.seq check: 2969 from: 1 to: 1566
MLVAALVMTSCGDGEPEPTSHQTSLFGYAVNSSLATTNAASLLGVANDAGLLAARVYPGV
YVQGPSGQMIPNTDLASTQVLPGINRQVIYTINEDATYSDGQPVVCDDFLLSATAGQMPE
LFQSHVPLTSQIERVDCVSGSKVATVVFKEDLGERWRYLFEQGDLLPAHAVASKAGMTLE
ELNQALKDKDPEALTEPARVWSEGFQLSQFDPELQTAFGPYKVDSVGEFGEVKLVRNEFY
SGDQAVEAEITMWPKGSDLSAIADNGNLQIAHVVAWESEPWVNRDDPLNPYDIKEEVGVL
TEQLTLASAGVFYAAEARQAFAACVDQEAVAAASSSISGIDVPAVGVHSVRHQNPVVHQI
GDLPAQHMAVDINAASALAGQSIRIGYDGPDERKAAMVEAIRQSCEPAGITVIDASQEAV
SLNDLSRTEVSEWGYEQYFEGTLDAVLRTVDPHREYENANTIGTDAESTRRTEEQLWAEV
PSIPLAAQPRVFVIDRTVGNVVVNTDLAGIGWNMDRWSRSEE

>RXN02781 TRANSLATE of: rxn02781.seq check: 9745 from: 1 to: 1191
VVAALVFGFLLPTWERGLSDAALKFVFEGGPDAAREVLGTIAASTISVTGLIFSITLVVL
QLVSSQFSPRMLNGFLRNRIVQATLAMFLGTFVFSLTVIRYVWSEDEDITGFVPRASVSV
AFLLVLGCLGLFLAFIRLITFSMRVANAISEIGEETMALAARIYPVQSDDAGPVQGPGWS
PRPGDPREEIRVGNHGSLVWIDYRKLVSWSTEHQAVITVDRPVGDFLVEGQPLLRVWWDG
ELSDRDRRVLHSAIEVRTERELHQDVAFGLRQLVDIADRALSPGINDPATAAQCVQEIHR
IFRYLVTVIEPSPYIADDDGRVRVVHQPQRIADMLYEVIREIHLYGADSAMIPRLLRTMV
EDLVTAAADHSLPAVERARGILDDETDEDRDSDTANV

>RXN02782 TRANSLATE of: rxn02782.seq check: 837 from: 1 to: 1299
MPTLLIDTHPHLAAQLLDPGLGELLTAGSNKKVQWQCPKHSNHIWTASVNNRTNAKNPRC
PYCAGTRVLAGFNDLATTHPHLAVQLVDQDIAVTISAGSGKRQLWQCVVNPKHQWLATPN
NRTSTKSASSGCPYCANRAVLVGDNDFATTYPELAAQLVDQSAATTFTAGHNKPVEWICC
KHEPPFIWKTSPILRVRQNTQCPVCSERTVAPALNDLATTHPKLAEQIADPQPSGVSAAA
IIPTISRGSHTQLTWQCSKNHDHQWVATVKDRVRGTDCPTCANTGTSRKEAELIEVIRAL
FPNTDVQQGALINGRTGNQGASPSTDVLIPSKNLAIEFNGLYWHSELFIKDKHYHANKSA
LAEQAGVQLIHVWEDDWNLRRDIVIRMIAHKLHATHNLSAVLPTETTDSRVATTAFAVHS
HCRWSLVHALLHS

>RXN02812 TRANSLATE of: rxn02812.seq check: 3189 from: 1 to: 339
VWAVAINAGNGISEDQARAASDFSSFSFDTGNADNSALESVLTQASSESAAETTEAQPSE
TPVEPAAASPSDTIINLDTSSNMDRVVDGSQETYHTVTSRTLANLARETGAQG

>RXN02817 TRANSLATE of: rxn02817.seq check: 7091 from: 1 to: 399
MILGVPIQYLLYSLWNWIVDTGFDVAIILVLAFLIPRIGRLAMRIIKRRVESAADADTTK
NQLAFAGVGVYIAQIVAFFMLAVSAMQAFGFSLAGAAIPATIASAAIGLGAQSIVADFLA
GFFILTEKQFGVG

>RXN02818 TRANSLATE of: rxn02818.seq check: 4037 from: 1 to: 606
SYSRKFLTQVWIRDNVGDYKGLTDTAFRKKLQRDLAYLRRVGVPIEQFTVTSGIAEGQQA
YRLAQDSYKLPEVEFTPDEAAVLGMAGEMGHNQELGAFARSGWTKLAAGGAQRDLSTSTA
LTNAGDLGSLSAKTLDAIIKARQLGKQISFEYRRAPKDAPSLRHMDPWGLVPERDRIYLV
GFDLDRQEARTFRITRVRNIKL

>RXN02825 TRANSLATE of: rxn02825.seq check: 7394 from: 1 to: 1839
MKLAPRMRMRSPKTFAALASLALVIGLGQVPIAQAQTEYRTASDGSLNWGFRQSFRNYIQ
TGVAKGSITLGDGASDNGGNFAFTPRTNGTTVTSDSQGTVEFNGSVHFLGHQAEDKWILD
TTMSDIKMVFNGSSAQLVVDLVAREFKGTTYDDIGEYIISDDIVLADVSLNSAADFSQDS
IDLSGTTDLTAAGAQAFGGFYETGEALDPTGGSLTISSTTTAPSTSTTSTSASTSGGTAD
CSSGALGVVTTGTNDGMLGTIQEVNNTFAIWNNLIVNTERMFCNIDTLKARFDTDDSSDS
ATSATSGTTASTGTTAATTAGTTGTTGTASTASGTSGTSGTSGTAATVAGTTPTDNGVCT
ASGSLGVTQASAQWGVKASFQNYIRGSIANGSWTLNGVGFDNQQFQFSGNSGAVDAENKT
GSINFPGSIHFTGHGGILDMQIANIEISFNGNSGELIADVVSSDMDGNSTNYGRTVVGTL
NFSALNVSATEASGSASVSLSQSGSQAFADFYTPGTQLDPISFSATLGGDASCATGSTST
TGAAATANTDNTEGVAGEESTTPANQNSQFQIRQAAADSTGLDTTTTMLLILAAFVVAGG
SMTRFTVGNPTGK

>RXN02838 TRANSLATE of: rxn02838.seq check: 4352 from: 1 to: 528
NTGKGGGLTVPLGDGQGRYIAKFPSTAFVGVSENEFANLALAEAIGMEVPARELVGRAQF
EGVPPEFEAMTDGLVLLVRRFDRAGDGVRVHMEDFAQVFGLYPARKYDGAASHDIAAVLG
SAVSIAAGLEFVRRLALSVVMGNGDMHLKNWSLIYRGRGDVPALAPVYYMMSTVTY

>RXN02840 TRANSLATE of: rxn02840.seq check: 7123 from: 1 to: 150
MTVISGALNVLLPDATDWQVYEAGSVFNVPGHSEFHLQVAEPTSYLCRYL

>RXN02841 TRANSLATE of: rxn02841.seq check: 2452 from: 1 to: 435
MFTAFKSNPTTIKKLVSELINGDDAALNELERHVTNESVRARELPNVQYKATAGRNFAIS
KLVQNLRRINKAQNNPRGVPTHATVILLKEDGSYDGEEQWRIPEKAITPFDMLRSPDFNH
NRLKNRPLMVESQYPWGVPGLIKMN

>RXN02846 TRANSLATE of: rxn02846.seq check: 4539 from: 1 to: 750
VLTIAIVLLASVLIGALLQRMTGLGVGLVTGPVLTSLLGPLAGVTMVNGLSIINAVNNAW
SVRKRTDWAKFRILAGALVLGSVPAVAVVYFLNGPWLLIFVGAMVLLALGVSLFPTEKFA
LKQEAKLPMVIFGMIGGFMSTVAGIAGPSLTVYARLSRWDYRDFVATLHPVLLVANTVSF
LLKVILIGGLDFGGAPAWLWIGAVAMIFVGAWLGEIVNAKVSTPMAKRIATLLAAAGAAV
VLFRGIMELV

>RXN02847 TRANSLATE of: rxn02847.seq check: 8481 from: 1 to: 1089
LALTARGFLNSERSQTRWKTHFTTQKVPRSGYRYDLDGLRGIAIAFVVLFHVFVGKVSGG
VDVFLLLSGYFFLGSQLRYADRPDSSINPWWPIWRTLRRLLPALVLVLGVSMVLILAWVP
RLQPIEIANQAVASLFYVQNWELASQGAAYGAASAEVSPFQHLWSMAVQGQFYLFAILLS
MAIILIRRYRPEYSAVRLATPVLAVLTSVSFFSAILWHFIDQSVNYYSTFTRFWELGLGA
LLVLHAPRILISAKTKSILAAVGLFMVLSTGFFMDGAETFPGFPALYPILGACLVILGDG
KISVFLSRKWMLWLGDIAYPLYLWHWPLLIIFTALFNQEEPSIWLGIAVIMLSLGLAQLT
NKY

>RXN02849 TRANSLATE of: rxn02849.seq check: 4597 from: 1 to: 282
SPYPVMISTSADASNVTVRIMGVDTTSVESINNGRWSTTQPNTVRVSGSDCVPSTGAPGF
TTSDTRIISDLSGNEITRETVTTVYDPSPNVVCS

>RXN02911 TRANSLATE of: rxn02911.seq check: 602 from: 1 to: 459
MRTSKKEMILRTAIDYIGEYSLETLSYDSLAEATGLSKSGLIYHFPSRHALLLGMHELLA
DDWDKELRDITRDPEDPLERLRAVVVTLAENVSRPELVLLMDAPSHPGFLNAWRTVNHQW
IPDTDDLENDAHKRAVYSGAARSRWPLRARLHS

>RXN02914 TRANSLATE of: rxn02914.seq check: 6261 from: 1 to: 543
MVGNSIWIIASLLGLSALISTYPAILNLLQLVGGGYLTWMGIGAVRSWWTKRSTQQAAAD
SQAVENTLVTATAASVGVWPAIRSGIATNLSNPKAVLFFGSVFAQFVRPDMGIGWSIFIG
VFLTLTGLLWFVGFAVLVRKLAAGLTRNGAIIDLLTGVIFIGLGMFMIFEGVVGIGGRVV
G

>RXN02921 TRANSLATE of: rxn02921.seq check: 4157 from: 1 to: 471
VSALEESIRIATIAAKAADEKKADDIAVIDVSDMIAITDCFVVASADNERQVGAIVEEIE
DEMTKAGFEPKRREGNRENRWVLLDYGLVVIHVQRQAEREFYGLDRLYRDCPLIEIEGLE
TFKRESSWSDEADIRNIDSIDELPPLPAEYEPGYEDD

>RXN02924 TRANSLATE of: rxn02924.seq check: 3999 from: 1 to: 549
VPSVASISERATFILTADHFLRSCSKVIYVRGENFTATATTSLSVFGTDLGLIKLDGKAP
TMPLPLFADKPLRVGMKTTTFGFGGLPSATVAKEIHGRVISAIPHGVSRNRITRVHHGAL
IFNSPEKAVKGDSGGPVLVNGRVAGIQSMISDPGGFNTGVATAASLIQHMPALAQALELL
EHS

>RXN02927 TRANSLATE of: rxn02927.seq check: 3221 from: 1 to: 468
VADEGSILAWFPCGDEAPVLVVTLCFAIFGEVVVAEVSATGLVAVEGVDTHEFAEVDVVG
YACCVFENLVHLIGAAGDAHVLPEVIAEGTDLVDAILEVFYVSGNATGEVQDIAKLAVVV
LRSVNVVTDPLWAVAHEAVNASLCTRNRCLCFWCIL

>RXN02928 TRANSLATE of: rxn02928.seq check: 382 from: 1 to: 693
VAGRCNTHWAGVWVLANCLFVHGEEVGVTLADGVLSEALGGVAEVQVCSVVQRSNTETSI
DLLGDRTGSNVTWDEVTECWVAALQEVVALILRDGVWIAVIVRFLRGPDAAVVTQRLGHQ
NGLGLPGGVHRQAGWVELDERWGREVCAGFVCTHDGRGVGVLGQGGHVVHVAVATGCQDN
GMAGVCGELAGDQVAHDQAFAALFTVTFGDNDVNHFVMGEDFYGAEVDLAL

>RXN02931 TRANSLATE of: rxn02931.seq check: 8393 from: 1 to: 225
MQPYPRNPIEKRKQEVRKNSRNAVVSVGGGIVGGAALWLVFGSAFFMGLGLIIAVVGGFY
YYNKVQKIINEKDRY

>RXN02932 TRANSLATE of: rxn02932.seq check: 938 from: 1 to: 972
VSKTEEGRSAAIIIYAFPTFILLGAIIAFIFPEPFIPLTNYINIFLTIIMFTMGLTLTVP
DFQMVLKRPLPILIGVVAQFVIMPFLAIVVAKMFNLNPALAVGLLMLGSVPGGTSSNVIA
FLARGDVALSVTMTSVSTIVSPIMTPFLMLMLAGTETAVDGGGMAWTLVQTVLLPVIIGL
VLRVFLNKWIDKILPILPYLSILGIGGVVFGAVAANAERLVSVGLIVFVAVIVHNVLGYV
VGYLTGRVFKFPEAANRTMAIEIGTQSAGLASGMAGRFFTPEAALPGAVAALVHNITGAV
YVGLVRNRPLTKASRKKESVAVSS

>RXN02934 TRANSLATE of: rxn02934.seq check: 3200 from: 1 to: 306
VGADEFDFIFEIDAPEAGFALVDAGGVSFFVEFPHAGFEGEVVFTVVGEGDLLAECVLSV
FCGVGLAFAAPDADEREEREESVVEVGAFAEVSGVVRDRKVT

>RXN02936 TRANSLATE of: rxn02936.seq check: 3720 from: 1 to: 198
VVAPFQLVGLVSVQLRSSFSEPATEEAEDTEAESPTTPTGLPAAAASIATLDNASARLFF
SRGIHV

>RXN02939 TRANSLATE of: rxn02939.seq check: 7866 from: 1 to: 1602
MNLHSLEIRQISSGTISERKTWIFPTAARSFNQNLVHPQSIEIDAQTGVILAMENRLQRT
EVESVEYPTDLPNPAWTGPAISWPLKDPSIDFPDPLPHSISELPPQSDNPRHLRVSISLD
AVEGAFPRYRIGDSIRIPLVFARDTPFMSGLETTRRAWIEAATEMDIHNTWPIILTGDGW
TALSHSDKPIRHEAELKGWFFHSLFGSEMPLTDLKIERIYGGLGTFDSGATRWQELTDTD
DAYTENGSWLLEVIVDATLDGAIPPPLQPQQFEASITHIVDEQLWVLGQMLPVLRCWDLE
TGKYLGQTYVPISVSHSSRLQFSEGLIHDYENAWSLNPGVRMLAEPQPWIEPVIELDVPA
PWELQESFPDGLYSLTDGEQTALGRSTPAGQLEICVISNDGSRILNAGRVEDLYFVQFWG
MTVFLNSNFQVQSAEEHQLGAKRERWITQEGVAAKFTEEDEIVFLDQISESEITRWKTPE
GYFTEVRILSPNHFNILVTPPTGSDYLKPVPSSVSVFRDGQWSNIKFEDVSVEI

>RXN02950 TRANSLATE of: rxn02950.seq check: 7742 from: 1 to: 324

MTVFNVLHDAPAPQPDKNRPGVKRLLQGDGANLIAFTFSPGQSLPDHRAAHPITVTAFSG
QLTFSYGEETFELSPGVTVHLEAGVTHRVDCPPEAPGDASNAVNYAHW

>RXN02951 TRANSLATE of: rxn02951.seq check: 852 from: 1 to: 609
MSSTLARKASGDGSEKKKPGLFRRALRFLTHPPHKQVDNSLADIREGLGLGVDDSHEGSK
PSNDHSLLHEKPEISVMPTESMARLIFYAPDMDGQTDPGEVVWIWAPADGPQQPPRKRAI
VVVGRNRNAILGLLISCNPEHRTDEDWIDIGSGSWDPRGRQSWVRLDRVLEVPELGIRRQ
GTVVPPGRFERIANRLRNDFNWV

>RXN02957 TRANSLATE of: rxn02957.seq check: 2405 from: 1 to: 291
MQTAQGGRVYTSLMDEKSLSPLIGLPGRENIGLGRHWHGLSTMLRVLNGIVYVVLLFATG
LWQGIIPTSWDVFPEAWETLKVYLGFRAPGIEHFTPL

>RXN02967 TRANSLATE of: rxn02967.seq check: 8901 from: 1 to: 318
MDLLVVAVHEGGQPRQSDCNAPGCAHTWLCAINFQLGAGVVEGGVEKRNVFFGGTFLGPE
YGGRALRAGGGGVDIGEQDPFDGGCGDVEFGGIDVIEVDEVGATGS

>RXN02971 TRANSLATE of: rxn02971.seq check: 4841 from: 1 to: 312
LIAIVALIVALVVWLFNRSDDSGSTTTTSQECISGNLSLPVGGDSTAAEELVNKFNDSSP
VSRDFCVEAEAVDGNVPAATYLFAGSRSDAATALAETGAVASSS

>RXN02978 TRANSLATE of: rxn02978.seq check: 8219 from: 1 to: 1509
VIDRPVWLFELYNTAKEVVYSLLIDQVTGENTILKKDDGWRDQFMIESFFAYDSEADATS
WSGKNMNSYWFVSDLISNISFAERSLESFSWALRDLEDLSSSETEFEGLEELNLKFSELQ
EWYTNLELPFQPSAADVDEVEQYLQAEVTRQRGDYQWSPEFWIPKPDSYYIDHALAVVTD
VLGAIEQGELREEVEVQQALDEVSENWNPLEDSDYYLQDHRGRPVQDLSREMEELVRCLM
LDQEWWGAEARIRKLVESVEWEDTQAISSLIEHEQYWEDGRFRPPLHKFSEGLDEPEPLP
MTRKMILATNHPDVLRVNIADYYQQHRRIATQKVECYKEVLALYPEILKKFDDSSFVNRH
WIYRAFDREGQLLYIGETINPLVRLREHAGLGSINHAHHRLVSPWFSTMATFHLESCFTQ
AEAKEKEALYIKLEQPRYNKTHNSARLAVSEEGVPVNEVPSRNDPRNVGWKGHRHVPPML
PIVARVVDESTTREGYAFYEDNR

>RXN02995 TRANSLATE of: rxn02995.seq check: 169 from: 1 to: 1566
LNHAKVNQHPGQATLPETAEGQVRTYEVKTYGCQMNVHDSERLSGLLEEAGYVAAPEDTT
PDLVVFNTCAVRENADMRLYGTLGNLRSVKEKNPGMQIAVGGCLAQKDKDTVVKKAPWVD
VVFGTHNIGSLPTLLQRAEHNAQAEVEIVDSLEQFPSVLPAKRESAYAGWVSVSVGCNNT
CTFCIVPSLRGKEQDRRPGDILAEVQALVDQGVTEVTLLGQNVNAYGVNFVDPELERDRS
AFSKLLRACGEIEGLERVRFTSPHPAEFTSDVIDAMAETPNICPQLHMPLQSGSDKVLKE
MRRSYRSKKFLSILDEVRAKIPHASITTDIIVGFPGETEEDFQATLDVVKKARFTSAYTF
QYSPRPGTPAAEYENQLPKEVVQERYERLMVVQEQVCEEENQKLIGTTVELLVQAGGGRK
NDATKRMSGRARDGRLVHFAPEGDIDGEIRPGDFVTVTVTEAKPFFLIADSGVQTHRRTK
AGDNSAVGQVPTTAPIGVGLGLPQIGAPKVAPATESACCSIN

>RXN02997 TRANSLATE of: rxn02997.seq check: 4243 from: 1 to: 729
PLPGQPFEGEALTLINALLHHAENVAASNPWKRTTFHTAHMHPPGSNADCDYCLVLQRRG
YVKAHEEIQQTIPLPSGDWSAGEFTVVDVEGTAFPSALIPSIVELQHRAALDVPHGNLSV
APAQWDEHRLAQQSERILKTGTKLFTVLFAEGSTVAAMSSIAIPPGSNPDIAEQGLTIVH
PDFRGRGLGTAVKLAGLSLLSRCHPEIQRVATSNAVDNHAMLAINRSIGATEIARTTLWE
KKL

>RXN03001 TRANSLATE of: rxn03001.seq check: 9853 from: 1 to: 453
MDWLTIPLFLVNEILAVPAFLIGIITAVGLGAMGRSVGQVIGGAIKATLGFLLIGAGATL
VTASLEPLGAMIMGATGMRGVVPTNEAIAGIAQAEYGAQVAWLMILGFAISLVLARFTNL
RYVLLNGHHVLLMCTMLTMVLATGRVDAWIF

>RXN03005 TRANSLATE of: rxn03005.seq check: 972 from: 1 to: 768
MSHKFSRRAFAVLTAAAISTSAFATTAPSAIAEPVLMSHCRRFQRRNFRKLPRLGLQGFL
AHLCHRTLDWWNRDATGGATVNEDGTYNFTLGTGSNYDVDTEKGQLNYEGTVAFASDAHG
FNITLSNPQITVEGDTATLSAELSDNAAPEETSTTRVDVAEFELTAPEVSETDADITYTW
TDASGTFLETLQPEELSRYAGQEADALSFSITVDKASENPSDDVATGSSSSFLSTILNFL
QQLASPLLKLFGSLSS

>RXN03009 TRANSLATE of: rxn03009.seq check: 8107 from: 1 to: 348
VANIASLYGLWEGSTSTPIEQLVPAKGSSFRLVRSFYRRIDGQAVQARLKEKILNTAENP
LPRLDIPGKERTAQYPENPDTFAQKAAQEILDEFRTPLIGEEAAAHVEKTKTIFWK

>RXN03010 TRANSLATE of: rxn03010.seq check: 697 from: 1 to: 237
VPTDNLFLIVAGIAWVLAGILSVLSIGKYMSAVNERKSTGFYTEVPWKKALFTATAVLLV
FAVVWSALDIALWVGKQSW

>RXN03011 TRANSLATE of: rxn03011.seq check: 6364 from: 1 to: 201
MAYETDSLNRRTLGPAIASAVVGIAVGAVAVVGVSMISGQDTVPTGNAVTADDALLGGPE
YGSREAD

>RXN03012 TRANSLATE of: rxn03012.seq check: 8240 from: 1 to: 570
TTINIIITNGAAPHPTNLNRAEIHDHLPLTASDSELTRPSQESVLYDHESETVLRTMVIP
ADLHVAMKHLAKKHNLTVTEISRILLQRYIDRNINHVEQNQAESDMVEVFASQPTNATAM
IPVPGTSFRQIFIKHSTGFWKNIDHDLVDLDASKTPRVRDRSVLPQPQLHRALLSDADMA
RLAAQLTDKH

>RXN03017 TRANSLATE of: rxn03017.seq check: 6478 from: 1 to: 1539
MLDSLKNRFTKAKGSHGVGEGAVSGDAAVKPLRKEERLASVIQETEPGAAVEVMRRNDAF
ALPGETGWVVMLLPTHDSQFGGLNAKEKNREDKGTIINLVVNDDIHSVVTPELLDSDVLG
VIPDADSFDRMDEFDLLRNKARWHYGVAAIEPDTGELVVFKVPAKNSASARGDIFSEVGD
VLSGAADLEDVVDFEVIATFLEVLNETSEVDIDDEDGDVPYGLEGVNAAGVITDDLIREK
LDVDSYPSSAEIIDNIVHVFTKLQGKHHVAPQPVLHSADVVDVDAQESHDTVVIESPDDV
ALAEQVDVPDFSDGFGIDDAEVTEPEDEEVVEATADADPFGDVAEDDPFGSDDEPDFGAS
DVVAAPAPVAGMSDEQIQALIRGVSESVQAKTGSELNALREELAQALAYNPVQDSQAALA
QVHAADARSFDADQVGDAVTKRYVNDDLGLYVDEANFNNALTRAPFQVAMPQFQETTPWL
GDQLRTLVAVFNGQLLDQHQRDYRRSARDVHCA

>RXN03018 TRANSLATE of: rxn03018.seq check: 6149 from: 1 to: 993
VTTEEVRAMYIALNDRSNLEIARDLGLDNKDSEFYEVYRAIERDRDVMAGDQQRVESERR
QQLQQEYEANREEYVMAKIAEQRVEYDRRHMPRHTASLEAVGRELTSLRDRTIEDYTARM
NTLRRARAGERANAAESRIIDELRPIVERQAELQRAAFDGFIVDLDKFIADHREDDLRLA
SVNEQKLAADNRVAQLTKEAEERIEGIRVETDKMIASQRKALERQEAEFAAELKRRDTIV
AASEERAEREITTARLDAEAALKRMEEQIRVNNEAHEAEIVIERDRATQAEANSMTFVES
VKQQDRSNNIILIAVLIVGLIAGMVAGAAFF

>RXN03024 TRANSLATE of: rxn03024.seq check: 8954 from: 1 to: 1416
MLERTQVFVDTSYLLASFYNSWETGARAQLEIDLPEVVGVLGRMIEQQLKQPVQRQMWYD
GIPDSGPHRYQRALRTCDGVQLRAGQLIEWGERRTQKAVDTRLVADLVLAGVRGQCSDIV
LVSGDADMIPGVQEAANAGLRVHLYGFGWDSMSSQLRHCCDTTTILDPREDFAECMQLQV
LEGPLPPVVRVKPINDAEPIEDLDFTPVPGVASPFEEVSAKDEKFSPRPSEPAEALSEQV
CEAQYEISKHEGQTADSGEITESFEAAEIKVTEFFGEPAAPVAESGVEAPTPEAPTVPEA
AKPTPAKPKTPKAEPQKQESPKPGTPKPKAPSPADIPPKAPADTEEHSEVEAEIEDSRPK
IPSPSMMAPRRKLRSRYVPLPNEVWATAGFQTPYDVGQQYASWWFENAATSTQRDQAHLL
SGGGLPPEIDRPLLQFACETLHEYTLTEAQRVALRDGFHSGIRGVLLNQRDS

>RXN03025 TRANSLATE of: rxn03025.seq check: 3655 from: 1 to: 873
MANPLSKGWKYLMASFDNKIDENADPKIQIQQATEAAQKQHQQIMQHASQIIGQQKQLEM
KLNRLVTDRDKLQEQARQAIQLADKSANEGDSVKAQEFNNTAEVFASQLVAVEQQLEQTT
ALHQQAEVAAKDAVAKSKESEMRLKEQMSQIDALRAQADQAKMQESVTKSMDSLNQFGTQ
DSSVPTLDAVREKIERRYADALGAQELTQNTVSDRMAEIAQSGTDMRASARLAELRAEAL
GTSATPKGQLEAGVEDAEELIDETSTPSATPETASPEADAPEASADESEKK

>RXN03027 TRANSLATE of: rxn03027.seq check: 7054 from: 1 to: 135
MENVYEFLGNLDVLSGSGLIGYVFDFLGASSKWAGAVADLIGLLG

>RXN03029 TRANSLATE of: rxn03029.seq check: 3295 from: 1 to: 513
MFGVGYYTTAHRLSTLQRPNLRGIPLTFVSVDRAGNMSKRQSATGFHFTHYGGTCPLWNV
FETFTNPGQVLRQFAQMPDGRNYLWISRTVRHHEARFGEVDKMFAIGLGCEARHADRTVY

SRGFNLQDLSTATPIGSGCRVCTRENCAQRAFPSVHGRINIDAHESTIAPY

>RXN03031 TRANSLATE of: rxn03031.seq check: 9392 from: 1 to: 789
NNGLNAMAAMTNLPHLRAIQERYYFLSIRYLASIMIAVAKADPTLWEELDLRITDALTPV
TAGEVMIQSSTLSKRIAAWIKELDPEPTPEPIPKEDYVHVHTTDEATYVRIKISGPNRLI
LNDIITQLKDTDTEDSLPEALMAFLMEKIQLKITKYLFTPHKHPEQVWSPDYGDIGPEAY
ANATLVCAKDLDEVAGATEKSYTPSEKMKALIRARDGHCRFPGCCVPASKCQVDHIIPWA
EGGPTAAWNLQLLCQRHHNMKTD

>RXN03032 TRANSLATE of: rxn03032.seq check: 9767 from: 1 to: 285
MTDGDLDADISPRQIGLMTTRTVVEIVRLRHMIAQQLERATIMENEYLKEIAALKKELAH
YKQKDHQNQMVIDILGKAIGTRPNPGEGLDEEDAT

>RXN03034 TRANSLATE of: rxn03034.seq check: 6067 from: 1 to: 660
FPPDRISANGRRYYEPQTRLEFMRIYTTLPHGYRQPFLKANNIGHCTVRTWLAAISTFSR
LPHAFDDAHRFGIERTTPVDDVTTLTADDKRDLVIGYLAQPHGQGQQFLTFYQLRKHTIM
AWCAAMTDGDLDADISPRQIGLMTTRTVVEIVRLRHMIAQQLERATIMENEYLKEIAALK
KELAHYKQKDHQNQMVIDILGKAIGTRPNPGEGLDEEDAT

>RXN03037 TRANSLATE of: rxn03037.seq check: 5439 from: 1 to: 186
MSVDDLYAVALDTHTGKPIPCVLCENAPQIVIYDGCCSLAYTQALGDLAEAEYYGADLAA
AA

>RXN03041 TRANSLATE of: rxn03041.seq check: 9452 from: 1 to: 498
MEGPEAFTVAAIAAAAGVSPRTFHNYFPSREDALVQFVVIRVQELTDQLYEFPTSVPPRD
AIEQLVINQLRDGDDAMDSFSAMFRIGEILENLDPIKCVIDKERLIAPLLEFMVERDKDL
DKFDXGNSDPFACSGNCNLAAYVLPSFRAPGHRRWSRIDPSGMRLD

>RXN03045 TRANSLATE of: rxn03045.seq check: 9805 from: 1 to: 996
MSITTHVQALTTALNAIDNHLASMLDHGVTPDQYKAIEPDLIALEHTINHHATIAAQTTA
LAERTNAAQSIGSTHLIDYLTTTFGLSKARAHHRINLAHSLYPIPKPNSGSGNGGNGGNP
DGGPDGGDSGDDDSGDDDPDPEPDKPEDGKPDSDKPRRPRISAEKHAIITDELARLNPNT
TPSAEELRNQALSQAIWRTPEDLRTWLRHQVTTANKNNPNPITAMKRRYLSVGKPDADNM
VRISGLVPAATAALITANTAPLTKRGNLVDLPAAEDMRTRGQRHADALHHIMEIYNHGIV
TPARGGTASIIISMTTDDLDEINHANSSGESL

>RXN03046 TRANSLATE of: rxn03046.seq check: 2540 from: 1 to: 336
ASIANSTLNIPVGLGGSNLLLKAQTATPSEPANAQDKLYRFCIANGKRAFSDAQRFLLNA
DELAELSDYERLAYAITLLDQPGKEAEGRELFPFGASPPGLPRCRFLGIPDC

>RXN03047 TRANSLATE of: rxn03047.seq check: 8954 from: 1 to: 1416
MLERTQVFVDTSYLLASFYNSWETGARAQLEIDLPEVVGVLGRMIEQQLKQPVQRQMWYD
GIPDSGPHRYQRALRTCDGVQLRAGQLIEWGERRTQKAVDTRLVADLVLAGVRGQCSDIV
LVSGDADMIPGVQEAANAGLRVHLYGFGWDSMSSQLRHCCDTTTILDPREDFAECMQLQV
LEGPLPPVVRVKPINDAEPIEDLDFTPVPGVASPFEEVSAKDEKFSPRPSEPAEALSEQV
CEAQYEISKHEGQTADSGEITESFEAAEIKVTEFFGEPAAPVAESGVEAPTPEAPTVPEA
AKPTPAKPKTPKAEPQKQESPKPGTPKPKAPSPADIPPKAPADTEEHSEVEAEIEDSRPK
IPSPSMMAPRRKLRSRYVPLPNEVWATAGFQTPYDVGQQYASWWFENAATSTQRDQAHLL
SGGGLPPEIDRPLLQFACETLHEYTLTEAQRVALRDGFHSGIRGVLLNQRDS

>RXN03048 TRANSLATE of: rxn03048.seq check: 3655 from: 1 to: 873
MANPLSKGWKYLMASFDNKIDENADPKIQIQQATEAAQKQHQQIMQHASQIIGQQKQLEM
KLNRLVTDRDKLQEQARQAIQLADKSANEGDSVKAQEFNNTAEVFASQLVAVEQQLEQTT
ALHQQAEVAAKDAVAKSKESEMRLKEQMSQIDALRAQADQAKMQESVTKSMDSLNQFGTQ
DSSVPTLDAVREKIERRYADALGAQELTQNTVSDRMAEIAQSGTDMRASARLAELRAEAL
GTSATPKGQLEAGVEDAEELIDETSTPSATPETASPEADAPEASADESEKK

>RXN03050 TRANSLATE of: rxn03050.seq check: 8926 from: 1 to: 966
MSITTHVQALTTALNAIDNHLASMLDHGVTPDQYKAIEPDLIALEHTINHHATIAAQTTA
LAERTNAAHTIGSTHLIDYLTTTFGLSKARAHHRINLAHSLYPIPKPNPGSGNGGNGGNP
DGGPDGGDSGDDDSGDDDPDPEPDKPEDGKPDGDKPRGPRISAEKHAIITDELARLNPNT

TPSAEELRTQALSQAIWRTPEDLRTWLRHHVTTANKNNPNPITAMKRRYLAVGKPDADNM
VRISGLVPAATAALITANTAPLTKRGNLVDLPAAEDMRTRGQRHADALHHIMEIYNHGIV
TPARGGTASIIISMTTDDLDEI

>RXN03053 TRANSLATE of: rxn03053.seq check: 9689 from: 1 to: 1524
FHFTSTEFAGSYSLVTNGLNDVAGEYVGVMRGDVNNSAVLFDVDRWSGHVVCADSSINTS
PLLKRPRVVDMWGSKISQAALLNNRRVVHLVLNGAKLDEMGPKLESMTAHVDMTSGDLNM
FELFGKQEDELSLYSTHMDKIVFMTEQALGDKTSELALLRGKLKEIITAFYVDMKMWALN
AGENRDKLRLVGVPHEQIPLLSVFVSYLDQEYERQKYEGTKDPEMFRAISVLRLTYKDLL
DTHGDLFNQHTADGIDSVNSARRVIYDFSGVLRRGAGVAMAQLVNVIGFAVETLGQGDVV
IIHGADGIVDVDVQDYLANQFAYMAERGGRVAYLYSSMDAMLGTVGFNQFQRAAYTILGP
MNVDSVDTYQSLINSQIPMDLARLVTTQNSGASYLRRGSTNVVFETNLALGVNPYMEQRR
KIEAQRGQRRSKRDKHYGGGTTMVGTADLDVVAIQAKAEHREERFDEKSARKMKELDDVE
AKELALKTGPKNLDDALAQVEKKRLAKR

>RXN03055 TRANSLATE of: rxn03055.seq check: 6322 from: 1 to: 429
MYSDKLILLFLSEQDSSYECCVGLLDGSDGRDYIEKLLKGRKLKNHFLEWEDINKADVAR
EEIYKGQLVHLVFVTALSTPGEISFVFPGQSLMSATLEEDFAALVLEEERTSFRPELSHL
WSLPVGWVAPGLEGFVERNSEAA

>RXN03059 TRANSLATE of: rxn03059.seq check: 9601 from: 1 to: 480
MNSGSTMRRISLRNIGAHKVRLFLTVLAVVLGTSFVSGAMMFTNALSSTFDEAIASSFDG
VDVVVSPNGASEVQGVPVETVESLREDSRINHLNINGSQTVVLADADSKAIQTTGGSSLS
IYYSADDAVAQAPELAEGEAPTGTEEVLASKAGAEANGLE

>RXN03062 TRANSLATE of: rxn03062.seq check: 8000 from: 1 to: 522
METPTQDMDVRWLYTQSQLKLREILPTNKTFDVIQISELVDPTDFIRPNSVVLSVGIAFA
ETPDGLRDWAHRLADAGVIAIGFGSGLTFPQVPQALIDASLHLGLGLFEVPREIPFISIT
SSVRDEQTRRAGRLQQELLLEQERLNSIAISGGIEALCRAAADYLGGAVTIVDS

>RXN03066 TRANSLATE of: rxn03066.seq check: 1968 from: 1 to: 663
MTSDKDTEQLEAAGTEILMPRRRPAQQRSRERFNRILTAARSVLVDLGFESFTFDEVAKR
AEVPIGTLYQFFANKYVLICELDRVDTAEAVAELKKFSDQVPALQWPDILDEFIEHLARL
WRDDPSRRAVWHAIQSTPATRATAAATEKEMLEIIAEVMRPLARGAGYEERMSLAGLLVH
TVSSLLNYAVRDVNSSEEDFDSIVEEIKRMLISYLFSVATG

>RXN03067 TRANSLATE of: rxn03067.seq check: 3872 from: 1 to: 171
VMTAWGAFGEKKNYGKIVQGVIRSTFLINADGTVGMAKYNVRATGHVERIVREITAA

>RXN03068 TRANSLATE of: rxn03068.seq check: 9072 from: 1 to: 120
TKEACDFRDSLSNLNDLDIAVVGISPDPVDKLVSSVRTMS

>RXN03073 TRANSLATE of: rxn03073.seq check: 8068 from: 1 to: 630
MDSVNVLLIGIIVAIAALLPRKGKYGPIATLLVAGDWLGVFLLSILVMLVFDGLEDLVQG
FLDSIWFGVILLVTGIVSFVATLVSKTDSTRKLDGFLAPVKTPSWKTVGAGLILGIVQSA
TSVPFYAGLGYLSVGNFSPEIRYGGLVVYATLALSLPIIVAILVGMVRKYPESPVGRLFE
LIGQNKERVTKWSGYLVSLVLCIMGITSIL

>RXN03085 TRANSLATE of: rxn03085.seq check: 6690 from: 1 to: 351
MSIHIAKVHDVLKGEKTYGTTILVDRLWPRGVKKDDLEPDLWLKSVAPTTELRKWFGHDP
AKFSEFSTRYTEELNASNDKDLETLVDATSRHPVTLLYGAADRDHNHAIVLAKWLKK

>RXN03089 TRANSLATE of: rxn03089.seq check: 2217 from: 1 to: 1158
HSLYPIPKPNSGSGNGGNGGNPDGGPDGGDSGDDDSGDDDPDPEPDKPEDGKPDSDKPRR
PRISAEKHAIITDELARLNPNTTPSAEELRTQALSQAIWRTPEDLRTWLRHQVTTANKNN
PNPITAMKRRYLSVGKPDADNMVRISGLVPAATAALITANTAPLTKRGNLVDLPAAEDMR
TRGQRHADALHHIMEIYNHGIVTPARGGTASIIISMTTDDLDEINHGDHGDGSLLNNLYP
TNTGYSLNLAEIMNLIAAKYDFAVLLDGETGQPLNVNRMQRSANLTQRIALFASELVCSA
PNCDRPQLECEVHHLDPWMRGGLTNLVNLTHQCFNHHPRNDDSRSGVNGKGFMDRDPVTG
RVGHYSASGEGPVFNRSAAADRSGGA

>RXN03098 TRANSLATE of: rxn03098.seq check: 3946 from: 1 to: 624
MPTTDVFNRVRLALEPLADPARATGMASYMRDQFSFLGIPSTPRKEACKPVLSALKELDT
DFVSDCFGAAEREYQYVACDHINRVGITDLGFAKALVQTKSWWDTVDSLAKPIGAKHDDD
LMKTWALDEDFWVRRIAIIHQLGRKKNTDAALLAWIIEQNLGSSEFFINKAIGWALRDFA
RHDPSWVRAFVDATDLSPLSRREALKNI

>RXN03099 TRANSLATE of: rxn03099.seq check: 8629 from: 1 to: 675
VVDAVHDVLQIALARRGEYNLGNALGLEVLGQAFAVTPAAGVVYHDGVIDAVFGVINGGW
VIGVDDLDWGAVGPDDVVVIIGGDGAIESTVDRITTQQGCALDQVFFTIFADHDGAQTST
VIQCLAGNQDAGQQATDAAETVQHDISWVDVGFRTNDRRESVLQEGTQVGAFGFFEAVGQ
LSQVDRCGTKVHIYQFAQNIQGAFQWKFLGYDVAGVAVRLDDIDV

>RXN03104 TRANSLATE of: rxn03104.seq check: 6257 from: 1 to: 177
LELNAWEDILDLLSWSGSGNGAQDQTVIQVLEGFNAIVILANKQSLVGKQVWATEVDGL

>RXN03106 TRANSLATE of: rxn03106.seq check: 1318 from: 1 to: 192
MSASFDDPNLISLAGLVPTMHLADAASLSTLAQDRLSITGDKGANAGAKIASLVAGMVAG
ADSI

>RXN03107 TRANSLATE of: rxn03107.seq check: 669 from: 1 to: 201
MSDFSNKAEDLTGKAKEGFGEATDNESLADEGRADQAKADIKDAVENAGEKVKDAANKVL
GAFKKDD

>RXN03113 TRANSLATE of: rxn03113.seq check: 5526 from: 1 to: 1599
VLDFLAANPLIALVVILAVGLAIGQIRVFGLSLGAAAVLFVALVVSTANTDIVIPMIVYQ
LGLAMFVYVIGLSAGPAFFSEFAKKGWKLTIFMLLLLATLIGLAWVLIKSLGLDAAIGTG
MFTGALTSTPGMAAVVELIEGIDPSLASEPVIGYSLAYPGAVLGSIVVAAVGAKLLKVNH
REDARKEGMITAPLVWKGVQLKPGITGRVGDLPRLAGESIIATRIVDDPHTHRLADPDLP
ITEGMELLINGTEEAVDRAIKALGEERETKIEDTELIYTRLTVSSPEVAGRTVAELDTVA
HGFMIARIRQGDSEVVPKPDTVINYSDRIRVVVAPGRVAEVRRFLGDSEKSLADVNLLPL
AIGLSLGLLLGAIPIPLPGGTTMSLGFGGGPIIAGLILGALKHTGPLTWQMPFHANRTIS
TLGLALFLAGVGTSAGAGFRAALTDSSSLIYMAGGLVITLASALLCAVIGMWVLRLRWDE
AMGVAAGTTTNPAIISYLNGQTGTDLANRGYATVYPTAMIGKILGAQILFLLL

>RXN03115 TRANSLATE of: rxn03115.seq check: 582 from: 1 to: 399
VGKQEKLRIPLDVPGVESEEVGVELLAEGYYLVATLPAVAQDCALGDVVRAHHVDEVLEF
QEVAVAGGNKTLRVLVDAIAADHVRAQLETLGLHVEAPMSEMLTVNIAPDSPSHGLEILL
DDLHAQGVIFRAL

>RXN03122 TRANSLATE of: rxn03122.seq check: 3973 from: 1 to: 147
MTAHHEGAVDMARDEVTDGQNPQAIALAEQVIEDQEAEIAEMEHMLNEL

>RXN03134 TRANSLATE of: rxn03134.seq check: 1542 from: 1 to: 351
VAWRVGPGSHEHDIVGSSGFGSEADGGFFPASEGLALDNGAGDAAVDVGVSDIDVVKPGA
DFVGVEGLESAGESEVVAVLEFDGFIEVGGFHQAEDWSEYFCEVEEGSWFDAFFDAG

>RXN03135 TRANSLATE of: rxn03135.seq check: 3240 from: 1 to: 729
LVLDERWVGVGLVDKWDEGGVEKRLFAAVLCVVGAGRGHVDERGEVRYGGAEAALLSLEG
RVVGVEVEDGGHEVFARGVFLEAAHEVRNGHVEFLWAHGWYVKQQLTDVNADGARLIGRH
ALQHFELHTVRYPTLHREQMCECYVEKVVAGNAQAQALHVFFAHRPIEDALVIGIGGLFG
RFCGNWPAGDLRVDVLHRQISTLDQANLNARPACVDALAAELRQVLDCTEGIGKVRLQHN
SGF

>RXN03138 TRANSLATE of: rxn03138.seq check: 608 from: 1 to: 471
LDIVPKDVAESFAVGEVVFLRVLGDGVVDDVPVHSIDGGSDFGGSVWGEGHSERAVVLGT
ARTGGSCVVKQISYFFYLASYGRRAWQNLVGAGGGEVFGEDCVGAGEVVGVDAGEFVANG
DQSGEVEVVQLLLQGFEFGQVGERGKRDGYAGDLRFC

>RXN03140 TRANSLATE of: rxn03140.seq check: 4447 from: 1 to: 249
VKGIHQEISRIERSHDYLWSVREDLHARFDNQLKAHFVDSVLDSIAEGYEGRINRFRKIF
IEMKAVEELRTIAATRPSHLLAA

>RXN03141 TRANSLATE of: rxn03141.seq check: 2295 from: 1 to: 330
VVEATGVAGGNHVATVWHAGVLGVEGCFVDEVDFDFVANEVIRHGADVVFDALVIGRVGN
HEALALVGLLSGKVAGFAAAGLFQGVFGWEGVLDCLLNARDASQSIGVAL

>RXN03146 TRANSLATE of: rxn03146.seq check: 6973 from: 1 to: 471
MNPRILMLLRIIFGAAFLALLVLQVLLAIKIVRDGLNSGELSPIPLTILASFVIIGFGLV
QFIIVCLFALLRLVEDDEIFDAHSLAWVDRIAITIAAGAVLLLPMAYIVAEVDDAPGAIV
FGLILAMLITGVSLLVKIMRALLARAIGFSTELESVI

>RXN03147 TRANSLATE of: rxn03147.seq check: 6179 from: 1 to: 252
LEILFKSGLGFVVIIGAVGEYFGADFCGAGAGGGGLLKLAEYIAGWIAGESADDVFGFVV
CVLRFETFLGVGVCQRGIVWEEHG

>RXN03149 TRANSLATE of: rxn03149.seq check: 777 from: 1 to: 267
VVIGELLPKSYSIVNTEKVVLFVVKPLHYFYKVMFPFIWVLNHSAAGLGKLLGVRLVSEG
EETLSQEELTLVALNSYEKGELPKKNIII

>RXN03152 TRANSLATE of: rxn03152.seq check: 1285 from: 1 to: 273
MKLFSRTPLVALGTAAAMAATSISVPAQAEEVAPAQVVYVADTVEEETGSSNGSSDIDSD
TILDYVVVITGIVGVLSAGLTFATAFQRSLQ

>RXN03153 TRANSLATE of: rxn03153.seq check: 7794 from: 1 to: 564
MRRIWLLVCGIALTVAGCTSGSTTPTTVTVTATPTSEEAASTEPTNDILASQFHPCEVLT
QEQFEEVGLGVLIVEDAYLGSTGLGCSFGKADREDFSGTWLISTDQANRQFVENQDLETL
DWGSNDNPDLYVHQMSETGRQCEAAVDYDWGRLTVDYLELGEGWEPEILCSDAVEILENL
IKELRGIP

>RXN03154 TRANSLATE of: rxn03154.seq check: 5495 from: 1 to: 912
MLKTTLITDTLGHVTSTEPTTTAHVPLPDGSSTPVQIWASDNKDSQLVMLWPGFGMGGYY
YRPLAAALNKAGFHVAIGELRGQGQSSAKASRKSQWGYHDLASVDFPLQIAAAKKALDLE
EGHPMRFLSHSMGGQISCLFAARPEAEKYNLRAIFGVGAGSPFRPTFSPKMGKRLGLGAV
LLGGIGGHIVGFWPGKVLGKDLVGYGRQSGTHMREWRRFHKHNSLDDLTAQDINYVEVMK
KVSIPITFSRCPDDEDCPQASIDGLASFVPAAQIKMIEIPEALGHNRWAREPESTVKLFL
EQAL

>RXN03156 TRANSLATE of: rxn03156.seq check: 5548 from: 1 to: 180
MARTTPPPADVLDIIISTVKQTIGIDLAELIQGRALGQAQGEAQGKASAAALEQAPHNEQ

>RXN03162 TRANSLATE of: rxn03162.seq check: 7855 from: 1 to: 396
VHDEHWVWSDEKDADFAFDDAWHETHINEHAVVADDVLVTEIHELAELADFSVVVDCFGA
LDFSVQWQCGAWLDGCSQFLVYQLDAPNAGAGGATVLLEHALTEGQGGWENLVEGLHVVV
RLGVGWHQVGLG

>RXN03167 TRANSLATE of: rxn03167.seq check: 749 from: 1 to: 630
MNTNLPNLYTAFDLDRSESSEALGVSLSARDLRLEQMGIAQDDPRRAQTVQAFAVLADPA
KRATYDAQLEAGVPLTWAQIQHLGNFGTLPSTPTAQPFAAPQPEPSPEPQQQWNSGQNYA
YGNPTMDYQTQQSYNPMQDQTQASMYAQPFANTPAPMYNSNQVFNRPTAGTRLWMAILDS
IFAGIAGGIVSGIFGFGSEFLTSVIMILVL

>RXN03170 TRANSLATE of: rxn03170.seq check: 4430 from: 1 to: 249
LPHAKELAHELCLLPTPAVPALPTDSGAQFDIHQALSASLATYARNLTLLSHTAENLGNR
ALTGLAEIEDTDDQLAHALERLT

>RXN03172 TRANSLATE of: rxn03172.seq check: 3870 from: 1 to: 1026
PEWKKFNSGDAARVVPDANAELDIIGAPALLADRPSYANVKTLSRIFAVMRSLGHVTAAS
PVTVFFSSHSVLSNVDRGSEHYSGPNGLGEWTSVGRAVATNWNGVVDALDEAITVKEVNS
LFTEDAATRIQEAQAAVQAAREAEEQIAKEEAEKVDPYDNSPWAAAGIDPIKVSIDGRTI
YTLRTYLGGQPVFLGKFGEISTFNSQKSLLRWLVEHDDHDLARASTWSDLMLGINAGETE
LLVHSDNVYSFNGLVKDINTSVDAVDTQQMARAYELMADTADWADDDSMNSYFLANPRMQ
DYISYMLGGSDTSGYVPHAPFNDHSESWRELEEMLIKRFSKF

>RXN03173 TRANSLATE of: rxn03173.seq check: 9151 from: 1 to: 1098
LNRDTHHLWVVLTTDSDDFDADSFTTEVIRITGYSRHEVNNGLNAMAAMTNLPHLRAIQE
RYYFLSIRYLASIMIAVAKADPTLWEELDLRITDALTPVTAGEVMIQSSTLSKRIAAWIK
ELDPEPTPEPTPKEDYVHVHTTDEATYVRIKISGPNRLILNDIITQLKDTDTEDSLPEAL
MAFLTEKIQLKITKYLFTPHKHPEQVWSPDYGDIDPEAYANATLVCAKDLDELAGATEKS
YTPSEKMKALIRARDGHCRFPGCCVPASKCQVDHIIPWAEGGPTAAWNLQLLCQRHHNMK
TDGRFTADANGLAEIRWIGPMDVPAVTRPTGPLVKAMPRGIWGQVLRDRIQARFERIRDR
ALNKED

>RXN03174 TRANSLATE of: rxn03174.seq check: 9763 from: 1 to: 456
MLLTILWAIGITAEGMTGALAAGRQKMDLFGVSVIACVTAIGGGSIRDMLLGHYPLVWVE
KPLYLLLIIGAAILTVSISFLMEHFRVLFLVLDAVGLSAFAVIGTQIALEMGYGFIIAVV
ASVLTGVFGGVMRDLLCDRIPLVFQKELYASI

>RXN03177 TRANSLATE of: rxn03177.seq check: 4510 from: 1 to: 666
VKKKLMLPLIVAALGLSACSSEPAAAPLEAEPLHNLLIDGSESGLDNATEGNDTSLSGQP
INLTVVNGALDIDGSCGKALQAVEDVNLDSVASASRALASGDKQVGIAMYSTAEDNDISP
MDLYADIANACEDPVVDSSDTTYTFGKLDDAPDGAVGFTLDIEVTPDNQGSTVMMIQELG
NHHIIVAGLETTPEETATVFEAQRTKLEEGLQLKQNWQLGWV

>RXN03182 TRANSLATE of: rxn03182.seq check: 2985 from: 1 to: 273
MTLQLFTDIVSLVFILSGAFLSFSASIGLIRFKDTMSRVHAMTKPQTTGLILTVVGAIIR
ILGHEHFDQSQRSDLGVLVLLVLFALLTSPV

>RXN03184 TRANSLATE of: rxn03184.seq check: 3926 from: 1 to: 498
MVGAFGGGVLGGYIPGTILMIAFALMMIATSTAMLRGRKQKKGASKSSLWRVLVDGLVVG
AVTGLVGAGGGFLVVPALALLGGLSMPVAVGTSLVVITMKSFAGLAGYLTSVQLDWGLVL
MVTAAAIVGSLAGSRLAGRVPETLLRKGFGVFVLVMGVFVLGLELL

>RXN03185 TRANSLATE of: rxn03185.seq check: 4886 from: 1 to: 189
MNDLAAEGENDPYRMVQQLRRKLSRFVEQKWKRQPVIMPTVIPMTAETTHIGDDEVRASR
ESL

SEQUENCE LISTING

<110> Pompejus, Markus
Kroger, Burkhard
Schroder, Hartwig
Zelder, Oskar
Haberhauer, Gregor
<120> CORYNEBACTERIUM GLUTAMICUM GENES ENCODING NOVEL PROTEINS
<130> BGI-129CP
<140>
<141>
<160> 2932

<210> 1
<211> 1023
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1000)
<223> RXN01638

<400> 1
aggcatcaaa cccacagcac aaccaccagg acgtgccacg atgtccatcc gtggtgaaaa 60

catcggtgtt gcacagatgg caccgcatag gtgatgactc atg agc acc caa aca 115
Met Ser Thr Gln Thr
1 5

atc acc atc aca gtc cta gaa acc gcc acc atc ttt gac ggc cct gaa 163
Ile Thr Ile Thr Val Leu Glu Thr Ala Thr Ile Phe Asp Gly Pro Glu
10 15 20

acc atc tac cgc tat gac ctg gct gcc gaa ggc atc ctt gat gga tgg 211
Thr Ile Tyr Arg Tyr Asp Leu Ala Ala Glu Gly Ile Leu Asp Gly Trp
25 30 35

gct cac tct gct gtg ctg gat caa gtg aaa caa ata gca ggt gaa aac 259
Ala His Ser Ala Val Leu Asp Gln Val Lys Gln Ile Ala Gly Glu Asn
40 45 50

tgg ccg act gtt gag atc gtg gtg gat ggc acc gac aac gta gtc aat 307
Trp Pro Thr Val Glu Ile Val Val Asp Gly Thr Asp Asn Val Val Asn
55 60 65

gca ctc acc tcc atg ttt gct tcc aaa ggc gtg acc tgc ggt ggg gtt 355
Ala Leu Thr Ser Met Phe Ala Ser Lys Gly Val Thr Cys Gly Gly Val
70 75 80 85

gga gta gaa gca cct ccc gtt gcg gag gaa cca ccg aaa att aaa cgg 403
Gly Val Glu Ala Pro Pro Val Ala Glu Glu Pro Pro Lys Ile Lys Arg
90 95 100

ccc acg agt gga aaa caa gtc cgc cag ttc tac ggc atc aag cca cta 451
Pro Thr Ser Gly Lys Gln Val Arg Gln Phe Tyr Gly Ile Lys Pro Leu
105 110 115

cac ctg ttg ttg gtc agc ata ttg gtt ggt tct att gct ggt att tgg 499
His Leu Leu Leu Val Ser Ile Leu Val Gly Ser Ile Ala Gly Ile Trp

```
        120                 125                 130

gtg att tcg ggt ttc act ggg cca gtg gac tca cgg ccg gta gat aag   547
Val Ile Ser Gly Phe Thr Gly Pro Val Asp Ser Arg Pro Val Asp Lys
    135                 140                 145

gtg gcg gag att tca acg cag ggg gag acg tcg ata agc aat caa ccc   595
Val Ala Glu Ile Ser Thr Gln Gly Glu Thr Ser Ile Ser Asn Gln Pro
150                 155                 160                 165

caa ccc cag ccc acc gtg ctc gtg acc gag gac ctg ctt att gag gcg   643
Gln Pro Gln Pro Thr Val Leu Val Thr Glu Asp Leu Leu Ile Glu Ala
                170                 175                 180

cca ttt ggt ttt gaa atg cga agc gac gaa cag tcg cgc tac ctg gaa   691
Pro Phe Gly Phe Glu Met Arg Ser Asp Glu Gln Ser Arg Tyr Leu Glu
            185                 190                 195

ggc ccc gac ccg aat ctg cgc atc cac gtg ggc gtc gat ccg ctg cac   739
Gly Pro Asp Pro Asn Leu Arg Ile His Val Gly Val Asp Pro Leu His
        200                 205                 210

ggc gcg gac gcc gcg ctg gtt gcc gaa gag ctg cgc cgc ctg atc acc   787
Gly Ala Asp Ala Ala Leu Val Ala Glu Glu Leu Arg Arg Leu Ile Thr
    215                 220                 225

gag gat cct tcg ctg gag gaa att ccc gca ggg gag tgg ggc gag aaa   835
Glu Asp Pro Ser Leu Glu Glu Ile Pro Ala Gly Glu Trp Gly Glu Lys
230                 235                 240                 245

acc acc atc gac tac cgc gaa aca ccc ggc gat ggc tct cat gtg ctg   883
Thr Thr Ile Asp Tyr Arg Glu Thr Pro Gly Asp Gly Ser His Val Leu
                250                 255                 260

tgg gtg acc tgg ttt gac acc gac cga caa ctc aac gtt ggg tgc cat   931
Trp Val Thr Trp Phe Asp Thr Asp Arg Gln Leu Asn Val Gly Cys His
            265                 270                 275

agc aaa gcc gcc gaa acc ctt gtt cac aag gca caa tgc cga aat gtg   979
Ser Lys Ala Ala Glu Thr Leu Val His Lys Ala Gln Cys Arg Asn Val
        280                 285                 290

att gag cat ctg acg ctg aaa tgatgccggt ttctatccgg aat            1023
Ile Glu His Leu Thr Leu Lys
    295                 300
```

<210> 2
<211> 300
<212> PRT
<213> Corynebacterium glutamicum

<400> 2

```
Met Ser Thr Gln Thr Ile Thr Ile Thr Val Leu Glu Thr Ala Thr Ile
  1               5                  10                  15

Phe Asp Gly Pro Glu Thr Ile Tyr Arg Tyr Asp Leu Ala Ala Glu Gly
             20                  25                  30

Ile Leu Asp Gly Trp Ala His Ser Ala Val Leu Asp Gln Val Lys Gln
         35                  40                  45
```

```
Ile Ala Gly Glu Asn Trp Pro Thr Val Glu Ile Val Val Asp Gly Thr
     50                  55                  60

Asp Asn Val Val Asn Ala Leu Thr Ser Met Phe Ala Ser Lys Gly Val
 65                  70                  75                  80

Thr Cys Gly Gly Val Gly Val Glu Ala Pro Pro Val Ala Glu Glu Pro
                85                  90                  95

Pro Lys Ile Lys Arg Pro Thr Ser Gly Lys Gln Val Arg Gln Phe Tyr
            100                 105                 110

Gly Ile Lys Pro Leu His Leu Leu Leu Val Ser Ile Leu Val Gly Ser
        115                 120                 125

Ile Ala Gly Ile Trp Val Ile Ser Gly Phe Thr Gly Pro Val Asp Ser
    130                 135                 140

Arg Pro Val Asp Lys Val Ala Glu Ile Ser Thr Gln Gly Glu Thr Ser
145                 150                 155                 160

Ile Ser Asn Gln Pro Gln Pro Gln Pro Thr Val Leu Val Thr Glu Asp
                165                 170                 175

Leu Leu Ile Glu Ala Pro Phe Gly Phe Glu Met Arg Ser Asp Glu Gln
            180                 185                 190

Ser Arg Tyr Leu Glu Gly Pro Asp Pro Asn Leu Arg Ile His Val Gly
        195                 200                 205

Val Asp Pro Leu His Gly Ala Asp Ala Ala Leu Val Ala Glu Glu Leu
    210                 215                 220

Arg Arg Leu Ile Thr Glu Asp Pro Ser Leu Glu Glu Ile Pro Ala Gly
225                 230                 235                 240

Glu Trp Gly Glu Lys Thr Thr Ile Asp Tyr Arg Glu Thr Pro Gly Asp
                245                 250                 255

Gly Ser His Val Leu Trp Val Thr Trp Phe Asp Thr Asp Arg Gln Leu
            260                 265                 270

Asn Val Gly Cys His Ser Lys Ala Ala Glu Thr Leu Val His Lys Ala
        275                 280                 285

Gln Cys Arg Asn Val Ile Glu His Leu Thr Leu Lys
    290                 295                 300
```

<210> 3
<211> 513
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(490)
<223> FRXA01638

<400> 3

```
tttcactggg ccagtggact cacggccggt agataaggtg gcggagattt caacgcaggg 60

ggagacgtcg ataagcaatc aaccccaacc ccagcccacc gtg ctc gtg acc gag   115
                                             Val Leu Val Thr Glu
                                               1               5

gac ctg ctt att gag gcg cca ttt ggt ttt gaa atg cga agc gac gaa   163
Asp Leu Leu Ile Glu Ala Pro Phe Gly Phe Glu Met Arg Ser Asp Glu
                 10                  15                  20

cag tcg cgc tac ctg gaa ggc ccc gac ccg aat ctg cgc atc cac gtg   211
Gln Ser Arg Tyr Leu Glu Gly Pro Asp Pro Asn Leu Arg Ile His Val
             25                  30                  35

ggc gtc gat ccg ctg cac ggc gcg gac gcc gcg ctg gtt gcc gaa gag   259
Gly Val Asp Pro Leu His Gly Ala Asp Ala Ala Leu Val Ala Glu Glu
         40                  45                  50

ctg cgc cgc ctg atc acc gag gat cct tcg ctg gag gaa att ccc gca   307
Leu Arg Arg Leu Ile Thr Glu Asp Pro Ser Leu Glu Glu Ile Pro Ala
     55                  60                  65

ggg gag tgg ggc gag aaa acc acc atc gac tac cgc gaa aca ccc ggc   355
Gly Glu Trp Gly Glu Lys Thr Thr Ile Asp Tyr Arg Glu Thr Pro Gly
 70                  75                  80                  85

gat ggc tct cat gtg ctg tgg gtg acc tgg ttt gac acc gac cga caa   403
Asp Gly Ser His Val Leu Trp Val Thr Trp Phe Asp Thr Asp Arg Gln
                 90                  95                 100

ctc aac gtt ggg tgc cat agc aaa gcc gcc gaa acc ctt gtt cac aag   451
Leu Asn Val Gly Cys His Ser Lys Ala Ala Glu Thr Leu Val His Lys
            105                 110                 115

gca caa tgc cga aat gtg att gag cat ctg acg ctg aaa tgatgccggt    500
Ala Gln Cys Arg Asn Val Ile Glu His Leu Thr Leu Lys
        120                 125                 130

ttctatccgg aat                                                   513
```

Sequence Listing - Page 4 of 5

<210> 4
<211> 130
<212> PRT
<213> Corynebacterium glutamicum

<400> 4

```
Val Leu Val Thr Glu Asp Leu Leu Ile Glu Ala Pro Phe Gly Phe Glu
  1               5                  10                  15

Met Arg Ser Asp Glu Gln Ser Arg Tyr Leu Glu Gly Pro Asp Pro Asn
             20                  25                  30

Leu Arg Ile His Val Gly Val Asp Pro Leu His Gly Ala Asp Ala Ala
         35                  40                  45

Leu Val Ala Glu Glu Leu Arg Arg Leu Ile Thr Glu Asp Pro Ser Leu
     50                  55                  60

Glu Glu Ile Pro Ala Gly Glu Trp Gly Glu Lys Thr Thr Ile Asp Tyr
 65                  70                  75                  80
```

```
Arg Glu Thr Pro Gly Asp Gly Ser His Val Leu Trp Val Thr Trp Phe
                85                  90                  95

Asp Thr Asp Arg Gln Leu Asn Val Gly Cys His Ser Lys Ala Ala Glu
            100                 105                 110

Thr Leu Val His Lys Ala Gln Cys Arg Asn Val Ile Glu His Leu Thr
        115                 120                 125

Leu Lys
    130
```

<210> 5
<211> 561
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(538)
<223> FRXA01639

<400> 5

```
aggcatcaaa cccacagcac aaccaccagg acgtgccacg atgtccatcc gtggtgaaaa 60

catcggtgtt gcacagatgg caccgcatag gtgatgactc atg agc acc caa aca   115
                                            Met Ser Thr Gln Thr
                                              1               5

atc acc atc aca gtc cta gaa acc gcc acc atc ttt gac ggc cct gaa   163
Ile Thr Ile Thr Val Leu Glu Thr Ala Thr Ile Phe Asp Gly Pro Glu
                10                  15                  20

acc atc tac cgc tat gac ctg gct gcc gaa ggc atc ctt gat gga tgg   211
Thr Ile Tyr Arg Tyr Asp Leu Ala Ala Glu Gly Ile Leu Asp Gly Trp
            25                  30                  35

gct cac tct gct gtg ctg gat caa gtg aaa caa ata gca ggt gaa aac   259
Ala His Ser Ala Val Leu Asp Gln Val Lys Gln Ile Ala Gly Glu Asn
        40                  45                  50

tgg ccg act gtt gag atc gtg gtg gat ggc acc gac aac gta gtc aat   307
Trp Pro Thr Val Glu Ile Val Val Asp Gly Thr Asp Asn Val Val Asn
    55                  60                  65

gca ctc acc tcc atg ttt gct tcc aaa ggc gtg acc tgc ggt ggg gtt   355
Ala Leu Thr Ser Met Phe Ala Ser Lys Gly Val Thr Cys Gly Gly Val
70                  75                  80                  85

gga gta gaa gca cct ccc gtt gcg gag gaa cca ccg aaa att aaa cgg   403
Gly Val Glu Ala Pro Pro Val Ala Glu Glu Pro Pro Lys Ile Lys Arg
                90                  95                 100

ccc acg agt gga aaa caa gtc cgc cag ttc tac ggc atc aag cca cta   451
Pro Thr Ser Gly Lys Gln Val Arg Gln Phe Tyr Gly Ile Lys Pro Leu
            105                 110                 115

cac ctg ttg ttg gtc agc ata ttg gtt ggt tct att gct ggt att tgg   499
His Leu Leu Leu Val Ser Ile Leu Val Gly Ser Ile Ala Gly Ile Trp
```

```
        120                 125                 130

gga ttt cgg gtt tca ctg ggc cag tgg act cac ggc cgg tagataaggt    548
Gly Phe Arg Val Ser Leu Gly Gln Trp Thr His Gly Arg
    135                 140                 145

ggcggagatt tca                                                  561


<210> 6
<211> 146
<212> PRT
<213> Corynebacterium glutamicum

<400> 6
Met Ser Thr Gln Thr Ile Thr Ile Thr Val Leu Glu Thr Ala Thr Ile
  1               5                  10                  15

Phe Asp Gly Pro Glu Thr Ile Tyr Arg Tyr Asp Leu Ala Ala Glu Gly
             20                  25                  30

Ile Leu Asp Gly Trp Ala His Ser Ala Val Leu Asp Gln Val Lys Gln
         35                  40                  45

Ile Ala Gly Glu Asn Trp Pro Thr Val Glu Ile Val Val Asp Gly Thr
     50                  55                  60

Asp Asn Val Val Asn Ala Leu Thr Ser Met Phe Ala Ser Lys Gly Val
 65                  70                  75                  80

Thr Cys Gly Gly Val Gly Val Glu Ala Pro Pro Val Ala Glu Glu Pro
                 85                  90                  95

Pro Lys Ile Lys Arg Pro Thr Ser Gly Lys Gln Val Arg Gln Phe Tyr
            100                 105                 110

Gly Ile Lys Pro Leu His Leu Leu Leu Val Ser Ile Leu Val Gly Ser
        115                 120                 125

Ile Ala Gly Ile Trp Gly Phe Arg Val Ser Leu Gly Gln Trp Thr His
    130                 135                 140

Gly Arg
145


<210> 7
<211> 6470
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(6447)
<223> RXN01590

<400> 7
tgg ggt caa aaa gat cac tgg ggc aaa gct cca ctg ggt gat cac gat   48
Trp Gly Gln Lys Asp His Trp Gly Lys Ala Pro Leu Gly Asp His Asp
  1               5                  10                  15
```

```
gct gtg cgt atc tat agg caa gca gaa gcc ttg atg aaa cag cgc gca   96
Ala Val Arg Ile Tyr Arg Gln Ala Glu Ala Leu Met Lys Gln Arg Ala
            20                  25                  30

gca aac aat aag ggc tta gac ctc aat gat gaa gcg acc tat ggc gcc  144
Ala Asn Asn Lys Gly Leu Asp Leu Asn Asp Glu Ala Thr Tyr Gly Ala
        35                  40                  45

atc atg ttt gcg tct ttc gat gat gcc ttc gcc gct gat gcc gaa gct  192
Ile Met Phe Ala Ser Phe Asp Asp Ala Phe Ala Ala Asp Ala Glu Ala
    50                  55                  60

cat ggc tgt gta cac cga cca cag ttc gcg aag gta act agg cga aat  240
His Gly Cys Val His Arg Pro Gln Phe Ala Lys Val Thr Arg Arg Asn
65                  70                  75                  80

att ctt aat tca ccg caa tac acg gcg att aag tca tct tat gac gcg  288
Ile Leu Asn Ser Pro Gln Tyr Thr Ala Ile Lys Ser Ser Tyr Asp Ala
                85                  90                  95

ctg gtg cag cag gat ctc gtg gcc caa cag cag cag gca caa gcg cta  336
Leu Val Gln Gln Asp Leu Val Ala Gln Gln Gln Gln Ala Gln Ala Leu
            100                 105                 110

cag caa gct gct tat gag caa gag cag gca gct att ttc cag gca cgt  384
Gln Gln Ala Ala Tyr Glu Gln Glu Gln Ala Ala Ile Phe Gln Ala Arg
        115                 120                 125

gat caa gca aca ttc cag gct gaa caa acg ctc gcg caa gag tcc gtt  432
Asp Gln Ala Thr Phe Gln Ala Glu Gln Thr Leu Ala Gln Glu Ser Val
    130                 135                 140

cgc caa tca gag ggt gtg ggt tta cct gtc att gat ccg atg gag agc  480
Arg Gln Ser Glu Gly Val Gly Leu Pro Val Ile Asp Pro Met Glu Ser
145                 150                 155                 160

tat ttc cgg gag tac gcc ttc tat gaa ggt gtc gag atg ttt ggt acc  528
Tyr Phe Arg Glu Tyr Ala Phe Tyr Glu Gly Val Glu Met Phe Gly Thr
                165                 170                 175

tgg ggt acg cac gtt gat gct ggt gtg tcg cag ttt agc acc tct gat  576
Trp Gly Thr His Val Asp Ala Gly Val Ser Gln Phe Ser Thr Ser Asp
            180                 185                 190

ggc cgt gcg atc cga gcg ctt gtt gat gag cat ctc gca acc tat gaa  624
Gly Arg Ala Ile Arg Ala Leu Val Asp Glu His Leu Ala Thr Tyr Glu
        195                 200                 205

cca gta gag cag cgg ggg agt act cag gca ttc ttc gcc tct gtc aat  672
Pro Val Glu Gln Arg Gly Ser Thr Gln Ala Phe Phe Ala Ser Val Asn
    210                 215                 220

gct gcc ttt gct gag gtg gca cct cac gca gca ccc atg ttt agt gcg  720
Ala Ala Phe Ala Glu Val Ala Pro His Ala Ala Pro Met Phe Ser Ala
225                 230                 235                 240

att gct cgc gag ggt gag ggt tca aag ggg tac cag gcg ctg cgt cac  768
Ile Ala Arg Glu Gly Glu Gly Ser Lys Gly Tyr Gln Ala Leu Arg His
                245                 250                 255

cgt ttc gac aag atg gtc ggc act gca att gga cct aat ggt ttg cct  816
```

```
Arg Phe Asp Lys Met Val Gly Thr Ala Ile Gly Pro Asn Gly Leu Pro
            260                 265                 270

gag gga cct gat ctg ggt ggt cgt cgt tta cct att tcg cct tat gat   864
Glu Gly Pro Asp Leu Gly Gly Arg Arg Leu Pro Ile Ser Pro Tyr Asp
        275                 280                 285

cca cgc tgg tca gac cgc gaa gta gtc cgt gtg cac ggt acc aag ctg   912
Pro Arg Trp Ser Asp Arg Glu Val Val Arg Val His Gly Thr Lys Leu
    290                 295                 300

cta tca ctg tcc gaa gag agt gtt ggc atg atc agg gac ctt gat cta   960
Leu Ser Leu Ser Glu Glu Ser Val Gly Met Ile Arg Asp Leu Asp Leu
305                 310                 315                 320

gca acg atc cac cta caa gat aat gat gtt tac gag ggc act cat cga  1008
Ala Thr Ile His Leu Gln Asp Asn Asp Val Tyr Glu Gly Thr His Arg
                325                 330                 335

gaa gac gac act aaa ggc ggt gtg cga ccg ttg act caa tgg gtc aat  1056
Glu Asp Asp Thr Lys Gly Gly Val Arg Pro Leu Thr Gln Trp Val Asn
            340                 345                 350

ggt gaa gct att gcc tgg cgc act atc acc gag aat gac cag atg cga  1104
Gly Glu Ala Ile Ala Trp Arg Thr Ile Thr Glu Asn Asp Gln Met Arg
        355                 360                 365

ctg ccc aat att ggt cag ttt atg acg gct aaa gaa tac cgt gcc gca  1152
Leu Pro Asn Ile Gly Gln Phe Met Thr Ala Lys Glu Tyr Arg Ala Ala
    370                 375                 380

gcg tca tgg ctg cgt gct gga ctc att gat acc gca gat gtt gcg agt  1200
Ala Ser Trp Leu Arg Ala Gly Leu Ile Asp Thr Ala Asp Val Ala Ser
385                 390                 395                 400

cag aaa att gac ccc aac aag gtc atg tct gat gag ggt atc gcg cgc  1248
Gln Lys Ile Asp Pro Asn Lys Val Met Ser Asp Glu Gly Ile Ala Arg
                405                 410                 415

tcg gaa gct att ttg acg tat ctg tcg gat gag ggt gtg gat ttt agg  1296
Ser Glu Ala Ile Leu Thr Tyr Leu Ser Asp Glu Gly Val Asp Phe Arg
            420                 425                 430

atc gag cca gat cgt gag ccg gga cag ctt aaa gtg cgt att gag ggc  1344
Ile Glu Pro Asp Arg Glu Pro Gly Gln Leu Lys Val Arg Ile Glu Gly
        435                 440                 445

acc cgt att gat att cgt ctc act gat act cgc gcc aat gaa cag tgg  1392
Thr Arg Ile Asp Ile Arg Leu Thr Asp Thr Arg Ala Asn Glu Gln Trp
    450                 455                 460

gtg ggt cgt gtc tat gat tct ggc act gtg att aag tat tcc gcc gaa  1440
Val Gly Arg Val Tyr Asp Ser Gly Thr Val Ile Lys Tyr Ser Ala Glu
465                 470                 475                 480

caa aca gcg gaa gaa cgt cta cga gct cgt gag cgc atg gag aac ggt  1488
Gln Thr Ala Glu Glu Arg Leu Arg Ala Arg Glu Arg Met Glu Asn Gly
                485                 490                 495

gat gga acg tgg aca ccg gct act gat tat gaa cca agc cca act gaa  1536
Asp Gly Thr Trp Thr Pro Ala Thr Asp Tyr Glu Pro Ser Pro Thr Glu
```

```
                500                 505                 510

gtt gtc gat ctc gtg aaa ttt gct ctc ggt cga gag gtt gag cga cag   1584
Val Val Asp Leu Val Lys Phe Ala Leu Gly Arg Glu Val Glu Arg Gln
        515                 520                 525

gat ggc aaa ggt ctt gtt ggt gtg cct aat gct cga cac cca cgt gct   1632
Asp Gly Lys Gly Leu Val Gly Val Pro Asn Ala Arg His Pro Arg Ala
    530                 535                 540

tta gag cag gca cag gat gca tat ttc act aag aat cgt tcc gca ttc   1680
Leu Glu Gln Ala Gln Asp Ala Tyr Phe Thr Lys Asn Arg Ser Ala Phe
545                 550                 555                 560

atg gtg cgt gaa ggg ctc tcg atc gtt cag gat gca cgt gat cga agt   1728
Met Val Arg Glu Gly Leu Ser Ile Val Gln Asp Ala Arg Asp Arg Ser
                565                 570                 575

gct ggt cct gga aag tgg ttt gat aat gaa gcg aaa gca tcg gag tgg   1776
Ala Gly Pro Gly Lys Trp Phe Asp Asn Glu Ala Lys Ala Ser Glu Trp
            580                 585                 590

ctt ggt aac aat atc gcc ctt act cgt gcg cgt gtg gcc gaa gag ctc   1824
Leu Gly Asn Asn Ile Ala Leu Thr Arg Ala Arg Val Ala Glu Glu Leu
        595                 600                 605

ggc gtt gaa gaa ctg att gcg ctt tct gca cag tac gcc gat gat cct   1872
Gly Val Glu Glu Leu Ile Ala Leu Ser Ala Gln Tyr Ala Asp Asp Pro
    610                 615                 620

gac ttc atg ccg gct ttt gct ggt gag gat gag ctc atg gcg ata aag   1920
Asp Phe Met Pro Ala Phe Ala Gly Glu Asp Glu Leu Met Ala Ile Lys
625                 630                 635                 640

cag gac tat tgg gcg atg ctg cga ggt gag gaa acc gat ctg ctt aac   1968
Gln Asp Tyr Trp Ala Met Leu Arg Gly Glu Glu Thr Asp Leu Leu Asn
                645                 650                 655

cct ggg gtt aac cgc gat gat tat atg gct gct atc cgc gat ggt gat   2016
Pro Gly Val Asn Arg Asp Asp Tyr Met Ala Ala Ile Arg Asp Gly Asp
            660                 665                 670

cat gag cag att gct gcg atg acc tca gca atg aat gct gtg acc gtg   2064
His Glu Gln Ile Ala Ala Met Thr Ser Ala Met Asn Ala Val Thr Val
        675                 680                 685

gag gat cgt gtg cgt cag cac gcg gcc ctt gtt ctt gat gat tat gtc   2112
Glu Asp Arg Val Arg Gln His Ala Ala Leu Val Leu Asp Asp Tyr Val
    690                 695                 700

ggc acg gtg gag cct gat cct gtt acc ggc ttg cgt ttt aat ccg gtg   2160
Gly Thr Val Glu Pro Asp Pro Val Thr Gly Leu Arg Phe Asn Pro Val
705                 710                 715                 720

aca gtt gct cag cac atg ccg agt gct aaa tcc ctg tgg tca aac cat   2208
Thr Val Ala Gln His Met Pro Ser Ala Lys Ser Leu Trp Ser Asn His
                725                 730                 735

gac gat att att gcc gcg ttg cga gcg act tcg att act ggc gat gaa   2256
Asp Asp Ile Ile Ala Ala Leu Arg Ala Thr Ser Ile Thr Gly Asp Glu
            740                 745                 750
```

```
ctg cgc ggt gac gaa ttc tat aac gat gtt att aat caa cag ttg ctc   2304
Leu Arg Gly Asp Glu Phe Tyr Asn Asp Val Ile Asn Gln Gln Leu Leu
        755                 760                 765

aaa ttt aat cct gag acc gcg cag aaa atg gtt aat aac cct gat ctt   2352
Lys Phe Asn Pro Glu Thr Ala Gln Lys Met Val Asn Asn Pro Asp Leu
    770                 775                 780

gac ccg cag ttg gct cga ttt ggc act gtc att gcc gag act att tcc   2400
Asp Pro Gln Leu Ala Arg Phe Gly Thr Val Ile Ala Glu Thr Ile Ser
785                 790                 795                 800

cgc aat ggt gct gat gtg gtc gat att gct gtt gac gat aac ggt gtg   2448
Arg Asn Gly Ala Asp Val Val Asp Ile Ala Val Asp Asp Asn Gly Val
                805                 810                 815

gtg cgg tgg acc gca cag cga cgt gtt ggt gcg aag gat agt cgt gca   2496
Val Arg Trp Thr Ala Gln Arg Arg Val Gly Ala Lys Asp Ser Arg Ala
            820                 825                 830

gta gat agt aag ggg cag gtt cgc ggt gaa cgc acc cgt cat gtg cag   2544
Val Asp Ser Lys Gly Gln Val Arg Gly Glu Arg Thr Arg His Val Gln
        835                 840                 845

ggt gag ata ggt cag att ttt act cgc ggt gag cat ggt gaa att gtc   2592
Gly Glu Ile Gly Gln Ile Phe Thr Arg Gly Glu His Gly Glu Ile Val
    850                 855                 860

acc aaa ttt aat ggt ggc gag aac tat atg ttt gcc cct ggc tac acc   2640
Thr Lys Phe Asn Gly Gly Glu Asn Tyr Met Phe Ala Pro Gly Tyr Thr
865                 870                 875                 880

gcg tct gtg gta cca caa aag cct ggt gag aca aag agt tta gaa gag   2688
Ala Ser Val Val Pro Gln Lys Pro Gly Glu Thr Lys Ser Leu Glu Glu
                885                 890                 895

cgt acc aag ctc aaa ggc tat gag cag gtg atg tca gag gcg ttg gtg   2736
Arg Thr Lys Leu Lys Gly Tyr Glu Gln Val Met Ser Glu Ala Leu Val
            900                 905                 910

tac cgt gtg cga gaa gat ttg atg ttc act gag cga tcc cga gtg ggt   2784
Tyr Arg Val Arg Glu Asp Leu Met Phe Thr Glu Arg Ser Arg Val Gly
        915                 920                 925

gct aca acc agc atc aac agt gca tat aag cga ctg tat gac aat cgc   2832
Ala Thr Thr Ser Ile Asn Ser Ala Tyr Lys Arg Leu Tyr Asp Asn Arg
    930                 935                 940

ttc cct gtg gac ttc ttc gag cgc agc gcc gaa gaa ggt ttg agc gat   2880
Phe Pro Val Asp Phe Phe Glu Arg Ser Ala Glu Glu Gly Leu Ser Asp
945                 950                 955                 960

gag tgg cgt gct gcg ttg ctt gag act gcg agt ttg cgt gtg cgc tac   2928
Glu Trp Arg Ala Ala Leu Leu Glu Thr Ala Ser Leu Arg Val Arg Tyr
                965                 970                 975

gac aac tct att cgt gat ggt gcg aat gtg atg gag gat att cga gca   2976
Asp Asn Ser Ile Arg Asp Gly Ala Asn Val Met Glu Asp Ile Arg Ala
            980                 985                 990
```

```
cag cag cgt ggt ttt gat gcg cgt aat gat aac tcc cgt gat gcg ctg   3024
Gln Gln Arg Gly Phe Asp Ala Arg Asn Asp Asn Ser Arg Asp Ala Leu
        995                 1000                1005

gtg ctt acc ggt ggg cgt aac att tct gta ctt gat gtt gat gcg ggt   3072
Val Leu Thr Gly Gly Arg Asn Ile Ser Val Leu Asp Val Asp Ala Gly
    1010                1015                1020

aaa ggt ttc ttt gat ccc atg atg act ggt atg gcg gcg aac cag ggt   3120
Lys Gly Phe Phe Asp Pro Met Met Thr Gly Met Ala Ala Asn Gln Gly
1025                1030                1035                1040

tct gtt cgc tat ttg ttg cct tct gcg aag gtg ggc gct gat ggc atg   3168
Ser Val Arg Tyr Leu Leu Pro Ser Ala Lys Val Gly Ala Asp Gly Met
                1045                1050                1055

att acc cct ggt gat ccg gct gat cga gta cct gtt gca gcg cat cca   3216
Ile Thr Pro Gly Asp Pro Ala Asp Arg Val Pro Val Ala Ala His Pro
            1060                1065                1070

gaa tca tgg gcg atg ggc ttt gac cca cat gac cgt cag aac atg act   3264
Glu Ser Trp Ala Met Gly Phe Asp Pro His Asp Arg Gln Asn Met Thr
        1075                1080                1085

ttc tcg aac atc atg cag gct agc gct gtg act ggt ggt gca cgc act   3312
Phe Ser Asn Ile Met Gln Ala Ser Ala Val Thr Gly Gly Ala Arg Thr
    1090                1095                1100

gcg atg ata cag ctg ggc ggt tgg aac ttt gaa gat ggc att att gtc   3360
Ala Met Ile Gln Leu Gly Gly Trp Asn Phe Glu Asp Gly Ile Ile Val
1105                1110                1115                1120

tct gcc gat ttt gcg aat acc cat gtt att cgc gat acg gaa gat gag   3408
Ser Ala Asp Phe Ala Asn Thr His Val Ile Arg Asp Thr Glu Asp Glu
                1125                1130                1135

atg cgc ccc ttg gtt gcc ggc gat aag ctg tct gat ttt cac ggt aat   3456
Met Arg Pro Leu Val Ala Gly Asp Lys Leu Ser Asp Phe His Gly Asn
            1140                1145                1150

aag ggt gtg acc gct ctt gtt gtt gat cca gcg atg agt gat gct gat   3504
Lys Gly Val Thr Ala Leu Val Val Asp Pro Ala Met Ser Asp Ala Asp
        1155                1160                1165

gca cgt gca gca ggg ctg gaa tca gag gtg gcg ttt ttc cga gac aac   3552
Ala Arg Ala Ala Gly Leu Glu Ser Glu Val Ala Phe Phe Arg Asp Asn
    1170                1175                1180

cct gat cta gag gtt gtc atg agt ccg ttt tct gcc att tct cgt ttt   3600
Pro Asp Leu Glu Val Val Met Ser Pro Phe Ser Ala Ile Ser Arg Phe
1185                1190                1195                1200

aat ggt ggc acg gca cgt gag ctc atg acc aac ccg cag gat gtg gtg   3648
Asn Gly Gly Thr Ala Arg Glu Leu Met Thr Asn Pro Gln Asp Val Val
                1205                1210                1215

ttc agg aat aat gat ggt tct act cgt gtt caa cca ggt gcc tct ggt   3696
Phe Arg Asn Asn Asp Gly Ser Thr Arg Val Gln Pro Gly Ala Ser Gly
            1220                1225                1230

gat ctc aac ttc atc gtc acg cat atg gct gtt gat gcg aaa acc aat   3744
```

```
Asp Leu Asn Phe Ile Val Thr His Met Ala Val Asp Ala Lys Thr Asn
        1235                1240                1245

gtc tat gat gaa gaa gct gtt cgt gag ggc caa gga cgt aaa gcg tct   3792
Val Tyr Asp Glu Glu Ala Val Arg Glu Gly Gln Gly Arg Lys Ala Ser
    1250                1255                1260

tct cag ctg gcg tgg gtg ctc caa gcc cag gaa tgt cat gag att atg   3840
Ser Gln Leu Ala Trp Val Leu Gln Ala Gln Glu Cys His Glu Ile Met
1265                1270                1275                1280

gag cac ttt tat ggc aac aac gtc tct gca ttg gct aac ttc cag gaa   3888
Glu His Phe Tyr Gly Asn Asn Val Ser Ala Leu Ala Asn Phe Gln Glu
                1285                1290                1295

tat ctt cgc gtc acg ggg ctt gat gtc acc ccg tat ggt gag ttg cgc   3936
Tyr Leu Arg Val Thr Gly Leu Asp Val Thr Pro Tyr Gly Glu Leu Arg
            1300                1305                1310

gag ggg ttc agc gag tcc aat gag cag cgc aat atc atc gag atg cca   3984
Glu Gly Phe Ser Glu Ser Asn Glu Gln Arg Asn Ile Ile Glu Met Pro
        1315                1320                1325

agc att tac gat gag aac ggt gag ctg aat aat cgt gtt aat cgt gca   4032
Ser Ile Tyr Asp Glu Asn Gly Glu Leu Asn Asn Arg Val Asn Arg Ala
    1330                1335                1340

cag gtg cgc gaa gct ttt gtt gag cag atc agt cgc gct ggt ggt gtt   4080
Gln Val Arg Glu Ala Phe Val Glu Gln Ile Ser Arg Ala Gly Gly Val
1345                1350                1355                1360

atg gag att cct ttc cag tta cag ttg cgc aat ggt gca cag cta gaa   4128
Met Glu Ile Pro Phe Gln Leu Gln Leu Arg Asn Gly Ala Gln Leu Glu
                1365                1370                1375

gag tca cct aat aat cca gac atg tat cag ttg cca cta ctg agc ccg   4176
Glu Ser Pro Asn Asn Pro Asp Met Tyr Gln Leu Pro Leu Leu Ser Pro
            1380                1385                1390

cat ttg cgc agt gat gag gat tta gcg gac ggt agt acc tct cga cat   4224
His Leu Arg Ser Asp Glu Asp Leu Ala Asp Gly Ser Thr Ser Arg His
        1395                1400                1405

gag tac acc acg cgg tat atg gct att ttt gat acg tgc tac aag ctg   4272
Glu Tyr Thr Thr Arg Tyr Met Ala Ile Phe Asp Thr Cys Tyr Lys Leu
    1410                1415                1420

gca gaa gag caa gcc aag att gac gca ttg cgc cag gag gaa gcg cag   4320
Ala Glu Glu Gln Ala Lys Ile Asp Ala Leu Arg Gln Glu Glu Ala Gln
1425                1430                1435                1440

cac ggc acg ttg cct cgt gct gcg gaa aag cga ctg agc gag tca cag   4368
His Gly Thr Leu Pro Arg Ala Ala Glu Lys Arg Leu Ser Glu Ser Gln
                1445                1450                1455

aag ttt gtt gat caa gca cag aaa aag gtg cag gca agc ttt gat gga   4416
Lys Phe Val Asp Gln Ala Gln Lys Lys Val Gln Ala Ser Phe Asp Gly
            1460                1465                1470

att gct aat gat att gtc gcc agc cgg atc gag acc aag aac aat gtg   4464
Ile Ala Asn Asp Ile Val Ala Ser Arg Ile Glu Thr Lys Asn Asn Val
```

```
        1475                1480                1485

ttc aag gac ggc ttt atg tcg gcg cga cag tca cac tcc gct act gct   4512
Phe Lys Asp Gly Phe Met Ser Ala Arg Gln Ser His Ser Ala Thr Ala
    1490                1495                1500

gtg tgg aca ggt gat cca cgc ctg tca gtt gat gaa gta gcc atg aac   4560
Val Trp Thr Gly Asp Pro Arg Leu Ser Val Asp Glu Val Ala Met Asn
1505                1510                1515                1520

tct tcg atg gca cgt gaa ctc ggc gtt ctc gat aac ggt tat gca atg   4608
Ser Ser Met Ala Arg Glu Leu Gly Val Leu Asp Asn Gly Tyr Ala Met
                1525                1530                1535

gtg tgg cgt gat ccg gtg atc cgc gat ggt ggt gtg cgc tat ttg cgt   4656
Val Trp Arg Asp Pro Val Ile Arg Asp Gly Gly Val Arg Tyr Leu Arg
            1540                1545                1550

gtg gtt att aat gat gat ctg cac ggt gtg gca gtc aac cct gtg tcg   4704
Val Val Ile Asn Asp Asp Leu His Gly Val Ala Val Asn Pro Val Ser
        1555                1560                1565

gtg aag agc ttt gac ggt gac ttc gat ggt gac tct gta ggt ctg gtc   4752
Val Lys Ser Phe Asp Gly Asp Phe Asp Gly Asp Ser Val Gly Leu Val
    1570                1575                1580

ggc aat ctg ccg aaa aag gcg cat gag gag gca ttg tcc agg ctc aca   4800
Gly Asn Leu Pro Lys Lys Ala His Glu Glu Ala Leu Ser Arg Leu Thr
1585                1590                1595                1600

gtt gag gca aac atg ctt gat ctt ggt gat ggt aag cgt atg gag gac   4848
Val Glu Ala Asn Met Leu Asp Leu Gly Asp Gly Lys Arg Met Glu Asp
                1605                1610                1615

ggc act atg ttt tat ggg cta act ctg cat gac agc ctc gat gta cag   4896
Gly Thr Met Phe Tyr Gly Leu Thr Leu His Asp Ser Leu Asp Val Gln
            1620                1625                1630

gta gcg cag cac cat gat ccg gca atg gcc gag aac atg aag gtt att   4944
Val Ala Gln His His Asp Pro Ala Met Ala Glu Asn Met Lys Val Ile
        1635                1640                1645

gtc tct gag ctt aac cgc tac cag cgt gaa tac gag gcc ggc gag att   4992
Val Ser Glu Leu Asn Arg Tyr Gln Arg Glu Tyr Glu Ala Gly Glu Ile
    1650                1655                1660

agc cgc gaa gaa ttg cta gag gtc aac cgt gca cac atg gat gat ctc   5040
Ser Arg Glu Glu Leu Leu Glu Val Asn Arg Ala His Met Asp Asp Leu
1665                1670                1675                1680

aat gag cac tat gca cag gct ttt gcc aac cgc gat ggt ttg gtg acc   5088
Asn Glu His Tyr Ala Gln Ala Phe Ala Asn Arg Asp Gly Leu Val Thr
                1685                1690                1695

ttg cgt ttt gac ggt atg gaa aac cat atg gct tct gtt gcg cag tgc   5136
Leu Arg Phe Asp Gly Met Glu Asn His Met Ala Ser Val Ala Gln Cys
            1700                1705                1710

ttc gag acg ggt gcg aaa ggt tcg cct ggc aag ctg aag gaa tat gcc   5184
Phe Glu Thr Gly Ala Lys Gly Ser Pro Gly Lys Leu Lys Glu Tyr Ala
        1715                1720                1725
```

```
acc tat atc ggc gct gat ccg gcg cag ggt ttt aaa gac gta ggt caa   5232
Thr Tyr Ile Gly Ala Asp Pro Ala Gln Gly Phe Lys Asp Val Gly Gln
    1730                1735                1740

cca acg cca gaa gcg ctg cgt agc cac tat gag ggt tcg cag aag gcg   5280
Pro Thr Pro Glu Ala Leu Arg Ser His Tyr Glu Gly Ser Gln Lys Ala
1745                1750                1755                1760

act gca att aag gtg ctc ttt acc ggt gtg gct ggt aaa aaa gag cag   5328
Thr Ala Ile Lys Val Leu Phe Thr Gly Val Ala Gly Lys Lys Glu Gln
                1765                1770                1775

gaa atg gtg gca ttg tgc cgc aat ctt ggt ctg acc aag gaa gct atg   5376
Glu Met Val Ala Leu Cys Arg Asn Leu Gly Leu Thr Lys Glu Ala Met
            1780                1785                1790

gct gca tca gca ccg gca cag cag tcg att ctg cag gcg aag cac gac   5424
Ala Ala Ser Ala Pro Ala Gln Gln Ser Ile Leu Gln Ala Lys His Asp
        1795                1800                1805

ccg att gac gcg ctc tat cgt gca gaa act ctt atg gga cca gta ggt   5472
Pro Ile Asp Ala Leu Tyr Arg Ala Glu Thr Leu Met Gly Pro Val Gly
    1810                1815                1820

gat ctc tac caa ggt cgc aag atg cgt cgt ggt gag aat gag caa ggt   5520
Asp Leu Tyr Gln Gly Arg Lys Met Arg Arg Gly Glu Asn Glu Gln Gly
1825                1830                1835                1840

cgc tat gag tgg gaa gtc gtt agg gac gag aac cac cag cct atc cag   5568
Arg Tyr Glu Trp Glu Val Val Arg Asp Glu Asn His Gln Pro Ile Gln
                1845                1850                1855

gcc acc aag gat gaa tgg gta cag cag tac atg gag atg tac gcc gat   5616
Ala Thr Lys Asp Glu Trp Val Gln Gln Tyr Met Glu Met Tyr Ala Asp
            1860                1865                1870

gac aag ggt atg ggt gtc tcg gtt ggc gtt gac cag gtg gag aag atc   5664
Asp Lys Gly Met Gly Val Ser Val Gly Val Asp Gln Val Glu Lys Ile
        1875                1880                1885

gcg gaa gaa ttc tct gat gag cag ggt tat atg cgt gtg ctt agc cat   5712
Ala Glu Glu Phe Ser Asp Glu Gln Gly Tyr Met Arg Val Leu Ser His
    1890                1895                1900

gat gag cta ccc act gag att aag cca cta gca ctt gat cag ctt gcc   5760
Asp Glu Leu Pro Thr Glu Ile Lys Pro Leu Ala Leu Asp Gln Leu Ala
1905                1910                1915                1920

tat ggc gat aag aag aac cgc ttt gat ttg ttg tgc gag atg gca aag   5808
Tyr Gly Asp Lys Lys Asn Arg Phe Asp Leu Leu Cys Glu Met Ala Lys
                1925                1930                1935

cag cag gtc aac atc tac gac ggt gat gct tat gac ttt gcc cct cgt   5856
Gln Gln Val Asn Ile Tyr Asp Gly Asp Ala Tyr Asp Phe Ala Pro Arg
            1940                1945                1950

gtg gtg cgc gcc aat atg aag gca atg gag gat gca gcg cgt ttt ggt   5904
Val Val Arg Ala Asn Met Lys Ala Met Glu Asp Ala Ala Arg Phe Gly
        1955                1960                1965
```

```
atc cct gat gtg gag att cag tcg att tct gca cag cag tca ttg gcg   5952
Ile Pro Asp Val Glu Ile Gln Ser Ile Ser Ala Gln Gln Ser Leu Ala
    1970                1975                1980

agc ttt gag cga gtc cca caa cgt tct ggt ttc cgt att gag cgt cgt   6000
Ser Phe Glu Arg Val Pro Gln Arg Ser Gly Phe Arg Ile Glu Arg Arg
1985                1990                1995                2000

gtg ccg gca gaa gta ggt aca ggg att gct gca cca gca ccg tta cct   6048
Val Pro Ala Glu Val Gly Thr Gly Ile Ala Ala Pro Ala Pro Leu Pro
                2005                2010                2015

gat gca ggt gta cag ggg aat tat gtt cag cag cag gtg cct gcg acc   6096
Asp Ala Gly Val Gln Gly Asn Tyr Val Gln Gln Gln Val Pro Ala Thr
            2020                2025                2030

ccg cca gtt atg cct gtc aca cct ccg gca cag caa cct gtt tcg cct   6144
Pro Pro Val Met Pro Val Thr Pro Pro Ala Gln Gln Pro Val Ser Pro
        2035                2040                2045

gct cag acg gac ttc cgg ggc gtt ggt cag cca ctc gac cag ggc gga   6192
Ala Gln Thr Asp Phe Arg Gly Val Gly Gln Pro Leu Asp Gln Gly Gly
    2050                2055                2060

aaa atc ggg aat tat gga cat cag gga cct gca atg ggg gcg caa cag   6240
Lys Ile Gly Asn Tyr Gly His Gln Gly Pro Ala Met Gly Ala Gln Gln
2065                2070                2075                2080

cca gtt gtg cct cag cag cag aat att ccg cct gtg cat aat ccg gta   6288
Pro Val Val Pro Gln Gln Gln Asn Ile Pro Pro Val His Asn Pro Val
                2085                2090                2095

cca cag aat tct gtt ccg cct act ccg gtt gtg ccg aag cca ggt aca   6336
Pro Gln Asn Ser Val Pro Pro Thr Pro Val Val Pro Lys Pro Gly Thr
            2100                2105                2110

gga aac ccg ttt act cat ggt ggt gcg aac aat cag ttt atg ggt cga   6384
Gly Asn Pro Phe Thr His Gly Gly Ala Asn Asn Gln Phe Met Gly Arg
        2115                2120                2125

ttt gat aca agc cgt tac aac caa cag gaa cca cca caa cga cag gat   6432
Phe Asp Thr Ser Arg Tyr Asn Gln Gln Glu Pro Pro Gln Arg Gln Asp
    2130                2135                2140

ggc ggg ttt gag ctc taaataatgg cagtagattt cag                    6470
Gly Gly Phe Glu Leu
2145
```

Confidential

<210> 8
<211> 2149
<212> PRT
<213> Corynebacterium glutamicum

<400> 8

```
Trp Gly Gln Lys Asp His Trp Gly Lys Ala Pro Leu Gly Asp His Asp
  1               5                  10                  15

Ala Val Arg Ile Tyr Arg Gln Ala Glu Ala Leu Met Lys Gln Arg Ala
             20                  25                  30
```

```
Ala Asn Asn Lys Gly Leu Asp Leu Asn Asp Glu Ala Thr Tyr Gly Ala
          35                  40                  45

Ile Met Phe Ala Ser Phe Asp Asp Ala Phe Ala Ala Asp Ala Glu Ala
      50                  55                  60

His Gly Cys Val His Arg Pro Gln Phe Ala Lys Val Thr Arg Arg Asn
 65                  70                  75                  80

Ile Leu Asn Ser Pro Gln Tyr Thr Ala Ile Lys Ser Ser Tyr Asp Ala
                 85                  90                  95

Leu Val Gln Gln Asp Leu Val Ala Gln Gln Gln Gln Ala Gln Ala Leu
            100                 105                 110

Gln Gln Ala Ala Tyr Glu Gln Glu Gln Ala Ala Ile Phe Gln Ala Arg
        115                 120                 125

Asp Gln Ala Thr Phe Gln Ala Glu Gln Thr Leu Ala Gln Glu Ser Val
    130                 135                 140

Arg Gln Ser Glu Gly Val Gly Leu Pro Val Ile Asp Pro Met Glu Ser
145                 150                 155                 160

Tyr Phe Arg Glu Tyr Ala Phe Tyr Glu Gly Val Glu Met Phe Gly Thr
                165                 170                 175

Trp Gly Thr His Val Asp Ala Gly Val Ser Gln Phe Ser Thr Ser Asp
            180                 185                 190

Gly Arg Ala Ile Arg Ala Leu Val Asp Glu His Leu Ala Thr Tyr Glu
        195                 200                 205

Pro Val Glu Gln Arg Gly Ser Thr Gln Ala Phe Phe Ala Ser Val Asn
    210                 215                 220

Ala Ala Phe Ala Glu Val Ala Pro His Ala Ala Pro Met Phe Ser Ala
225                 230                 235                 240

Ile Ala Arg Glu Gly Glu Gly Ser Lys Gly Tyr Gln Ala Leu Arg His
                245                 250                 255

Arg Phe Asp Lys Met Val Gly Thr Ala Ile Gly Pro Asn Gly Leu Pro
            260                 265                 270

Glu Gly Pro Asp Leu Gly Gly Arg Arg Leu Pro Ile Ser Pro Tyr Asp
        275                 280                 285

Pro Arg Trp Ser Asp Arg Glu Val Val Arg Val His Gly Thr Lys Leu
    290                 295                 300

Leu Ser Leu Ser Glu Glu Ser Val Gly Met Ile Arg Asp Leu Asp Leu
305                 310                 315                 320

Ala Thr Ile His Leu Gln Asp Asn Asp Val Tyr Glu Gly Thr His Arg
                325                 330                 335

Glu Asp Asp Thr Lys Gly Gly Val Arg Pro Leu Thr Gln Trp Val Asn
            340                 345                 350

Gly Glu Ala Ile Ala Trp Arg Thr Ile Thr Glu Asn Asp Gln Met Arg
```

```
        355                 360                 365

Leu Pro Asn Ile Gly Gln Phe Met Thr Ala Lys Glu Tyr Arg Ala Ala
    370                 375                 380

Ala Ser Trp Leu Arg Ala Gly Leu Ile Asp Thr Ala Asp Val Ala Ser
385                 390                 395                 400

Gln Lys Ile Asp Pro Asn Lys Val Met Ser Asp Glu Gly Ile Ala Arg
                405                 410                 415

Ser Glu Ala Ile Leu Thr Tyr Leu Ser Asp Glu Gly Val Asp Phe Arg
            420                 425                 430

Ile Glu Pro Asp Arg Glu Pro Gly Gln Leu Lys Val Arg Ile Glu Gly
        435                 440                 445

Thr Arg Ile Asp Ile Arg Leu Thr Asp Thr Arg Ala Asn Glu Gln Trp
    450                 455                 460

Val Gly Arg Val Tyr Asp Ser Gly Thr Val Ile Lys Tyr Ser Ala Glu
465                 470                 475                 480

Gln Thr Ala Glu Glu Arg Leu Arg Ala Arg Glu Arg Met Glu Asn Gly
                485                 490                 495

Asp Gly Thr Trp Thr Pro Ala Thr Asp Tyr Glu Pro Ser Pro Thr Glu
            500                 505                 510

Val Val Asp Leu Val Lys Phe Ala Leu Gly Arg Glu Val Glu Arg Gln
        515                 520                 525

Asp Gly Lys Gly Leu Val Gly Val Pro Asn Ala Arg His Pro Arg Ala
    530                 535                 540

Leu Glu Gln Ala Gln Asp Ala Tyr Phe Thr Lys Asn Arg Ser Ala Phe
545                 550                 555                 560

Met Val Arg Glu Gly Leu Ser Ile Val Gln Asp Ala Arg Asp Arg Ser
                565                 570                 575

Ala Gly Pro Gly Lys Trp Phe Asp Asn Glu Ala Lys Ala Ser Glu Trp
            580                 585                 590

Leu Gly Asn Asn Ile Ala Leu Thr Arg Ala Arg Val Ala Glu Glu Leu
        595                 600                 605

Gly Val Glu Glu Leu Ile Ala Leu Ser Ala Gln Tyr Ala Asp Asp Pro
    610                 615                 620

Asp Phe Met Pro Ala Phe Ala Gly Glu Asp Glu Leu Met Ala Ile Lys
625                 630                 635                 640

Gln Asp Tyr Trp Ala Met Leu Arg Gly Glu Glu Thr Asp Leu Leu Asn
                645                 650                 655

Pro Gly Val Asn Arg Asp Asp Tyr Met Ala Ala Ile Arg Asp Gly Asp
            660                 665                 670

His Glu Gln Ile Ala Ala Met Thr Ser Ala Met Asn Ala Val Thr Val
        675                 680                 685
```

```
Glu Asp Arg Val Arg Gln His Ala Ala Leu Val Leu Asp Asp Tyr Val
    690                 695                 700

Gly Thr Val Glu Pro Asp Pro Val Thr Gly Leu Arg Phe Asn Pro Val
705                 710                 715                 720

Thr Val Ala Gln His Met Pro Ser Ala Lys Ser Leu Trp Ser Asn His
                725                 730                 735

Asp Asp Ile Ile Ala Ala Leu Arg Ala Thr Ser Ile Thr Gly Asp Glu
            740                 745                 750

Leu Arg Gly Asp Glu Phe Tyr Asn Asp Val Ile Asn Gln Gln Leu Leu
        755                 760                 765

Lys Phe Asn Pro Glu Thr Ala Gln Lys Met Val Asn Asn Pro Asp Leu
    770                 775                 780

Asp Pro Gln Leu Ala Arg Phe Gly Thr Val Ile Ala Glu Thr Ile Ser
785                 790                 795                 800

Arg Asn Gly Ala Asp Val Val Asp Ile Ala Val Asp Asp Asn Gly Val
                805                 810                 815

Val Arg Trp Thr Ala Gln Arg Arg Val Gly Ala Lys Asp Ser Arg Ala
            820                 825                 830

Val Asp Ser Lys Gly Gln Val Arg Gly Glu Arg Thr Arg His Val Gln
        835                 840                 845

Gly Glu Ile Gly Gln Ile Phe Thr Arg Gly Glu His Gly Glu Ile Val
    850                 855                 860

Thr Lys Phe Asn Gly Gly Glu Asn Tyr Met Phe Ala Pro Gly Tyr Thr
865                 870                 875                 880

Ala Ser Val Val Pro Gln Lys Pro Gly Glu Thr Lys Ser Leu Glu Glu
                885                 890                 895

Arg Thr Lys Leu Lys Gly Tyr Glu Gln Val Met Ser Glu Ala Leu Val
            900                 905                 910

Tyr Arg Val Arg Glu Asp Leu Met Phe Thr Glu Arg Ser Arg Val Gly
        915                 920                 925

Ala Thr Thr Ser Ile Asn Ser Ala Tyr Lys Arg Leu Tyr Asp Asn Arg
    930                 935                 940

Phe Pro Val Asp Phe Phe Glu Arg Ser Ala Glu Glu Gly Leu Ser Asp
945                 950                 955                 960

Glu Trp Arg Ala Ala Leu Leu Glu Thr Ala Ser Leu Arg Val Arg Tyr
                965                 970                 975

Asp Asn Ser Ile Arg Asp Gly Ala Asn Val Met Glu Asp Ile Arg Ala
            980                 985                 990

Gln Gln Arg Gly Phe Asp Ala Arg Asn Asp Asn Ser Arg Asp Ala Leu
        995                 1000                1005
```

```
Val Leu Thr Gly Gly Arg Asn Ile Ser Val Leu Asp Val Asp Ala Gly
    1010                1015                1020

Lys Gly Phe Phe Asp Pro Met Met Thr Gly Met Ala Ala Asn Gln Gly
1025                1030                1035                1040

Ser Val Arg Tyr Leu Leu Pro Ser Ala Lys Val Gly Ala Asp Gly Met
                1045                1050                1055

Ile Thr Pro Gly Asp Pro Ala Asp Arg Val Pro Val Ala Ala His Pro
            1060                1065                1070

Glu Ser Trp Ala Met Gly Phe Asp Pro His Asp Arg Gln Asn Met Thr
        1075                1080                1085

Phe Ser Asn Ile Met Gln Ala Ser Ala Val Thr Gly Gly Ala Arg Thr
    1090                1095                1100

Ala Met Ile Gln Leu Gly Gly Trp Asn Phe Glu Asp Gly Ile Ile Val
1105                1110                1115                1120

Ser Ala Asp Phe Ala Asn Thr His Val Ile Arg Asp Thr Glu Asp Glu
                1125                1130                1135

Met Arg Pro Leu Val Ala Gly Asp Lys Leu Ser Asp Phe His Gly Asn
            1140                1145                1150

Lys Gly Val Thr Ala Leu Val Val Asp Pro Ala Met Ser Asp Ala Asp
        1155                1160                1165

Ala Arg Ala Ala Gly Leu Glu Ser Glu Val Ala Phe Phe Arg Asp Asn
    1170                1175                1180

Pro Asp Leu Glu Val Val Met Ser Pro Phe Ser Ala Ile Ser Arg Phe
1185                1190                1195                1200

Asn Gly Gly Thr Ala Arg Glu Leu Met Thr Asn Pro Gln Asp Val Val
                1205                1210                1215

Phe Arg Asn Asn Asp Gly Ser Thr Arg Val Gln Pro Gly Ala Ser Gly
            1220                1225                1230

Asp Leu Asn Phe Ile Val Thr His Met Ala Val Asp Ala Lys Thr Asn
        1235                1240                1245

Val Tyr Asp Glu Glu Ala Val Arg Glu Gly Gln Gly Arg Lys Ala Ser
    1250                1255                1260

Ser Gln Leu Ala Trp Val Leu Gln Ala Gln Glu Cys His Glu Ile Met
1265                1270                1275                1280

Glu His Phe Tyr Gly Asn Asn Val Ser Ala Leu Ala Asn Phe Gln Glu
                1285                1290                1295

Tyr Leu Arg Val Thr Gly Leu Asp Val Thr Pro Tyr Gly Glu Leu Arg
            1300                1305                1310

Glu Gly Phe Ser Glu Ser Asn Glu Gln Arg Asn Ile Ile Glu Met Pro
        1315                1320                1325

Ser Ile Tyr Asp Glu Asn Gly Glu Leu Asn Asn Arg Val Asn Arg Ala
```

```
    1330                1335                1340

Gln Val Arg Glu Ala Phe Val Glu Gln Ile Ser Arg Ala Gly Gly Val
1345                1350                1355                1360

Met Glu Ile Pro Phe Gln Leu Gln Leu Arg Asn Gly Ala Gln Leu Glu
                1365                1370                1375

Glu Ser Pro Asn Asn Pro Asp Met Tyr Gln Leu Pro Leu Leu Ser Pro
            1380                1385                1390

His Leu Arg Ser Asp Glu Asp Leu Ala Asp Gly Ser Thr Ser Arg His
        1395                1400                1405

Glu Tyr Thr Thr Arg Tyr Met Ala Ile Phe Asp Thr Cys Tyr Lys Leu
    1410                1415                1420

Ala Glu Glu Gln Ala Lys Ile Asp Ala Leu Arg Gln Glu Glu Ala Gln
1425                1430                1435                1440

His Gly Thr Leu Pro Arg Ala Ala Glu Lys Arg Leu Ser Glu Ser Gln
                1445                1450                1455

Lys Phe Val Asp Gln Ala Gln Lys Lys Val Gln Ala Ser Phe Asp Gly
            1460                1465                1470

Ile Ala Asn Asp Ile Val Ala Ser Arg Ile Glu Thr Lys Asn Asn Val
        1475                1480                1485

Phe Lys Asp Gly Phe Met Ser Ala Arg Gln Ser His Ser Ala Thr Ala
    1490                1495                1500

Val Trp Thr Gly Asp Pro Arg Leu Ser Val Asp Glu Val Ala Met Asn
1505                1510                1515                1520

Ser Ser Met Ala Arg Glu Leu Gly Val Leu Asp Asn Gly Tyr Ala Met
                1525                1530                1535

Val Trp Arg Asp Pro Val Ile Arg Asp Gly Gly Val Arg Tyr Leu Arg
            1540                1545                1550

Val Val Ile Asn Asp Asp Leu His Gly Val Ala Val Asn Pro Val Ser
        1555                1560                1565

Val Lys Ser Phe Asp Gly Asp Phe Asp Gly Asp Ser Val Gly Leu Val
    1570                1575                1580

Gly Asn Leu Pro Lys Lys Ala His Glu Glu Ala Leu Ser Arg Leu Thr
1585                1590                1595                1600

Val Glu Ala Asn Met Leu Asp Leu Gly Asp Gly Lys Arg Met Glu Asp
                1605                1610                1615

Gly Thr Met Phe Tyr Gly Leu Thr Leu His Asp Ser Leu Asp Val Gln
            1620                1625                1630

Val Ala Gln His His Asp Pro Ala Met Ala Glu Asn Met Lys Val Ile
        1635                1640                1645

Val Ser Glu Leu Asn Arg Tyr Gln Arg Glu Tyr Glu Ala Gly Glu Ile
    1650                1655                1660
```

Ser Arg Glu Glu Leu Leu Glu Val Asn Arg Ala His Met Asp Asp Leu
1665 1670 1675 1680

Asn Glu His Tyr Ala Gln Ala Phe Ala Asn Arg Asp Gly Leu Val Thr
1685 1690 1695

Leu Arg Phe Asp Gly Met Glu Asn His Met Ala Ser Val Ala Gln Cys
1700 1705 1710

Phe Glu Thr Gly Ala Lys Gly Ser Pro Gly Lys Leu Lys Glu Tyr Ala
1715 1720 1725

Thr Tyr Ile Gly Ala Asp Pro Ala Gln Gly Phe Lys Asp Val Gly Gln
1730 1735 1740

Pro Thr Pro Glu Ala Leu Arg Ser His Tyr Glu Gly Ser Gln Lys Ala
1745 1750 1755 1760

Thr Ala Ile Lys Val Leu Phe Thr Gly Val Ala Gly Lys Lys Glu Gln
1765 1770 1775

Glu Met Val Ala Leu Cys Arg Asn Leu Gly Leu Thr Lys Glu Ala Met
1780 1785 1790

Ala Ala Ser Ala Pro Ala Gln Gln Ser Ile Leu Gln Ala Lys His Asp
1795 1800 1805

Pro Ile Asp Ala Leu Tyr Arg Ala Glu Thr Leu Met Gly Pro Val Gly
1810 1815 1820

Asp Leu Tyr Gln Gly Arg Lys Met Arg Arg Gly Glu Asn Glu Gln Gly
1825 1830 1835 1840

Arg Tyr Glu Trp Glu Val Val Arg Asp Glu Asn His Gln Pro Ile Gln
1845 1850 1855

Ala Thr Lys Asp Glu Trp Val Gln Gln Tyr Met Glu Met Tyr Ala Asp
1860 1865 1870

Asp Lys Gly Met Gly Val Ser Val Gly Val Asp Gln Val Glu Lys Ile
1875 1880 1885

Ala Glu Glu Phe Ser Asp Glu Gln Gly Tyr Met Arg Val Leu Ser His
1890 1895 1900

Asp Glu Leu Pro Thr Glu Ile Lys Pro Leu Ala Leu Asp Gln Leu Ala
1905 1910 1915 1920

Tyr Gly Asp Lys Lys Asn Arg Phe Asp Leu Leu Cys Glu Met Ala Lys
1925 1930 1935

Gln Gln Val Asn Ile Tyr Asp Gly Asp Ala Tyr Asp Phe Ala Pro Arg
1940 1945 1950

Val Val Arg Ala Asn Met Lys Ala Met Glu Asp Ala Ala Arg Phe Gly
1955 1960 1965

Ile Pro Asp Val Glu Ile Gln Ser Ile Ser Ala Gln Gln Ser Leu Ala
1970 1975 1980

```
Ser Phe Glu Arg Val Pro Gln Arg Ser Gly Phe Arg Ile Glu Arg Arg
1985                1990                1995                2000

Val Pro Ala Glu Val Gly Thr Gly Ile Ala Ala Pro Ala Pro Leu Pro
                2005                2010                2015

Asp Ala Gly Val Gln Gly Asn Tyr Val Gln Gln Gln Val Pro Ala Thr
            2020                2025                2030

Pro Pro Val Met Pro Val Thr Pro Pro Ala Gln Gln Pro Val Ser Pro
        2035                2040                2045

Ala Gln Thr Asp Phe Arg Gly Val Gly Gln Pro Leu Asp Gln Gly Gly
    2050                2055                2060

Lys Ile Gly Asn Tyr Gly His Gln Gly Pro Ala Met Gly Ala Gln Gln
2065                2070                2075                2080

Pro Val Val Pro Gln Gln Gln Asn Ile Pro Pro Val His Asn Pro Val
                2085                2090                2095

Pro Gln Asn Ser Val Pro Pro Thr Pro Val Val Pro Lys Pro Gly Thr
            2100                2105                2110

Gly Asn Pro Phe Thr His Gly Gly Ala Asn Asn Gln Phe Met Gly Arg
        2115                2120                2125

Phe Asp Thr Ser Arg Tyr Asn Gln Gln Glu Pro Pro Gln Arg Gln Asp
    2130                2135                2140

Gly Gly Phe Glu Leu
2145
```

<210> 9
<211> 1307
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1284)
<223> FRXA01590

<400> 9

```
ggc aag ttg aag gaa tat gcc acc tat atc ggc gct gat ccg gcg cag   48
Gly Lys Leu Lys Glu Tyr Ala Thr Tyr Ile Gly Ala Asp Pro Ala Gln
  1               5                  10                  15

ggt ttt aaa gac gta ggt caa cca acg cca gaa gcg ctg cgt agc cac   96
Gly Phe Lys Asp Val Gly Gln Pro Thr Pro Glu Ala Leu Arg Ser His
             20                  25                  30

tat gag ggt tcg cag aag gcg act gca att aag gtg ctc ttt acc ggt   144
Tyr Glu Gly Ser Gln Lys Ala Thr Ala Ile Lys Val Leu Phe Thr Gly
         35                  40                  45

gtg gct ggt aaa aaa gag cag gaa atg gtg gca ttg tgc cgc aat ctt   192
Val Ala Gly Lys Lys Glu Gln Glu Met Val Ala Leu Cys Arg Asn Leu
     50                  55                  60
```

```
ggt ctg acc aag gaa gct atg gct gca tca gca ccg gca cag cag tcg   240
Gly Leu Thr Lys Glu Ala Met Ala Ala Ser Ala Pro Ala Gln Gln Ser
 65                  70                  75                  80

att ctg cag gcg aag cac gac ccg att gac gcg ctc tat cgt gca gaa   288
Ile Leu Gln Ala Lys His Asp Pro Ile Asp Ala Leu Tyr Arg Ala Glu
                85                  90                  95

act ctt atg gga cca gta ggt gat ctc tac caa ggt cgc aag atg cgt   336
Thr Leu Met Gly Pro Val Gly Asp Leu Tyr Gln Gly Arg Lys Met Arg
            100                 105                 110

cgt ggt gag aat gag caa ggt cgc tat gag tgg gaa gtc gtt agg gac   384
Arg Gly Glu Asn Glu Gln Gly Arg Tyr Glu Trp Glu Val Val Arg Asp
        115                 120                 125

gag aac cac cag cct atc cag gcc acc aag gat gaa tgg gta cag cag   432
Glu Asn His Gln Pro Ile Gln Ala Thr Lys Asp Glu Trp Val Gln Gln
    130                 135                 140

tac atg gag atg tac gcc gat gac aag ggt atg ggt gtc tcg gtt ggc   480
Tyr Met Glu Met Tyr Ala Asp Asp Lys Gly Met Gly Val Ser Val Gly
145                 150                 155                 160

gtt gac cag gtg gag aag atc gcg gaa gaa ttc tct gat gag cag ggt   528
Val Asp Gln Val Glu Lys Ile Ala Glu Glu Phe Ser Asp Glu Gln Gly
                165                 170                 175

tat atg cgt gtg ctt agc cat gat gag cta ccc act gag att aag cca   576
Tyr Met Arg Val Leu Ser His Asp Glu Leu Pro Thr Glu Ile Lys Pro
            180                 185                 190

cta gca ctt gat cag ctt gcc tat ggc gat aag aag aac cgc ttt gat   624
Leu Ala Leu Asp Gln Leu Ala Tyr Gly Asp Lys Lys Asn Arg Phe Asp
        195                 200                 205

ttg ttg tgc gag atg gca aag cag cag gtc aac atc tac gac ggt gat   672
Leu Leu Cys Glu Met Ala Lys Gln Gln Val Asn Ile Tyr Asp Gly Asp
    210                 215                 220

gct tat gac ttt gcc cct cgt gtg gtg cgc gcc aat atg aag gca atg   720
Ala Tyr Asp Phe Ala Pro Arg Val Val Arg Ala Asn Met Lys Ala Met
225                 230                 235                 240

gag gat gca gcg cgt ttt ggt atc cct gat gtg gag att cag tcg att   768
Glu Asp Ala Ala Arg Phe Gly Ile Pro Asp Val Glu Ile Gln Ser Ile
                245                 250                 255

tct gca cag cag tca ttg gcg agc ttt gag cga gtc cca caa cgt tct   816
Ser Ala Gln Gln Ser Leu Ala Ser Phe Glu Arg Val Pro Gln Arg Ser
            260                 265                 270

ggt ttc cgt att gag cgt cgt gtg ccg gca gaa gta ggt aca ggg att   864
Gly Phe Arg Ile Glu Arg Arg Val Pro Ala Glu Val Gly Thr Gly Ile
        275                 280                 285

gct gca cca gca ccg tta cct gat gca ggt gta cag ggg aat tat gtt   912
Ala Ala Pro Ala Pro Leu Pro Asp Ala Gly Val Gln Gly Asn Tyr Val
    290                 295                 300

cag cag cag gtg cct gcg acc ccg cca gtt atg cct gtc aca cct ccg   960
```

```
Gln Gln Gln Val Pro Ala Thr Pro Pro Val Met Pro Val Thr Pro Pro
305                 310                 315                 320

gca cag caa cct gtt tcg cct gct cag acg gac ttc cgg ggc gtt ggt   1008
Ala Gln Gln Pro Val Ser Pro Ala Gln Thr Asp Phe Arg Gly Val Gly
                325                 330                 335

cag cca ctc gac cag ggc gga aaa atc ggg aat tat gga cat cag gga   1056
Gln Pro Leu Asp Gln Gly Gly Lys Ile Gly Asn Tyr Gly His Gln Gly
            340                 345                 350

cct gca atg ggg gcg caa cag cca gtt gtg cct cag cag cag aat att   1104
Pro Ala Met Gly Ala Gln Gln Pro Val Val Pro Gln Gln Gln Asn Ile
        355                 360                 365

ccg cct gtg cat aat ccg gta cca cag aat tct gtt ccg cct act ccg   1152
Pro Pro Val His Asn Pro Val Pro Gln Asn Ser Val Pro Pro Thr Pro
    370                 375                 380

gtt gtg ccg aag cca ggt aca gga aac ccg ttt act cat ggt ggt gcg   1200
Val Val Pro Lys Pro Gly Thr Gly Asn Pro Phe Thr His Gly Gly Ala
385                 390                 395                 400

aac aat cag ttt atg ggt cga ttt gat aca agc cgt tac aac caa cag   1248
Asn Asn Gln Phe Met Gly Arg Phe Asp Thr Ser Arg Tyr Asn Gln Gln
                405                 410                 415

gaa cca cca caa cga cag gat ggc ggg ttt gag ctc taaataatgg        1294
Glu Pro Pro Gln Arg Gln Asp Gly Gly Phe Glu Leu
            420                 425

cagtagattt cag                                                   1307
```

<210> 10
<211> 428
<212> PRT
<213> Corynebacterium glutamicum

<400> 10

```
Gly Lys Leu Lys Glu Tyr Ala Thr Tyr Ile Gly Ala Asp Pro Ala Gln
  1               5                  10                  15

Gly Phe Lys Asp Val Gly Gln Pro Thr Pro Glu Ala Leu Arg Ser His
             20                  25                  30

Tyr Glu Gly Ser Gln Lys Ala Thr Ala Ile Lys Val Leu Phe Thr Gly
         35                  40                  45

Val Ala Gly Lys Lys Glu Gln Glu Met Val Ala Leu Cys Arg Asn Leu
     50                  55                  60

Gly Leu Thr Lys Glu Ala Met Ala Ala Ser Ala Pro Ala Gln Gln Ser
 65                  70                  75                  80

Ile Leu Gln Ala Lys His Asp Pro Ile Asp Ala Leu Tyr Arg Ala Glu
                 85                  90                  95

Thr Leu Met Gly Pro Val Gly Asp Leu Tyr Gln Gly Arg Lys Met Arg
            100                 105                 110
```

```
Arg Gly Glu Asn Glu Gln Gly Arg Tyr Glu Trp Glu Val Val Arg Asp
        115                 120                 125

Glu Asn His Gln Pro Ile Gln Ala Thr Lys Asp Glu Trp Val Gln Gln
    130                 135                 140

Tyr Met Glu Met Tyr Ala Asp Asp Lys Gly Met Gly Val Ser Val Gly
145                 150                 155                 160

Val Asp Gln Val Glu Lys Ile Ala Glu Glu Phe Ser Asp Glu Gln Gly
                165                 170                 175

Tyr Met Arg Val Leu Ser His Asp Glu Leu Pro Thr Glu Ile Lys Pro
            180                 185                 190

Leu Ala Leu Asp Gln Leu Ala Tyr Gly Asp Lys Lys Asn Arg Phe Asp
        195                 200                 205

Leu Leu Cys Glu Met Ala Lys Gln Gln Val Asn Ile Tyr Asp Gly Asp
    210                 215                 220

Ala Tyr Asp Phe Ala Pro Arg Val Val Arg Ala Asn Met Lys Ala Met
225                 230                 235                 240

Glu Asp Ala Ala Arg Phe Gly Ile Pro Asp Val Glu Ile Gln Ser Ile
                245                 250                 255

Ser Ala Gln Gln Ser Leu Ala Ser Phe Glu Arg Val Pro Gln Arg Ser
            260                 265                 270

Gly Phe Arg Ile Glu Arg Arg Val Pro Ala Glu Val Gly Thr Gly Ile
        275                 280                 285

Ala Ala Pro Ala Pro Leu Pro Asp Ala Gly Val Gln Gly Asn Tyr Val
    290                 295                 300

Gln Gln Gln Val Pro Ala Thr Pro Pro Val Met Pro Val Thr Pro Pro
305                 310                 315                 320

Ala Gln Gln Pro Val Ser Pro Ala Gln Thr Asp Phe Arg Gly Val Gly
                325                 330                 335

Gln Pro Leu Asp Gln Gly Gly Lys Ile Gly Asn Tyr Gly His Gln Gly
            340                 345                 350

Pro Ala Met Gly Ala Gln Gln Pro Val Val Pro Gln Gln Gln Asn Ile
        355                 360                 365

Pro Pro Val His Asn Pro Val Pro Gln Asn Ser Val Pro Pro Thr Pro
    370                 375                 380

Val Val Pro Lys Pro Gly Thr Gly Asn Pro Phe Thr His Gly Gly Ala
385                 390                 395                 400

Asn Asn Gln Phe Met Gly Arg Phe Asp Thr Ser Arg Tyr Asn Gln Gln
                405                 410                 415

Glu Pro Pro Gln Arg Gln Asp Gly Gly Phe Glu Leu
            420                 425
```

<210> 11
<211> 5061
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(5061)
<223> FRXA01542

<400> 11

```
tgg ggt caa aaa gat cac tgg ggc aaa gct cca ctg ggt gat cac gat   48
Trp Gly Gln Lys Asp His Trp Gly Lys Ala Pro Leu Gly Asp His Asp
  1               5                  10                  15

gct gtg cgt atc tat agg caa gca gaa gcc ttg atg aaa cag cgc gca   96
Ala Val Arg Ile Tyr Arg Gln Ala Glu Ala Leu Met Lys Gln Arg Ala
             20                  25                  30

gca aac aat aag ggc tta gac ctc aat gat gaa gcg acc tat ggc gcc   144
Ala Asn Asn Lys Gly Leu Asp Leu Asn Asp Glu Ala Thr Tyr Gly Ala
         35                  40                  45

atc atg ttt gcg tct ttc gat gat gcc ttc gcc gct gat gcc gaa gct   192
Ile Met Phe Ala Ser Phe Asp Asp Ala Phe Ala Ala Asp Ala Glu Ala
     50                  55                  60

cat ggc tgt gta cac cga cca cag ttc gcg aag gta act agg cga aat   240
His Gly Cys Val His Arg Pro Gln Phe Ala Lys Val Thr Arg Arg Asn
 65                  70                  75                  80

att ctt aat tca ccg caa tac acg gcg att aag tca tct tat gac gcg   288
Ile Leu Asn Ser Pro Gln Tyr Thr Ala Ile Lys Ser Ser Tyr Asp Ala
                 85                  90                  95

ctg gtg cag cag gat ctc gtg gcc caa cag cag cag gca caa gcg cta   336
Leu Val Gln Gln Asp Leu Val Ala Gln Gln Gln Gln Ala Gln Ala Leu
            100                 105                 110

cag caa gct gct tat gag caa gag cag gca gct att ttc cag gca cgt   384
Gln Gln Ala Ala Tyr Glu Gln Glu Gln Ala Ala Ile Phe Gln Ala Arg
        115                 120                 125

gat caa gca aca ttc cag gct gaa caa acg ctc gcg caa gag tcc gtt   432
Asp Gln Ala Thr Phe Gln Ala Glu Gln Thr Leu Ala Gln Glu Ser Val
    130                 135                 140

cgc caa tca gag ggt gtg ggt tta cct gtc att gat ccg atg gag agc   480
Arg Gln Ser Glu Gly Val Gly Leu Pro Val Ile Asp Pro Met Glu Ser
145                 150                 155                 160

tat ttc cgg gag tac gcc ttc tat gaa ggt gtc gag atg ttt ggt acc   528
Tyr Phe Arg Glu Tyr Ala Phe Tyr Glu Gly Val Glu Met Phe Gly Thr
                165                 170                 175

tgg ggt acg cac gtt gat gct ggt gtg tcg cag ttt agc acc tct gat   576
Trp Gly Thr His Val Asp Ala Gly Val Ser Gln Phe Ser Thr Ser Asp
            180                 185                 190

ggc cgt gcg atc cga gcg ctt gtt gat gag cat ctc gca acc tat gaa   624
Gly Arg Ala Ile Arg Ala Leu Val Asp Glu His Leu Ala Thr Tyr Glu
```

```
        195                 200                 205

cca gta gag cag cgg ggg agt act cag gca ttc ttc gcc tct gtc aat   672
Pro Val Glu Gln Arg Gly Ser Thr Gln Ala Phe Phe Ala Ser Val Asn
    210                 215                 220

gct gcc ttt gct gag gtg gca cct cac gca gca ccc atg ttt agt gcg   720
Ala Ala Phe Ala Glu Val Ala Pro His Ala Ala Pro Met Phe Ser Ala
225                 230                 235                 240

att gct cgc gag ggt gag ggt tca aag ggg tac cag gcg ctg cgt cac   768
Ile Ala Arg Glu Gly Glu Gly Ser Lys Gly Tyr Gln Ala Leu Arg His
                245                 250                 255

cgt ttc gac aag atg gtc ggc act gca att gga cct aat ggt ttg cct   816
Arg Phe Asp Lys Met Val Gly Thr Ala Ile Gly Pro Asn Gly Leu Pro
            260                 265                 270

gag gga cct gat ctg ggt ggt cgt cgt tta cct att tcg cct tat gat   864
Glu Gly Pro Asp Leu Gly Gly Arg Arg Leu Pro Ile Ser Pro Tyr Asp
        275                 280                 285

cca cgc tgg tca gac cgc gaa gta gtc cgt gtg cac ggt acc aag ctg   912
Pro Arg Trp Ser Asp Arg Glu Val Val Arg Val His Gly Thr Lys Leu
    290                 295                 300

cta tca ctg tcc gaa gag agt gtt ggc atg atc agg gac ctt gat cta   960
Leu Ser Leu Ser Glu Glu Ser Val Gly Met Ile Arg Asp Leu Asp Leu
305                 310                 315                 320

gca acg atc cac cta caa gat aat gat gtt tac gag ggc act cat cga  1008
Ala Thr Ile His Leu Gln Asp Asn Asp Val Tyr Glu Gly Thr His Arg
                325                 330                 335

gaa gac gac act aaa ggc ggt gtg cga ccg ttg act caa tgg gtc aat  1056
Glu Asp Asp Thr Lys Gly Gly Val Arg Pro Leu Thr Gln Trp Val Asn
            340                 345                 350

ggt gaa gct att gcc tgg cgc act atc acc gag aat gac cag atg cga  1104
Gly Glu Ala Ile Ala Trp Arg Thr Ile Thr Glu Asn Asp Gln Met Arg
        355                 360                 365

ctg ccc aat att ggt cag ttt atg acg gct aaa gaa tac cgt gcc gca  1152
Leu Pro Asn Ile Gly Gln Phe Met Thr Ala Lys Glu Tyr Arg Ala Ala
    370                 375                 380

gcg tca tgg ctg cgt gct gga ctc att gat acc gca gat gtt gcg agt  1200
Ala Ser Trp Leu Arg Ala Gly Leu Ile Asp Thr Ala Asp Val Ala Ser
385                 390                 395                 400

cag aaa att gac ccc aac aag gtc atg tct gat gag ggt atc gcg cgc  1248
Gln Lys Ile Asp Pro Asn Lys Val Met Ser Asp Glu Gly Ile Ala Arg
                405                 410                 415

tcg gaa gct att ttg acg tat ctg tcg gat gag ggt gtg gat ttt agg  1296
Ser Glu Ala Ile Leu Thr Tyr Leu Ser Asp Glu Gly Val Asp Phe Arg
            420                 425                 430

atc gag cca gat cgt gag ccg gga cag ctt aaa gtg cgt att gag ggc  1344
Ile Glu Pro Asp Arg Glu Pro Gly Gln Leu Lys Val Arg Ile Glu Gly
        435                 440                 445
```

```
acc cgt att gat att cgt ctc act gat act cgc gcc aat gaa cag tgg   1392
Thr Arg Ile Asp Ile Arg Leu Thr Asp Thr Arg Ala Asn Glu Gln Trp
    450                 455                 460

gtg ggt cgt gtc tat gat tct ggc act gtg att aag tat tcc gcc gaa   1440
Val Gly Arg Val Tyr Asp Ser Gly Thr Val Ile Lys Tyr Ser Ala Glu
465                 470                 475                 480

caa aca gcg gaa gaa cgt cta cga gct cgt gag cgc atg gag aac ggt   1488
Gln Thr Ala Glu Glu Arg Leu Arg Ala Arg Glu Arg Met Glu Asn Gly
                485                 490                 495

gat gga acg tgg aca ccg gct act gat tat gaa cca agc cca act gaa   1536
Asp Gly Thr Trp Thr Pro Ala Thr Asp Tyr Glu Pro Ser Pro Thr Glu
            500                 505                 510

gtt gtc gat ctc gtg aaa ttt gct ctc ggt cga gag gtt gag cga cag   1584
Val Val Asp Leu Val Lys Phe Ala Leu Gly Arg Glu Val Glu Arg Gln
        515                 520                 525

gat ggc aaa ggt ctt gtt ggt gtg cct aat gct cga cac cca cgt gct   1632
Asp Gly Lys Gly Leu Val Gly Val Pro Asn Ala Arg His Pro Arg Ala
    530                 535                 540

tta gag cag gca cag gat gca tat ttc act aag aat cgt tcc gca ttc   1680
Leu Glu Gln Ala Gln Asp Ala Tyr Phe Thr Lys Asn Arg Ser Ala Phe
545                 550                 555                 560

atg gtg cgt gaa ggg ctc tcg atc gtt cag gat gca cgt gat cga agt   1728
Met Val Arg Glu Gly Leu Ser Ile Val Gln Asp Ala Arg Asp Arg Ser
                565                 570                 575

gct ggt cct gga aag tgg ttt gat aat gaa gcg aaa gca tcg gag tgg   1776
Ala Gly Pro Gly Lys Trp Phe Asp Asn Glu Ala Lys Ala Ser Glu Trp
            580                 585                 590

ctt ggt aac aat atc gcc ctt act cgt gcg cgt gtg gcc gaa gag ctc   1824
Leu Gly Asn Asn Ile Ala Leu Thr Arg Ala Arg Val Ala Glu Glu Leu
        595                 600                 605

ggc gtt gaa gaa ctg att gcg ctt tct gca cag tac gcc gat gat cct   1872
Gly Val Glu Glu Leu Ile Ala Leu Ser Ala Gln Tyr Ala Asp Asp Pro
    610                 615                 620

gac ttc atg ccg gct ttt gct ggt gag gat gag ctc atg gcg ata aag   1920
Asp Phe Met Pro Ala Phe Ala Gly Glu Asp Glu Leu Met Ala Ile Lys
625                 630                 635                 640

cag gac tat tgg gcg atg ctg cga ggt gag gaa acc gat ctg ctt aac   1968
Gln Asp Tyr Trp Ala Met Leu Arg Gly Glu Glu Thr Asp Leu Leu Asn
                645                 650                 655

cct ggg gtt aac cgc gat gat tat atg gct gct atc cgc gat ggt gat   2016
Pro Gly Val Asn Arg Asp Asp Tyr Met Ala Ala Ile Arg Asp Gly Asp
            660                 665                 670

cat gag cag att gct gcg atg acc tca gca atg aat gct gtg acc gtg   2064
His Glu Gln Ile Ala Ala Met Thr Ser Ala Met Asn Ala Val Thr Val
        675                 680                 685
```

```
gag gat cgt gtg cgt cag cac gcg gcc ctt gtt ctt gat gat tat gtc   2112
Glu Asp Arg Val Arg Gln His Ala Ala Leu Val Leu Asp Asp Tyr Val
    690                 695                 700

ggc acg gtg gag cct gat cct gtt acc ggc ttg cgt ttt aat ccg gtg   2160
Gly Thr Val Glu Pro Asp Pro Val Thr Gly Leu Arg Phe Asn Pro Val
705                 710                 715                 720

aca gtt gct cag cac atg ccg agt gct aaa tcc ctg tgg tca aac cat   2208
Thr Val Ala Gln His Met Pro Ser Ala Lys Ser Leu Trp Ser Asn His
                725                 730                 735

gac gat att att gcc gcg ttg cga gcg act tcg att act ggc gat gaa   2256
Asp Asp Ile Ile Ala Ala Leu Arg Ala Thr Ser Ile Thr Gly Asp Glu
            740                 745                 750

ctg cgc ggt gac gaa ttc tat aac gat gtt att aat caa cag ttg ctc   2304
Leu Arg Gly Asp Glu Phe Tyr Asn Asp Val Ile Asn Gln Gln Leu Leu
        755                 760                 765

aaa ttt aat cct gag acc gcg cag aaa atg gtt aat aac cct gat ctt   2352
Lys Phe Asn Pro Glu Thr Ala Gln Lys Met Val Asn Asn Pro Asp Leu
    770                 775                 780

gac ccg cag ttg gct cga ttt ggc act gtc att gcc gag act att tcc   2400
Asp Pro Gln Leu Ala Arg Phe Gly Thr Val Ile Ala Glu Thr Ile Ser
785                 790                 795                 800

cgc aat ggt gct gat gtg gtc gat att gct gtt gac gat aac ggt gtg   2448
Arg Asn Gly Ala Asp Val Val Asp Ile Ala Val Asp Asp Asn Gly Val
                805                 810                 815

gtg cgg tgg acc gca cag cga cgt gtt ggt gcg aag gat agt cgt gca   2496
Val Arg Trp Thr Ala Gln Arg Arg Val Gly Ala Lys Asp Ser Arg Ala
            820                 825                 830

gta gat agt aag ggg cag gtt cgc ggt gaa cgc acc cgt cat gtg cag   2544
Val Asp Ser Lys Gly Gln Val Arg Gly Glu Arg Thr Arg His Val Gln
        835                 840                 845

ggt gag ata ggt cag att ttt act cgc ggt gag cat ggt gaa att gtc   2592
Gly Glu Ile Gly Gln Ile Phe Thr Arg Gly Glu His Gly Glu Ile Val
    850                 855                 860

acc aaa ttt aat ggt ggc gag aac tat atg ttt gcc cct ggc tac acc   2640
Thr Lys Phe Asn Gly Gly Glu Asn Tyr Met Phe Ala Pro Gly Tyr Thr
865                 870                 875                 880

gcg tct gtg gta cca caa aag cct ggt gag aca aag agt tta gaa gag   2688
Ala Ser Val Val Pro Gln Lys Pro Gly Glu Thr Lys Ser Leu Glu Glu
                885                 890                 895

cgt acc aag ctc aaa ggc tat gag cag gtg atg tca gag gcg ttg gtg   2736
Arg Thr Lys Leu Lys Gly Tyr Glu Gln Val Met Ser Glu Ala Leu Val
            900                 905                 910

tac cgt gtg cga gaa gat ttg atg ttc act gag cga tcc cga gtg ggt   2784
Tyr Arg Val Arg Glu Asp Leu Met Phe Thr Glu Arg Ser Arg Val Gly
        915                 920                 925

gct aca acc agc atc aac agt gca tat aag cga ctg tat gac aat cgc   2832
```

```
Ala Thr Thr Ser Ile Asn Ser Ala Tyr Lys Arg Leu Tyr Asp Asn Arg
    930                 935                 940

ttc cct gtg gac ttc ttc gag cgc agc gcc gaa gaa ggt ttg agc gat   2880
Phe Pro Val Asp Phe Phe Glu Arg Ser Ala Glu Glu Gly Leu Ser Asp
945                 950                 955                 960

gag tgg cgt gct gcg ttg ctt gag act gcg agt ttg cgt gtg cgc tac   2928
Glu Trp Arg Ala Ala Leu Leu Glu Thr Ala Ser Leu Arg Val Arg Tyr
                965                 970                 975

gac aac tct att cgt gat ggt gcg aat gtg atg gag gat att cga gca   2976
Asp Asn Ser Ile Arg Asp Gly Ala Asn Val Met Glu Asp Ile Arg Ala
            980                 985                 990

cag cag cgt ggt ttt gat gcg cgt aat gat aac tcc cgt gat gcg ctg   3024
Gln Gln Arg Gly Phe Asp Ala Arg Asn Asp Asn Ser Arg Asp Ala Leu
        995                 1000                1005

gtg ctt acc ggt ggg cgt aac att tct gta ctt gat gtt gat gcg ggt   3072
Val Leu Thr Gly Gly Arg Asn Ile Ser Val Leu Asp Val Asp Ala Gly
    1010                1015                1020

aaa ggt ttc ttt gat ccc atg atg act ggt atg gcg gcg aac cag ggt   3120
Lys Gly Phe Phe Asp Pro Met Met Thr Gly Met Ala Ala Asn Gln Gly
1025                1030                1035                1040

tct gtt cgc tat ttg ttg cct tct gcg aag gtg ggc gct gat ggc atg   3168
Ser Val Arg Tyr Leu Leu Pro Ser Ala Lys Val Gly Ala Asp Gly Met
                1045                1050                1055

att acc cct ggt gat ccg gct gat cga gta cct gtt gca gcg cat cca   3216
Ile Thr Pro Gly Asp Pro Ala Asp Arg Val Pro Val Ala Ala His Pro
            1060                1065                1070

gaa tca tgg gcg atg ggc ttt gac cca cat gac cgt cag aac atg act   3264
Glu Ser Trp Ala Met Gly Phe Asp Pro His Asp Arg Gln Asn Met Thr
        1075                1080                1085

ttc tcg aac atc atg cag gct agc gct gtg act ggt ggt gca cgc act   3312
Phe Ser Asn Ile Met Gln Ala Ser Ala Val Thr Gly Gly Ala Arg Thr
    1090                1095                1100

gcg atg ata cag ctg ggc ggt tgg aac ttt gaa gat ggc att att gtc   3360
Ala Met Ile Gln Leu Gly Gly Trp Asn Phe Glu Asp Gly Ile Ile Val
1105                1110                1115                1120

tct gcc gat ttt gcg aat acc cat gtt att cgc gat acg gaa gat gag   3408
Ser Ala Asp Phe Ala Asn Thr His Val Ile Arg Asp Thr Glu Asp Glu
                1125                1130                1135

atg cgc ccc ttg gtt gcc ggc gat aag ctg tct gat ttt cac ggt aat   3456
Met Arg Pro Leu Val Ala Gly Asp Lys Leu Ser Asp Phe His Gly Asn
            1140                1145                1150

aag ggt gtg acc gct ctt gtt gtt gat cca gcg atg agt gat gct gat   3504
Lys Gly Val Thr Ala Leu Val Val Asp Pro Ala Met Ser Asp Ala Asp
        1155                1160                1165

gca cgt gca gca ggg ctg gaa tca gag gtg gcg ttt ttc cga gac aac   3552
Ala Arg Ala Ala Gly Leu Glu Ser Glu Val Ala Phe Phe Arg Asp Asn
```

```
    1170                1175                1180

cct gat cta gag gtt gtc atg agt ccg ttt tct gcc att tct cgt ttt   3600
Pro Asp Leu Glu Val Val Met Ser Pro Phe Ser Ala Ile Ser Arg Phe
1185                1190                1195                1200

aat ggt ggc acg gca cgt gag ctc atg acc aac ccg cag gat gtg gtg   3648
Asn Gly Gly Thr Ala Arg Glu Leu Met Thr Asn Pro Gln Asp Val Val
                1205                1210                1215

ttc agg aat aat gat ggt tct act cgt gtt caa cca ggt gcc tct ggt   3696
Phe Arg Asn Asn Asp Gly Ser Thr Arg Val Gln Pro Gly Ala Ser Gly
            1220                1225                1230

gat ctc aac ttc atc gtc acg cat atg gct gtt gat gcg aaa acc aat   3744
Asp Leu Asn Phe Ile Val Thr His Met Ala Val Asp Ala Lys Thr Asn
        1235                1240                1245

gtc tat gat gaa gaa gct gtt cgt gag ggc caa gga cgt aaa gcg tct   3792
Val Tyr Asp Glu Glu Ala Val Arg Glu Gly Gln Gly Arg Lys Ala Ser
    1250                1255                1260

tct cag ctg gcg tgg gtg ctc caa gcc cag gaa tgt cat gag att atg   3840
Ser Gln Leu Ala Trp Val Leu Gln Ala Gln Glu Cys His Glu Ile Met
1265                1270                1275                1280

gag cac ttt tat ggc aac aac gtc tct gca ttg gct aac ttc cag gaa   3888
Glu His Phe Tyr Gly Asn Asn Val Ser Ala Leu Ala Asn Phe Gln Glu
                1285                1290                1295

tat ctt cgc gtc acg ggg ctt gat gtc acc ccg tat ggt gag ttg cgc   3936
Tyr Leu Arg Val Thr Gly Leu Asp Val Thr Pro Tyr Gly Glu Leu Arg
            1300                1305                1310

gag ggg ttc agc gag tcc aat gag cag cgc aat atc atc gag atg cca   3984
Glu Gly Phe Ser Glu Ser Asn Glu Gln Arg Asn Ile Ile Glu Met Pro
        1315                1320                1325

agc att tac gat gag aac ggt gag ctg aat aat cgt gtt aat cgt gca   4032
Ser Ile Tyr Asp Glu Asn Gly Glu Leu Asn Asn Arg Val Asn Arg Ala
    1330                1335                1340

cag gtg cgc gaa gct ttt gtt gag cag atc agt cgc gct ggt ggt gtt   4080
Gln Val Arg Glu Ala Phe Val Glu Gln Ile Ser Arg Ala Gly Gly Val
1345                1350                1355                1360

atg gag att cct ttc cag tta cag ttg cgc aat ggt gca cag cta gaa   4128
Met Glu Ile Pro Phe Gln Leu Gln Leu Arg Asn Gly Ala Gln Leu Glu
                1365                1370                1375

gag tca cct aat aat cca gac atg tat cag ttg cca cta ctg agc ccg   4176
Glu Ser Pro Asn Asn Pro Asp Met Tyr Gln Leu Pro Leu Leu Ser Pro
            1380                1385                1390

cat ttg cgc agt gat gag gat tta gcg gac ggt agt acc tct cga cat   4224
His Leu Arg Ser Asp Glu Asp Leu Ala Asp Gly Ser Thr Ser Arg His
        1395                1400                1405

gag tac acc acg cgg tat atg gct att ttt gat acg tgc tac aag ctg   4272
Glu Tyr Thr Thr Arg Tyr Met Ala Ile Phe Asp Thr Cys Tyr Lys Leu
    1410                1415                1420
```

```
gca gaa gag caa gcc aag att gac gca ttg cgc cag gag gaa gcg cag   4320
Ala Glu Glu Gln Ala Lys Ile Asp Ala Leu Arg Gln Glu Glu Ala Gln
1425                1430                1435                1440

cac ggc acg ttg cct cgt gct gcg gaa aag cga ctg agc gag tca cag   4368
His Gly Thr Leu Pro Arg Ala Ala Glu Lys Arg Leu Ser Glu Ser Gln
                1445                1450                1455

aag ttt gtt gat caa gca cag aaa aag gtg cag gca agc ttt gat gga   4416
Lys Phe Val Asp Gln Ala Gln Lys Lys Val Gln Ala Ser Phe Asp Gly
            1460                1465                1470

att gct aat gat att gtc gcc agc cgg atc gag acc aag aac aat gtg   4464
Ile Ala Asn Asp Ile Val Ala Ser Arg Ile Glu Thr Lys Asn Asn Val
        1475                1480                1485

ttc aag gac ggc ttt atg tcg gcg cga cag tca cac tcc gct act gct   4512
Phe Lys Asp Gly Phe Met Ser Ala Arg Gln Ser His Ser Ala Thr Ala
    1490                1495                1500

gtg tgg aca ggt gat cca cgc ctg tca gtt gat gaa gta gcc atg aac   4560
Val Trp Thr Gly Asp Pro Arg Leu Ser Val Asp Glu Val Ala Met Asn
1505                1510                1515                1520

tct tcg atg gca cgt gaa ctc ggc gtt ctc gat aac ggt tat gca atg   4608
Ser Ser Met Ala Arg Glu Leu Gly Val Leu Asp Asn Gly Tyr Ala Met
                1525                1530                1535

gtg tgg cgt gat ccg gtg atc cgc gat ggt ggt gtg cgc tat ttg cgt   4656
Val Trp Arg Asp Pro Val Ile Arg Asp Gly Gly Val Arg Tyr Leu Arg
            1540                1545                1550

gtg gtt att aat gat gat ctg cac ggt gtg gca gtc aac cct gtg tcg   4704
Val Val Ile Asn Asp Asp Leu His Gly Val Ala Val Asn Pro Val Ser
        1555                1560                1565

gtg aag agc ttt gac ggt gac ttc gat ggt gac tct gta ggt ctg gtc   4752
Val Lys Ser Phe Asp Gly Asp Phe Asp Gly Asp Ser Val Gly Leu Val
    1570                1575                1580

ggc aat ctg ccg aaa aag gcg cat gag gag gca ttg tcc agg ctc aca   4800
Gly Asn Leu Pro Lys Lys Ala His Glu Glu Ala Leu Ser Arg Leu Thr
1585                1590                1595                1600

gtt gag gca aac atg ctt gat ctt ggt gat ggt aag cgt atg gag gac   4848
Val Glu Ala Asn Met Leu Asp Leu Gly Asp Gly Lys Arg Met Glu Asp
                1605                1610                1615

ggc act atg ttt tat ggg cta act ctg cat gac agc ctc gat gta cag   4896
Gly Thr Met Phe Tyr Gly Leu Thr Leu His Asp Ser Leu Asp Val Gln
            1620                1625                1630

gta gcg cag cac cat gat ccg gca atg gcc gag aac atg aag gtt att   4944
Val Ala Gln His His Asp Pro Ala Met Ala Glu Asn Met Lys Val Ile
        1635                1640                1645

gtc tct gag ctt aac cgc tac cag cgt gaa tac gag gcc ggc gag att   4992
Val Ser Glu Leu Asn Arg Tyr Gln Arg Glu Tyr Glu Ala Gly Glu Ile
    1650                1655                1660
```

```
agc cgc gaa gaa ttg cta gag gtc aac cgt gca cac atg gat gat ctc   5040
Ser Arg Glu Glu Leu Leu Glu Val Asn Arg Ala His Met Asp Asp Leu
1665                 1670                 1675                 1680

aat gag cac tat gca cag gct                                      5061
Asn Glu His Tyr Ala Gln Ala
                1685
```

<210> 12
<211> 1687
<212> PRT
<213> Corynebacterium glutamicum

<400> 12

```
Trp Gly Gln Lys Asp His Trp Gly Lys Ala Pro Leu Gly Asp His Asp
  1               5                  10                  15

Ala Val Arg Ile Tyr Arg Gln Ala Glu Ala Leu Met Lys Gln Arg Ala
             20                  25                  30

Ala Asn Asn Lys Gly Leu Asp Leu Asn Asp Glu Ala Thr Tyr Gly Ala
         35                  40                  45

Ile Met Phe Ala Ser Phe Asp Asp Ala Phe Ala Ala Asp Ala Glu Ala
     50                  55                  60

His Gly Cys Val His Arg Pro Gln Phe Ala Lys Val Thr Arg Arg Asn
 65                  70                  75                  80

Ile Leu Asn Ser Pro Gln Tyr Thr Ala Ile Lys Ser Ser Tyr Asp Ala
                 85                  90                  95

Leu Val Gln Gln Asp Leu Val Ala Gln Gln Gln Gln Ala Gln Ala Leu
            100                 105                 110

Gln Gln Ala Ala Tyr Glu Gln Glu Gln Ala Ala Ile Phe Gln Ala Arg
        115                 120                 125

Asp Gln Ala Thr Phe Gln Ala Glu Gln Thr Leu Ala Gln Glu Ser Val
    130                 135                 140

Arg Gln Ser Glu Gly Val Gly Leu Pro Val Ile Asp Pro Met Glu Ser
145                 150                 155                 160

Tyr Phe Arg Glu Tyr Ala Phe Tyr Glu Gly Val Glu Met Phe Gly Thr
                165                 170                 175

Trp Gly Thr His Val Asp Ala Gly Val Ser Gln Phe Ser Thr Ser Asp
            180                 185                 190

Gly Arg Ala Ile Arg Ala Leu Val Asp Glu His Leu Ala Thr Tyr Glu
        195                 200                 205

Pro Val Glu Gln Arg Gly Ser Thr Gln Ala Phe Phe Ala Ser Val Asn
    210                 215                 220

Ala Ala Phe Ala Glu Val Ala Pro His Ala Ala Pro Met Phe Ser Ala
225                 230                 235                 240

Ile Ala Arg Glu Gly Glu Gly Ser Lys Gly Tyr Gln Ala Leu Arg His
```

```
                245                 250                 255

Arg Phe Asp Lys Met Val Gly Thr Ala Ile Gly Pro Asn Gly Leu Pro
            260                 265                 270

Glu Gly Pro Asp Leu Gly Gly Arg Arg Leu Pro Ile Ser Pro Tyr Asp
        275                 280                 285

Pro Arg Trp Ser Asp Arg Glu Val Val Arg Val His Gly Thr Lys Leu
    290                 295                 300

Leu Ser Leu Ser Glu Glu Ser Val Gly Met Ile Arg Asp Leu Asp Leu
305                 310                 315                 320

Ala Thr Ile His Leu Gln Asp Asn Asp Val Tyr Glu Gly Thr His Arg
                325                 330                 335

Glu Asp Asp Thr Lys Gly Gly Val Arg Pro Leu Thr Gln Trp Val Asn
            340                 345                 350

Gly Glu Ala Ile Ala Trp Arg Thr Ile Thr Glu Asn Asp Gln Met Arg
        355                 360                 365

Leu Pro Asn Ile Gly Gln Phe Met Thr Ala Lys Glu Tyr Arg Ala Ala
    370                 375                 380

Ala Ser Trp Leu Arg Ala Gly Leu Ile Asp Thr Ala Asp Val Ala Ser
385                 390                 395                 400

Gln Lys Ile Asp Pro Asn Lys Val Met Ser Asp Glu Gly Ile Ala Arg
                405                 410                 415

Ser Glu Ala Ile Leu Thr Tyr Leu Ser Asp Glu Gly Val Asp Phe Arg
            420                 425                 430

Ile Glu Pro Asp Arg Glu Pro Gly Gln Leu Lys Val Arg Ile Glu Gly
        435                 440                 445

Thr Arg Ile Asp Ile Arg Leu Thr Asp Thr Arg Ala Asn Glu Gln Trp
    450                 455                 460

Val Gly Arg Val Tyr Asp Ser Gly Thr Val Ile Lys Tyr Ser Ala Glu
465                 470                 475                 480

Gln Thr Ala Glu Glu Arg Leu Arg Ala Arg Glu Arg Met Glu Asn Gly
                485                 490                 495

Asp Gly Thr Trp Thr Pro Ala Thr Asp Tyr Glu Pro Ser Pro Thr Glu
            500                 505                 510

Val Val Asp Leu Val Lys Phe Ala Leu Gly Arg Glu Val Glu Arg Gln
        515                 520                 525

Asp Gly Lys Gly Leu Val Gly Val Pro Asn Ala Arg His Pro Arg Ala
    530                 535                 540

Leu Glu Gln Ala Gln Asp Ala Tyr Phe Thr Lys Asn Arg Ser Ala Phe
545                 550                 555                 560

Met Val Arg Glu Gly Leu Ser Ile Val Gln Asp Ala Arg Asp Arg Ser
                565                 570                 575
```

Ala Gly Pro Gly Lys Trp Phe Asp Asn Glu Ala Lys Ala Ser Glu Trp
580 585 590

Leu Gly Asn Asn Ile Ala Leu Thr Arg Ala Arg Val Ala Glu Glu Leu
595 600 605

Gly Val Glu Glu Leu Ile Ala Leu Ser Ala Gln Tyr Ala Asp Asp Pro
610 615 620

Asp Phe Met Pro Ala Phe Ala Gly Glu Asp Glu Leu Met Ala Ile Lys
625 630 635 640

Gln Asp Tyr Trp Ala Met Leu Arg Gly Glu Glu Thr Asp Leu Leu Asn
645 650 655

Pro Gly Val Asn Arg Asp Asp Tyr Met Ala Ala Ile Arg Asp Gly Asp
660 665 670

His Glu Gln Ile Ala Ala Met Thr Ser Ala Met Asn Ala Val Thr Val
675 680 685

Glu Asp Arg Val Arg Gln His Ala Ala Leu Val Leu Asp Asp Tyr Val
690 695 700

Gly Thr Val Glu Pro Asp Pro Val Thr Gly Leu Arg Phe Asn Pro Val
705 710 715 720

Thr Val Ala Gln His Met Pro Ser Ala Lys Ser Leu Trp Ser Asn His
725 730 735

Asp Asp Ile Ile Ala Ala Leu Arg Ala Thr Ser Ile Thr Gly Asp Glu
740 745 750

Leu Arg Gly Asp Glu Phe Tyr Asn Asp Val Ile Asn Gln Gln Leu Leu
755 760 765

Lys Phe Asn Pro Glu Thr Ala Gln Lys Met Val Asn Asn Pro Asp Leu
770 775 780

Asp Pro Gln Leu Ala Arg Phe Gly Thr Val Ile Ala Glu Thr Ile Ser
785 790 795 800

Arg Asn Gly Ala Asp Val Val Asp Ile Ala Val Asp Asp Asn Gly Val
805 810 815

Val Arg Trp Thr Ala Gln Arg Arg Val Gly Ala Lys Asp Ser Arg Ala
820 825 830

Val Asp Ser Lys Gly Gln Val Arg Gly Glu Arg Thr Arg His Val Gln
835 840 845

Gly Glu Ile Gly Gln Ile Phe Thr Arg Gly Glu His Gly Glu Ile Val
850 855 860

Thr Lys Phe Asn Gly Gly Glu Asn Tyr Met Phe Ala Pro Gly Tyr Thr
865 870 875 880

Ala Ser Val Val Pro Gln Lys Pro Gly Glu Thr Lys Ser Leu Glu Glu
885 890 895

```
Arg Thr Lys Leu Lys Gly Tyr Glu Gln Val Met Ser Glu Ala Leu Val
            900                 905                 910

Tyr Arg Val Arg Glu Asp Leu Met Phe Thr Glu Arg Ser Arg Val Gly
        915                 920                 925

Ala Thr Thr Ser Ile Asn Ser Ala Tyr Lys Arg Leu Tyr Asp Asn Arg
    930                 935                 940

Phe Pro Val Asp Phe Phe Glu Arg Ser Ala Glu Glu Gly Leu Ser Asp
945                 950                 955                 960

Glu Trp Arg Ala Ala Leu Leu Glu Thr Ala Ser Leu Arg Val Arg Tyr
                965                 970                 975

Asp Asn Ser Ile Arg Asp Gly Ala Asn Val Met Glu Asp Ile Arg Ala
            980                 985                 990

Gln Gln Arg Gly Phe Asp Ala Arg Asn Asp Asn Ser Arg Asp Ala Leu
        995                 1000                1005

Val Leu Thr Gly Gly Arg Asn Ile Ser Val Leu Asp Val Asp Ala Gly
    1010                1015                1020

Lys Gly Phe Phe Asp Pro Met Met Thr Gly Met Ala Ala Asn Gln Gly
1025                1030                1035                1040

Ser Val Arg Tyr Leu Leu Pro Ser Ala Lys Val Gly Ala Asp Gly Met
                1045                1050                1055

Ile Thr Pro Gly Asp Pro Ala Asp Arg Val Pro Val Ala Ala His Pro
            1060                1065                1070

Glu Ser Trp Ala Met Gly Phe Asp Pro His Asp Arg Gln Asn Met Thr
        1075                1080                1085

Phe Ser Asn Ile Met Gln Ala Ser Ala Val Thr Gly Gly Ala Arg Thr
    1090                1095                1100

Ala Met Ile Gln Leu Gly Gly Trp Asn Phe Glu Asp Gly Ile Ile Val
1105                1110                1115                1120

Ser Ala Asp Phe Ala Asn Thr His Val Ile Arg Asp Thr Glu Asp Glu
                1125                1130                1135

Met Arg Pro Leu Val Ala Gly Asp Lys Leu Ser Asp Phe His Gly Asn
            1140                1145                1150

Lys Gly Val Thr Ala Leu Val Val Asp Pro Ala Met Ser Asp Ala Asp
        1155                1160                1165

Ala Arg Ala Ala Gly Leu Glu Ser Glu Val Ala Phe Phe Arg Asp Asn
    1170                1175                1180

Pro Asp Leu Glu Val Val Met Ser Pro Phe Ser Ala Ile Ser Arg Phe
1185                1190                1195                1200

Asn Gly Gly Thr Ala Arg Glu Leu Met Thr Asn Pro Gln Asp Val Val
                1205                1210                1215

Phe Arg Asn Asn Asp Gly Ser Thr Arg Val Gln Pro Gly Ala Ser Gly
```

```
            1220                1225                1230

Asp Leu Asn Phe Ile Val Thr His Met Ala Val Asp Ala Lys Thr Asn
        1235                1240                1245

Val Tyr Asp Glu Glu Ala Val Arg Glu Gly Gln Gly Arg Lys Ala Ser
    1250                1255                1260

Ser Gln Leu Ala Trp Val Leu Gln Ala Gln Glu Cys His Glu Ile Met
1265                1270                1275                1280

Glu His Phe Tyr Gly Asn Asn Val Ser Ala Leu Ala Asn Phe Gln Glu
                1285                1290                1295

Tyr Leu Arg Val Thr Gly Leu Asp Val Thr Pro Tyr Gly Glu Leu Arg
            1300                1305                1310

Glu Gly Phe Ser Glu Ser Asn Glu Gln Arg Asn Ile Ile Glu Met Pro
        1315                1320                1325

Ser Ile Tyr Asp Glu Asn Gly Glu Leu Asn Asn Arg Val Asn Arg Ala
    1330                1335                1340

Gln Val Arg Glu Ala Phe Val Glu Gln Ile Ser Arg Ala Gly Gly Val
1345                1350                1355                1360

Met Glu Ile Pro Phe Gln Leu Gln Leu Arg Asn Gly Ala Gln Leu Glu
                1365                1370                1375

Glu Ser Pro Asn Asn Pro Asp Met Tyr Gln Leu Pro Leu Leu Ser Pro
            1380                1385                1390

His Leu Arg Ser Asp Glu Asp Leu Ala Asp Gly Ser Thr Ser Arg His
        1395                1400                1405

Glu Tyr Thr Thr Arg Tyr Met Ala Ile Phe Asp Thr Cys Tyr Lys Leu
    1410                1415                1420

Ala Glu Glu Gln Ala Lys Ile Asp Ala Leu Arg Gln Glu Glu Ala Gln
1425                1430                1435                1440

His Gly Thr Leu Pro Arg Ala Ala Glu Lys Arg Leu Ser Glu Ser Gln
                1445                1450                1455

Lys Phe Val Asp Gln Ala Gln Lys Lys Val Gln Ala Ser Phe Asp Gly
            1460                1465                1470

Ile Ala Asn Asp Ile Val Ala Ser Arg Ile Glu Thr Lys Asn Asn Val
        1475                1480                1485

Phe Lys Asp Gly Phe Met Ser Ala Arg Gln Ser His Ser Ala Thr Ala
    1490                1495                1500

Val Trp Thr Gly Asp Pro Arg Leu Ser Val Asp Glu Val Ala Met Asn
1505                1510                1515                1520

Ser Ser Met Ala Arg Glu Leu Gly Val Leu Asp Asn Gly Tyr Ala Met
                1525                1530                1535

Val Trp Arg Asp Pro Val Ile Arg Asp Gly Gly Val Arg Tyr Leu Arg
            1540                1545                1550
```

```
Val Val Ile Asn Asp Asp Leu His Gly Val Ala Val Asn Pro Val Ser
        1555                1560                1565

Val Lys Ser Phe Asp Gly Asp Phe Asp Gly Asp Ser Val Gly Leu Val
    1570                1575                1580

Gly Asn Leu Pro Lys Lys Ala His Glu Glu Ala Leu Ser Arg Leu Thr
1585                1590                1595                1600

Val Glu Ala Asn Met Leu Asp Leu Gly Asp Gly Lys Arg Met Glu Asp
                1605                1610                1615

Gly Thr Met Phe Tyr Gly Leu Thr Leu His Asp Ser Leu Asp Val Gln
            1620                1625                1630

Val Ala Gln His His Asp Pro Ala Met Ala Glu Asn Met Lys Val Ile
        1635                1640                1645

Val Ser Glu Leu Asn Arg Tyr Gln Arg Glu Tyr Glu Ala Gly Glu Ile
    1650                1655                1660

Ser Arg Glu Glu Leu Leu Glu Val Asn Arg Ala His Met Asp Asp Leu
1665                1670                1675                1680

Asn Glu His Tyr Ala Gln Ala
                1685
```

Sequence Listing.ST25.txt

<210> 13
<211> 2289
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2266)
<223> RXN01539

<400> 13

```
gaacagcacg gttgggtgcc gcagaattgt tgcgtcgttt tgaacgcaca ggtgcagcag 60

ctcagaataa tcagtttgac gatatggact tttaaggagt gtg gtg aca gtg gct   115
                                            Val Val Thr Val Ala
                                              1               5

ggg aat gag aag aat aag ata cga gaa gag cgg gtg gct cgg cgt gcc   163
Gly Asn Glu Lys Asn Lys Ile Arg Glu Glu Arg Val Ala Arg Arg Ala
                 10                  15                  20

cag gca gtc gta gag gcg gag att agt ctt gct gca caa gca agt gag   211
Gln Ala Val Val Glu Ala Glu Ile Ser Leu Ala Ala Gln Ala Ser Glu
             25                  30                  35

cag gtg cgt gaa caa gca gag gcg cct gat gta aat gaa cag gta gaa   259
Gln Val Arg Glu Gln Ala Glu Ala Pro Asp Val Asn Glu Gln Val Glu
         40                  45                  50

gag gtt agt gtc gag gta tct tct gtc cag tca tta acc cag cct aag   307
Glu Val Ser Val Glu Val Ser Ser Val Gln Ser Leu Thr Gln Pro Lys
     55                  60                  65
```

```
acg ttg ggg cag ctg cat gac cca agg aaa aat gtc atg agt agc agc   355
Thr Leu Gly Gln Leu His Asp Pro Arg Lys Asn Val Met Ser Ser Ser
 70                  75                  80                  85

gac ttg gct tct att att ggt gta gag caa cag cct gtt gct tat ggt   403
Asp Leu Ala Ser Ile Ile Gly Val Glu Gln Gln Pro Val Ala Tyr Gly
                 90                  95                 100

gag tct gag gaa cca gaa aca ctg cgt gat gtg ttg cct cgg cga aag   451
Glu Ser Glu Glu Pro Glu Thr Leu Arg Asp Val Leu Pro Arg Arg Lys
            105                 110                 115

ctt cac cca tct gag ata aca ccg agt tat gag gtt gct gat ggt gaa   499
Leu His Pro Ser Glu Ile Thr Pro Ser Tyr Glu Val Ala Asp Gly Glu
        120                 125                 130

cag cgc agc att ttt ggt gaa tca gct ccg tct gat ttt gat gac ctc   547
Gln Arg Ser Ile Phe Gly Glu Ser Ala Pro Ser Asp Phe Asp Asp Leu
    135                 140                 145

agt gat gtc gaa gaa ttt gat acc agt cat tgg gtg cgt gct gga caa   595
Ser Asp Val Glu Glu Phe Asp Thr Ser His Trp Val Arg Ala Gly Gln
150                 155                 160                 165

gat gat cgt agt gat gat gat cga ctc gct gat gag gct ggt gta ccg   643
Asp Asp Arg Ser Asp Asp Asp Arg Leu Ala Asp Glu Ala Gly Val Pro
                170                 175                 180

cgt agt ggc gca caa gat gta gct gat aat gag gct aat ctt tct ggt   691
Arg Ser Gly Ala Gln Asp Val Ala Asp Asn Glu Ala Asn Leu Ser Gly
            185                 190                 195

gtg gat gag cag ctg cac atg cgt gaa gtc cat gca cag agt ttt gac   739
Val Asp Glu Gln Leu His Met Arg Glu Val His Ala Gln Ser Phe Asp
        200                 205                 210

cct att gac gtt gcc aaa aag gaa cgc aaa gca gcg gaa aag aag tat   787
Pro Ile Asp Val Ala Lys Lys Glu Arg Lys Ala Ala Glu Lys Lys Tyr
    215                 220                 225

gcc aag cca cca aaa agt gat aat ccg tac cta gca cgg gat gcc aaa   835
Ala Lys Pro Pro Lys Ser Asp Asn Pro Tyr Leu Ala Arg Asp Ala Lys
230                 235                 240                 245

gat gca gct gct cgt aag cgg aag atc aat gca gct cat gat aat ttt   883
Asp Ala Ala Ala Arg Lys Arg Lys Ile Asn Ala Ala His Asp Asn Phe
                250                 255                 260

gcc caa gag atg gca cag gct gcg atg gga cca ctg cgc aaa ggg gtc   931
Ala Gln Glu Met Ala Gln Ala Ala Met Gly Pro Leu Arg Lys Gly Val
            265                 270                 275

aac act caa acg gtg atg gcc gcg tgt acg act gct gcg gtg atg tgg   979
Asn Thr Gln Thr Val Met Ala Ala Cys Thr Thr Ala Ala Val Met Trp
        280                 285                 290

tgc atg agc cca cgt atg acc ggt gtg aac gtg gat atg aag cgc aag   1027
Cys Met Ser Pro Arg Met Thr Gly Val Asn Val Asp Met Lys Arg Lys
    295                 300                 305
```

```
ttt aac aag gat ctg gaa cag gct aaa gac act aag ttg tcg aag tat   1075
Phe Asn Lys Asp Leu Glu Gln Ala Lys Asp Thr Lys Leu Ser Lys Tyr
310                 315                 320                 325

gtg tcc aaa gat ttt tgg aag tca aag ctg acg cgc gat aag acg gag   1123
Val Ser Lys Asp Phe Trp Lys Ser Lys Leu Thr Arg Asp Lys Thr Glu
                330                 335                 340

aag gaa gcg aag tcg ctc tct gat gcg ttc atg cag cag aaa aca gcg   1171
Lys Glu Ala Lys Ser Leu Ser Asp Ala Phe Met Gln Gln Lys Thr Ala
            345                 350                 355

atc atc agc aac cgt gaa cga atc ccc atg agt gtt gct tct gcc gcg   1219
Ile Ile Ser Asn Arg Glu Arg Ile Pro Met Ser Val Ala Ser Ala Ala
        360                 365                 370

cag acc gtg gtt cgg ttg tct gat caa gcg tat gag gcg atg cgt gaa   1267
Gln Thr Val Val Arg Leu Ser Asp Gln Ala Tyr Glu Ala Met Arg Glu
    375                 380                 385

gta gat acg gat ggt caa gcg ata gtg gat gcg aag gat gtc tct gca   1315
Val Asp Thr Asp Gly Gln Ala Ile Val Asp Ala Lys Asp Val Ser Ala
390                 395                 400                 405

cag gtg gca gaa gat att gac atg gtg gtc aag cag ggt gaa gag cat   1363
Gln Val Ala Glu Asp Ile Asp Met Val Val Lys Gln Gly Glu Glu His
                410                 415                 420

ggc ctg aag tcg aag gat att tat ggc gct gcc cgc gat att gtg ggt   1411
Gly Leu Lys Ser Lys Asp Ile Tyr Gly Ala Ala Arg Asp Ile Val Gly
            425                 430                 435

cgt cgc atg gag cgc gat cca ggc tat gct gcc cgg ttt aat gag acg   1459
Arg Arg Met Glu Arg Asp Pro Gly Tyr Ala Ala Arg Phe Asn Glu Thr
        440                 445                 450

gct ttt ggc acc gtg cgc ctg ggt gaa caa cga cgt ggc atg gtg att   1507
Ala Phe Gly Thr Val Arg Leu Gly Glu Gln Arg Arg Gly Met Val Ile
    455                 460                 465

tca aag acc ccg aca tgg caa ttc cct gat ggt gca ggt ttg agt aaa   1555
Ser Lys Thr Pro Thr Trp Gln Phe Pro Asp Gly Ala Gly Leu Ser Lys
470                 475                 480                 485

aac gcc ggc tgg ttt agt gtt cgt gag ccg atg ggt aat gcg cag aac   1603
Asn Ala Gly Trp Phe Ser Val Arg Glu Pro Met Gly Asn Ala Gln Asn
                490                 495                 500

ttc gct gac aac ctg gct gcg act ttg gcg aca gaa atg cgg gta gct   1651
Phe Ala Asp Asn Leu Ala Ala Thr Leu Ala Thr Glu Met Arg Val Ala
            505                 510                 515

ggt gag cag tac ggt tcc gat ggc gtt cgt gat gta gtt gcc ggc ttc   1699
Gly Glu Gln Tyr Gly Ser Asp Gly Val Arg Asp Val Val Ala Gly Phe
        520                 525                 530

atg aca gcg act gat gtc tca gaa agt ggc ctc gcc tct gcg aag aaa   1747
Met Thr Ala Thr Asp Val Ser Glu Ser Gly Leu Ala Ser Ala Lys Lys
    535                 540                 545

ctg tta cct gac ttt gat aca cgt ggt cgc agt gct tct cgg gtg cgc   1795
```

```
Leu Leu Pro Asp Phe Asp Thr Arg Gly Arg Ser Ala Ser Arg Val Arg
550                 555                 560                 565

cag att gct atg gca cag cgc aca cag gca gcg atc aag gtg ttg cag   1843
Gln Ile Ala Met Ala Gln Arg Thr Gln Ala Ala Ile Lys Val Leu Gln
                570                 575                 580

gat gat ggt aat cag acc gcg atg acg act gag cag gtc aag gag gtt   1891
Asp Asp Gly Asn Gln Thr Ala Met Thr Thr Glu Gln Val Lys Glu Val
            585                 590                 595

cag gta tgg gcg atg gat cag gct gag aag gtg atg cag cgt gat cat   1939
Gln Val Trp Ala Met Asp Gln Ala Glu Lys Val Met Gln Arg Asp His
        600                 605                 610

cca gcg att ctg gat aag ttt gtg cgc aaa cat ggg cag aca ttt ggg   1987
Pro Ala Ile Leu Asp Lys Phe Val Arg Lys His Gly Gln Thr Phe Gly
    615                 620                 625

cag gat gcg gac gct ttt gtt aaa tcc ata act atg gaa aaa gac acg   2035
Gln Asp Ala Asp Ala Phe Val Lys Ser Ile Thr Met Glu Lys Asp Thr
630                 635                 640                 645

agc agc gag tac act gat gct atg gtt cga cct caa gaa aat cgt gga   2083
Ser Ser Glu Tyr Thr Asp Ala Met Val Arg Pro Gln Glu Asn Arg Gly
                650                 655                 660

tca ggt cga gaa ctg gca gct cgt cgt cgt gta caa gca gcg caa atc   2131
Ser Gly Arg Glu Leu Ala Ala Arg Arg Arg Val Gln Ala Ala Gln Ile
            665                 670                 675

aat cag gca gca cag ctg gat atg aat gtt cat gat ttc cgt gaa tcg   2179
Asn Gln Ala Ala Gln Leu Asp Met Asn Val His Asp Phe Arg Glu Ser
        680                 685                 690

aat ctg cca gag gaa cga ccc gcg aat cct tat gaa gcg tat gtt cgt   2227
Asn Leu Pro Glu Glu Arg Pro Ala Asn Pro Tyr Glu Ala Tyr Val Arg
    695                 700                 705

gag act gaa gcg aaa acc aat gat ccg cag tac ggt tat taatagaaaa   2276
Glu Thr Glu Ala Lys Thr Asn Asp Pro Gln Tyr Gly Tyr
710                 715                 720

tgatagaaag aag                                                  2289


<210> 14
<211> 722
<212> PRT
<213> Corynebacterium glutamicum

<400> 14
Val Val Thr Val Ala Gly Asn Glu Lys Asn Lys Ile Arg Glu Glu Arg
  1               5                  10                  15

Val Ala Arg Arg Ala Gln Ala Val Val Glu Ala Glu Ile Ser Leu Ala
             20                  25                  30

Ala Gln Ala Ser Glu Gln Val Arg Glu Gln Ala Glu Ala Pro Asp Val
         35                  40                  45
```

```
Asn Glu Gln Val Glu Glu Val Ser Val Glu Val Ser Ser Val Gln Ser
     50                  55                  60

Leu Thr Gln Pro Lys Thr Leu Gly Gln Leu His Asp Pro Arg Lys Asn
 65                  70                  75                  80

Val Met Ser Ser Ser Asp Leu Ala Ser Ile Ile Gly Val Glu Gln Gln
                 85                  90                  95

Pro Val Ala Tyr Gly Glu Ser Glu Glu Pro Glu Thr Leu Arg Asp Val
            100                 105                 110

Leu Pro Arg Arg Lys Leu His Pro Ser Glu Ile Thr Pro Ser Tyr Glu
        115                 120                 125

Val Ala Asp Gly Glu Gln Arg Ser Ile Phe Gly Glu Ser Ala Pro Ser
    130                 135                 140

Asp Phe Asp Asp Leu Ser Asp Val Glu Glu Phe Asp Thr Ser His Trp
145                 150                 155                 160

Val Arg Ala Gly Gln Asp Asp Arg Ser Asp Asp Asp Arg Leu Ala Asp
                165                 170                 175

Glu Ala Gly Val Pro Arg Ser Gly Ala Gln Asp Val Ala Asp Asn Glu
            180                 185                 190

Ala Asn Leu Ser Gly Val Asp Glu Gln Leu His Met Arg Glu Val His
        195                 200                 205

Ala Gln Ser Phe Asp Pro Ile Asp Val Ala Lys Lys Glu Arg Lys Ala
    210                 215                 220

Ala Glu Lys Lys Tyr Ala Lys Pro Pro Lys Ser Asp Asn Pro Tyr Leu
225                 230                 235                 240

Ala Arg Asp Ala Lys Asp Ala Ala Ala Arg Lys Arg Lys Ile Asn Ala
                245                 250                 255

Ala His Asp Asn Phe Ala Gln Glu Met Ala Gln Ala Ala Met Gly Pro
            260                 265                 270

Leu Arg Lys Gly Val Asn Thr Gln Thr Val Met Ala Ala Cys Thr Thr
        275                 280                 285

Ala Ala Val Met Trp Cys Met Ser Pro Arg Met Thr Gly Val Asn Val
    290                 295                 300

Asp Met Lys Arg Lys Phe Asn Lys Asp Leu Glu Gln Ala Lys Asp Thr
305                 310                 315                 320

Lys Leu Ser Lys Tyr Val Ser Lys Asp Phe Trp Lys Ser Lys Leu Thr
                325                 330                 335

Arg Asp Lys Thr Glu Lys Glu Ala Lys Ser Leu Ser Asp Ala Phe Met
            340                 345                 350

Gln Gln Lys Thr Ala Ile Ile Ser Asn Arg Glu Arg Ile Pro Met Ser
        355                 360                 365

Val Ala Ser Ala Ala Gln Thr Val Val Arg Leu Ser Asp Gln Ala Tyr
```

```
    370                 375                 380

Glu Ala Met Arg Glu Val Asp Thr Asp Gly Gln Ala Ile Val Asp Ala
385                 390                 395                 400

Lys Asp Val Ser Ala Gln Val Ala Glu Asp Ile Asp Met Val Val Lys
                405                 410                 415

Gln Gly Glu Glu His Gly Leu Lys Ser Lys Asp Ile Tyr Gly Ala Ala
            420                 425                 430

Arg Asp Ile Val Gly Arg Arg Met Glu Arg Asp Pro Gly Tyr Ala Ala
        435                 440                 445

Arg Phe Asn Glu Thr Ala Phe Gly Thr Val Arg Leu Gly Glu Gln Arg
    450                 455                 460

Arg Gly Met Val Ile Ser Lys Thr Pro Thr Trp Gln Phe Pro Asp Gly
465                 470                 475                 480

Ala Gly Leu Ser Lys Asn Ala Gly Trp Phe Ser Val Arg Glu Pro Met
                485                 490                 495

Gly Asn Ala Gln Asn Phe Ala Asp Asn Leu Ala Ala Thr Leu Ala Thr
            500                 505                 510

Glu Met Arg Val Ala Gly Glu Gln Tyr Gly Ser Asp Gly Val Arg Asp
        515                 520                 525

Val Val Ala Gly Phe Met Thr Ala Thr Asp Val Ser Glu Ser Gly Leu
    530                 535                 540

Ala Ser Ala Lys Lys Leu Leu Pro Asp Phe Asp Thr Arg Gly Arg Ser
545                 550                 555                 560

Ala Ser Arg Val Arg Gln Ile Ala Met Ala Gln Arg Thr Gln Ala Ala
                565                 570                 575

Ile Lys Val Leu Gln Asp Asp Gly Asn Gln Thr Ala Met Thr Thr Glu
            580                 585                 590

Gln Val Lys Glu Val Gln Val Trp Ala Met Asp Gln Ala Glu Lys Val
        595                 600                 605

Met Gln Arg Asp His Pro Ala Ile Leu Asp Lys Phe Val Arg Lys His
    610                 615                 620

Gly Gln Thr Phe Gly Gln Asp Ala Asp Ala Phe Val Lys Ser Ile Thr
625                 630                 635                 640

Met Glu Lys Asp Thr Ser Ser Glu Tyr Thr Asp Ala Met Val Arg Pro
                645                 650                 655

Gln Glu Asn Arg Gly Ser Gly Arg Glu Leu Ala Ala Arg Arg Arg Val
            660                 665                 670

Gln Ala Ala Gln Ile Asn Gln Ala Ala Gln Leu Asp Met Asn Val His
        675                 680                 685

Asp Phe Arg Glu Ser Asn Leu Pro Glu Glu Arg Pro Ala Asn Pro Tyr
    690                 695                 700
```

```
Glu Ala Tyr Val Arg Glu Thr Glu Ala Lys Thr Asn Asp Pro Gln Tyr
705                 710                 715                 720

Gly Tyr
```

<210> 15
<211> 2046
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2023)
<223> FRXA01539

<400> 15

```
aaatgaacag gtagaagagg ttagtgtcga ggtatcttct gtccagtcat taacccagcc 60

taagacgttg gggcagctgc atgacccaag gaaaaatgtc atg agt agc agc gac   115
                                            Met Ser Ser Ser Asp
                                              1               5

ttg gct tct att att ggt gta gag caa cag cct gtt gct tat ggt gag   163
Leu Ala Ser Ile Ile Gly Val Glu Gln Gln Pro Val Ala Tyr Gly Glu
                 10                  15                  20

tct gag gaa cca gaa aca ctg cgt gat gtg ttg cct cgg cga aag ctt   211
Ser Glu Glu Pro Glu Thr Leu Arg Asp Val Leu Pro Arg Arg Lys Leu
             25                  30                  35

cac cca tct gag ata aca ccg agt tat gag gtt gct gat ggt gaa cag   259
His Pro Ser Glu Ile Thr Pro Ser Tyr Glu Val Ala Asp Gly Glu Gln
         40                  45                  50

cgc agc att ttt ggt gaa tca gct ccg tct gat ttt gat gac ctc agt   307
Arg Ser Ile Phe Gly Glu Ser Ala Pro Ser Asp Phe Asp Asp Leu Ser
     55                  60                  65

gat gtc gaa gaa ttt gat acc agt cat tgg gtg cgt gct gga caa gat   355
Asp Val Glu Glu Phe Asp Thr Ser His Trp Val Arg Ala Gly Gln Asp
 70                  75                  80                  85

gat cgt agt gat gat gat cga ctc gct gat gag gct ggt gta ccg cct   403
Asp Arg Ser Asp Asp Asp Arg Leu Ala Asp Glu Ala Gly Val Pro Pro
                 90                  95                 100

agt ggc gca caa gat gta gct gat aat gag gct aat ctt tct ggt gtg   451
Ser Gly Ala Gln Asp Val Ala Asp Asn Glu Ala Asn Leu Ser Gly Val
             105                 110                 115

gat gag cag ctg cac atg cgt gaa gtc cat gca cag agt ttt gac cct   499
Asp Glu Gln Leu His Met Arg Glu Val His Ala Gln Ser Phe Asp Pro
         120                 125                 130

att gac gtt gcc aaa aag gaa cgc aaa gca gcg gaa aag aag tat gcc   547
Ile Asp Val Ala Lys Lys Glu Arg Lys Ala Ala Glu Lys Lys Tyr Ala
     135                 140                 145
```

```
aag cca cca aaa agt gat aat ccg tac cta gca cgg gat gcc aaa gat   595
Lys Pro Pro Lys Ser Asp Asn Pro Tyr Leu Ala Arg Asp Ala Lys Asp
150                 155                 160                 165

gca gct gct cgt aag cgg aag atc aat gca gct cat gat aat ttt gcc   643
Ala Ala Ala Arg Lys Arg Lys Ile Asn Ala Ala His Asp Asn Phe Ala
                170                 175                 180

caa gag atg gca cag gct gcg atg gga cca ctg cgc aaa ggg gtc aac   691
Gln Glu Met Ala Gln Ala Ala Met Gly Pro Leu Arg Lys Gly Val Asn
            185                 190                 195

act caa acg gtg atg gcc gcg tgt acg act gct gcg gtg atg tgg tgc   739
Thr Gln Thr Val Met Ala Ala Cys Thr Thr Ala Ala Val Met Trp Cys
        200                 205                 210

atg agc cca cgt atg acc ggt gtg aac gtg gat atg aag cgc aag ttt   787
Met Ser Pro Arg Met Thr Gly Val Asn Val Asp Met Lys Arg Lys Phe
    215                 220                 225

aac aag gat ctg gaa cag gct aaa gac act aag ttg tcg aag tat gtg   835
Asn Lys Asp Leu Glu Gln Ala Lys Asp Thr Lys Leu Ser Lys Tyr Val
230                 235                 240                 245

tcc aaa gat ttt tgg aag tca aag ctg acg cgc gat aag acg gag aag   883
Ser Lys Asp Phe Trp Lys Ser Lys Leu Thr Arg Asp Lys Thr Glu Lys
                250                 255                 260

gaa gcg aag tcg ctc tct gat gcg ttc atg cag cag aaa aca gcg atc   931
Glu Ala Lys Ser Leu Ser Asp Ala Phe Met Gln Gln Lys Thr Ala Ile
            265                 270                 275

atc agc aac cgt gaa cga atc ccc atg agt gtt gct tct gcc gcg cag   979
Ile Ser Asn Arg Glu Arg Ile Pro Met Ser Val Ala Ser Ala Ala Gln
        280                 285                 290

acc gtg gtt cgg ttg tct gat caa gcg tat gag gcg atg cgt gaa gta   1027
Thr Val Val Arg Leu Ser Asp Gln Ala Tyr Glu Ala Met Arg Glu Val
    295                 300                 305

gat acg gat ggt caa gcg ata gtg gat gcg aag gat gtc tct gca cag   1075
Asp Thr Asp Gly Gln Ala Ile Val Asp Ala Lys Asp Val Ser Ala Gln
310                 315                 320                 325

gtg gca gaa gat att gac atg gtg gtc aag cag ggt gaa gag cat ggc   1123
Val Ala Glu Asp Ile Asp Met Val Val Lys Gln Gly Glu Glu His Gly
                330                 335                 340

ctg aag tcg aag gat att tat ggc gct gcc cgc gat att gtg ggt cgt   1171
Leu Lys Ser Lys Asp Ile Tyr Gly Ala Ala Arg Asp Ile Val Gly Arg
            345                 350                 355

cgc atg gag cgc gat cca ggc tat gct gcc cgg ttt aat gag acg gct   1219
Arg Met Glu Arg Asp Pro Gly Tyr Ala Ala Arg Phe Asn Glu Thr Ala
        360                 365                 370

ttt ggc acc gtg cgc ctg ggt gaa caa cga cgt ggc atg gtg att tca   1267
Phe Gly Thr Val Arg Leu Gly Glu Gln Arg Arg Gly Met Val Ile Ser
    375                 380                 385

aag acc ccg aca tgg caa ttc cct gat ggt gca ggt ttg agt aaa aac   1315
```

```
Lys Thr Pro Thr Trp Gln Phe Pro Asp Gly Ala Gly Leu Ser Lys Asn
390                 395                 400                 405

gcc ggc tgg ttt agt gtt cgt gag ccg atg ggt aat gcg cag aac ttc   1363
Ala Gly Trp Phe Ser Val Arg Glu Pro Met Gly Asn Ala Gln Asn Phe
                410                 415                 420

gct gac aac ctg gct gcg act ttg gcg aca gaa atg cgg gta gct ggt   1411
Ala Asp Asn Leu Ala Ala Thr Leu Ala Thr Glu Met Arg Val Ala Gly
            425                 430                 435

gag cag tac ggt tcc gat ggc gtt cgt gat gta gtt gcc ggc ttc atg   1459
Glu Gln Tyr Gly Ser Asp Gly Val Arg Asp Val Val Ala Gly Phe Met
        440                 445                 450

aca gcg act gat gtc tca gaa agt ggc ctc gcc tct gcg aag aaa ctg   1507
Thr Ala Thr Asp Val Ser Glu Ser Gly Leu Ala Ser Ala Lys Lys Leu
    455                 460                 465

tta cct gac ttt gat aca cgt ggt cgc agt gct tct cgg gtg cgc cag   1555
Leu Pro Asp Phe Asp Thr Arg Gly Arg Ser Ala Ser Arg Val Arg Gln
470                 475                 480                 485

att gct atg gca cag cgc aca cag gca gcg atc aag gtg ttg cag gat   1603
Ile Ala Met Ala Gln Arg Thr Gln Ala Ala Ile Lys Val Leu Gln Asp
                490                 495                 500

gat ggt aat cag acc gcg atg acg act gag cag gtc aag gag gtt cag   1651
Asp Gly Asn Gln Thr Ala Met Thr Thr Glu Gln Val Lys Glu Val Gln
            505                 510                 515

gta tgg gcg atg gat cag gct gag aag gtg atg cag cgt gat cat cca   1699
Val Trp Ala Met Asp Gln Ala Glu Lys Val Met Gln Arg Asp His Pro
        520                 525                 530

gcg att ctg gat aag ttt gtg cgc aaa cat ggg cag aca ttt ggg cag   1747
Ala Ile Leu Asp Lys Phe Val Arg Lys His Gly Gln Thr Phe Gly Gln
    535                 540                 545

gat gcg gac gct ttt gtt aaa tcc ata act atg gaa aaa gac acg agc   1795
Asp Ala Asp Ala Phe Val Lys Ser Ile Thr Met Glu Lys Asp Thr Ser
550                 555                 560                 565

agc gag tac act gat gct atg gtt cga cct caa gaa aat cgt gga tca   1843
Ser Glu Tyr Thr Asp Ala Met Val Arg Pro Gln Glu Asn Arg Gly Ser
                570                 575                 580

ggt cga gaa ctg gca gct cgt cgt cgt gta caa gca gcg caa atc aat   1891
Gly Arg Glu Leu Ala Ala Arg Arg Arg Val Gln Ala Ala Gln Ile Asn
            585                 590                 595

cag gca gca cag ctg gat atg aat gtt cat gat ttc cgt gaa tcg aat   1939
Gln Ala Ala Gln Leu Asp Met Asn Val His Asp Phe Arg Glu Ser Asn
        600                 605                 610

ctg cca gag gaa cga ccc gcg aat cct tat gaa gcg tat gtt cgt gag   1987
Leu Pro Glu Glu Arg Pro Ala Asn Pro Tyr Glu Ala Tyr Val Arg Glu
    615                 620                 625

act gaa gcg aaa acc aat gat ccg cag tac ggt tat taatagaaaa        2033
Thr Glu Ala Lys Thr Asn Asp Pro Gln Tyr Gly Tyr
```

630 635 640

tgatagaaag aag 2046

<210> 16
<211> 641
<212> PRT
<213> Corynebacterium glutamicum

<400> 16

```
Met Ser Ser Ser Asp Leu Ala Ser Ile Ile Gly Val Glu Gln Gln Pro
  1               5                  10                  15

Val Ala Tyr Gly Glu Ser Glu Glu Pro Glu Thr Leu Arg Asp Val Leu
             20                  25                  30

Pro Arg Arg Lys Leu His Pro Ser Glu Ile Thr Pro Ser Tyr Glu Val
         35                  40                  45

Ala Asp Gly Glu Gln Arg Ser Ile Phe Gly Glu Ser Ala Pro Ser Asp
     50                  55                  60

Phe Asp Asp Leu Ser Asp Val Glu Glu Phe Asp Thr Ser His Trp Val
 65                  70                  75                  80

Arg Ala Gly Gln Asp Asp Arg Ser Asp Asp Asp Arg Leu Ala Asp Glu
                 85                  90                  95

Ala Gly Val Pro Pro Ser Gly Ala Gln Asp Val Ala Asp Asn Glu Ala
            100                 105                 110

Asn Leu Ser Gly Val Asp Glu Gln Leu His Met Arg Glu Val His Ala
        115                 120                 125

Gln Ser Phe Asp Pro Ile Asp Val Ala Lys Lys Glu Arg Lys Ala Ala
    130                 135                 140

Glu Lys Lys Tyr Ala Lys Pro Pro Lys Ser Asp Asn Pro Tyr Leu Ala
145                 150                 155                 160

Arg Asp Ala Lys Asp Ala Ala Ala Arg Lys Arg Lys Ile Asn Ala Ala
                165                 170                 175

His Asp Asn Phe Ala Gln Glu Met Ala Gln Ala Ala Met Gly Pro Leu
            180                 185                 190

Arg Lys Gly Val Asn Thr Gln Thr Val Met Ala Ala Cys Thr Thr Ala
        195                 200                 205

Ala Val Met Trp Cys Met Ser Pro Arg Met Thr Gly Val Asn Val Asp
    210                 215                 220

Met Lys Arg Lys Phe Asn Lys Asp Leu Glu Gln Ala Lys Asp Thr Lys
225                 230                 235                 240

Leu Ser Lys Tyr Val Ser Lys Asp Phe Trp Lys Ser Lys Leu Thr Arg
                245                 250                 255

Asp Lys Thr Glu Lys Glu Ala Lys Ser Leu Ser Asp Ala Phe Met Gln
            260                 265                 270
```

```
Gln Lys Thr Ala Ile Ile Ser Asn Arg Glu Arg Ile Pro Met Ser Val
        275                 280                 285

Ala Ser Ala Ala Gln Thr Val Val Arg Leu Ser Asp Gln Ala Tyr Glu
    290                 295                 300

Ala Met Arg Glu Val Asp Thr Asp Gly Gln Ala Ile Val Asp Ala Lys
305                 310                 315                 320

Asp Val Ser Ala Gln Val Ala Glu Asp Ile Asp Met Val Val Lys Gln
                325                 330                 335

Gly Glu Glu His Gly Leu Lys Ser Lys Asp Ile Tyr Gly Ala Ala Arg
            340                 345                 350

Asp Ile Val Gly Arg Arg Met Glu Arg Asp Pro Gly Tyr Ala Ala Arg
        355                 360                 365

Phe Asn Glu Thr Ala Phe Gly Thr Val Arg Leu Gly Glu Gln Arg Arg
    370                 375                 380

Gly Met Val Ile Ser Lys Thr Pro Thr Trp Gln Phe Pro Asp Gly Ala
385                 390                 395                 400

Gly Leu Ser Lys Asn Ala Gly Trp Phe Ser Val Arg Glu Pro Met Gly
                405                 410                 415

Asn Ala Gln Asn Phe Ala Asp Asn Leu Ala Ala Thr Leu Ala Thr Glu
            420                 425                 430

Met Arg Val Ala Gly Glu Gln Tyr Gly Ser Asp Gly Val Arg Asp Val
        435                 440                 445

Val Ala Gly Phe Met Thr Ala Thr Asp Val Ser Glu Ser Gly Leu Ala
    450                 455                 460

Ser Ala Lys Lys Leu Leu Pro Asp Phe Asp Thr Arg Gly Arg Ser Ala
465                 470                 475                 480

Ser Arg Val Arg Gln Ile Ala Met Ala Gln Arg Thr Gln Ala Ala Ile
                485                 490                 495

Lys Val Leu Gln Asp Asp Gly Asn Gln Thr Ala Met Thr Thr Glu Gln
            500                 505                 510

Val Lys Glu Val Gln Val Trp Ala Met Asp Gln Ala Glu Lys Val Met
        515                 520                 525

Gln Arg Asp His Pro Ala Ile Leu Asp Lys Phe Val Arg Lys His Gly
    530                 535                 540

Gln Thr Phe Gly Gln Asp Ala Asp Ala Phe Val Lys Ser Ile Thr Met
545                 550                 555                 560

Glu Lys Asp Thr Ser Ser Glu Tyr Thr Asp Ala Met Val Arg Pro Gln
                565                 570                 575

Glu Asn Arg Gly Ser Gly Arg Glu Leu Ala Ala Arg Arg Arg Val Gln
            580                 585                 590
```

```
Ala Ala Gln Ile Asn Gln Ala Ala Gln Leu Asp Met Asn Val His Asp
        595                 600                 605

Phe Arg Glu Ser Asn Leu Pro Glu Glu Arg Pro Ala Asn Pro Tyr Glu
    610                 615                 620

Ala Tyr Val Arg Glu Thr Glu Ala Lys Thr Asn Asp Pro Gln Tyr Gly
625                 630                 635                 640

Tyr
```

<210> 17
<211> 1095
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1072)
<223> RXN01422

<400> 17

```
aatgcattga aatcgtgatc gcctgttatt gttttgtacg tcgaataaca gtcccacaac 60

agttccccaa aaggtgcgag cgggaaaagg agaagcaaac atg gct cag cga aaa   115
                                            Met Ala Gln Arg Lys
                                              1               5

ctg gcc tct gtg atc ggt gca gca ttg gca gca tct gct gta ctg gtt   163
Leu Ala Ser Val Ile Gly Ala Ala Leu Ala Ala Ser Ala Val Leu Val
                10                  15                  20

gga tta atg aca ccc gca aca gca caa agt agt ggc agc tca tca aca   211
Gly Leu Met Thr Pro Ala Thr Ala Gln Ser Ser Gly Ser Ser Ser Thr
            25                  30                  35

gac atc act cga gca ctc acc tca agt ggt ggt gtg gct gat agc cgt   259
Asp Ile Thr Arg Ala Leu Thr Ser Ser Gly Gly Val Ala Asp Ser Arg
        40                  45                  50

gct cct gaa ggt ggc gca aag gtc gtt gtt ttc ggt gac tcc cac acc   307
Ala Pro Glu Gly Gly Ala Lys Val Val Val Phe Gly Asp Ser His Thr
    55                  60                  65

tct ggc acc aat gct cca ttc cgt acc gat gag cgt ggc tgc ctc aag   355
Ser Gly Thr Asn Ala Pro Phe Arg Thr Asp Glu Arg Gly Cys Leu Lys
70                  75                  80                  85

ggt gca aac aac tgg gca gat cag ctg cag tct cag ctg gga ctt ggc   403
Gly Ala Asn Asn Trp Ala Asp Gln Leu Gln Ser Gln Leu Gly Leu Gly
                90                  95                  100

gcg gga gac ctc att gat gtc tcc tgc tcc ggt gca tcg atc aac tct   451
Ala Gly Asp Leu Ile Asp Val Ser Cys Ser Gly Ala Ser Ile Asn Ser
            105                 110                 115

gat gga ttc cac ttc tct gat gaa gtc cgc cat gct gaa gct cgt ggc   499
Asp Gly Phe His Phe Ser Asp Glu Val Arg His Ala Glu Ala Arg Gly
        120                 125                 130
```

```
gca atc ggc cca aac acc acc gat att ttt gtt cag ttg ggc aag aat   547
Ala Ile Gly Pro Asn Thr Thr Asp Ile Phe Val Gln Leu Gly Lys Asn
    135                 140                 145

gat cag tgg ggc ctt tcc aat gtg aac ctt ctg cag tct gtt cag acc   595
Asp Gln Trp Gly Leu Ser Asn Val Asn Leu Leu Gln Ser Val Gln Thr
150                 155                 160                 165

tgc ttg act gat gtg ttc gct ggt tgt ggc gat gct gcg gtt gct gct   643
Cys Leu Thr Asp Val Phe Ala Gly Cys Gly Asp Ala Ala Val Ala Ala
                170                 175                 180

ggc aag atg cag gat cca aat gca gtt act gct gaa aac tat gca gag   691
Gly Lys Met Gln Asp Pro Asn Ala Val Thr Ala Glu Asn Tyr Ala Glu
            185                 190                 195

cgc atg aag cca gtc att gac tac ttg aag tac tac gca cca aac gca   739
Arg Met Lys Pro Val Ile Asp Tyr Leu Lys Tyr Tyr Ala Pro Asn Ala
        200                 205                 210

gag atc acc ttg gtt ggt tac cag gaa tac acc gct cgc agc gga agt   787
Glu Ile Thr Leu Val Gly Tyr Gln Glu Tyr Thr Ala Arg Ser Gly Ser
    215                 220                 225

cag gta tgt gtt cgc ctt ggt gga acc cca ctg gtg aaa aat gat gca   835
Gln Val Cys Val Arg Leu Gly Gly Thr Pro Leu Val Lys Asn Asp Ala
230                 235                 240                 245

cct gcg ctg gtt tcg ttc atg aac aag ttg gac atg gcg att gat ggt   883
Pro Ala Leu Val Ser Phe Met Asn Lys Leu Asp Met Ala Ile Asp Gly
                250                 255                 260

gct gct gga atc ctc ggc gtc agc cac gtt gat ctg cgt agc gcg act   931
Ala Ala Gly Ile Leu Gly Val Ser His Val Asp Leu Arg Ser Ala Thr
            265                 270                 275

gaa ggg cac gac agc tgc tcc aac gat cct tgg gtc aac ggt gtc ttt   979
Glu Gly His Asp Ser Cys Ser Asn Asp Pro Trp Val Asn Gly Val Phe
        280                 285                 290

gat gca cgt gca gaa atc gtc ggc ggt ccg tgg cac cca tct gtt aag   1027
Asp Ala Arg Ala Glu Ile Val Gly Gly Pro Trp His Pro Ser Val Lys
    295                 300                 305

gga gac tcg gtt act gca ggg atc ctg cga gat cga gta aac gcc       1072
Gly Asp Ser Val Thr Ala Gly Ile Leu Arg Asp Arg Val Asn Ala
310                 315                 320

taaagatgac gtcgaaaagc att                                        1095
```

<210> 18
<211> 324
<212> PRT
<213> Corynebacterium glutamicum

<400> 18

```
Met Ala Gln Arg Lys Leu Ala Ser Val Ile Gly Ala Ala Leu Ala Ala
  1               5                  10                  15
```

```
Ser Ala Val Leu Val Gly Leu Met Thr Pro Ala Thr Ala Gln Ser Ser
            20                  25                  30

Gly Ser Ser Ser Thr Asp Ile Thr Arg Ala Leu Thr Ser Ser Gly Gly
        35                  40                  45

Val Ala Asp Ser Arg Ala Pro Glu Gly Gly Ala Lys Val Val Val Phe
    50                  55                  60

Gly Asp Ser His Thr Ser Gly Thr Asn Ala Pro Phe Arg Thr Asp Glu
65                  70                  75                  80

Arg Gly Cys Leu Lys Gly Ala Asn Asn Trp Ala Asp Gln Leu Gln Ser
                85                  90                  95

Gln Leu Gly Leu Gly Ala Gly Asp Leu Ile Asp Val Ser Cys Ser Gly
            100                 105                 110

Ala Ser Ile Asn Ser Asp Gly Phe His Phe Ser Asp Glu Val Arg His
        115                 120                 125

Ala Glu Ala Arg Gly Ala Ile Gly Pro Asn Thr Thr Asp Ile Phe Val
    130                 135                 140

Gln Leu Gly Lys Asn Asp Gln Trp Gly Leu Ser Asn Val Asn Leu Leu
145                 150                 155                 160

Gln Ser Val Gln Thr Cys Leu Thr Asp Val Phe Ala Gly Cys Gly Asp
                165                 170                 175

Ala Ala Val Ala Ala Gly Lys Met Gln Asp Pro Asn Ala Val Thr Ala
            180                 185                 190

Glu Asn Tyr Ala Glu Arg Met Lys Pro Val Ile Asp Tyr Leu Lys Tyr
        195                 200                 205

Tyr Ala Pro Asn Ala Glu Ile Thr Leu Val Gly Tyr Gln Glu Tyr Thr
    210                 215                 220

Ala Arg Ser Gly Ser Gln Val Cys Val Arg Leu Gly Gly Thr Pro Leu
225                 230                 235                 240

Val Lys Asn Asp Ala Pro Ala Leu Val Ser Phe Met Asn Lys Leu Asp
                245                 250                 255

Met Ala Ile Asp Gly Ala Ala Gly Ile Leu Gly Val Ser His Val Asp
            260                 265                 270

Leu Arg Ser Ala Thr Glu Gly His Asp Ser Cys Ser Asn Asp Pro Trp
        275                 280                 285

Val Asn Gly Val Phe Asp Ala Arg Ala Glu Ile Val Gly Gly Pro Trp
    290                 295                 300

His Pro Ser Val Lys Gly Asp Ser Val Thr Ala Gly Ile Leu Arg Asp
305                 310                 315                 320

Arg Val Asn Ala
```

<210> 19
<211> 806
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(783)
<223> FRXA01422

<400> 19

```
ttc ggt gac tcc cac acc tct ggc acc aat gct cca ttc cgt acc gat   48
Phe Gly Asp Ser His Thr Ser Gly Thr Asn Ala Pro Phe Arg Thr Asp
  1               5                  10                  15

gag cgt ggc tgc ctc aag ggt gca aac aac tgg gca gat cag ctg cag   96
Glu Arg Gly Cys Leu Lys Gly Ala Asn Asn Trp Ala Asp Gln Leu Gln
             20                  25                  30

tct cag ctg gga ctt ggc gcg gga gac ctc att gat gtc tcc tgc tcc  144
Ser Gln Leu Gly Leu Gly Ala Gly Asp Leu Ile Asp Val Ser Cys Ser
         35                  40                  45

ggt gca tcg atc aac tct gat gga ttc cac ttc tct gat gaa gtc cgc  192
Gly Ala Ser Ile Asn Ser Asp Gly Phe His Phe Ser Asp Glu Val Arg
     50                  55                  60

cat gct gaa gct cgt ggc gca atc ggc cca aac acc acc gat att ttt  240
His Ala Glu Ala Arg Gly Ala Ile Gly Pro Asn Thr Thr Asp Ile Phe
 65                  70                  75                  80

gtt cag ttg ggc aag aat gat cag tgg ggc ctt tcc aat gtg aac ctt  288
Val Gln Leu Gly Lys Asn Asp Gln Trp Gly Leu Ser Asn Val Asn Leu
                 85                  90                  95

ctg cag tct gtt cag acc tgc ttg act gat gtg ttc gct ggt tgt ggc  336
Leu Gln Ser Val Gln Thr Cys Leu Thr Asp Val Phe Ala Gly Cys Gly
            100                 105                 110

gat gct gcg gtt gct gct ggc aag atg cag gat cca aat gca gtt act  384
Asp Ala Ala Val Ala Ala Gly Lys Met Gln Asp Pro Asn Ala Val Thr
        115                 120                 125

gct gaa aac tat gca gag cgc atg aag cca gtc att gac tac ttg aag  432
Ala Glu Asn Tyr Ala Glu Arg Met Lys Pro Val Ile Asp Tyr Leu Lys
    130                 135                 140

tac tac gca cca aac gca gag atc acc ttg gtt ggt tac cag gaa tac  480
Tyr Tyr Ala Pro Asn Ala Glu Ile Thr Leu Val Gly Tyr Gln Glu Tyr
145                 150                 155                 160

acc gct cgc agc gga agt cag gta tgt gtt cgc ctt ggt gga acc cca  528
Thr Ala Arg Ser Gly Ser Gln Val Cys Val Arg Leu Gly Gly Thr Pro
                165                 170                 175

ctg gtg aaa aat gat gca cct gcg ctg gtt tcg ttc atg aac aag ttg  576
Leu Val Lys Asn Asp Ala Pro Ala Leu Val Ser Phe Met Asn Lys Leu
            180                 185                 190

gac atg gcg att gat ggt gct gct gga atc ctc ggc gtc agc cac gtt  624
Asp Met Ala Ile Asp Gly Ala Ala Gly Ile Leu Gly Val Ser His Val
```

```
        195                 200                 205

gat ctg cgt agc gcg act gaa ggg cac gac agc tgc tcc aac gat cct   672
Asp Leu Arg Ser Ala Thr Glu Gly His Asp Ser Cys Ser Asn Asp Pro
    210                 215                 220

tgg gtc aac ggt gtc ttt gat gca cgt gca gaa atc gtc ggc ggt ccg   720
Trp Val Asn Gly Val Phe Asp Ala Arg Ala Glu Ile Val Gly Gly Pro
225                 230                 235                 240

tgg cac cca tct gtt aag gga gac tcg gtt act gca ggg atc ctg cga   768
Trp His Pro Ser Val Lys Gly Asp Ser Val Thr Ala Gly Ile Leu Arg
                245                 250                 255

gat cga gta aac gcc taaagatgac gtcgaaaagc att                    806
Asp Arg Val Asn Ala
            260
```

<210> 20
<211> 261
<212> PRT
<213> Corynebacterium glutamicum

<400> 20

```
Phe Gly Asp Ser His Thr Ser Gly Thr Asn Ala Pro Phe Arg Thr Asp
  1               5                  10                  15

Glu Arg Gly Cys Leu Lys Gly Ala Asn Asn Trp Ala Asp Gln Leu Gln
             20                  25                  30

Ser Gln Leu Gly Leu Gly Ala Gly Asp Leu Ile Asp Val Ser Cys Ser
         35                  40                  45

Gly Ala Ser Ile Asn Ser Asp Gly Phe His Phe Ser Asp Glu Val Arg
     50                  55                  60

His Ala Glu Ala Arg Gly Ala Ile Gly Pro Asn Thr Thr Asp Ile Phe
 65                  70                  75                  80

Val Gln Leu Gly Lys Asn Asp Gln Trp Gly Leu Ser Asn Val Asn Leu
                 85                  90                  95

Leu Gln Ser Val Gln Thr Cys Leu Thr Asp Val Phe Ala Gly Cys Gly
            100                 105                 110

Asp Ala Ala Val Ala Ala Gly Lys Met Gln Asp Pro Asn Ala Val Thr
        115                 120                 125

Ala Glu Asn Tyr Ala Glu Arg Met Lys Pro Val Ile Asp Tyr Leu Lys
    130                 135                 140

Tyr Tyr Ala Pro Asn Ala Glu Ile Thr Leu Val Gly Tyr Gln Glu Tyr
145                 150                 155                 160

Thr Ala Arg Ser Gly Ser Gln Val Cys Val Arg Leu Gly Gly Thr Pro
                165                 170                 175

Leu Val Lys Asn Asp Ala Pro Ala Leu Val Ser Phe Met Asn Lys Leu
            180                 185                 190
```

```
Asp Met Ala Ile Asp Gly Ala Ala Gly Ile Leu Gly Val Ser His Val
        195                 200                 205

Asp Leu Arg Ser Ala Thr Glu Gly His Asp Ser Cys Ser Asn Asp Pro
    210                 215                 220

Trp Val Asn Gly Val Phe Asp Ala Arg Ala Glu Ile Val Gly Gly Pro
225                 230                 235                 240

Trp His Pro Ser Val Lys Gly Asp Ser Val Thr Ala Gly Ile Leu Arg
                245                 250                 255

Asp Arg Val Asn Ala
            260


<210> 21
<211> 771
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(748)
<223> RXN01403

<400> 21
gtgcgtcgca tacggtgaat tatctttcgg cggatcgttt ccgcacggtg tcgagtttcg 60

tagagtttgc ggccgatcgc ggtattcagg aattcagcca ttg gtg cgc ggt cgg   115
                                        Leu Val Arg Gly Arg
                                          1               5

ggc tat ttc aat gcg gtg gat att tat gag acc tcc acg caa cct gac   163
Gly Tyr Phe Asn Ala Val Asp Ile Tyr Glu Thr Ser Thr Gln Pro Asp
                10                  15                  20

cag gaa ttt cct ttc gat ttt gac act ttt tca gcc gac ccc acg ccg   211
Gln Glu Phe Pro Phe Asp Phe Asp Thr Phe Ser Ala Asp Pro Thr Pro
            25                  30                  35

ttt caa ctc tct gcg gtg cgt gcc gat acc ggc gag acc gtt ttt tgg   259
Phe Gln Leu Ser Ala Val Arg Ala Asp Thr Gly Glu Thr Val Phe Trp
        40                  45                  50

ggc agg gaa gac acc ccg gat ttg agc gct ctg atg aag cgg gtt cgc   307
Gly Arg Glu Asp Thr Pro Asp Leu Ser Ala Leu Met Lys Arg Val Arg
    55                  60                  65

gcg tcg tcg acc atg cct ggt ttc atg ccg atc acc tac atc gac ggc   355
Ala Ser Ser Thr Met Pro Gly Phe Met Pro Ile Thr Tyr Ile Asp Gly
70                  75                  80                  85

cat cca tat gtc gat ggc gcg gtc ggg gag acc ggc ggt ttg atg cta   403
His Pro Tyr Val Asp Gly Ala Val Gly Glu Thr Gly Gly Leu Met Leu
                90                  95                  100

cag ccg gcc atc gat gcg ggc ttc acc cgc ttt ttc gtt atc gcc tcc   451
Gln Pro Ala Ile Asp Ala Gly Phe Thr Arg Phe Phe Val Ile Ala Ser
            105                 110                 115
```

```
cgt ccg cgc gat tat tgg cgc aag gag atc ggg cgc ccg ggt ttc atc   499
Arg Pro Arg Asp Tyr Trp Arg Lys Glu Ile Gly Arg Pro Gly Phe Ile
        120                 125                 130

aaa gct gct tta cga cgt ttc ccc aca atc gcc gac ctc acc atc gcg   547
Lys Ala Ala Leu Arg Arg Phe Pro Thr Ile Ala Asp Leu Thr Ile Ala
    135                 140                 145

cgt cct gca ctg tat aac tcg gta aag caa cag atc ctc gac cta gag   595
Arg Pro Ala Leu Tyr Asn Ser Val Lys Gln Gln Ile Leu Asp Leu Glu
150                 155                 160                 165

aaa caa ggc agc gcc tat gtg ttc ttt gcg gac aac atg aac atc cag   643
Lys Gln Gly Ser Ala Tyr Val Phe Phe Ala Asp Asn Met Asn Ile Gln
                170                 175                 180

aac acg gaa atc aat ctg aag aaa ctc cgt gca tct ttc gat gca ggc   691
Asn Thr Glu Ile Asn Leu Lys Lys Leu Arg Ala Ser Phe Asp Ala Gly
            185                 190                 195

atg cag cag acc cgc aaa gat tgg ccg gag atc atg agc ttc ctg aac   739
Met Gln Gln Thr Arg Lys Asp Trp Pro Glu Ile Met Ser Phe Leu Asn
        200                 205                 210

caa acc aga taatgaaggt ttttagtcca act                            771
Gln Thr Arg
    215
```

Sequence Listing Page 55 of 76

<210> 22
<211> 216
<212> PRT
<213> Corynebacterium glutamicum

<400> 22

```
Leu Val Arg Gly Arg Gly Tyr Phe Asn Ala Val Asp Ile Tyr Glu Thr
  1               5                  10                  15

Ser Thr Gln Pro Asp Gln Glu Phe Pro Phe Asp Phe Asp Thr Phe Ser
             20                  25                  30

Ala Asp Pro Thr Pro Phe Gln Leu Ser Ala Val Arg Ala Asp Thr Gly
         35                  40                  45

Glu Thr Val Phe Trp Gly Arg Glu Asp Thr Pro Asp Leu Ser Ala Leu
     50                  55                  60

Met Lys Arg Val Arg Ala Ser Ser Thr Met Pro Gly Phe Met Pro Ile
 65                  70                  75                  80

Thr Tyr Ile Asp Gly His Pro Tyr Val Asp Gly Ala Val Gly Glu Thr
                 85                  90                  95

Gly Gly Leu Met Leu Gln Pro Ala Ile Asp Ala Gly Phe Thr Arg Phe
            100                 105                 110

Phe Val Ile Ala Ser Arg Pro Arg Asp Tyr Trp Arg Lys Glu Ile Gly
        115                 120                 125

Arg Pro Gly Phe Ile Lys Ala Ala Leu Arg Arg Phe Pro Thr Ile Ala
    130                 135                 140
```

```
Asp Leu Thr Ile Ala Arg Pro Ala Leu Tyr Asn Ser Val Lys Gln Gln
145                 150                 155                 160

Ile Leu Asp Leu Glu Lys Gln Gly Ser Ala Tyr Val Phe Phe Ala Asp
                165                 170                 175

Asn Met Asn Ile Gln Asn Thr Glu Ile Asn Leu Lys Lys Leu Arg Ala
            180                 185                 190

Ser Phe Asp Ala Gly Met Gln Gln Thr Arg Lys Asp Trp Pro Glu Ile
        195                 200                 205

Met Ser Phe Leu Asn Gln Thr Arg
    210                 215
```

<210> 23
<211> 437
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(414)
<223> FRXA01403

<400> 23

```
ccg atc acc tac atc gac ggc cat cca tat gtc gat ggc gcg gtc ggg   48
Pro Ile Thr Tyr Ile Asp Gly His Pro Tyr Val Asp Gly Ala Val Gly
  1               5                  10                  15

gag acc ggc ggt ttg atg cta cag ccg gcc atc gat gcg ggc ttc acc   96
Glu Thr Gly Gly Leu Met Leu Gln Pro Ala Ile Asp Ala Gly Phe Thr
             20                  25                  30

cgc ttt ttc gtt atc gcc tcc cgt ccg cgc gat tat tgg cgc aag gag   144
Arg Phe Phe Val Ile Ala Ser Arg Pro Arg Asp Tyr Trp Arg Lys Glu
         35                  40                  45

atc ggg cgc ccg ggt ttc atc aaa gct gct tta cga cgt ttc ccc aca   192
Ile Gly Arg Pro Gly Phe Ile Lys Ala Ala Leu Arg Arg Phe Pro Thr
     50                  55                  60

atc gcc gac ctc acc atc gcg cgt cct gca ctg tat aac tcg gta aag   240
Ile Ala Asp Leu Thr Ile Ala Arg Pro Ala Leu Tyr Asn Ser Val Lys
 65                  70                  75                  80

caa cag atc ctc gac cta gag aaa caa ggc agc gcc tat gtg ttc ttt   288
Gln Gln Ile Leu Asp Leu Glu Lys Gln Gly Ser Ala Tyr Val Phe Phe
                 85                  90                  95

gcg gac aac atg aac atc cag aac acg gaa atc aat ctg aag aaa ctc   336
Ala Asp Asn Met Asn Ile Gln Asn Thr Glu Ile Asn Leu Lys Lys Leu
            100                 105                 110

cgt gca tct ttc gat gca ggc atg cag cag acc cgc aaa gat tgg ccg   384
Arg Ala Ser Phe Asp Ala Gly Met Gln Gln Thr Arg Lys Asp Trp Pro
        115                 120                 125

gag atc atg agc ttc ctg aac caa acc aga taatgaaggt ttttagtcca     434
```

Glu Ile Met Ser Phe Leu Asn Gln Thr Arg
130 135

act 437

<210> 24
<211> 138
<212> PRT
<213> Corynebacterium glutamicum

<400> 24
Pro Ile Thr Tyr Ile Asp Gly His Pro Tyr Val Asp Gly Ala Val Gly
1 5 10 15

Glu Thr Gly Gly Leu Met Leu Gln Pro Ala Ile Asp Ala Gly Phe Thr
20 25 30

Arg Phe Phe Val Ile Ala Ser Arg Pro Arg Asp Tyr Trp Arg Lys Glu
35 40 45

Ile Gly Arg Pro Gly Phe Ile Lys Ala Ala Leu Arg Arg Phe Pro Thr
50 55 60

Ile Ala Asp Leu Thr Ile Ala Arg Pro Ala Leu Tyr Asn Ser Val Lys
65 70 75 80

Gln Gln Ile Leu Asp Leu Glu Lys Gln Gly Ser Ala Tyr Val Phe Phe
85 90 95

Ala Asp Asn Met Asn Ile Gln Asn Thr Glu Ile Asn Leu Lys Lys Leu
100 105 110

Arg Ala Ser Phe Asp Ala Gly Met Gln Gln Thr Arg Lys Asp Trp Pro
115 120 125

Glu Ile Met Ser Phe Leu Asn Gln Thr Arg
130 135

<210> 25
<211> 489
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(466)
<223> RXN01326

<400> 25
gtccttgagg ctgcttacac tctacttatt gtagaaatgg gagggtcgtg gcgtcgaaaa 60

gcaaacatct tttaacgctt ttggcccgta ttatggtggc atg gct ttc ccc gtg 115
Met Ala Phe Pro Val
1 5

aca gaa gac aaa atc ctg gca gct gag gaa acc ctt ggc agg cgc ctc 163
Thr Glu Asp Lys Ile Leu Ala Ala Glu Glu Thr Leu Gly Arg Arg Leu
10 15 20

```
ccc gaa act ttg cgc gaa cga cta ctt caa aac aat ggt ggc gaa gtc   211
Pro Glu Thr Leu Arg Glu Arg Leu Leu Gln Asn Asn Gly Gly Glu Val
            25                  30                  35

atc gac aat gaa aac aac gac tgg att ctc cat cca gtt cgt gat gac   259
Ile Asp Asn Glu Asn Asn Asp Trp Ile Leu His Pro Val Arg Asp Asp
        40                  45                  50

agc gac cga aaa agg ctt gtc cga act gcc aac gac atc atc cgc gag   307
Ser Asp Arg Lys Arg Leu Val Arg Thr Ala Asn Asp Ile Ile Arg Glu
    55                  60                  65

acc gaa tct gca cgt gaa tgg gac aat ttc ccc gaa aat gcg atc gca   355
Thr Glu Ser Ala Arg Glu Trp Asp Asn Phe Pro Glu Asn Ala Ile Ala
70                  75                  80                  85

att gca aat gac gga acg ggc gac tta ata att ctg ctt ccc gac gat   403
Ile Ala Asn Asp Gly Thr Gly Asp Leu Ile Ile Leu Leu Pro Asp Asp
                90                  95                  100

gat gct ttc tac atc tgg tcg cac gaa gat gaa ccc ctg atc gaa act   451
Asp Ala Phe Tyr Ile Trp Ser His Glu Asp Glu Pro Leu Ile Glu Thr
            105                 110                 115

gaa ctt gag gat gcc taaaacagct ggacagaatt cga                    489
Glu Leu Glu Asp Ala
        120
```

<210> 26
<211> 122
<212> PRT
<213> Corynebacterium glutamicum

<400> 26

```
Met Ala Phe Pro Val Thr Glu Asp Lys Ile Leu Ala Ala Glu Glu Thr
  1               5                  10                  15

Leu Gly Arg Arg Leu Pro Glu Thr Leu Arg Glu Arg Leu Leu Gln Asn
            20                  25                  30

Asn Gly Gly Glu Val Ile Asp Asn Glu Asn Asn Asp Trp Ile Leu His
        35                  40                  45

Pro Val Arg Asp Asp Ser Asp Arg Lys Arg Leu Val Arg Thr Ala Asn
    50                  55                  60

Asp Ile Ile Arg Glu Thr Glu Ser Ala Arg Glu Trp Asp Asn Phe Pro
65                  70                  75                  80

Glu Asn Ala Ile Ala Ile Ala Asn Asp Gly Thr Gly Asp Leu Ile Ile
                85                  90                  95

Leu Leu Pro Asp Asp Asp Ala Phe Tyr Ile Trp Ser His Glu Asp Glu
            100                 105                 110

Pro Leu Ile Glu Thr Glu Leu Glu Asp Ala
        115                 120
```

<210> 27

<211> 361
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (45)..(338)
<223> FRXA01326

<400> 27
ccggctggcg ctgaggaaac cttggcaggc gcctccccga actttg cgc gaa cga 56
Leu Arg Glu Arg
1

cta ctt caa aac aat ggt ggc gaa gtc atc gac aat gaa aac aac gac 104
Leu Leu Gln Asn Asn Gly Gly Glu Val Ile Asp Asn Glu Asn Asn Asp
5 10 15 20

tgg att ctc cat cca gtt cgt gat gac agc gac cga aaa agg ctt gtc 152
Trp Ile Leu His Pro Val Arg Asp Asp Ser Asp Arg Lys Arg Leu Val
25 30 35

cga act gcc aac gac atc atc cgc gag acc gaa tct gca cgt gaa tgg 200
Arg Thr Ala Asn Asp Ile Ile Arg Glu Thr Glu Ser Ala Arg Glu Trp
40 45 50

gac aat ttc ccc gaa aat gcg atc gca att gca aat gac gga acg ggc 248
Asp Asn Phe Pro Glu Asn Ala Ile Ala Ile Ala Asn Asp Gly Thr Gly
55 60 65

gac tta ata att ctg ctt ccc gac gat gat gct ttc tac atc tgg tcg 296
Asp Leu Ile Ile Leu Leu Pro Asp Asp Asp Ala Phe Tyr Ile Trp Ser
70 75 80

cac gaa gat gaa ccc ctg atc gaa act gaa ctt gag gat gcc 338
His Glu Asp Glu Pro Leu Ile Glu Thr Glu Leu Glu Asp Ala
85 90 95

taaaacagct ggacagaatt cga 361

<210> 28
<211> 98
<212> PRT
<213> Corynebacterium glutamicum

<400> 28
Leu Arg Glu Arg Leu Leu Gln Asn Asn Gly Gly Glu Val Ile Asp Asn
1 5 10 15

Glu Asn Asn Asp Trp Ile Leu His Pro Val Arg Asp Asp Ser Asp Arg
20 25 30

Lys Arg Leu Val Arg Thr Ala Asn Asp Ile Ile Arg Glu Thr Glu Ser
35 40 45

Ala Arg Glu Trp Asp Asn Phe Pro Glu Asn Ala Ile Ala Ile Ala Asn
50 55 60

Asp Gly Thr Gly Asp Leu Ile Ile Leu Leu Pro Asp Asp Asp Ala Phe
65 70 75 80

```
Tyr Ile Trp Ser His Glu Asp Glu Pro Leu Ile Glu Thr Glu Leu Glu
                 85                  90                  95

Asp Ala
```

<210> 29
<211> 648
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(625)
<223> RXN01301

<400> 29

```
aggcaagaac gcaaagttct agtacgctgc taaagtatgc agcttggccc gcacggtttc 60

cgcgtgcggg acgtgttcat ttctgtatag gaaaactacc ttg atc gtt gat acc   115
                                            Leu Ile Val Asp Thr
                                              1               5

cag ttt gag aag atc cct gct cac gac gtc gtg ggc atc cgg gta atc   163
Gln Phe Glu Lys Ile Pro Ala His Asp Val Val Gly Ile Arg Val Ile
                10                  15                  20

ctt tcc tct gag gat ctc cct gag ctc ttt aaa cgc ggc tac gcg gaa   211
Leu Ser Ser Glu Asp Leu Pro Glu Leu Phe Lys Arg Gly Tyr Ala Glu
            25                  30                  35

gta aag aaa ttc ctc cgc cta gaa ggc atc gaa cct aaa ggt cct gcc   259
Val Lys Lys Phe Leu Arg Leu Glu Gly Ile Glu Pro Lys Gly Pro Ala
        40                  45                  50

cgc gcc tac tac ttt ggc gat gtc tct gac acc gta gac atc ctg att   307
Arg Ala Tyr Tyr Phe Gly Asp Val Ser Asp Thr Val Asp Ile Leu Ile
    55                  60                  65

ggt ttc ccc gtc agc ccc gcg caa gca gaa tcc ctg cgc cgc ggc gca   355
Gly Phe Pro Val Ser Pro Ala Gln Ala Glu Ser Leu Arg Arg Gly Ala
70                  75                  80                  85

ttg agc caa tcc ggt ggc gac atc gat gac gtt gtc ctc cac cac ttc   403
Leu Ser Gln Ser Gly Gly Asp Ile Asp Asp Val Val Leu His His Phe
                90                  95                 100

cgc gac atg aaa acc atg cac agc cgc cac tcc ggc ccc ttc gat gga   451
Arg Asp Met Lys Thr Met His Ser Arg His Ser Gly Pro Phe Asp Gly
            105                 110                 115

gtc gag cgc gtc tgg gac gaa atc ctc gat gaa gtc gaa gac ctc gga   499
Val Glu Arg Val Trp Asp Glu Ile Leu Asp Glu Val Glu Asp Leu Gly
        120                 125                 130

tgc act ctg cca tcc agc agc atc ggt tgg gaa gaa tac atc gag ggc   547
Cys Thr Leu Pro Ser Ser Ser Ile Gly Trp Glu Glu Tyr Ile Glu Gly
    135                 140                 145
```

```
cca gcc acc gct gat acc tgc gac caa ctg gcc tct gaa gtt tat gtt   595
Pro Ala Thr Ala Asp Thr Cys Asp Gln Leu Ala Ser Glu Val Tyr Val
150                 155                 160                 165

cag gtg tgc caa gca ccg gtg aag tct gca taaagattca cccggaattt     645
Gln Val Cys Gln Ala Pro Val Lys Ser Ala
                170                 175

ccc                                                               648


<210> 30
<211> 175
<212> PRT
<213> Corynebacterium glutamicum

<400> 30
Leu Ile Val Asp Thr Gln Phe Glu Lys Ile Pro Ala His Asp Val Val
  1               5                  10                  15

Gly Ile Arg Val Ile Leu Ser Ser Glu Asp Leu Pro Glu Leu Phe Lys
             20                  25                  30

Arg Gly Tyr Ala Glu Val Lys Lys Phe Leu Arg Leu Glu Gly Ile Glu
         35                  40                  45

Pro Lys Gly Pro Ala Arg Ala Tyr Tyr Phe Gly Asp Val Ser Asp Thr
     50                  55                  60

Val Asp Ile Leu Ile Gly Phe Pro Val Ser Pro Ala Gln Ala Glu Ser
 65                  70                  75                  80

Leu Arg Arg Gly Ala Leu Ser Gln Ser Gly Gly Asp Ile Asp Asp Val
                 85                  90                  95

Val Leu His His Phe Arg Asp Met Lys Thr Met His Ser Arg His Ser
            100                 105                 110

Gly Pro Phe Asp Gly Val Glu Arg Val Trp Asp Glu Ile Leu Asp Glu
        115                 120                 125

Val Glu Asp Leu Gly Cys Thr Leu Pro Ser Ser Ser Ile Gly Trp Glu
    130                 135                 140

Glu Tyr Ile Glu Gly Pro Ala Thr Ala Asp Thr Cys Asp Gln Leu Ala
145                 150                 155                 160

Ser Glu Val Tyr Val Gln Val Cys Gln Ala Pro Val Lys Ser Ala
                165                 170                 175


<210> 31
<211> 428
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(405)
<223> FRXA01301
```

<400> 31
ttc ctc cgc cta gaa ggc atc gaa cct aaa ggt cct gcc cgc gcc tac 48
Phe Leu Arg Leu Glu Gly Ile Glu Pro Lys Gly Pro Ala Arg Ala Tyr
1 5 10 15

tac ttt ggc gat gtc tct gac acc gta gac atc ctg att ggt ttc ccc 96
Tyr Phe Gly Asp Val Ser Asp Thr Val Asp Ile Leu Ile Gly Phe Pro
20 25 30

gtc agc ccc gcg caa gca gaa tcc ctg cgc cgc ggc gca ttg agc caa 144
Val Ser Pro Ala Gln Ala Glu Ser Leu Arg Arg Gly Ala Leu Ser Gln
35 40 45

tcc ggt ggc gac atc gat gac gtt gtc ctc cac cac ttc cgc gac atg 192
Ser Gly Gly Asp Ile Asp Asp Val Val Leu His His Phe Arg Asp Met
50 55 60

aaa acc atg cac agc cgc cac tcc ggc ccc ttc gat gga gtc gag cgc 240
Lys Thr Met His Ser Arg His Ser Gly Pro Phe Asp Gly Val Glu Arg
65 70 75 80

gtc tgg gac gaa atc ctc gat gaa gtc gaa gac ctc gga tgc act ctg 288
Val Trp Asp Glu Ile Leu Asp Glu Val Glu Asp Leu Gly Cys Thr Leu
85 90 95

cca tcc agc agc atc ggt tgg gaa gaa tac atc gag ggc cca gcc acc 336
Pro Ser Ser Ser Ile Gly Trp Glu Glu Tyr Ile Glu Gly Pro Ala Thr
100 105 110

gct gat acc tgc gac caa ctg gcc tct gaa gtt tat gtt cag gtg tgc 384
Ala Asp Thr Cys Asp Gln Leu Ala Ser Glu Val Tyr Val Gln Val Cys
115 120 125

caa gca ccg gtg aag tct gca taaagattca cccggaattt ccc 428
Gln Ala Pro Val Lys Ser Ala
130 135

<210> 32
<211> 135
<212> PRT
<213> Corynebacterium glutamicum

<400> 32
Phe Leu Arg Leu Glu Gly Ile Glu Pro Lys Gly Pro Ala Arg Ala Tyr
1 5 10 15

Tyr Phe Gly Asp Val Ser Asp Thr Val Asp Ile Leu Ile Gly Phe Pro
20 25 30

Val Ser Pro Ala Gln Ala Glu Ser Leu Arg Arg Gly Ala Leu Ser Gln
35 40 45

Ser Gly Gly Asp Ile Asp Asp Val Val Leu His His Phe Arg Asp Met
50 55 60

Lys Thr Met His Ser Arg His Ser Gly Pro Phe Asp Gly Val Glu Arg
65 70 75 80

Val Trp Asp Glu Ile Leu Asp Glu Val Glu Asp Leu Gly Cys Thr Leu
85 90 95

```
Pro Ser Ser Ser Ile Gly Trp Glu Glu Tyr Ile Glu Gly Pro Ala Thr
            100                 105                 110

Ala Asp Thr Cys Asp Gln Leu Ala Ser Glu Val Tyr Val Gln Val Cys
        115                 120                 125

Gln Ala Pro Val Lys Ser Ala
    130                 135


<210> 33
<211> 567
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(544)
<223> RXN01276

<400> 33
tgcgtaaaac cctcatcacc atgctcgcga ccaccgcgat cgccttttcc gccatctcac 60

cagtgcaggc gcaaaccgtg gacacagaca ctgacgcctc gtg tca tct gag ctg   115
                                            Val Ser Ser Glu Leu
                                              1               5

agc agc ggc aca agc tca gga agt tca gag gat tcc gaa gat tct gac   163
Ser Ser Gly Thr Ser Ser Gly Ser Ser Glu Asp Ser Glu Asp Ser Asp
                10                  15                  20

atc tcc aac cgg gac atc atc ttc ggc atc gca gct atc gct gca gtc   211
Ile Ser Asn Arg Asp Ile Ile Phe Gly Ile Ala Ala Ile Ala Ala Val
            25                  30                  35

ggc gga ctt atc gca agt ggt gtg cac tgg gca gta caa cag cgc atg   259
Gly Gly Leu Ile Ala Ser Gly Val His Trp Ala Val Gln Gln Arg Met
        40                  45                  50

atc cca aat ccc ctc cca gga atc att cca aat ccc cct gca ctg gca   307
Ile Pro Asn Pro Leu Pro Gly Ile Ile Pro Asn Pro Pro Ala Leu Ala
    55                  60                  65

cct cag gcg cct gcc cca gca cct gct ccc gct cct gcc cct cag gca   355
Pro Gln Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Gln Ala
70                  75                  80                  85

gtc gcg ccc cag gtt gtc gct ccc cag gtt gtc gcg cct gct cca gcc   403
Val Ala Pro Gln Val Val Ala Pro Gln Val Val Ala Pro Ala Pro Ala
                90                  95                  100

cca gta cag acc aac cgc acc tac aaa aac tgc acc gaa gta tgg aac   451
Pro Val Gln Thr Asn Arg Thr Tyr Lys Asn Cys Thr Glu Val Trp Asn
            105                 110                 115

gtc ctg gga agg tcc atc cgc caa agc gat cca ggc tac ggc aca cac   499
Val Leu Gly Arg Ser Ile Arg Gln Ser Asp Pro Gly Tyr Gly Thr His
        120                 125                 130

ctc gac cgc gac cgc gac ggc atc ggc tgc gaa tca cgc cct agg       544
```

Leu Asp Arg Asp Arg Asp Gly Ile Gly Cys Glu Ser Arg Pro Arg
135 140 145

tagtttgggt tttggggatc ttc 567

<210> 34
<211> 148
<212> PRT
<213> Corynebacterium glutamicum

<400> 34
Val Ser Ser Glu Leu Ser Ser Gly Thr Ser Ser Gly Ser Ser Glu Asp
1 5 10 15

Ser Glu Asp Ser Asp Ile Ser Asn Arg Asp Ile Ile Phe Gly Ile Ala
20 25 30

Ala Ile Ala Ala Val Gly Gly Leu Ile Ala Ser Gly Val His Trp Ala
35 40 45

Val Gln Gln Arg Met Ile Pro Asn Pro Leu Pro Gly Ile Ile Pro Asn
50 55 60

Pro Pro Ala Leu Ala Pro Gln Ala Pro Ala Pro Ala Pro Ala Pro Ala
65 70 75 80

Pro Ala Pro Gln Ala Val Ala Pro Gln Val Val Ala Pro Gln Val Val
85 90 95

Ala Pro Ala Pro Ala Pro Val Gln Thr Asn Arg Thr Tyr Lys Asn Cys
100 105 110

Thr Glu Val Trp Asn Val Leu Gly Arg Ser Ile Arg Gln Ser Asp Pro
115 120 125

Gly Tyr Gly Thr His Leu Asp Arg Asp Arg Asp Gly Ile Gly Cys Glu
130 135 140

Ser Arg Pro Arg
145

<210> 35
<211> 669
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(646)
<223> FRXA01276

<400> 35
ctagatgccc ggaaaatagc atctcctata cacccaaaaa aaaggggagc gctgacagaa 60

aatagtaata attttgacag ctcgtgcaaa gatgattggc atg cgt aaa acc ctc 115
Met Arg Lys Thr Leu
1 5

atc acc atg ctc gcg acc acc gcg atc gcc ttt tcc gcc atc tca cca 163

```
Ile Thr Met Leu Ala Thr Thr Ala Ile Ala Phe Ser Ala Ile Ser Pro
                10                  15                  20

gtg cag gcg caa acc gtg gac aca gac act gac gcc tcc gtg tca tct   211
Val Gln Ala Gln Thr Val Asp Thr Asp Thr Asp Ala Ser Val Ser Ser
            25                  30                  35

gag ctg agc agc ggc aca agc tca gga agt tca gag gat tcc gaa gat   259
Glu Leu Ser Ser Gly Thr Ser Ser Gly Ser Ser Glu Asp Ser Glu Asp
        40                  45                  50

tct gac atc tcc aac cgg gac atc atc ttc ggc atc gca gct atc gct   307
Ser Asp Ile Ser Asn Arg Asp Ile Ile Phe Gly Ile Ala Ala Ile Ala
    55                  60                  65

gca gtc ggc gga ctt atc gca ggt ggt gtg cac tgg gca gta caa cag   355
Ala Val Gly Gly Leu Ile Ala Gly Gly Val His Trp Ala Val Gln Gln
70                  75                  80                  85

cgc atg atc cca aat ccc ctc cca gga atc att cca aat ccc cct gca   403
Arg Met Ile Pro Asn Pro Leu Pro Gly Ile Ile Pro Asn Pro Pro Ala
                90                  95                  100

ctg gca cct cag gcg cct gcc cca gca cct gct ccc gct cct gcc cct   451
Leu Ala Pro Gln Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro
            105                 110                 115

cag gca gtc gcg ccc cag gtt gtc gct ccc cag gtt gtc gcg cct gct   499
Gln Ala Val Ala Pro Gln Val Val Ala Pro Gln Val Val Ala Pro Ala
        120                 125                 130

cca gcc cca gta cag acc aac cgc acc tac aaa aac tgc acc gaa gta   547
Pro Ala Pro Val Gln Thr Asn Arg Thr Tyr Lys Asn Cys Thr Glu Val
    135                 140                 145

tgg aac gtc ctg gga agg tcc atc cgc caa agc gat cca ggc tac ggc   595
Trp Asn Val Leu Gly Arg Ser Ile Arg Gln Ser Asp Pro Gly Tyr Gly
150                 155                 160                 165

aca cac ctc gac cgc gac cgc gac ggc atc ggc tgc gaa tca cgc cct   643
Thr His Leu Asp Arg Asp Arg Asp Gly Ile Gly Cys Glu Ser Arg Pro
                170                 175                 180

agg tagtttgggt tttggggatc ttc                                    669
Arg
```

Application Copy

<210> 36
<211> 182
<212> PRT
<213> Corynebacterium glutamicum

<400> 36

```
Met Arg Lys Thr Leu Ile Thr Met Leu Ala Thr Thr Ala Ile Ala Phe
  1               5                  10                  15

Ser Ala Ile Ser Pro Val Gln Ala Gln Thr Val Asp Thr Asp Thr Asp
            20                  25                  30

Ala Ser Val Ser Ser Glu Leu Ser Ser Gly Thr Ser Ser Gly Ser Ser
```

```
         35                  40                  45

Glu Asp Ser Glu Asp Ser Asp Ile Ser Asn Arg Asp Ile Ile Phe Gly
     50                  55                  60

Ile Ala Ala Ile Ala Ala Val Gly Gly Leu Ile Ala Gly Gly Val His
 65                  70                  75                  80

Trp Ala Val Gln Gln Arg Met Ile Pro Asn Pro Leu Pro Gly Ile Ile
                 85                  90                  95

Pro Asn Pro Pro Ala Leu Ala Pro Gln Ala Pro Ala Pro Ala Pro Ala
            100                 105                 110

Pro Ala Pro Ala Pro Gln Ala Val Ala Pro Gln Val Val Ala Pro Gln
        115                 120                 125

Val Val Ala Pro Ala Pro Ala Pro Val Gln Thr Asn Arg Thr Tyr Lys
    130                 135                 140

Asn Cys Thr Glu Val Trp Asn Val Leu Gly Arg Ser Ile Arg Gln Ser
145                 150                 155                 160

Asp Pro Gly Tyr Gly Thr His Leu Asp Arg Asp Arg Asp Gly Ile Gly
                165                 170                 175

Cys Glu Ser Arg Pro Arg
            180
```

Application Filed with the Chinese Patent Office on 2007-07-20

<210> 37
<211> 366
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(343)
<223> RXN01231

<400> 37
tcctgggacg tcttccccga ggcgtgggag acattgaagg tttacctggg ctttcgtgcc 60

ccaggcatcg agcacttcac ccccctatga cgccttgcaa atg ctg ggc tac acc 115
                                                Met Leu Gly Tyr Thr
                                                  1   5

ttc gtc atc ttt atc ctg gcg ccg ttt ctc atc ctc acc gga ata gcg 163
Phe Val Ile Phe Ile Leu Ala Pro Phe Leu Ile Leu Thr Gly Ile Ala
                 10   15   20

atg gcc ccg gcc atc cgg tcc cgc ttc ccg tgg tac gtc aaa ctc ttc 211
Met Ala Pro Ala Ile Arg Ser Arg Phe Pro Trp Tyr Val Lys Leu Phe
             25   30   35

ggc ggc cac cag ggt gca cgt tcc ctg cac ttc atc gcc atg gtg ttg 259
Gly Gly His Gln Gly Ala Arg Ser Leu His Phe Ile Ala Met Val Leu
         40   45   50

atg acg ggc ttt gtc atc atg cac gtc ggc ctg gtt ttt tgg tcc atg 307
Met Thr Gly Phe Val Ile Met His Val Gly Leu Val Phe Trp Ser Met
```
```

```
     55                  60                  65

gcg act aca aca tgg tcc aca tgg tct tcg gcg ata tgaacactga        353
Ala Thr Thr Thr Trp Ser Thr Trp Ser Ser Ala Ile
 70                  75                  80

ccgtgcggcg cag                                                    366


<210> 38
<211> 81
<212> PRT
<213> Corynebacterium glutamicum

<400> 38
Met Leu Gly Tyr Thr Phe Val Ile Phe Ile Leu Ala Pro Phe Leu Ile
  1               5                  10                  15

Leu Thr Gly Ile Ala Met Ala Pro Ala Ile Arg Ser Arg Phe Pro Trp
            20                  25                  30

Tyr Val Lys Leu Phe Gly Gly His Gln Gly Ala Arg Ser Leu His Phe
         35                  40                  45

Ile Ala Met Val Leu Met Thr Gly Phe Val Ile Met His Val Gly Leu
     50                  55                  60

Val Phe Trp Ser Met Ala Thr Thr Thr Trp Ser Thr Trp Ser Ser Ala
 65                  70                  75                  80

Ile



<210> 39
<211> 627
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(604)
<223> FRXA01231

<400> 39
cctgggacgt cttccccgag gcgtgggang acattgaagg tttacctggg ctttcgtgcc 60

ccaggcatcg agcacttcac ccccctatga cgccttgcaa atg ctg ggc tac acc   115
                                              Met Leu Gly Tyr Thr
                                                1               5

ttc gtc atc ttt atc ctg gcg ccg ttt ctc atc ctc acc gga ata gcg   163
Phe Val Ile Phe Ile Leu Ala Pro Phe Leu Ile Leu Thr Gly Ile Ala
                10                  15                  20

atg gcc ccg gcc atc cgg tcc cgc ttc ccg tgg tac gtc aaa ctc ttc   211
Met Ala Pro Ala Ile Arg Ser Arg Phe Pro Trp Tyr Val Lys Leu Phe
            25                  30                  35

ggc ggc cac cag ggt gca cgt tcc ctg cac ttc atc gcc atg gtg ttg   259
Gly Gly His Gln Gly Ala Arg Ser Leu His Phe Ile Ala Met Val Leu
```

```
         40                  45                  50

atg acg ggc ttt gtc atc atg cac ngt cgg cct ggt ttt ttg gtc cat   307
Met Thr Gly Phe Val Ile Met His Xaa Arg Pro Gly Phe Leu Val His
     55                  60                  65

ggc gac tac aac atg gtc cac atg gtc ttc ggc gat atg aac act gac   355
Gly Asp Tyr Asn Met Val His Met Val Phe Gly Asp Met Asn Thr Asp
 70                  75                  80                  85

cgt gcg gcg cag gcc tac atc atc gtg atc acc acc atc gtc ant ggt   403
Arg Ala Ala Gln Ala Tyr Ile Ile Val Ile Thr Thr Ile Val Xaa Gly
                 90                  95                 100

ggt gtt ktt ctg rat cgk gct cag tat att kgt mrc tgg ctk acc grg   451
Gly Val Xaa Leu Xaa Xaa Ala Gln Tyr Ile Xaa Xaa Trp Xaa Thr Xaa
            105                 110                 115

mcc gcg ccm wgc ggt tya ccg cca gcw tca tck gag wtm ggw cgc aaa   499
Xaa Ala Xaa Xaa Gly Xaa Pro Pro Xaa Ser Xaa Glu Xaa Xaa Arg Lys
        120                 125                 130

atc ttt nct caw ccg gct gcg tcc ccg gat gag cag gca gan nan cac   547
Ile Phe Xaa Xaa Pro Ala Ala Ser Pro Asp Glu Gln Ala Xaa Xaa His
    135                 140                 145

cta cac gga caa gga cat ctc gca gtt cca ctg gac caa tgg cct gcc   595
Leu His Gly Gln Gly His Leu Ala Val Pro Leu Asp Gln Trp Pro Ala
150                 155                 160                 165

gcc gac cga tgatgaatcc cccgagtgga tcg                            627
Ala Asp Arg
```

<210> 40
<211> 168
<212> PRT
<213> Corynebacterium glutamicum

<400> 40

```
Met Leu Gly Tyr Thr Phe Val Ile Phe Ile Leu Ala Pro Phe Leu Ile
  1               5                  10                  15

Leu Thr Gly Ile Ala Met Ala Pro Ala Ile Arg Ser Arg Phe Pro Trp
             20                  25                  30

Tyr Val Lys Leu Phe Gly Gly His Gln Gly Ala Arg Ser Leu His Phe
         35                  40                  45

Ile Ala Met Val Leu Met Thr Gly Phe Val Ile Met His Xaa Arg Pro
     50                  55                  60

Gly Phe Leu Val His Gly Asp Tyr Asn Met Val His Met Val Phe Gly
 65                  70                  75                  80

Asp Met Asn Thr Asp Arg Ala Ala Gln Ala Tyr Ile Ile Val Ile Thr
                 85                  90                  95

Thr Ile Val Xaa Gly Gly Val Xaa Leu Xaa Xaa Ala Gln Tyr Ile Xaa
            100                 105                 110
```

```
Xaa Trp Xaa Thr Xaa Xaa Ala Xaa Xaa Gly Xaa Pro Pro Xaa Ser Xaa
        115                 120                 125

Glu Xaa Xaa Arg Lys Ile Phe Xaa Xaa Pro Ala Ala Ser Pro Asp Glu
    130                 135                 140

Gln Ala Xaa Xaa His Leu His Gly Gln Gly His Leu Ala Val Pro Leu
145                 150                 155                 160

Asp Gln Trp Pro Ala Ala Asp Arg
                165
```

<210> 41
<211> 954
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(931)
<223> RXN01210

<400> 41
ttcgctgcaa aacccgccac cttggaatcc gtattcatgg acatcgcctc actcgagaac 60

```
acctcgctgc aaaccgccta gaatctttaa ggagaccaca atg acc acg tca cac   115
                                              Met Thr Thr Ser His
                                                1               5

acc gcc cgc ggg ctg caa cat gca acc ccg gag cgc cgc aag act tca   163
Thr Ala Arg Gly Leu Gln His Ala Thr Pro Glu Arg Arg Lys Thr Ser
                10                  15                  20

ttt ttc aaa acc tct ctg ttt aag gcc gaa tgg ctc cag ttc cgc aga   211
Phe Phe Lys Thr Ser Leu Phe Lys Ala Glu Trp Leu Gln Phe Arg Arg
            25                  30                  35

aat aaa acc ctg ttg ttc atg gcc acc gta ttc cca gtc gga atc cct   259
Asn Lys Thr Leu Leu Phe Met Ala Thr Val Phe Pro Val Gly Ile Pro
        40                  45                  50

ttg ttg ctc ttt ctc atc gga aat ggt ggg gca gca gag tcc gcg aac   307
Leu Leu Leu Phe Leu Ile Gly Asn Gly Gly Ala Ala Glu Ser Ala Asn
    55                  60                  65

tcc ttc gac tac ttc gtc atg tac acc ctg cta ttt gtg cag ttc tac   355
Ser Phe Asp Tyr Phe Val Met Tyr Thr Leu Leu Phe Val Gln Phe Tyr
70                  75                  80                  85

acg gtg ctg tcc atg gca acc acc cgc cgt gat gaa cgt gtg ctg aaa   403
Thr Val Leu Ser Met Ala Thr Thr Arg Arg Asp Glu Arg Val Leu Lys
                90                  95                  100

agg ctg cgc acg gga gaa gcc cgc gac atc gat atc atc ggt gcc atc   451
Arg Leu Arg Thr Gly Glu Ala Arg Asp Ile Asp Ile Ile Gly Ala Ile
            105                 110                 115

tgt ttc ccc ggc gcg ctc ctc aca ctg atc ttc acc gtg gtg atc att   499
Cys Phe Pro Gly Ala Leu Leu Thr Leu Ile Phe Thr Val Val Ile Ile
```

```
        120                 125                 130

cca ttg ctc atg gtt ttg gga gct ccc gcg ccc atc aac ctt gtg ccc   547
Pro Leu Leu Met Val Leu Gly Ala Pro Ala Pro Ile Asn Leu Val Pro
    135                 140                 145

att gtg ttt gcc gta ctg atc gga cta ctt ctt tgt agt gct ctt gcc   595
Ile Val Phe Ala Val Leu Ile Gly Leu Leu Leu Cys Ser Ala Leu Ala
150                 155                 160                 165

ttg atg acc agc ggt ttc acc cga aac gcc gaa gcc gca cag atg acc   643
Leu Met Thr Ser Gly Phe Thr Arg Asn Ala Glu Ala Ala Gln Met Thr
                170                 175                 180

tcc atg ccc gtg ttc atg ctt gcg atg ggt gga ctt gga tca atc cgc   691
Ser Met Pro Val Phe Met Leu Ala Met Gly Gly Leu Gly Ser Ile Arg
            185                 190                 195

ttc gta ttc ggc gac agc att gtg gct gat atc ttg gcc tac acc cca   739
Phe Val Phe Gly Asp Ser Ile Val Ala Asp Ile Leu Ala Tyr Thr Pro
        200                 205                 210

ttc gcc gcg atc agt gac ctt gtc caa atc ggc tgg gct ggc gcc acc   787
Phe Ala Ala Ile Ser Asp Leu Val Gln Ile Gly Trp Ala Gly Ala Thr
    215                 220                 225

ttc gcc gac agc gtt ggt gga gta gag gca gca aac ttc gct gga att   835
Phe Ala Asp Ser Val Gly Gly Val Glu Ala Ala Asn Phe Ala Gly Ile
230                 235                 240                 245

ttc caa gac atg ctc ata cca ctt gga att ctg gca gcg tgg aca gct   883
Phe Gln Asp Met Leu Ile Pro Leu Gly Ile Leu Ala Ala Trp Thr Ala
                250                 255                 260

gca gcg gtg tgg gcg gcg aac cgc tac atg cgc tgg gac tcg tac cgc   931
Ala Ala Val Trp Ala Ala Asn Arg Tyr Met Arg Trp Asp Ser Tyr Arg
            265                 270                 275

taagcctgca gccgacggga tta                                        954
```

FA Global | 2009-12-17 09:57:08 | Page 70

<210> 42
<211> 277
<212> PRT
<213> Corynebacterium glutamicum

<400> 42

```
Met Thr Thr Ser His Thr Ala Arg Gly Leu Gln His Ala Thr Pro Glu
  1               5                  10                  15

Arg Arg Lys Thr Ser Phe Phe Lys Thr Ser Leu Phe Lys Ala Glu Trp
             20                  25                  30

Leu Gln Phe Arg Arg Asn Lys Thr Leu Leu Phe Met Ala Thr Val Phe
         35                  40                  45

Pro Val Gly Ile Pro Leu Leu Leu Phe Leu Ile Gly Asn Gly Gly Ala
     50                  55                  60

Ala Glu Ser Ala Asn Ser Phe Asp Tyr Phe Val Met Tyr Thr Leu Leu
 65                  70                  75                  80
```

```
Phe Val Gln Phe Tyr Thr Val Leu Ser Met Ala Thr Thr Arg Arg Asp
                85                  90                  95

Glu Arg Val Leu Lys Arg Leu Arg Thr Gly Glu Ala Arg Asp Ile Asp
            100                 105                 110

Ile Ile Gly Ala Ile Cys Phe Pro Gly Ala Leu Leu Thr Leu Ile Phe
        115                 120                 125

Thr Val Val Ile Ile Pro Leu Leu Met Val Leu Gly Ala Pro Ala Pro
    130                 135                 140

Ile Asn Leu Val Pro Ile Val Phe Ala Val Leu Ile Gly Leu Leu Leu
145                 150                 155                 160

Cys Ser Ala Leu Ala Leu Met Thr Ser Gly Phe Thr Arg Asn Ala Glu
                165                 170                 175

Ala Ala Gln Met Thr Ser Met Pro Val Phe Met Leu Ala Met Gly Gly
            180                 185                 190

Leu Gly Ser Ile Arg Phe Val Phe Gly Asp Ser Ile Val Ala Asp Ile
        195                 200                 205

Leu Ala Tyr Thr Pro Phe Ala Ala Ile Ser Asp Leu Val Gln Ile Gly
    210                 215                 220

Trp Ala Gly Ala Thr Phe Ala Asp Ser Val Gly Gly Val Glu Ala Ala
225                 230                 235                 240

Asn Phe Ala Gly Ile Phe Gln Asp Met Leu Ile Pro Leu Gly Ile Leu
                245                 250                 255

Ala Ala Trp Thr Ala Ala Ala Val Trp Ala Ala Asn Arg Tyr Met Arg
            260                 265                 270

Trp Asp Ser Tyr Arg
        275
```

Sequence Listing

<210> 43
<211> 716
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(693)
<223> FRXA01210

<400> 43

```
gta ttc cca gtc gga atc cct ttg ttg ctc ttt ctc atc gga aat ggt   48
Val Phe Pro Val Gly Ile Pro Leu Leu Leu Phe Leu Ile Gly Asn Gly
  1               5                  10                  15

ggg gca gca gag tcc gcg aac tcc ttc gac tac ttc gtc atg tac acc   96
Gly Ala Ala Glu Ser Ala Asn Ser Phe Asp Tyr Phe Val Met Tyr Thr
             20                  25                  30

ctg cta ttt gtg cag ttc tac acg gtg ctg tcc atg gca acc acc cgc   144
```

```
Leu Leu Phe Val Gln Phe Tyr Thr Val Leu Ser Met Ala Thr Thr Arg
         35                  40                  45

cgt gat gaa cgt gtg ctg aaa agg ctg cgc acg gga gaa gcc cgc gac   192
Arg Asp Glu Arg Val Leu Lys Arg Leu Arg Thr Gly Glu Ala Arg Asp
     50                  55                  60

atc gat atc atc ggt gcc atc tgt ttc ccc ggc gcg ctc ctc aca ctg   240
Ile Asp Ile Ile Gly Ala Ile Cys Phe Pro Gly Ala Leu Leu Thr Leu
 65                  70                  75                  80

atc ttc acc gtg gtg atc att cca ttg ctc atg gtt ttg gga gct ccc   288
Ile Phe Thr Val Val Ile Ile Pro Leu Leu Met Val Leu Gly Ala Pro
                 85                  90                  95

gcg ccc atc aac ctt gtg ccc att gtg ttt gcc gta ctg atc gga cta   336
Ala Pro Ile Asn Leu Val Pro Ile Val Phe Ala Val Leu Ile Gly Leu
            100                 105                 110

ctt ctt tgt agt gct ctt gcc ttg atg acc agc ggt ttc acc cga aac   384
Leu Leu Cys Ser Ala Leu Ala Leu Met Thr Ser Gly Phe Thr Arg Asn
        115                 120                 125

gcc gaa gcc gca cag atg acc tcc atg ccc gtg ttc atg ctt gcg atg   432
Ala Glu Ala Ala Gln Met Thr Ser Met Pro Val Phe Met Leu Ala Met
    130                 135                 140

ggt gga ctt gga tca atc cgc ttc gta ttc ggc gac agc att gtg gct   480
Gly Gly Leu Gly Ser Ile Arg Phe Val Phe Gly Asp Ser Ile Val Ala
145                 150                 155                 160

gat atc ttg gcc tac acc cca ttc gcc gcg atc agt gac ctt gtc caa   528
Asp Ile Leu Ala Tyr Thr Pro Phe Ala Ala Ile Ser Asp Leu Val Gln
                165                 170                 175

atc ggc tgg gct ggc gcc acc ttc gcc gac agc gtt ggt gga gta gag   576
Ile Gly Trp Ala Gly Ala Thr Phe Ala Asp Ser Val Gly Gly Val Glu
            180                 185                 190

gca gca aac ttc gct gga att ttc caa gac atg ctc ata cca ctt gga   624
Ala Ala Asn Phe Ala Gly Ile Phe Gln Asp Met Leu Ile Pro Leu Gly
        195                 200                 205

att ctg gca gcg tgg aca gct gca gcg gtg tgg gcg gcg aac cgc tac   672
Ile Leu Ala Ala Trp Thr Ala Ala Ala Val Trp Ala Ala Asn Arg Tyr
    210                 215                 220

atg cgc tgg gac tcg tac cgc taagcctgca gccgacggga tta             716
Met Arg Trp Asp Ser Tyr Arg
225                 230
```

<210> 44
<211> 231
<212> PRT
<213> Corynebacterium glutamicum

<400> 44

```
Val Phe Pro Val Gly Ile Pro Leu Leu Leu Phe Leu Ile Gly Asn Gly
  1               5                  10                  15
```

```
Gly Ala Ala Glu Ser Ala Asn Ser Phe Asp Tyr Phe Val Met Tyr Thr
            20                  25                  30

Leu Leu Phe Val Gln Phe Tyr Thr Val Leu Ser Met Ala Thr Thr Arg
        35                  40                  45

Arg Asp Glu Arg Val Leu Lys Arg Leu Arg Thr Gly Glu Ala Arg Asp
    50                  55                  60

Ile Asp Ile Ile Gly Ala Ile Cys Phe Pro Gly Ala Leu Leu Thr Leu
65                  70                  75                  80

Ile Phe Thr Val Val Ile Ile Pro Leu Leu Met Val Leu Gly Ala Pro
                85                  90                  95

Ala Pro Ile Asn Leu Val Pro Ile Val Phe Ala Val Leu Ile Gly Leu
            100                 105                 110

Leu Leu Cys Ser Ala Leu Ala Leu Met Thr Ser Gly Phe Thr Arg Asn
        115                 120                 125

Ala Glu Ala Ala Gln Met Thr Ser Met Pro Val Phe Met Leu Ala Met
    130                 135                 140

Gly Gly Leu Gly Ser Ile Arg Phe Val Phe Gly Asp Ser Ile Val Ala
145                 150                 155                 160

Asp Ile Leu Ala Tyr Thr Pro Phe Ala Ala Ile Ser Asp Leu Val Gln
                165                 170                 175

Ile Gly Trp Ala Gly Ala Thr Phe Ala Asp Ser Val Gly Gly Val Glu
            180                 185                 190

Ala Ala Asn Phe Ala Gly Ile Phe Gln Asp Met Leu Ile Pro Leu Gly
        195                 200                 205

Ile Leu Ala Ala Trp Thr Ala Ala Ala Val Trp Ala Ala Asn Arg Tyr
    210                 215                 220

Met Arg Trp Asp Ser Tyr Arg
225                 230


<210> 45
<211> 400
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(400)
<223> RXN01206

<400> 45
ccgtgccagt gatgaaaagc cggcgagccg ccaaacttga ttaagtgatt gtcactttgg 60

attgtcatat tgggcgaata aaccggtagg attccccttc gtg agc gcc gaa aat   115
                                               Val Ser Ala Glu Asn
                                                 1               5

acc gag aac aca gat tcc cca ttt gaa atc tcc gag ttt gat gat cac   163
```

```
Thr Glu Asn Thr Asp Ser Pro Phe Glu Ile Ser Glu Phe Asp Asp His
                10                  15                  20

cga cgc ccc ctc cag cgg gcc ctc aaa ttc ggt tcc atc gcc cta att   211
Arg Arg Pro Leu Gln Arg Ala Leu Lys Phe Gly Ser Ile Ala Leu Ile
            25                  30                  35

gtc ttc acc ctg atc tcc cta gcg atc tgg ggt gca act cgt ggc gta   259
Val Phe Thr Leu Ile Ser Leu Ala Ile Trp Gly Ala Thr Arg Gly Val
        40                  45                  50

ccc ggc gta tca gca gtt gtt atc ggc gca gca gtt ggc gca ggc ttt   307
Pro Gly Val Ser Ala Val Val Ile Gly Ala Ala Val Gly Ala Gly Phe
    55                  60                  65

gtc ctc tta acg gct ctc agc gtc ctg ttt aca act aat tcc aac gtc   355
Val Leu Leu Thr Ala Leu Ser Val Leu Phe Thr Thr Asn Ser Asn Val
70                  75                  80                  85

acc acc acc ggt gcg gtg gtg ctc ggt ggc tgg ctg ctg aag atc       400
Thr Thr Thr Gly Ala Val Val Leu Gly Gly Trp Leu Leu Lys Ile
                90                  95                  100
```

Translation Request Form

<210> 46
<211> 100
<212> PRT
<213> Corynebacterium glutamicum

<400> 46

```
Val Ser Ala Glu Asn Thr Glu Asn Thr Asp Ser Pro Phe Glu Ile Ser
  1               5                  10                  15

Glu Phe Asp Asp His Arg Arg Pro Leu Gln Arg Ala Leu Lys Phe Gly
            20                  25                  30

Ser Ile Ala Leu Ile Val Phe Thr Leu Ile Ser Leu Ala Ile Trp Gly
        35                  40                  45

Ala Thr Arg Gly Val Pro Gly Val Ser Ala Val Val Ile Gly Ala Ala
    50                  55                  60

Val Gly Ala Gly Phe Val Leu Leu Thr Ala Leu Ser Val Leu Phe Thr
65                  70                  75                  80

Thr Asn Ser Asn Val Thr Thr Thr Gly Ala Val Val Leu Gly Gly Trp
                85                  90                  95

Leu Leu Lys Ile
            100
```

<210> 47
<211> 361
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(361)
<223> FRXA01206

<400> 47
ccgtgccagt gatgaaaagc cggcgagccg ccaaacttga ttaagtgatt gtcactttgg 60

attgtcatat tgggcgaata aaccggtagg attccccttc gtg agc gcc gaa aat 115
Val Ser Ala Glu Asn
1 5

acc gag aac aca gat tcc cca ttt gaa atc tcc gag ttt gat gat cac 163
Thr Glu Asn Thr Asp Ser Pro Phe Glu Ile Ser Glu Phe Asp Asp His
10 15 20

cga cgc ccc ctc cag cgg gcc ctc aaa ttc ggt tcc atc gcc cta att 211
Arg Arg Pro Leu Gln Arg Ala Leu Lys Phe Gly Ser Ile Ala Leu Ile
25 30 35

gtc ttc acc ctg atc tcc cta gcg atc tgg ggt gca act cgt ggc gta 259
Val Phe Thr Leu Ile Ser Leu Ala Ile Trp Gly Ala Thr Arg Gly Val
40 45 50

ccc ggc gta tca gca gtt gtt atc ggc gca gca gtt ggc gca ggc ttt 307
Pro Gly Val Ser Ala Val Val Ile Gly Ala Ala Val Gly Ala Gly Phe
55 60 65

gtc ctc tta acg gct ctc agc gtc ctg ttt aca act aat tcc aac gtc 355
Val Leu Leu Thr Ala Leu Ser Val Leu Phe Thr Thr Asn Ser Asn Val
70 75 80 85

acc acc 361
Thr Thr

<210> 48
<211> 87
<212> PRT
<213> Corynebacterium glutamicum

<400> 48
Val Ser Ala Glu Asn Thr Glu Asn Thr Asp Ser Pro Phe Glu Ile Ser
1 5 10 15

Glu Phe Asp Asp His Arg Arg Pro Leu Gln Arg Ala Leu Lys Phe Gly
20 25 30

Ser Ile Ala Leu Ile Val Phe Thr Leu Ile Ser Leu Ala Ile Trp Gly
35 40 45

Ala Thr Arg Gly Val Pro Gly Val Ser Ala Val Val Ile Gly Ala Ala
50 55 60

Val Gly Ala Gly Phe Val Leu Leu Thr Ala Leu Ser Val Leu Phe Thr
65 70 75 80

Thr Asn Ser Asn Val Thr Thr
85

<210> 49
<211> 1209
<212> DNA

<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1186)
<223> RXN01121

<400> 49
aaagatttac tgcgtacaac tctaaccaac aatattggca atgggttgtt ccatcttagc 60

gctttacctg tgaactctgc agagcggtac gcttaagcta atg aat ccc gaa ttt 115
Met Asn Pro Glu Phe
1 5

att cac ggc gca acc gaa att gaa acc aca aac agg ggc ctt cgc ccg 163
Ile His Gly Ala Thr Glu Ile Glu Thr Thr Asn Arg Gly Leu Arg Pro
10 15 20

cat cga ctc agc aaa gaa ata gta gaa cgc tac tgt gat ccc cag ttt 211
His Arg Leu Ser Lys Glu Ile Val Glu Arg Tyr Cys Asp Pro Gln Phe
25 30 35

agc gcg atg gaa cgc caa cca tcg ggc gtg cgc gtt gtg tgt cgc acc 259
Ser Ala Met Glu Arg Gln Pro Ser Gly Val Arg Val Val Cys Arg Thr
40 45 50

acc gcc acc tcc gtc acg ctg acc acg tat tcc acg cgg gtg gtg tac 307
Thr Ala Thr Ser Val Thr Leu Thr Thr Tyr Ser Thr Arg Val Val Tyr
55 60 65

ctc gat tcc ggc cgg ccg ggc ggc aag att gat gtg ctt atc gac ggc 355
Leu Asp Ser Gly Arg Pro Gly Gly Lys Ile Asp Val Leu Ile Asp Gly
70 75 80 85

gcc ccc aca tct tcc acg cca act tcc ggg ggc gag acc acg gaa gtc 403
Ala Pro Thr Ser Ser Thr Pro Thr Ser Gly Gly Glu Thr Thr Glu Val
90 95 100

aat ttc atc acc ggc gcc acg gaa cgg cgc ctg aaa gat ccg cag gtg 451
Asn Phe Ile Thr Gly Ala Thr Glu Arg Arg Leu Lys Asp Pro Gln Val
105 110 115

ctc aca gtg gat gga ctt tca gag cag gaa aag gtg gtg gag ttc tgg 499
Leu Thr Val Asp Gly Leu Ser Glu Gln Glu Lys Val Val Glu Phe Trp
120 125 130

ctg cct cac aat gaa gaa att gaa gtg atc tcc ctt aaa gcc aac gca 547
Leu Pro His Asn Glu Glu Ile Glu Val Ile Ser Leu Lys Ala Asn Ala
135 140 145

gct tta aac act gtc gaa gac acc cgt ccc gtg tgg atc aat tac ggc 595
Ala Leu Asn Thr Val Glu Asp Thr Arg Pro Val Trp Ile Asn Tyr Gly
150 155 160 165

agc tcc att agc cac ggt tcg gtt gcc act gcc cca acc aaa att tgg 643
Ser Ser Ile Ser His Gly Ser Val Ala Thr Ala Pro Thr Lys Ile Trp
170 175 180

cca gcc att gtt gcc cag tcc aaa aac tac aac ctg cgt aac ttc ggt 691
Pro Ala Ile Val Ala Gln Ser Lys Asn Tyr Asn Leu Arg Asn Phe Gly
185 190 195

```
ttt ggt ggc agc gcc atg ttg gat cct ttt atg gcg agg cta atc agg   739
Phe Gly Gly Ser Ala Met Leu Asp Pro Phe Met Ala Arg Leu Ile Arg
        200                 205                 210

gat act cca gct gat ctg atc acc ttg gaa att ggc atc aat att gtc   787
Asp Thr Pro Ala Asp Leu Ile Thr Leu Glu Ile Gly Ile Asn Ile Val
    215                 220                 225

aat ggt gat gtg atg cgt cgc cgc gga cta gag gct gct gtg gat ggg   835
Asn Gly Asp Val Met Arg Arg Arg Gly Leu Glu Ala Ala Val Asp Gly
230                 235                 240                 245

ttc atc aat acc atc cgc gat ggc cac ccc acc acg ccg atc aag att   883
Phe Ile Asn Thr Ile Arg Asp Gly His Pro Thr Thr Pro Ile Lys Ile
                250                 255                 260

gtg tcg ccg ttc tac tgc ccc att cat gag aaa act cca gga ccc ggc   931
Val Ser Pro Phe Tyr Cys Pro Ile His Glu Lys Thr Pro Gly Pro Gly
            265                 270                 275

gcg ttt gat acc tca tcg ttt ggc agt ggt cag att agg ttc atc gcc   979
Ala Phe Asp Thr Ser Ser Phe Gly Ser Gly Gln Ile Arg Phe Ile Ala
        280                 285                 290

act ggt gaa cct gat gag cat ggt cga ctg acg ctg gag atg gtg cgt   1027
Thr Gly Glu Pro Asp Glu His Gly Arg Leu Thr Leu Glu Met Val Arg
    295                 300                 305

gag gtg ttg gag ggg ttc gtc gaa aag caa aaa gac ccg cac ctg acc   1075
Glu Val Leu Glu Gly Phe Val Glu Lys Gln Lys Asp Pro His Leu Thr
310                 315                 320                 325

tac gtc gat ggt gcg agc ctt tat cag gcc agc gat gcg ccg ttg ctg   1123
Tyr Val Asp Gly Ala Ser Leu Tyr Gln Ala Ser Asp Ala Pro Leu Leu
                330                 335                 340

gat aat ttg cac cca gac gag gcg tcg cac gcc tta att gcg cag cgt   1171
Asp Asn Leu His Pro Asp Glu Ala Ser His Ala Leu Ile Ala Gln Arg
            345                 350                 355

ttg ctt aag caa ctt tgaaatcggc ttcggtgatt tcg                    1209
Leu Leu Lys Gln Leu
        360
```

<210> 50
<211> 362
<212> PRT
<213> Corynebacterium glutamicum

<400> 50

```
Met Asn Pro Glu Phe Ile His Gly Ala Thr Glu Ile Glu Thr Thr Asn
  1               5                  10                  15

Arg Gly Leu Arg Pro His Arg Leu Ser Lys Glu Ile Val Glu Arg Tyr
             20                  25                  30

Cys Asp Pro Gln Phe Ser Ala Met Glu Arg Gln Pro Ser Gly Val Arg
         35                  40                  45
```

```
Val Val Cys Arg Thr Thr Ala Thr Ser Val Thr Leu Thr Thr Tyr Ser
     50                  55                  60

Thr Arg Val Val Tyr Leu Asp Ser Gly Arg Pro Gly Gly Lys Ile Asp
 65                  70                  75                  80

Val Leu Ile Asp Gly Ala Pro Thr Ser Ser Thr Pro Thr Ser Gly Gly
                 85                  90                  95

Glu Thr Thr Glu Val Asn Phe Ile Thr Gly Ala Thr Glu Arg Arg Leu
            100                 105                 110

Lys Asp Pro Gln Val Leu Thr Val Asp Gly Leu Ser Glu Gln Glu Lys
        115                 120                 125

Val Val Glu Phe Trp Leu Pro His Asn Glu Glu Ile Glu Val Ile Ser
    130                 135                 140

Leu Lys Ala Asn Ala Ala Leu Asn Thr Val Glu Asp Thr Arg Pro Val
145                 150                 155                 160

Trp Ile Asn Tyr Gly Ser Ser Ile Ser His Gly Ser Val Ala Thr Ala
                165                 170                 175

Pro Thr Lys Ile Trp Pro Ala Ile Val Ala Gln Ser Lys Asn Tyr Asn
            180                 185                 190

Leu Arg Asn Phe Gly Phe Gly Gly Ser Ala Met Leu Asp Pro Phe Met
        195                 200                 205

Ala Arg Leu Ile Arg Asp Thr Pro Ala Asp Leu Ile Thr Leu Glu Ile
    210                 215                 220

Gly Ile Asn Ile Val Asn Gly Asp Val Met Arg Arg Arg Gly Leu Glu
225                 230                 235                 240

Ala Ala Val Asp Gly Phe Ile Asn Thr Ile Arg Asp Gly His Pro Thr
                245                 250                 255

Thr Pro Ile Lys Ile Val Ser Pro Phe Tyr Cys Pro Ile His Glu Lys
            260                 265                 270

Thr Pro Gly Pro Gly Ala Phe Asp Thr Ser Ser Phe Gly Ser Gly Gln
        275                 280                 285

Ile Arg Phe Ile Ala Thr Gly Glu Pro Asp Glu His Gly Arg Leu Thr
    290                 295                 300

Leu Glu Met Val Arg Glu Val Leu Glu Gly Phe Val Glu Lys Gln Lys
305                 310                 315                 320

Asp Pro His Leu Thr Tyr Val Asp Gly Ala Ser Leu Tyr Gln Ala Ser
                325                 330                 335

Asp Ala Pro Leu Leu Asp Asn Leu His Pro Asp Glu Ala Ser His Ala
            340                 345                 350

Leu Ile Ala Gln Arg Leu Leu Lys Gln Leu
        355                 360
```

<210> 51
<211> 778
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(778)
<223> FRXA01121

<400> 51
aaagatttac tgcgtacaac tctaaccaac aatattggca atgggttgtt ccatcttagc 60

gctttacctg tgaactctgc agagcggtac gcttaagcta atg aat ccc gaa ttt 115
Met Asn Pro Glu Phe
1 5

att cac ggc gca acc gaa att gaa acc aca aac agg ggc ctt cgc ccg 163
Ile His Gly Ala Thr Glu Ile Glu Thr Thr Asn Arg Gly Leu Arg Pro
10 15 20

cat cga ctc agc aaa gaa ata gta gaa cgc tac tgt gat ccc cag ttt 211
His Arg Leu Ser Lys Glu Ile Val Glu Arg Tyr Cys Asp Pro Gln Phe
25 30 35

agc gcg atg gaa cgc caa cca tcg ggc gtg cgc gtt gtg tgt cgc acc 259
Ser Ala Met Glu Arg Gln Pro Ser Gly Val Arg Val Val Cys Arg Thr
40 45 50

acc gcc acc tcc gtc acg ctg acc acg tat tcc acg cgg gtg gtg tac 307
Thr Ala Thr Ser Val Thr Leu Thr Thr Tyr Ser Thr Arg Val Val Tyr
55 60 65

ctc gat tcc ggc cgg ccg ggc ggc aag att gat gtg ctt atc gac ggc 355
Leu Asp Ser Gly Arg Pro Gly Gly Lys Ile Asp Val Leu Ile Asp Gly
70 75 80 85

gcc ccc aca tct tcc acg cca act tcc ggg ggc gag acc acg gaa gtc 403
Ala Pro Thr Ser Ser Thr Pro Thr Ser Gly Gly Glu Thr Thr Glu Val
90 95 100

aat ttc atc acc ggc gcc acg gaa cgg cgc ctg aaa gat ccg cag gtg 451
Asn Phe Ile Thr Gly Ala Thr Glu Arg Arg Leu Lys Asp Pro Gln Val
105 110 115

ctc aca gtg gat gga ctt tca gag cag gaa aag gtg gtg gag ttc tgg 499
Leu Thr Val Asp Gly Leu Ser Glu Gln Glu Lys Val Val Glu Phe Trp
120 125 130

ctg cct cac aat gaa gaa att gaa gtg atc tcc ctt aaa gcc aac gca 547
Leu Pro His Asn Glu Glu Ile Glu Val Ile Ser Leu Lys Ala Asn Ala
135 140 145

gct tta aac act gtc gaa gac acc cgt ccc gtg tgg atc aat tac ggc 595
Ala Leu Asn Thr Val Glu Asp Thr Arg Pro Val Trp Ile Asn Tyr Gly
150 155 160 165

agc tcc att agc cac ggt tcg gtt gcc act gcc cca acc aaa att tgg 643
Ser Ser Ile Ser His Gly Ser Val Ala Thr Ala Pro Thr Lys Ile Trp
170 175 180

```
cca gcc att gtt gcc cag tcc aaa aac tac aac ctg cgt aac ttc ggt   691
Pro Ala Ile Val Ala Gln Ser Lys Asn Tyr Asn Leu Arg Asn Phe Gly
            185                 190                 195

ttt ggt ggc agc gcc atg ttg gat cct ttt atg gcg agg cta atc agg   739
Phe Gly Gly Ser Ala Met Leu Asp Pro Phe Met Ala Arg Leu Ile Arg
        200                 205                 210

gat act cca gct gat ctg atc acc ttg gaa att ggc atc               778
Asp Thr Pro Ala Asp Leu Ile Thr Leu Glu Ile Gly Ile
    215                 220                 225


<210> 52
<211> 226
<212> PRT
<213> Corynebacterium glutamicum

<400> 52
Met Asn Pro Glu Phe Ile His Gly Ala Thr Glu Ile Glu Thr Thr Asn
  1               5                  10                  15

Arg Gly Leu Arg Pro His Arg Leu Ser Lys Glu Ile Val Glu Arg Tyr
             20                  25                  30

Cys Asp Pro Gln Phe Ser Ala Met Glu Arg Gln Pro Ser Gly Val Arg
         35                  40                  45

Val Val Cys Arg Thr Thr Ala Thr Ser Val Thr Leu Thr Thr Tyr Ser
     50                  55                  60

Thr Arg Val Val Tyr Leu Asp Ser Gly Arg Pro Gly Gly Lys Ile Asp
 65                  70                  75                  80

Val Leu Ile Asp Gly Ala Pro Thr Ser Ser Thr Pro Thr Ser Gly Gly
                 85                  90                  95

Glu Thr Thr Glu Val Asn Phe Ile Thr Gly Ala Thr Glu Arg Arg Leu
            100                 105                 110

Lys Asp Pro Gln Val Leu Thr Val Asp Gly Leu Ser Glu Gln Glu Lys
        115                 120                 125

Val Val Glu Phe Trp Leu Pro His Asn Glu Glu Ile Glu Val Ile Ser
    130                 135                 140

Leu Lys Ala Asn Ala Ala Leu Asn Thr Val Glu Asp Thr Arg Pro Val
145                 150                 155                 160

Trp Ile Asn Tyr Gly Ser Ser Ile Ser His Gly Ser Val Ala Thr Ala
                165                 170                 175

Pro Thr Lys Ile Trp Pro Ala Ile Val Ala Gln Ser Lys Asn Tyr Asn
            180                 185                 190

Leu Arg Asn Phe Gly Phe Gly Gly Ser Ala Met Leu Asp Pro Phe Met
        195                 200                 205

Ala Arg Leu Ile Arg Asp Thr Pro Ala Asp Leu Ile Thr Leu Glu Ile
    210                 215                 220
```

Gly Ile
225

<210> 53
<211> 902
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(879)
<223> RXN01085

<400> 53

```
cga aag cgt ggt gaa gga ctt gat ccc aac tca cca gaa gct att gag   48
Arg Lys Arg Gly Glu Gly Leu Asp Pro Asn Ser Pro Glu Ala Ile Glu
  1               5                  10                  15

cag gcg aag aag aaa ggg gaa cgg aag gct cgt aat gag cgt tgc cgc   96
Gln Ala Lys Lys Lys Gly Glu Arg Lys Ala Arg Asn Glu Arg Cys Arg
             20                  25                  30

aaa aac ttc aaa ggt ggt ggc acc aaa gat ctt aag cag act gat cgg   144
Lys Asn Phe Lys Gly Gly Gly Thr Lys Asp Leu Lys Gln Thr Asp Arg
         35                  40                  45

acc ttt gat cag ctg cga aaa cag cgg gtg acg gat aaa gcc cgc aac   192
Thr Phe Asp Gln Leu Arg Lys Gln Arg Val Thr Asp Lys Ala Arg Asn
     50                  55                  60

cgt gac gta cac aat gag cag caa ctg gca cgc ggt gaa atc gga gaa   240
Arg Asp Val His Asn Glu Gln Gln Leu Ala Arg Gly Glu Ile Gly Glu
 65                  70                  75                  80

atg cgc tca ccg atg tgg gtt gag gtg ggt gct gcg att ctg ggc gtg   288
Met Arg Ser Pro Met Trp Val Glu Val Gly Ala Ala Ile Leu Gly Val
                 85                  90                  95

ttt gtc ctg gtt gtg atg tgg ctg gcc tgg ggc ggt atc ggg ctg ctg   336
Phe Val Leu Val Val Met Trp Leu Ala Trp Gly Gly Ile Gly Leu Leu
            100                 105                 110

atc cag acc atg atg aat act ggc tca cct aat gac aaa gag ctt ttt   384
Ile Gln Thr Met Met Asn Thr Gly Ser Pro Asn Asp Lys Glu Leu Phe
        115                 120                 125

gat gag ctt ggt gtg aga ccc tat tat gtt gct gtc gaa cag caa atc   432
Asp Glu Leu Gly Val Arg Pro Tyr Tyr Val Ala Val Glu Gln Gln Ile
    130                 135                 140

ggc acc agt agt gct cac acc acg tgc tac caa ccg ctt gat gaa ttt   480
Gly Thr Ser Ser Ala His Thr Thr Cys Tyr Gln Pro Leu Asp Glu Phe
145                 150                 155                 160

ggc aat aat ttt ggc gac tgt acg cgt agc gtg cct aaa gag cca gtg   528
Gly Asn Asn Phe Gly Asp Cys Thr Arg Ser Val Pro Lys Glu Pro Val
                165                 170                 175

tgg tac gcc gat tat gta gct agt gtg ttc gca gaa cat ggc ttt gat   576
Trp Tyr Ala Asp Tyr Val Ala Ser Val Phe Ala Glu His Gly Phe Asp
```

```
            180                 185                 190

gca cca gaa cct att gat aat tcg gtg ggt agc tgg ctg tta ttt ggt   624
Ala Pro Glu Pro Ile Asp Asn Ser Val Gly Ser Trp Leu Leu Phe Gly
        195                 200                 205

cat gtg ggc att att cgg gtg acg ttt gtg att gcg gtt gca gcg ggt   672
His Val Gly Ile Ile Arg Val Thr Phe Val Ile Ala Val Ala Ala Gly
    210                 215                 220

gtg tat gcg atg tca cgc gca gca atg atg cgt cag cta gaa aca caa   720
Val Tyr Ala Met Ser Arg Ala Ala Met Met Arg Gln Leu Glu Thr Gln
225                 230                 235                 240

aac gtc gct gtg gac acc acc gat att aac cag cac acc aat gac gca   768
Asn Val Ala Val Asp Thr Thr Asp Ile Asn Gln His Thr Asn Asp Ala
                245                 250                 255

cgt ttg gcg att ccg cag gag att gtg cgc gat ttg agt ctg ttc ccc   816
Arg Leu Ala Ile Pro Gln Glu Ile Val Arg Asp Leu Ser Leu Phe Pro
            260                 265                 270

gat gtc ggt gca cac ttc acc agt cca gcc ctc aag cat gat ttc cca   864
Asp Val Gly Ala His Phe Thr Ser Pro Ala Leu Lys His Asp Phe Pro
        275                 280                 285

tgt gat gct gtc gaa taagggcttt gaaaaaggtg gat                    902
Cys Asp Ala Val Glu
    290
```

Application Filed Under 37 CFR 1.821(c)

<210> 54
<211> 293
<212> PRT
<213> Corynebacterium glutamicum

<400> 54

```
Arg Lys Arg Gly Glu Gly Leu Asp Pro Asn Ser Pro Glu Ala Ile Glu
  1               5                  10                  15

Gln Ala Lys Lys Lys Gly Glu Arg Lys Ala Arg Asn Glu Arg Cys Arg
             20                  25                  30

Lys Asn Phe Lys Gly Gly Gly Thr Lys Asp Leu Lys Gln Thr Asp Arg
         35                  40                  45

Thr Phe Asp Gln Leu Arg Lys Gln Arg Val Thr Asp Lys Ala Arg Asn
     50                  55                  60

Arg Asp Val His Asn Glu Gln Gln Leu Ala Arg Gly Glu Ile Gly Glu
 65                  70                  75                  80

Met Arg Ser Pro Met Trp Val Glu Val Gly Ala Ala Ile Leu Gly Val
                 85                  90                  95

Phe Val Leu Val Val Met Trp Leu Ala Trp Gly Gly Ile Gly Leu Leu
            100                 105                 110

Ile Gln Thr Met Met Asn Thr Gly Ser Pro Asn Asp Lys Glu Leu Phe
        115                 120                 125
```

```
Asp Glu Leu Gly Val Arg Pro Tyr Tyr Val Ala Val Glu Gln Gln Ile
    130                 135                 140

Gly Thr Ser Ser Ala His Thr Thr Cys Tyr Gln Pro Leu Asp Glu Phe
145                 150                 155                 160

Gly Asn Asn Phe Gly Asp Cys Thr Arg Ser Val Pro Lys Glu Pro Val
                165                 170                 175

Trp Tyr Ala Asp Tyr Val Ala Ser Val Phe Ala Glu His Gly Phe Asp
            180                 185                 190

Ala Pro Glu Pro Ile Asp Asn Ser Val Gly Ser Trp Leu Leu Phe Gly
        195                 200                 205

His Val Gly Ile Ile Arg Val Thr Phe Val Ile Ala Val Ala Ala Gly
    210                 215                 220

Val Tyr Ala Met Ser Arg Ala Ala Met Met Arg Gln Leu Glu Thr Gln
225                 230                 235                 240

Asn Val Ala Val Asp Thr Thr Asp Ile Asn Gln His Thr Asn Asp Ala
                245                 250                 255

Arg Leu Ala Ile Pro Gln Glu Ile Val Arg Asp Leu Ser Leu Phe Pro
            260                 265                 270

Asp Val Gly Ala His Phe Thr Ser Pro Ala Leu Lys His Asp Phe Pro
        275                 280                 285

Cys Asp Ala Val Glu
    290
```

Application Filed

<210> 55
<211> 1057
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1057)
<223> FRXA01085

<400> 55
gaagggtcgt aatgagcgtt gccgcaaaaa cttcaaaggt ggtggcacca aagatcttaa 60

```
gcagactgat cggacctttg atcagctgcg aaaacagcgg gtg acg gat aaa gcc   115
                                          Val Thr Asp Lys Ala
                                            1               5

cgc aac cgt gac gta cac aat gag cag caa ctg gca cgc ggt gaa atc   163
Arg Asn Arg Asp Val His Asn Glu Gln Gln Leu Ala Arg Gly Glu Ile
                 10                  15                  20

gga gaa atg cgc tca ccg atg tgg gtt gag gtg ggt gct gcg att ctg   211
Gly Glu Met Arg Ser Pro Met Trp Val Glu Val Gly Ala Ala Ile Leu
             25                  30                  35

ggc gtg ttt gtc ctg gtt gtg atg tgg ctg gcc tgg ggc ggt atc ggg   259
Gly Val Phe Val Leu Val Val Met Trp Leu Ala Trp Gly Gly Ile Gly
```

```
         40                  45                  50

ctg ctg atc cag acc atg atg aat act ggc tca cct aat gac aaa gag   307
Leu Leu Ile Gln Thr Met Met Asn Thr Gly Ser Pro Asn Asp Lys Glu
     55                  60                  65

ctt ttt gat gag ctt ggt gtg aga ccc tat tat gtt gct gtc gaa cag   355
Leu Phe Asp Glu Leu Gly Val Arg Pro Tyr Tyr Val Ala Val Glu Gln
 70                  75                  80                  85

caa atc ggc acc agt agt gct cac acc acg tgc tac caa ccg ctt gat   403
Gln Ile Gly Thr Ser Ser Ala His Thr Thr Cys Tyr Gln Pro Leu Asp
                 90                  95                 100

gaa ttt ggc aat aat ttt ggc gac tgt acg cgt agc gtg cct aaa gag   451
Glu Phe Gly Asn Asn Phe Gly Asp Cys Thr Arg Ser Val Pro Lys Glu
            105                 110                 115

cca gtg tgg tac gcc gat tat gta gct agt gtg ttc gca gaa cat ggc   499
Pro Val Trp Tyr Ala Asp Tyr Val Ala Ser Val Phe Ala Glu His Gly
        120                 125                 130

ttt gat gca cca gaa cct att gat aat tcg gtg ggt agc tgg ctg tta   547
Phe Asp Ala Pro Glu Pro Ile Asp Asn Ser Val Gly Ser Trp Leu Leu
    135                 140                 145

ttt ggt cat gtg ggc att att cgg gtg acg ttt gtg att gcg gtt gca   595
Phe Gly His Val Gly Ile Ile Arg Val Thr Phe Val Ile Ala Val Ala
150                 155                 160                 165

gcg ggt gtg tat gcg atg tca cgc gca gca atg atg cgt cag cta gaa   643
Ala Gly Val Tyr Ala Met Ser Arg Ala Ala Met Met Arg Gln Leu Glu
                170                 175                 180

aca caa aac gtc gct gtg gac acc acc gat att aac cag cac acc aat   691
Thr Gln Asn Val Ala Val Asp Thr Thr Asp Ile Asn Gln His Thr Asn
            185                 190                 195

gac gca cgt ttg gcg att ccg cag gag att gtg cgc gat ttg agt ctg   739
Asp Ala Arg Leu Ala Ile Pro Gln Glu Ile Val Arg Asp Leu Ser Leu
        200                 205                 210

ttc ccc gat gtc ggt gca cac tca cca gtc cag ccc tca agc atg att   787
Phe Pro Asp Val Gly Ala His Ser Pro Val Gln Pro Ser Ser Met Ile
    215                 220                 225

tcc cat gtg atg ctg tcg aat aag ggc ttg aaa aag gtg gat gta acg   835
Ser His Val Met Leu Ser Asn Lys Gly Leu Lys Lys Val Asp Val Thr
230                 235                 240                 245

cag ttt gca cag gag aca att atc gac aat gac act ggt gaa att gtc   883
Gln Phe Ala Gln Glu Thr Ile Ile Asp Asn Asp Thr Gly Glu Ile Val
                250                 255                 260

tct gaa aag ggt gaa gtg ctc tat gac ggt gca gga caa ccg atc aca   931
Ser Glu Lys Gly Glu Val Leu Tyr Asp Gly Ala Gly Gln Pro Ile Thr
            265                 270                 275

aag agc ttg ccg atg att gac aac gaa ttt agc cat gcg att ttt gac   979
Lys Ser Leu Pro Met Ile Asp Asn Glu Phe Ser His Ala Ile Phe Asp
        280                 285                 290
```

```
aaa tca gat gtc ccg aat ctt ccc gag ctg cga cgg ttc ttt aat cca   1027
Lys Ser Asp Val Pro Asn Leu Pro Glu Leu Arg Arg Phe Phe Asn Pro
    295                 300                 305

gca aag att gag tgg aat cct ggt ggt agt                          1057
Ala Lys Ile Glu Trp Asn Pro Gly Gly Ser
310                 315
```

<210> 56
<211> 319
<212> PRT
<213> Corynebacterium glutamicum

<400> 56

```
Val Thr Asp Lys Ala Arg Asn Arg Asp Val His Asn Glu Gln Gln Leu
  1               5                  10                  15

Ala Arg Gly Glu Ile Gly Glu Met Arg Ser Pro Met Trp Val Glu Val
            20                  25                  30

Gly Ala Ala Ile Leu Gly Val Phe Val Leu Val Val Met Trp Leu Ala
        35                  40                  45

Trp Gly Gly Ile Gly Leu Leu Ile Gln Thr Met Met Asn Thr Gly Ser
    50                  55                  60

Pro Asn Asp Lys Glu Leu Phe Asp Glu Leu Gly Val Arg Pro Tyr Tyr
65                  70                  75                  80

Val Ala Val Glu Gln Gln Ile Gly Thr Ser Ser Ala His Thr Thr Cys
                85                  90                  95

Tyr Gln Pro Leu Asp Glu Phe Gly Asn Asn Phe Gly Asp Cys Thr Arg
            100                 105                 110

Ser Val Pro Lys Glu Pro Val Trp Tyr Ala Asp Tyr Val Ala Ser Val
        115                 120                 125

Phe Ala Glu His Gly Phe Asp Ala Pro Glu Pro Ile Asp Asn Ser Val
    130                 135                 140

Gly Ser Trp Leu Leu Phe Gly His Val Gly Ile Ile Arg Val Thr Phe
145                 150                 155                 160

Val Ile Ala Val Ala Ala Gly Val Tyr Ala Met Ser Arg Ala Ala Met
                165                 170                 175

Met Arg Gln Leu Glu Thr Gln Asn Val Ala Val Asp Thr Thr Asp Ile
            180                 185                 190

Asn Gln His Thr Asn Asp Ala Arg Leu Ala Ile Pro Gln Glu Ile Val
        195                 200                 205

Arg Asp Leu Ser Leu Phe Pro Asp Val Gly Ala His Ser Pro Val Gln
    210                 215                 220

Pro Ser Ser Met Ile Ser His Val Met Leu Ser Asn Lys Gly Leu Lys
225                 230                 235                 240
```

```
Lys Val Asp Val Thr Gln Phe Ala Gln Glu Thr Ile Ile Asp Asn Asp
               245                 250                 255

Thr Gly Glu Ile Val Ser Glu Lys Gly Glu Val Leu Tyr Asp Gly Ala
            260                 265                 270

Gly Gln Pro Ile Thr Lys Ser Leu Pro Met Ile Asp Asn Glu Phe Ser
        275                 280                 285

His Ala Ile Phe Asp Lys Ser Asp Val Pro Asn Leu Pro Glu Leu Arg
    290                 295                 300

Arg Phe Phe Asn Pro Ala Lys Ile Glu Trp Asn Pro Gly Gly Ser
305                 310                 315


<210> 57
<211> 1824
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1801)
<223> RXN00022

<400> 57
aggactgctc cgcaaacctc taacaacacc tgctactccc cctgcagcgc cggtcaaccc 60

cacaccaccc acccttaac aaccacaaga aagatttatc atg tcc gct cca acc   115
                                            Met Ser Ala Pro Thr
                                              1               5

atc tac ccc ggc acc aaa aca tct att gat ccg atc acc atg gat gac   163
Ile Tyr Pro Gly Thr Lys Thr Ser Ile Asp Pro Ile Thr Met Asp Asp
                10                  15                  20

gct cgc atc atc ttt ttc gat att gag tcg ctc cac aat att ttc acg   211
Ala Arg Ile Ile Phe Phe Asp Ile Glu Ser Leu His Asn Ile Phe Thr
            25                  30                  35

gta gca acc tac gat tct ctg tcc cac cac gtc gat gtc ttt tac ctg   259
Val Ala Thr Tyr Asp Ser Leu Ser His His Val Asp Val Phe Tyr Leu
        40                  45                  50

ctc gat cac aca acc agc cct cag atc acg gtg ctg ccg cac tca atg   307
Leu Asp His Thr Thr Ser Pro Gln Ile Thr Val Leu Pro His Ser Met
    55                  60                  65

gat tat ttc gat caa acg cgc agc gat gct gtt atg gct gcc atc att   355
Asp Tyr Phe Asp Gln Thr Arg Ser Asp Ala Val Met Ala Ala Ile Ile
70                  75                  80                  85

gag caa aac cct gcg ttc gca gaa att aaa ggc tca ccc att aca acc   403
Glu Gln Asn Pro Ala Phe Ala Glu Ile Lys Gly Ser Pro Ile Thr Thr
                90                  95                  100

gca gat gta gcc ctc cac aat ctc ggt gac acc aac gcc aac cga cgc   451
Ala Asp Val Ala Leu His Asn Leu Gly Asp Thr Asn Ala Asn Arg Arg
            105                 110                 115
```

```
tgg cag tct aac gtg ctg ctt gcc cgg cta ctc ggg ggt att agt gtg   499
Trp Gln Ser Asn Val Leu Leu Ala Arg Leu Leu Gly Gly Ile Ser Val
        120                 125                 130

cgc gga gag gta cct gag cac cag agc cac aac cat ctc gcc aag cag   547
Arg Gly Glu Val Pro Glu His Gln Ser His Asn His Leu Ala Lys Gln
    135                 140                 145

ttt gcc gag gca acc ttg gtc acc agg gac ttc gat gtg aat tat gat   595
Phe Ala Glu Ala Thr Leu Val Thr Arg Asp Phe Asp Val Asn Tyr Asp
150                 155                 160                 165

cca aca agc gct cac cct ttt act gct ggc ttc aac tcg atc aac tat   643
Pro Thr Ser Ala His Pro Phe Thr Ala Gly Phe Asn Ser Ile Asn Tyr
                170                 175                 180

gac acc acc ttg ctc agc ctg tac ttc gca atg ttg acc tca aat atc   691
Asp Thr Thr Leu Leu Ser Leu Tyr Phe Ala Met Leu Thr Ser Asn Ile
            185                 190                 195

gga agt aca ccg acg tat ttc ccg gtg atc acc gca cag gaa ctt cgt   739
Gly Ser Thr Pro Thr Tyr Phe Pro Val Ile Thr Ala Gln Glu Leu Arg
        200                 205                 210

gcg cat aac gac aag ctc ttt agc cct gag ttc atc aaa aac atg cca   787
Ala His Asn Asp Lys Leu Phe Ser Pro Glu Phe Ile Lys Asn Met Pro
    215                 220                 225

aag tat ctc tgg gat cgc gac agc ggt gct gga ctc aga gct gca tcg   835
Lys Tyr Leu Trp Asp Arg Asp Ser Gly Ala Gly Leu Arg Ala Ala Ser
230                 235                 240                 245

ggt ttc cgc aac gcc atg ctc aaa tcg ggt cgc cac att gat att caa   883
Gly Phe Arg Asn Ala Met Leu Lys Ser Gly Arg His Ile Asp Ile Gln
                250                 255                 260

cgc ctc aat gaa aaa cag ctc ttt gtt gga ctc aag cgc ctg ctt ggt   931
Arg Leu Asn Glu Lys Gln Leu Phe Val Gly Leu Lys Arg Leu Leu Gly
            265                 270                 275

ctc ctc ggt cac cag att ctc gaa tct gat cgt ctc tct ggt gat gat   979
Leu Leu Gly His Gln Ile Leu Glu Ser Asp Arg Leu Ser Gly Asp Asp
        280                 285                 290

gcc cat gtt gat act aac gag gat gta ctt gat ctc att gcc tac aac   1027
Ala His Val Asp Thr Asn Glu Asp Val Leu Asp Leu Ile Ala Tyr Asn
    295                 300                 305

gtc tca gac gtg gtg ggc acc aga ctg ctc gct gag gac ccg gtg tac   1075
Val Ser Asp Val Val Gly Thr Arg Leu Leu Ala Glu Asp Pro Val Tyr
310                 315                 320                 325

tcc ggc tct ttc gat ctg cgg gca ggt cta ctg agc acc tac cca gag   1123
Ser Gly Ser Phe Asp Leu Arg Ala Gly Leu Leu Ser Thr Tyr Pro Glu
                330                 335                 340

act gtt ttt gat cat gat ggt act ttc cgt cag cca tcc acg cag atg   1171
Thr Val Phe Asp His Asp Gly Thr Phe Arg Gln Pro Ser Thr Gln Met
            345                 350                 355

cgt aaa gat cgc cta acg att aat acc tca tca gct cag ttc gca gcg   1219
```

```
Arg Lys Asp Arg Leu Thr Ile Asn Thr Ser Ser Ala Gln Phe Ala Ala
        360                 365                 370

cgt att ttg gcg cca tat cgc cca ctc cgc gat gtc cct gat gcg att   1267
Arg Ile Leu Ala Pro Tyr Arg Pro Leu Arg Asp Val Pro Asp Ala Ile
    375                 380                 385

ggc gac atg ccg gtg gtg tct tac ttg tac ccg gat gca gca gtc gcc   1315
Gly Asp Met Pro Val Val Ser Tyr Leu Tyr Pro Asp Ala Ala Val Ala
390                 395                 400                 405

gaa gca aca ggt caa aaa caa gtc aac gtg ctt gat gag tca aag aag   1363
Glu Ala Thr Gly Gln Lys Gln Val Asn Val Leu Asp Glu Ser Lys Lys
                410                 415                 420

ttc ttc tat gac aac atc acc gac ccg gaa gca cgt gct gcc ttt gat   1411
Phe Phe Tyr Asp Asn Ile Thr Asp Pro Glu Ala Arg Ala Ala Phe Asp
            425                 430                 435

gag gtc ttt gct ttt tac gct gat att gag ggt cgc aac ttc aac agt   1459
Glu Val Phe Ala Phe Tyr Ala Asp Ile Glu Gly Arg Asn Phe Asn Ser
        440                 445                 450

cac aat gag gct att gat acc cag att aac caa tta cgt gct tat ctc   1507
His Asn Glu Ala Ile Asp Thr Gln Ile Asn Gln Leu Arg Ala Tyr Leu
    455                 460                 465

aac cag gtt gtc gca ttc gat gca gct ggg tat gcg ctc tat gat gta   1555
Asn Gln Val Val Ala Phe Asp Ala Ala Gly Tyr Ala Leu Tyr Asp Val
470                 475                 480                 485

cgt aca cgt ttt gag cag atc ttc ccc aag gat cgc agc tac atc aac   1603
Arg Thr Arg Phe Glu Gln Ile Phe Pro Lys Asp Arg Ser Tyr Ile Asn
                490                 495                 500

gat gct acg gat atg acc cct cgc gca gta tcg agc ttt gac gat ctg   1651
Asp Ala Thr Asp Met Thr Pro Arg Ala Val Ser Ser Phe Asp Asp Leu
            505                 510                 515

gtt gca ctc tgt gat gat att cgc ggt gta ctt gat cga ggt tta gag   1699
Val Ala Leu Cys Asp Asp Ile Arg Gly Val Leu Asp Arg Gly Leu Glu
        520                 525                 530

atc tca tct ccg aat cat cat gag atg gtg gat gct atg cgc aag cag   1747
Ile Ser Ser Pro Asn His His Glu Met Val Asp Ala Met Arg Lys Gln
    535                 540                 545

ctg cac tat att cag gca ttt tac cgt gcc tgg gac cca tca acg ccg   1795
Leu His Tyr Ile Gln Ala Phe Tyr Arg Ala Trp Asp Pro Ser Thr Pro
550                 555                 560                 565

ctt caa tgacgctgac ccagcggtga ccc                                1824
Leu Gln
```

Application Filed 2004-07-27 00:00:00

<210> 58
<211> 567
<212> PRT
<213> Corynebacterium glutamicum

<400> 58

```
Met Ser Ala Pro Thr Ile Tyr Pro Gly Thr Lys Thr Ser Ile Asp Pro
 1               5                  10                  15

Ile Thr Met Asp Asp Ala Arg Ile Ile Phe Phe Asp Ile Glu Ser Leu
            20                  25                  30

His Asn Ile Phe Thr Val Ala Thr Tyr Asp Ser Leu Ser His His Val
        35                  40                  45

Asp Val Phe Tyr Leu Leu Asp His Thr Thr Ser Pro Gln Ile Thr Val
    50                  55                  60

Leu Pro His Ser Met Asp Tyr Phe Asp Gln Thr Arg Ser Asp Ala Val
65                  70                  75                  80

Met Ala Ala Ile Ile Glu Gln Asn Pro Ala Phe Ala Glu Ile Lys Gly
                85                  90                  95

Ser Pro Ile Thr Thr Ala Asp Val Ala Leu His Asn Leu Gly Asp Thr
            100                 105                 110

Asn Ala Asn Arg Arg Trp Gln Ser Asn Val Leu Leu Ala Arg Leu Leu
        115                 120                 125

Gly Gly Ile Ser Val Arg Gly Glu Val Pro Glu His Gln Ser His Asn
    130                 135                 140

His Leu Ala Lys Gln Phe Ala Glu Ala Thr Leu Val Thr Arg Asp Phe
145                 150                 155                 160

Asp Val Asn Tyr Asp Pro Thr Ser Ala His Pro Phe Thr Ala Gly Phe
                165                 170                 175

Asn Ser Ile Asn Tyr Asp Thr Thr Leu Leu Ser Leu Tyr Phe Ala Met
            180                 185                 190

Leu Thr Ser Asn Ile Gly Ser Thr Pro Thr Tyr Phe Pro Val Ile Thr
        195                 200                 205

Ala Gln Glu Leu Arg Ala His Asn Asp Lys Leu Phe Ser Pro Glu Phe
    210                 215                 220

Ile Lys Asn Met Pro Lys Tyr Leu Trp Asp Arg Asp Ser Gly Ala Gly
225                 230                 235                 240

Leu Arg Ala Ala Ser Gly Phe Arg Asn Ala Met Leu Lys Ser Gly Arg
                245                 250                 255

His Ile Asp Ile Gln Arg Leu Asn Glu Lys Gln Leu Phe Val Gly Leu
            260                 265                 270

Lys Arg Leu Leu Gly Leu Leu Gly His Gln Ile Leu Glu Ser Asp Arg
        275                 280                 285

Leu Ser Gly Asp Asp Ala His Val Asp Thr Asn Glu Asp Val Leu Asp
    290                 295                 300

Leu Ile Ala Tyr Asn Val Ser Asp Val Val Gly Thr Arg Leu Leu Ala
305                 310                 315                 320
```

Glu Asp Pro Val Tyr Ser Gly Ser Phe Asp Leu Arg Ala Gly Leu Leu
325 330 335

Ser Thr Tyr Pro Glu Thr Val Phe Asp His Asp Gly Thr Phe Arg Gln
340 345 350

Pro Ser Thr Gln Met Arg Lys Asp Arg Leu Thr Ile Asn Thr Ser Ser
355 360 365

Ala Gln Phe Ala Ala Arg Ile Leu Ala Pro Tyr Arg Pro Leu Arg Asp
370 375 380

Val Pro Asp Ala Ile Gly Asp Met Pro Val Val Ser Tyr Leu Tyr Pro
385 390 395 400

Asp Ala Ala Val Ala Glu Ala Thr Gly Gln Lys Gln Val Asn Val Leu
405 410 415

Asp Glu Ser Lys Lys Phe Phe Tyr Asp Asn Ile Thr Asp Pro Glu Ala
420 425 430

Arg Ala Ala Phe Asp Glu Val Phe Ala Phe Tyr Ala Asp Ile Glu Gly
435 440 445

Arg Asn Phe Asn Ser His Asn Glu Ala Ile Asp Thr Gln Ile Asn Gln
450 455 460

Leu Arg Ala Tyr Leu Asn Gln Val Val Ala Phe Asp Ala Ala Gly Tyr
465 470 475 480

Ala Leu Tyr Asp Val Arg Thr Arg Phe Glu Gln Ile Phe Pro Lys Asp
485 490 495

Arg Ser Tyr Ile Asn Asp Ala Thr Asp Met Thr Pro Arg Ala Val Ser
500 505 510

Ser Phe Asp Asp Leu Val Ala Leu Cys Asp Asp Ile Arg Gly Val Leu
515 520 525

Asp Arg Gly Leu Glu Ile Ser Ser Pro Asn His His Glu Met Val Asp
530 535 540

Ala Met Arg Lys Gln Leu His Tyr Ile Gln Ala Phe Tyr Arg Ala Trp
545 550 555 560

Asp Pro Ser Thr Pro Leu Gln
565

<210> 59
<211> 835
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(835)
<223> FRXA00022

<400> 59
aggactgctc cgcaaacctc taacaacacc tgctactccc cctgcagcgc cggtcaaccc 60

```
cacaccaccc acccccttaac aaccacaaga aagatttatc atg tcc gct cca acc   115
                                            Met Ser Ala Pro Thr
                                              1               5

atc tac ccc ggc acc aaa aca tct att gat ccg atc acc atg gat gac   163
Ile Tyr Pro Gly Thr Lys Thr Ser Ile Asp Pro Ile Thr Met Asp Asp
                10                  15                  20

gct cgc atc atc ttt ttc gat att gag tcg ctc cac aat att ttc acg   211
Ala Arg Ile Ile Phe Phe Asp Ile Glu Ser Leu His Asn Ile Phe Thr
            25                  30                  35

gta gca acc tac gat tct ctg tcc cac cac gtc gat gtc ttt tac ctg   259
Val Ala Thr Tyr Asp Ser Leu Ser His His Val Asp Val Phe Tyr Leu
        40                  45                  50

ctc gat cac aca acc agc cct cag atc acg gtg ctg ccg cac tca atg   307
Leu Asp His Thr Thr Ser Pro Gln Ile Thr Val Leu Pro His Ser Met
    55                  60                  65

gat tat ttc gat caa acg cgc agc gat gct gtt atg gct gcc atc att   355
Asp Tyr Phe Asp Gln Thr Arg Ser Asp Ala Val Met Ala Ala Ile Ile
70                  75                  80                  85

gag caa aac cct gcg ttc gca gaa att aaa ggc tca ccc att aca acc   403
Glu Gln Asn Pro Ala Phe Ala Glu Ile Lys Gly Ser Pro Ile Thr Thr
                90                  95                  100

gca gat gta gcc ctc cac aat ctc ggt gac acc aac gcc aac cga cgc   451
Ala Asp Val Ala Leu His Asn Leu Gly Asp Thr Asn Ala Asn Arg Arg
            105                 110                 115

tgg cag tct aac gtg ctg ctt gcc cgg cta ctc ggg ggt att agt gtg   499
Trp Gln Ser Asn Val Leu Leu Ala Arg Leu Leu Gly Gly Ile Ser Val
        120                 125                 130

cgc gga gag gta cct gag cac cag agc cac aac cat ctc gcc aag cag   547
Arg Gly Glu Val Pro Glu His Gln Ser His Asn His Leu Ala Lys Gln
    135                 140                 145

ttt gcc gag gca acc ttg gtc acc agg gac ttc gat gtg aat tat gat   595
Phe Ala Glu Ala Thr Leu Val Thr Arg Asp Phe Asp Val Asn Tyr Asp
150                 155                 160                 165

cca aca agc gct cac cct ttt act gct ggc ttc aac tcg atc aac tat   643
Pro Thr Ser Ala His Pro Phe Thr Ala Gly Phe Asn Ser Ile Asn Tyr
                170                 175                 180

gac acc acc ttg ctc agc ctg tac ttc gca atg ttg acc tca aat atc   691
Asp Thr Thr Leu Leu Ser Leu Tyr Phe Ala Met Leu Thr Ser Asn Ile
            185                 190                 195

gga agt aca ccg acg tat ttc ccg gtg atc acc gca caa gaa ctt cgt   739
Gly Ser Thr Pro Thr Tyr Phe Pro Val Ile Thr Ala Gln Glu Leu Arg
        200                 205                 210

gcg cat aac gac aag ctc ttt agc cct gag ttc atc aaa aac atg cca   787
Ala His Asn Asp Lys Leu Phe Ser Pro Glu Phe Ile Lys Asn Met Pro
    215                 220                 225
```

```
aag tat ttc tgg gat cgc gac agc ggt gct gga ctc aga gct gca tcg   835
Lys Tyr Phe Trp Asp Arg Asp Ser Gly Ala Gly Leu Arg Ala Ala Ser
230                 235                 240                 245


<210> 60
<211> 245
<212> PRT
<213> Corynebacterium glutamicum

<400> 60
Met Ser Ala Pro Thr Ile Tyr Pro Gly Thr Lys Thr Ser Ile Asp Pro
  1               5                  10                  15

Ile Thr Met Asp Asp Ala Arg Ile Ile Phe Phe Asp Ile Glu Ser Leu
             20                  25                  30

His Asn Ile Phe Thr Val Ala Thr Tyr Asp Ser Leu Ser His His Val
         35                  40                  45

Asp Val Phe Tyr Leu Leu Asp His Thr Thr Ser Pro Gln Ile Thr Val
     50                  55                  60

Leu Pro His Ser Met Asp Tyr Phe Asp Gln Thr Arg Ser Asp Ala Val
 65                  70                  75                  80

Met Ala Ala Ile Ile Glu Gln Asn Pro Ala Phe Ala Glu Ile Lys Gly
                 85                  90                  95

Ser Pro Ile Thr Thr Ala Asp Val Ala Leu His Asn Leu Gly Asp Thr
            100                 105                 110

Asn Ala Asn Arg Arg Trp Gln Ser Asn Val Leu Leu Ala Arg Leu Leu
        115                 120                 125

Gly Gly Ile Ser Val Arg Gly Glu Val Pro Glu His Gln Ser His Asn
    130                 135                 140

His Leu Ala Lys Gln Phe Ala Glu Ala Thr Leu Val Thr Arg Asp Phe
145                 150                 155                 160

Asp Val Asn Tyr Asp Pro Thr Ser Ala His Pro Phe Thr Ala Gly Phe
                165                 170                 175

Asn Ser Ile Asn Tyr Asp Thr Thr Leu Leu Ser Leu Tyr Phe Ala Met
            180                 185                 190

Leu Thr Ser Asn Ile Gly Ser Thr Pro Thr Tyr Phe Pro Val Ile Thr
        195                 200                 205

Ala Gln Glu Leu Arg Ala His Asn Asp Lys Leu Phe Ser Pro Glu Phe
    210                 215                 220

Ile Lys Asn Met Pro Lys Tyr Phe Trp Asp Arg Asp Ser Gly Ala Gly
225                 230                 235                 240

Leu Arg Ala Ala Ser
                245


<210> 61
```

<211> 939
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(939)
<223> FRXA01921

<400> 61

```
cac att gat att caa cgc ctc aat gaa aaa cag ctc ttt gtt gga ctc   48
His Ile Asp Ile Gln Arg Leu Asn Glu Lys Gln Leu Phe Val Gly Leu
  1               5                  10                  15

aag cgc ctg ctt ggt ctc ctc ggt cac cag att ctc gaa tct gat cgt   96
Lys Arg Leu Leu Gly Leu Leu Gly His Gln Ile Leu Glu Ser Asp Arg
             20                  25                  30

ctc tct ggt gat gat gcc cat gtt gat act aac gag gat gta ctt gat   144
Leu Ser Gly Asp Asp Ala His Val Asp Thr Asn Glu Asp Val Leu Asp
         35                  40                  45

ctc att gcc tac aac gtc tca gac gtg gtg ggc acc aga ctg ctc gct   192
Leu Ile Ala Tyr Asn Val Ser Asp Val Val Gly Thr Arg Leu Leu Ala
     50                  55                  60

gag gac ccg gtg tac tcc ggc tct ttc gat ctg cgg gca ggt cta ctg   240
Glu Asp Pro Val Tyr Ser Gly Ser Phe Asp Leu Arg Ala Gly Leu Leu
 65                  70                  75                  80

agc acc tac cca gag act gtt ttt gat cat gat ggt act ttc cgt cag   288
Ser Thr Tyr Pro Glu Thr Val Phe Asp His Asp Gly Thr Phe Arg Gln
                 85                  90                  95

cca tcc acg cag atg cgt aaa gat cgc cta acg att aat acc tca tca   336
Pro Ser Thr Gln Met Arg Lys Asp Arg Leu Thr Ile Asn Thr Ser Ser
            100                 105                 110

gct cag ttc gca gcg cgt att ttg gcg cca tat cgc cca ctc cgc gat   384
Ala Gln Phe Ala Ala Arg Ile Leu Ala Pro Tyr Arg Pro Leu Arg Asp
        115                 120                 125

gtc cct gat gcg att ggc gac atg ccg gtg gtg tct tac ttg tac ccg   432
Val Pro Asp Ala Ile Gly Asp Met Pro Val Val Ser Tyr Leu Tyr Pro
    130                 135                 140

gat gca gca gtc gcc gaa gca aca ggt caa aaa caa gtc aac gtg ctt   480
Asp Ala Ala Val Ala Glu Ala Thr Gly Gln Lys Gln Val Asn Val Leu
145                 150                 155                 160

gat gag tca aag aag ttc ttc tat gac aac atc acc gac ccg gaa gca   528
Asp Glu Ser Lys Lys Phe Phe Tyr Asp Asn Ile Thr Asp Pro Glu Ala
                165                 170                 175

cgt gct gcc ttt gat gag gtc ttt gct ttt tac gct gat att gag ggt   576
Arg Ala Ala Phe Asp Glu Val Phe Ala Phe Tyr Ala Asp Ile Glu Gly
            180                 185                 190

cgc aac ttc aac agt cac aat gag gct att gat acc cag att aac caa   624
Arg Asn Phe Asn Ser His Asn Glu Ala Ile Asp Thr Gln Ile Asn Gln
        195                 200                 205
```

```
tta cgt gct tat ctc aac cag gtt gtc gca ttc gat gca gct ggg tat   672
Leu Arg Ala Tyr Leu Asn Gln Val Val Ala Phe Asp Ala Ala Gly Tyr
    210                 215                 220

gcg ctc tat gat gta cgt aca cgt ttt gag cag atc ttc ccc aag gat   720
Ala Leu Tyr Asp Val Arg Thr Arg Phe Glu Gln Ile Phe Pro Lys Asp
225                 230                 235                 240

cgc agc tac atc aac gat gct acg gat atg acc cct cgc gca gta tcg   768
Arg Ser Tyr Ile Asn Asp Ala Thr Asp Met Thr Pro Arg Ala Val Ser
                245                 250                 255

agc ttt gac gat ctg gtt gca ctc tgt gat gat att cgc ggt gta ctt   816
Ser Phe Asp Asp Leu Val Ala Leu Cys Asp Asp Ile Arg Gly Val Leu
            260                 265                 270

gat cga ggt tta gag atc tca tct ccg aat cat cat gag atg gtg gat   864
Asp Arg Gly Leu Glu Ile Ser Ser Pro Asn His His Glu Met Val Asp
        275                 280                 285

gct atg cgc aag cag ctg cac tat att cag gca ttt acc gtg cct ggg   912
Ala Met Arg Lys Gln Leu His Tyr Ile Gln Ala Phe Thr Val Pro Gly
    290                 295                 300

acc cat caa cgc cgc ttc aat gac gct                              939
Thr His Gln Arg Arg Phe Asn Asp Ala
305                 310


<210> 62
<211> 313
<212> PRT
<213> Corynebacterium glutamicum

<400> 62
His Ile Asp Ile Gln Arg Leu Asn Glu Lys Gln Leu Phe Val Gly Leu
  1               5                  10                  15

Lys Arg Leu Leu Gly Leu Leu Gly His Gln Ile Leu Glu Ser Asp Arg
             20                  25                  30

Leu Ser Gly Asp Asp Ala His Val Asp Thr Asn Glu Asp Val Leu Asp
         35                  40                  45

Leu Ile Ala Tyr Asn Val Ser Asp Val Val Gly Thr Arg Leu Leu Ala
     50                  55                  60

Glu Asp Pro Val Tyr Ser Gly Ser Phe Asp Leu Arg Ala Gly Leu Leu
 65                  70                  75                  80

Ser Thr Tyr Pro Glu Thr Val Phe Asp His Asp Gly Thr Phe Arg Gln
                 85                  90                  95

Pro Ser Thr Gln Met Arg Lys Asp Arg Leu Thr Ile Asn Thr Ser Ser
            100                 105                 110

Ala Gln Phe Ala Ala Arg Ile Leu Ala Pro Tyr Arg Pro Leu Arg Asp
        115                 120                 125

Val Pro Asp Ala Ile Gly Asp Met Pro Val Val Ser Tyr Leu Tyr Pro
```

```
    130                 135                 140

Asp Ala Ala Val Ala Glu Ala Thr Gly Gln Lys Gln Val Asn Val Leu
145                 150                 155                 160

Asp Glu Ser Lys Lys Phe Phe Tyr Asp Asn Ile Thr Asp Pro Glu Ala
                165                 170                 175

Arg Ala Ala Phe Asp Glu Val Phe Ala Phe Tyr Ala Asp Ile Glu Gly
            180                 185                 190

Arg Asn Phe Asn Ser His Asn Glu Ala Ile Asp Thr Gln Ile Asn Gln
        195                 200                 205

Leu Arg Ala Tyr Leu Asn Gln Val Val Ala Phe Asp Ala Ala Gly Tyr
    210                 215                 220

Ala Leu Tyr Asp Val Arg Thr Arg Phe Glu Gln Ile Phe Pro Lys Asp
225                 230                 235                 240

Arg Ser Tyr Ile Asn Asp Ala Thr Asp Met Thr Pro Arg Ala Val Ser
                245                 250                 255

Ser Phe Asp Asp Leu Val Ala Leu Cys Asp Asp Ile Arg Gly Val Leu
            260                 265                 270

Asp Arg Gly Leu Glu Ile Ser Ser Pro Asn His His Glu Met Val Asp
        275                 280                 285

Ala Met Arg Lys Gln Leu His Tyr Ile Gln Ala Phe Thr Val Pro Gly
    290                 295                 300

Thr His Gln Arg Arg Phe Asn Asp Ala
305                 310


<210> 63
<211> 489
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(466)
<223> RXN00027

<400> 63
ttaggcaacg actccgaaac cttcaagaac gtgtggcact aacaattgcg gactatcctt 60

gggaactgtt ttagatttta ttcagggtag ggagattgtt gtg gat gaa cga agc   115
                                               Val Asp Glu Arg Ser
                                                 1               5

cgg ttt gcg cgc agc gtt ttc ccg gac ggt gaa gaa cca gat cca cgt   163
Arg Phe Ala Arg Ser Val Phe Pro Asp Gly Glu Glu Pro Asp Pro Arg
                 10                  15                  20

ttc act ttg gcc aat gag cgc acg ttt cta gca tgg acg cgt acg tct   211
Phe Thr Leu Ala Asn Glu Arg Thr Phe Leu Ala Trp Thr Arg Thr Ser
             25                  30                  35
```

```
ttg gcg ttt ctt gcc ggt ggt att gct ttt gag gcg ttc cag atc agt   259
Leu Ala Phe Leu Ala Gly Gly Ile Ala Phe Glu Ala Phe Gln Ile Ser
         40                  45                  50

gga cta tcg gat act gtc cgt aca aca atc gcg gtt ttt atc att gcg   307
Gly Leu Ser Asp Thr Val Arg Thr Thr Ile Ala Val Phe Ile Ile Ala
     55                  60                  65

gtt ggc atg atc att gcc gct ggt gct gcg gtg agg tgg atg aat gtg   355
Val Gly Met Ile Ile Ala Ala Gly Ala Ala Val Arg Trp Met Asn Val
 70                  75                  80                  85

gag cgt gca atg cgt aaa cag aag cca ctt ccc gta cct gcg att att   403
Glu Arg Ala Met Arg Lys Gln Lys Pro Leu Pro Val Pro Ala Ile Ile
                 90                  95                 100

ccg ttt ctg tct att gcg gct ttg gtg gcc tct gcg gct gtc ttg gtt   451
Pro Phe Leu Ser Ile Ala Ala Leu Val Ala Ser Ala Ala Val Leu Val
            105                 110                 115

ctg att att gtt cag tagctatgcg cattcatgag gat                    489
Leu Ile Ile Val Gln
        120
```

Sequence Listing.ST25.txt

<210> 64
<211> 122
<212> PRT
<213> Corynebacterium glutamicum

<400> 64

```
Val Asp Glu Arg Ser Arg Phe Ala Arg Ser Val Phe Pro Asp Gly Glu
  1               5                  10                  15

Glu Pro Asp Pro Arg Phe Thr Leu Ala Asn Glu Arg Thr Phe Leu Ala
             20                  25                  30

Trp Thr Arg Thr Ser Leu Ala Phe Leu Ala Gly Gly Ile Ala Phe Glu
         35                  40                  45

Ala Phe Gln Ile Ser Gly Leu Ser Asp Thr Val Arg Thr Thr Ile Ala
     50                  55                  60

Val Phe Ile Ile Ala Val Gly Met Ile Ile Ala Ala Gly Ala Ala Val
 65                  70                  75                  80

Arg Trp Met Asn Val Glu Arg Ala Met Arg Lys Gln Lys Pro Leu Pro
                 85                  90                  95

Val Pro Ala Ile Ile Pro Phe Leu Ser Ile Ala Ala Leu Val Ala Ser
            100                 105                 110

Ala Ala Val Leu Val Leu Ile Ile Val Gln
        115                 120
```

<210> 65
<211> 489
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(466)
<223> FRXA00027

<400> 65
ttaggcaacg actccgaaac cttcaagaac gtgtggcact aacaattgcg gactatcctt 60

gggaactgtt ttagatttta ttcagggtag ggagattgtt gtg gat gaa cga agc 115
Val Asp Glu Arg Ser
1 5

cgg ttt gcg cgc agc gtt ttc ccg gac ggt gaa gaa cca gat cca cgt 163
Arg Phe Ala Arg Ser Val Phe Pro Asp Gly Glu Glu Pro Asp Pro Arg
10 15 20

ttc act ttg gcc aat gag cgc acg ttt cta gca tgg acg cgt acg tct 211
Phe Thr Leu Ala Asn Glu Arg Thr Phe Leu Ala Trp Thr Arg Thr Ser
25 30 35

ttg gcg ttt ctt gcc ggt ggt att gct ttt gag gcg ttc cag atc agt 259
Leu Ala Phe Leu Ala Gly Gly Ile Ala Phe Glu Ala Phe Gln Ile Ser
40 45 50

gga cta tcg gat act gtc cgt aca aca atc gcg gtt ttt atc att gcg 307
Gly Leu Ser Asp Thr Val Arg Thr Thr Ile Ala Val Phe Ile Ile Ala
55 60 65

gtt ggc atg atc att gcc gct ggt gct gcg gtg agg tgg atg aat gtg 355
Val Gly Met Ile Ile Ala Ala Gly Ala Ala Val Arg Trp Met Asn Val
70 75 80 85

gag cgt gca atg cgt aaa cag aag cca ctt ccc gta cct gcg att att 403
Glu Arg Ala Met Arg Lys Gln Lys Pro Leu Pro Val Pro Ala Ile Ile
90 95 100

ccg ttt ctg tct att gcg gct ttg gtg gcc tct gcg gct gtc ttg gtt 451
Pro Phe Leu Ser Ile Ala Ala Leu Val Ala Ser Ala Ala Val Leu Val
105 110 115

ctg att att gtt cag tagctatgcg cattcatgag gat 489
Leu Ile Ile Val Gln
120

<210> 66
<211> 122
<212> PRT
<213> Corynebacterium glutamicum

<400> 66
Val Asp Glu Arg Ser Arg Phe Ala Arg Ser Val Phe Pro Asp Gly Glu
1 5 10 15

Glu Pro Asp Pro Arg Phe Thr Leu Ala Asn Glu Arg Thr Phe Leu Ala
20 25 30

Trp Thr Arg Thr Ser Leu Ala Phe Leu Ala Gly Gly Ile Ala Phe Glu
35 40 45

Ala Phe Gln Ile Ser Gly Leu Ser Asp Thr Val Arg Thr Thr Ile Ala

```
     50                  55                  60

Val Phe Ile Ile Ala Val Gly Met Ile Ile Ala Ala Gly Ala Ala Val
 65                  70                  75                  80

Arg Trp Met Asn Val Glu Arg Ala Met Arg Lys Gln Lys Pro Leu Pro
                85                  90                  95

Val Pro Ala Ile Ile Pro Phe Leu Ser Ile Ala Ala Leu Val Ala Ser
            100                 105                 110

Ala Ala Val Leu Val Leu Ile Ile Val Gln
        115                 120


<210> 67
<211> 2070
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2047)
<223> RXN00028

<400> 67
aaaagtcctg gccagaaaac tctctatact gtgcagcatg gcaccaacga tcaccgacat 60

ccatgttctg cttcgtcgcg gtgagcgaca atcagtgatc atg acc ctc act gcc   115
                                            Met Thr Leu Thr Ala
                                              1               5

tct tcc ttg gag gcc ggg aaa atg tct ttt agt ggc ggg tat atc gtg   163
Ser Ser Leu Glu Ala Gly Lys Met Ser Phe Ser Gly Gly Tyr Ile Val
                10                  15                  20

ggc gag acg atg atc ttc ctc gtc gat ccc gat gaa gtc gag ata cga   211
Gly Glu Thr Met Ile Phe Leu Val Asp Pro Asp Glu Val Glu Ile Arg
            25                  30                  35

cgc agc cct aac agc ctc cac gtc ctg cgt aac ggt agc gat att ctg   259
Arg Ser Pro Asn Ser Leu His Val Leu Arg Asn Gly Ser Asp Ile Leu
        40                  45                  50

cgc cgc aac gag cat cat tgc tgg gta ttt gag aat ttc aat aaa ccc   307
Arg Arg Asn Glu His His Cys Trp Val Phe Glu Asn Phe Asn Lys Pro
    55                  60                  65

att gac cca cct gtt cga ttg ggt cct cgg gat atc atc tgc ccg agc   355
Ile Asp Pro Pro Val Arg Leu Gly Pro Arg Asp Ile Ile Cys Pro Ser
70                  75                  80                  85

gcc ttg gcc tgg gtt ctt caa cag cat tcc atc tcc cgg tcc tta tcc   403
Ala Leu Ala Trp Val Leu Gln Gln His Ser Ile Ser Arg Ser Leu Ser
                90                  95                  100

cac cac ctt cac gcg gat aag atc act gcg gga gag att gct gga cgc   451
His His Leu His Ala Asp Lys Ile Thr Ala Gly Glu Ile Ala Gly Arg
            105                 110                 115

ccc acc tgg atc ctc cgt gag gaa cct act tca gga ggg cag gac cca   499
```

```
Pro Thr Trp Ile Leu Arg Glu Glu Pro Thr Ser Gly Gly Gln Asp Pro
        120                 125                 130

agt cga ttg gtc agt ctt gaa atc gac cag gaa cac ggt gtc atc ctt   547
Ser Arg Leu Val Ser Leu Glu Ile Asp Gln Glu His Gly Val Ile Leu
    135                 140                 145

gca gtg gag act gga caa gaa cga ctc gaa gcc acg gag att tct ttt   595
Ala Val Glu Thr Gly Gln Glu Arg Leu Glu Ala Thr Glu Ile Ser Phe
150                 155                 160                 165

cct gac act ctt cct aat cct tcc tgg gac gga gcc tgg gaa cca ttc   643
Pro Asp Thr Leu Pro Asn Pro Ser Trp Asp Gly Ala Trp Glu Pro Phe
                170                 175                 180

cat tat cca gat tcg aca cca cac act gcc cct gat gtt gct gaa ata   691
His Tyr Pro Asp Ser Thr Pro His Thr Ala Pro Asp Val Ala Glu Ile
            185                 190                 195

ccc ggt tac att cag tca ctg ccg ccg cag tct gaa gat cct cgc aga   739
Pro Gly Tyr Ile Gln Ser Leu Pro Pro Gln Ser Glu Asp Pro Arg Arg
        200                 205                 210

cta cga gtc ttc gtc aat gag ata gca ctc gaa ggt gat ttc cct gac   787
Leu Arg Val Phe Val Asn Glu Ile Ala Leu Glu Gly Asp Phe Pro Asp
    215                 220                 225

tac cgt caa gga caa tct gtg cga ctt act ttg gga att agc tcc tcc   835
Tyr Arg Gln Gly Gln Ser Val Arg Leu Thr Leu Gly Ile Ser Ser Ser
230                 235                 240                 245

cct gtg cca ctc gaa gga atg aca acc aga cgc cgg ggc cgg gta cgc   883
Pro Val Pro Leu Glu Gly Met Thr Thr Arg Arg Arg Gly Arg Val Arg
                250                 255                 260

aac ctt ggg gaa gaa gct agt cca ggc gat gac ggt atg ccc cag tgg   931
Asn Leu Gly Glu Glu Ala Ser Pro Gly Asp Asp Gly Met Pro Gln Trp
            265                 270                 275

cca atc ctg ctc act ggt gat ggg tgg acg gcg ctg gcc tac act ccc   979
Pro Ile Leu Leu Thr Gly Asp Gly Trp Thr Ala Leu Ala Tyr Thr Pro
        280                 285                 290

atc cca aaa cgt gga gat gca gag atc cag ggg tgg ttt tat tat tcc   1027
Ile Pro Lys Arg Gly Asp Ala Glu Ile Gln Gly Trp Phe Tyr Tyr Ser
    295                 300                 305

gcc tac gga att gtt gat gtt ccc aca gat cta cgg gta gag cgt att   1075
Ala Tyr Gly Ile Val Asp Val Pro Thr Asp Leu Arg Val Glu Arg Ile
310                 315                 320                 325

ttc gct ggt atc ggc aca agt ggc acc aac gag cgt ttg tgg cag gag   1123
Phe Ala Gly Ile Gly Thr Ser Gly Thr Asn Glu Arg Leu Trp Gln Glu
                330                 335                 340

ata gac aat act tct tcg gct tat cac tcg gaa gat tgg tgg atc cgc   1171
Ile Asp Asn Thr Ser Ser Ala Tyr His Ser Glu Asp Trp Trp Ile Arg
            345                 350                 355

gat gtc gtt tta gac gtc acg ttg gat gga gct gtt ccg cct ccg ctt   1219
Asp Val Val Leu Asp Val Thr Leu Asp Gly Ala Val Pro Pro Pro Leu
```

```
        360                 365                 370

aga cgt gac gtc ttc act gct gtc gat cct att gtg gcg ggt gac aaa   1267
Arg Arg Asp Val Phe Thr Ala Val Asp Pro Ile Val Ala Gly Asp Lys
    375                 380                 385

ttg tgg ctg tgt gac gtg cac ttt ccg gta gcc cgc tgc tgg gag acc   1315
Leu Trp Leu Cys Asp Val His Phe Pro Val Ala Arg Cys Trp Glu Thr
390                 395                 400                 405

acg acc ggc cga tac ttg ggg cag act tta gtc cca gca cca ctg cga   1363
Thr Thr Gly Arg Tyr Leu Gly Gln Thr Leu Val Pro Ala Pro Leu Arg
                410                 415                 420

gat cga tcg tac gtc ctt gag ctg cac agc gac caa caa tta gga gcc   1411
Asp Arg Ser Tyr Val Leu Glu Leu His Ser Asp Gln Gln Leu Gly Ala
            425                 430                 435

gta gcg gca agt ggg aag agt ggt tgg att ctc aca cct ggt caa gca   1459
Val Ala Ala Ser Gly Lys Ser Gly Trp Ile Leu Thr Pro Gly Gln Ala
        440                 445                 450

gta gcc act aaa gct cct gat tgg act cct ccc acc cgg gca acc gat   1507
Val Ala Thr Lys Ala Pro Asp Trp Thr Pro Pro Thr Arg Ala Thr Asp
    455                 460                 465

ctg cct cag gtc ccc tcc ccc tgg gag atc gtc gct gtc cgt ggc caa   1555
Leu Pro Gln Val Pro Ser Pro Trp Glu Ile Val Ala Val Arg Gly Gln
470                 475                 480                 485

ggt ctg ttt gag ctg cag gtg gaa act agt aga cgc acc gcc ctc ggt   1603
Gly Leu Phe Glu Leu Gln Val Glu Thr Ser Arg Arg Thr Ala Leu Gly
                490                 495                 500

cga gtt aat gcg acc ggt ggc gtc gac atc ggt gaa ctc ccg ccc aac   1651
Arg Val Asn Ala Thr Gly Gly Val Asp Ile Gly Glu Leu Pro Pro Asn
            505                 510                 515

ggc tat acc atc agt tct gtg gtt cag atc ggt gat gaa tac atc gtg   1699
Gly Tyr Thr Ile Ser Ser Val Val Gln Ile Gly Asp Glu Tyr Ile Val
        520                 525                 530

ggc agg tgg gta gag gaa tac cgg ctc aac tcc aaa ctg gag gtc att   1747
Gly Arg Trp Val Glu Glu Tyr Arg Leu Asn Ser Lys Leu Glu Val Ile
    535                 540                 545

tct acc aaa gag cta gat atc tcc gca tcc gga tgg aag agc aag ggg   1795
Ser Thr Lys Glu Leu Asp Ile Ser Ala Ser Gly Trp Lys Ser Lys Gly
550                 555                 560                 565

acg gtt gct tat ctg tcg gaa gac act cac ata tgt ttc ttc gac cag   1843
Thr Val Ala Tyr Leu Ser Glu Asp Thr His Ile Cys Phe Phe Asp Gln
                570                 575                 580

gtc agc ggg gcc gag ctt ccc agc ctg ggt atc gcc gag gga cac cag   1891
Val Ser Gly Ala Glu Leu Pro Ser Leu Gly Ile Ala Glu Gly His Gln
            585                 590                 595

ggc gag gtt atg tca gca act tct tca gag agc atc gtg ctt atc tac   1939
Gly Glu Val Met Ser Ala Thr Ser Ser Glu Ser Ile Val Leu Ile Tyr
        600                 605                 610
```

```
cgg cgc aac ccg aac aat tca atg tcg att gtc ccg act tcc gtt gcc   1987
Arg Arg Asn Pro Asn Asn Ser Met Ser Ile Val Pro Thr Ser Val Ala
    615                 620                 625

acc tat gac aat ggc acc tgg acg act atg ccg cta cag gaa gct cca   2035
Thr Tyr Asp Asn Gly Thr Trp Thr Thr Met Pro Leu Gln Glu Ala Pro
630                 635                 640                 645

gcg gaa ctg tcc taaactgctc atagactgct gag                        2070
Ala Glu Leu Ser
```

<210> 68
<211> 649
<212> PRT
<213> Corynebacterium glutamicum

<400> 68

```
Met Thr Leu Thr Ala Ser Ser Leu Glu Ala Gly Lys Met Ser Phe Ser
  1               5                  10                  15

Gly Gly Tyr Ile Val Gly Glu Thr Met Ile Phe Leu Val Asp Pro Asp
             20                  25                  30

Glu Val Glu Ile Arg Arg Ser Pro Asn Ser Leu His Val Leu Arg Asn
         35                  40                  45

Gly Ser Asp Ile Leu Arg Arg Asn Glu His His Cys Trp Val Phe Glu
     50                  55                  60

Asn Phe Asn Lys Pro Ile Asp Pro Pro Val Arg Leu Gly Pro Arg Asp
 65                  70                  75                  80

Ile Ile Cys Pro Ser Ala Leu Ala Trp Val Leu Gln Gln His Ser Ile
                 85                  90                  95

Ser Arg Ser Leu Ser His His Leu His Ala Asp Lys Ile Thr Ala Gly
            100                 105                 110

Glu Ile Ala Gly Arg Pro Thr Trp Ile Leu Arg Glu Glu Pro Thr Ser
        115                 120                 125

Gly Gly Gln Asp Pro Ser Arg Leu Val Ser Leu Glu Ile Asp Gln Glu
    130                 135                 140

His Gly Val Ile Leu Ala Val Glu Thr Gly Gln Glu Arg Leu Glu Ala
145                 150                 155                 160

Thr Glu Ile Ser Phe Pro Asp Thr Leu Pro Asn Pro Ser Trp Asp Gly
                165                 170                 175

Ala Trp Glu Pro Phe His Tyr Pro Asp Ser Thr Pro His Thr Ala Pro
            180                 185                 190

Asp Val Ala Glu Ile Pro Gly Tyr Ile Gln Ser Leu Pro Pro Gln Ser
        195                 200                 205

Glu Asp Pro Arg Arg Leu Arg Val Phe Val Asn Glu Ile Ala Leu Glu
    210                 215                 220
```

```
Gly Asp Phe Pro Asp Tyr Arg Gln Gly Gln Ser Val Arg Leu Thr Leu
225                 230                 235                 240

Gly Ile Ser Ser Ser Pro Val Pro Leu Glu Gly Met Thr Thr Arg Arg
                245                 250                 255

Arg Gly Arg Val Arg Asn Leu Gly Glu Glu Ala Ser Pro Gly Asp Asp
            260                 265                 270

Gly Met Pro Gln Trp Pro Ile Leu Leu Thr Gly Asp Gly Trp Thr Ala
        275                 280                 285

Leu Ala Tyr Thr Pro Ile Pro Lys Arg Gly Asp Ala Glu Ile Gln Gly
    290                 295                 300

Trp Phe Tyr Tyr Ser Ala Tyr Gly Ile Val Asp Val Pro Thr Asp Leu
305                 310                 315                 320

Arg Val Glu Arg Ile Phe Ala Gly Ile Gly Thr Ser Gly Thr Asn Glu
                325                 330                 335

Arg Leu Trp Gln Glu Ile Asp Asn Thr Ser Ser Ala Tyr His Ser Glu
            340                 345                 350

Asp Trp Trp Ile Arg Asp Val Val Leu Asp Val Thr Leu Asp Gly Ala
        355                 360                 365

Val Pro Pro Pro Leu Arg Arg Asp Val Phe Thr Ala Val Asp Pro Ile
    370                 375                 380

Val Ala Gly Asp Lys Leu Trp Leu Cys Asp Val His Phe Pro Val Ala
385                 390                 395                 400

Arg Cys Trp Glu Thr Thr Thr Gly Arg Tyr Leu Gly Gln Thr Leu Val
                405                 410                 415

Pro Ala Pro Leu Arg Asp Arg Ser Tyr Val Leu Glu Leu His Ser Asp
            420                 425                 430

Gln Gln Leu Gly Ala Val Ala Ala Ser Gly Lys Ser Gly Trp Ile Leu
        435                 440                 445

Thr Pro Gly Gln Ala Val Ala Thr Lys Ala Pro Asp Trp Thr Pro Pro
    450                 455                 460

Thr Arg Ala Thr Asp Leu Pro Gln Val Pro Ser Pro Trp Glu Ile Val
465                 470                 475                 480

Ala Val Arg Gly Gln Gly Leu Phe Glu Leu Gln Val Glu Thr Ser Arg
                485                 490                 495

Arg Thr Ala Leu Gly Arg Val Asn Ala Thr Gly Gly Val Asp Ile Gly
            500                 505                 510

Glu Leu Pro Pro Asn Gly Tyr Thr Ile Ser Ser Val Val Gln Ile Gly
        515                 520                 525

Asp Glu Tyr Ile Val Gly Arg Trp Val Glu Glu Tyr Arg Leu Asn Ser
    530                 535                 540
```

```
Lys Leu Glu Val Ile Ser Thr Lys Glu Leu Asp Ile Ser Ala Ser Gly
545                 550                 555                 560

Trp Lys Ser Lys Gly Thr Val Ala Tyr Leu Ser Glu Asp Thr His Ile
                565                 570                 575

Cys Phe Phe Asp Gln Val Ser Gly Ala Glu Leu Pro Ser Leu Gly Ile
            580                 585                 590

Ala Glu Gly His Gln Gly Glu Val Met Ser Ala Thr Ser Ser Glu Ser
        595                 600                 605

Ile Val Leu Ile Tyr Arg Arg Asn Pro Asn Asn Ser Met Ser Ile Val
    610                 615                 620

Pro Thr Ser Val Ala Thr Tyr Asp Asn Gly Thr Trp Thr Thr Met Pro
625                 630                 635                 640

Leu Gln Glu Ala Pro Ala Glu Leu Ser
                645
```

<210> 69
<211> 2070
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2047)
<223> FRXA00028

<400> 69

```
aaaagtcctg gccagaaaac tctctatact gtgcagcatg gcaccaacga tcaccgacat 60

ccatgttctg cttcgtcgcg gtgagcgaca atcagtgatc atg acc ctc act gcc   115
                                            Met Thr Leu Thr Ala
                                              1               5

tct tcc ttg gag gcc ggg aaa atg tct ttt agt ggc ggg tat atc gtg   163
Ser Ser Leu Glu Ala Gly Lys Met Ser Phe Ser Gly Gly Tyr Ile Val
                 10                  15                  20

ggc gag acg atg atc ttc ctc gtc gat ccc gat gaa gtc gag ata cga   211
Gly Glu Thr Met Ile Phe Leu Val Asp Pro Asp Glu Val Glu Ile Arg
             25                  30                  35

cgc agc cct aac agc ctc cac gtc ctg cgt aac ggt agc gat att ctg   259
Arg Ser Pro Asn Ser Leu His Val Leu Arg Asn Gly Ser Asp Ile Leu
         40                  45                  50

cgc cgc aac gag cat cat tgc tgg gta ttt gag aat ttc aat aaa ccc   307
Arg Arg Asn Glu His His Cys Trp Val Phe Glu Asn Phe Asn Lys Pro
     55                  60                  65

att gac cca cct gtt cga ttg ggt cct cgg gat atc atc tgc ccg agc   355
Ile Asp Pro Pro Val Arg Leu Gly Pro Arg Asp Ile Ile Cys Pro Ser
 70                  75                  80                  85

gcc ttg gcc tgg gtt ctt caa cag cat tcc atc tcc cgg tcc tta tcc   403
Ala Leu Ala Trp Val Leu Gln Gln His Ser Ile Ser Arg Ser Leu Ser
```

```
                    90                  95                 100

cac cac ctt cac gcg gat aag atc act gcg gga gag att gct gga cgc   451
His His Leu His Ala Asp Lys Ile Thr Ala Gly Glu Ile Ala Gly Arg
            105                 110                 115

ccc acc tgg atc ctc cgt gag gaa cct act tca gga ggg cag gac cca   499
Pro Thr Trp Ile Leu Arg Glu Glu Pro Thr Ser Gly Gly Gln Asp Pro
        120                 125                 130

agt cga ttg gtc agt ctt gaa atc gac cag gaa cac ggt gtc atc ctt   547
Ser Arg Leu Val Ser Leu Glu Ile Asp Gln Glu His Gly Val Ile Leu
    135                 140                 145

gca gtg gag act gga caa gaa cga ctc gaa gcc acg gag att tct ttt   595
Ala Val Glu Thr Gly Gln Glu Arg Leu Glu Ala Thr Glu Ile Ser Phe
150                 155                 160                 165

cct gac act ctt cct aat cct tcc tgg gac gga gcc tgg gaa cca ttc   643
Pro Asp Thr Leu Pro Asn Pro Ser Trp Asp Gly Ala Trp Glu Pro Phe
                170                 175                 180

cat tat cca gat tcg aca cca cac act gcc cct gat gtt gct gaa ata   691
His Tyr Pro Asp Ser Thr Pro His Thr Ala Pro Asp Val Ala Glu Ile
            185                 190                 195

ccc ggt tac att cag tca ctg ccg ccg cag tct gaa gat cct cgc aga   739
Pro Gly Tyr Ile Gln Ser Leu Pro Pro Gln Ser Glu Asp Pro Arg Arg
        200                 205                 210

cta cga gtc ttc gtc aat gag ata gca ctc gaa ggt gat ttc cct gac   787
Leu Arg Val Phe Val Asn Glu Ile Ala Leu Glu Gly Asp Phe Pro Asp
    215                 220                 225

tac cgt caa gga caa tct gtg cga ctt act ttg gga att agc tcc tcc   835
Tyr Arg Gln Gly Gln Ser Val Arg Leu Thr Leu Gly Ile Ser Ser Ser
230                 235                 240                 245

cct gtg cca ctc gaa gga atg aca acc aga cgc cgg ggc cgg gta cgc   883
Pro Val Pro Leu Glu Gly Met Thr Thr Arg Arg Arg Gly Arg Val Arg
                250                 255                 260

aac ctt ggg gaa gaa gct agt cca ggc gat gac ggt atg ccc cag tgg   931
Asn Leu Gly Glu Glu Ala Ser Pro Gly Asp Asp Gly Met Pro Gln Trp
            265                 270                 275

cca atc ctg ctc act ggt gat ggg tgg acg gcg ctg gcc tac act ccc   979
Pro Ile Leu Leu Thr Gly Asp Gly Trp Thr Ala Leu Ala Tyr Thr Pro
        280                 285                 290

atc cca aaa cgt gga gat gca gag atc cag ggg tgg ttt tat tat tcc   1027
Ile Pro Lys Arg Gly Asp Ala Glu Ile Gln Gly Trp Phe Tyr Tyr Ser
    295                 300                 305

gcc tac gga att gtt gat gtt ccc aca gat cta cgg gta gag cgt att   1075
Ala Tyr Gly Ile Val Asp Val Pro Thr Asp Leu Arg Val Glu Arg Ile
310                 315                 320                 325

ttc gct ggt atc ggc aca agt ggc acc aac gag cgt ttg tgg cag gag   1123
Phe Ala Gly Ile Gly Thr Ser Gly Thr Asn Glu Arg Leu Trp Gln Glu
                330                 335                 340
```

```
ata gac aat act tct tcg gct tat cac tcg gaa gat tgg tgg atc cgc   1171
Ile Asp Asn Thr Ser Ser Ala Tyr His Ser Glu Asp Trp Trp Ile Arg
            345                 350                 355

gat gtc gtt tta gac gtc acg ttg gat gga gct gtt ccg cct ccg ctt   1219
Asp Val Val Leu Asp Val Thr Leu Asp Gly Ala Val Pro Pro Pro Leu
        360                 365                 370

aga cgt gac gtc ttc act gct gtc gat cct att gtg gcg ggt gac aaa   1267
Arg Arg Asp Val Phe Thr Ala Val Asp Pro Ile Val Ala Gly Asp Lys
    375                 380                 385

ttg tgg ctg tgt gac gtg cac ttt ccg gta gcc cgc tgc tgg gag acc   1315
Leu Trp Leu Cys Asp Val His Phe Pro Val Ala Arg Cys Trp Glu Thr
390                 395                 400                 405

acg acc ggc cga tac ttg ggg cag act tta ktc cca gca cca ctg cga   1363
Thr Thr Gly Arg Tyr Leu Gly Gln Thr Leu Xaa Pro Ala Pro Leu Arg
                410                 415                 420

gat cga tcg tac gtc ctt gag ctg cac agc gac caa caa tta gga gcc   1411
Asp Arg Ser Tyr Val Leu Glu Leu His Ser Asp Gln Gln Leu Gly Ala
            425                 430                 435

gta gcg gca agt ggg aag agt ggt tgg att ctc aca cct ggt caa gca   1459
Val Ala Ala Ser Gly Lys Ser Gly Trp Ile Leu Thr Pro Gly Gln Ala
        440                 445                 450

gta gcc act aaa gct cct gat tgg act cct ccc acc cgg gca acc gat   1507
Val Ala Thr Lys Ala Pro Asp Trp Thr Pro Pro Thr Arg Ala Thr Asp
    455                 460                 465

ctg cct cag gtc ccc tcc ccc tgg gag atc gtc gct gtc cgt ggc caa   1555
Leu Pro Gln Val Pro Ser Pro Trp Glu Ile Val Ala Val Arg Gly Gln
470                 475                 480                 485

ggt ctg ttt gag ctg cag gtg gaa act agt aga cgc acc gcc ctc ggt   1603
Gly Leu Phe Glu Leu Gln Val Glu Thr Ser Arg Arg Thr Ala Leu Gly
                490                 495                 500

cga gtt aat gcg acc ggt ggc gtc gac atc ggt gaa ctc ccg ccc aac   1651
Arg Val Asn Ala Thr Gly Gly Val Asp Ile Gly Glu Leu Pro Pro Asn
            505                 510                 515

ggc tat acc atc agt tct gtg gtt cag atc ggt gat gaa tac atc gtg   1699
Gly Tyr Thr Ile Ser Ser Val Val Gln Ile Gly Asp Glu Tyr Ile Val
        520                 525                 530

ggc agg tgg gta gag gaa tac cgg ctc aac tcc aaa ctg gag gtc att   1747
Gly Arg Trp Val Glu Glu Tyr Arg Leu Asn Ser Lys Leu Glu Val Ile
    535                 540                 545

tct acc aaa gag cta gat atc tcc gca tcc gga tgg aag agc aag ggg   1795
Ser Thr Lys Glu Leu Asp Ile Ser Ala Ser Gly Trp Lys Ser Lys Gly
550                 555                 560                 565

acg gtt gct tat ctg tcg gaa gac act cac ata tgt ttc ttc gac cag   1843
Thr Val Ala Tyr Leu Ser Glu Asp Thr His Ile Cys Phe Phe Asp Gln
                570                 575                 580
```

```
gtc agc ggg gcc gag ctt ccc agc ctg ggt atc gcc gag gga cac cag   1891
Val Ser Gly Ala Glu Leu Pro Ser Leu Gly Ile Ala Glu Gly His Gln
            585                 590                 595

ggc gag gtt atg tca gca act tct tca gag agc atc gtg ctt atc tac   1939
Gly Glu Val Met Ser Ala Thr Ser Ser Glu Ser Ile Val Leu Ile Tyr
        600                 605                 610

cgg cgc aac ccg aac aat tca atg tcg att gtc ccg act tcc gtt gcc   1987
Arg Arg Asn Pro Asn Asn Ser Met Ser Ile Val Pro Thr Ser Val Ala
    615                 620                 625

acc tat gac aat ggc acc tgg acg act atg ccg cta cag gaa gct cca   2035
Thr Tyr Asp Asn Gly Thr Trp Thr Thr Met Pro Leu Gln Glu Ala Pro
630                 635                 640                 645

gcg gaa ctg tcc taaactgctc atagactgct gag                        2070
Ala Glu Leu Ser
```

<210> 70
<211> 649
<212> PRT
<213> Corynebacterium glutamicum

<400> 70

```
Met Thr Leu Thr Ala Ser Ser Leu Glu Ala Gly Lys Met Ser Phe Ser
  1               5                  10                  15

Gly Gly Tyr Ile Val Gly Glu Thr Met Ile Phe Leu Val Asp Pro Asp
             20                  25                  30

Glu Val Glu Ile Arg Arg Ser Pro Asn Ser Leu His Val Leu Arg Asn
         35                  40                  45

Gly Ser Asp Ile Leu Arg Arg Asn Glu His His Cys Trp Val Phe Glu
     50                  55                  60

Asn Phe Asn Lys Pro Ile Asp Pro Pro Val Arg Leu Gly Pro Arg Asp
 65                  70                  75                  80

Ile Ile Cys Pro Ser Ala Leu Ala Trp Val Leu Gln Gln His Ser Ile
                 85                  90                  95

Ser Arg Ser Leu Ser His His Leu His Ala Asp Lys Ile Thr Ala Gly
            100                 105                 110

Glu Ile Ala Gly Arg Pro Thr Trp Ile Leu Arg Glu Glu Pro Thr Ser
        115                 120                 125

Gly Gly Gln Asp Pro Ser Arg Leu Val Ser Leu Glu Ile Asp Gln Glu
    130                 135                 140

His Gly Val Ile Leu Ala Val Glu Thr Gly Gln Glu Arg Leu Glu Ala
145                 150                 155                 160

Thr Glu Ile Ser Phe Pro Asp Thr Leu Pro Asn Pro Ser Trp Asp Gly
                165                 170                 175

Ala Trp Glu Pro Phe His Tyr Pro Asp Ser Thr Pro His Thr Ala Pro
```

```
            180                 185                 190

Asp Val Ala Glu Ile Pro Gly Tyr Ile Gln Ser Leu Pro Pro Gln Ser
        195                 200                 205

Glu Asp Pro Arg Arg Leu Arg Val Phe Val Asn Glu Ile Ala Leu Glu
    210                 215                 220

Gly Asp Phe Pro Asp Tyr Arg Gln Gly Gln Ser Val Arg Leu Thr Leu
225                 230                 235                 240

Gly Ile Ser Ser Ser Pro Val Pro Leu Glu Gly Met Thr Thr Arg Arg
                245                 250                 255

Arg Gly Arg Val Arg Asn Leu Gly Glu Glu Ala Ser Pro Gly Asp Asp
            260                 265                 270

Gly Met Pro Gln Trp Pro Ile Leu Leu Thr Gly Asp Gly Trp Thr Ala
        275                 280                 285

Leu Ala Tyr Thr Pro Ile Pro Lys Arg Gly Asp Ala Glu Ile Gln Gly
    290                 295                 300

Trp Phe Tyr Tyr Ser Ala Tyr Gly Ile Val Asp Val Pro Thr Asp Leu
305                 310                 315                 320

Arg Val Glu Arg Ile Phe Ala Gly Ile Gly Thr Ser Gly Thr Asn Glu
                325                 330                 335

Arg Leu Trp Gln Glu Ile Asp Asn Thr Ser Ser Ala Tyr His Ser Glu
            340                 345                 350

Asp Trp Trp Ile Arg Asp Val Val Leu Asp Val Thr Leu Asp Gly Ala
        355                 360                 365

Val Pro Pro Pro Leu Arg Arg Asp Val Phe Thr Ala Val Asp Pro Ile
    370                 375                 380

Val Ala Gly Asp Lys Leu Trp Leu Cys Asp Val His Phe Pro Val Ala
385                 390                 395                 400

Arg Cys Trp Glu Thr Thr Thr Gly Arg Tyr Leu Gly Gln Thr Leu Xaa
                405                 410                 415

Pro Ala Pro Leu Arg Asp Arg Ser Tyr Val Leu Glu Leu His Ser Asp
            420                 425                 430

Gln Gln Leu Gly Ala Val Ala Ala Ser Gly Lys Ser Gly Trp Ile Leu
        435                 440                 445

Thr Pro Gly Gln Ala Val Ala Thr Lys Ala Pro Asp Trp Thr Pro Pro
    450                 455                 460

Thr Arg Ala Thr Asp Leu Pro Gln Val Pro Ser Pro Trp Glu Ile Val
465                 470                 475                 480

Ala Val Arg Gly Gln Gly Leu Phe Glu Leu Gln Val Glu Thr Ser Arg
                485                 490                 495

Arg Thr Ala Leu Gly Arg Val Asn Ala Thr Gly Gly Val Asp Ile Gly
            500                 505                 510
```

```
Glu Leu Pro Pro Asn Gly Tyr Thr Ile Ser Ser Val Val Gln Ile Gly
        515                 520                 525

Asp Glu Tyr Ile Val Gly Arg Trp Val Glu Glu Tyr Arg Leu Asn Ser
    530                 535                 540

Lys Leu Glu Val Ile Ser Thr Lys Glu Leu Asp Ile Ser Ala Ser Gly
545                 550                 555                 560

Trp Lys Ser Lys Gly Thr Val Ala Tyr Leu Ser Glu Asp Thr His Ile
                565                 570                 575

Cys Phe Phe Asp Gln Val Ser Gly Ala Glu Leu Pro Ser Leu Gly Ile
            580                 585                 590

Ala Glu Gly His Gln Gly Glu Val Met Ser Ala Thr Ser Ser Glu Ser
        595                 600                 605

Ile Val Leu Ile Tyr Arg Arg Asn Pro Asn Asn Ser Met Ser Ile Val
    610                 615                 620

Pro Thr Ser Val Ala Thr Tyr Asp Asn Gly Thr Trp Thr Thr Met Pro
625                 630                 635                 640

Leu Gln Glu Ala Pro Ala Glu Leu Ser
                645
```

Application Filed with the EPO on 23 Dec 2009

<210> 71
<211> 1458
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1435)
<223> RXN00033

<400> 71

```
acacggattt aacgtgacgg tttctcagtg tttttagctt ctggcttttg gcttctgatg 60

ctttagcgct ggactcaaca tttaaaacaa aggtgaacac atg tca gta cag caa   115
                                            Met Ser Val Gln Gln
                                              1               5

agc ggg ttg ctc gaa cgt ctc ggc att ccc cga ccc ttg att ttc gga   163
Ser Gly Leu Leu Glu Arg Leu Gly Ile Pro Arg Pro Leu Ile Phe Gly
                 10                  15                  20

ttt atc ggc ctc acc atc ttc atg atc ggt gac ggt gtc gaa acc aac   211
Phe Ile Gly Leu Thr Ile Phe Met Ile Gly Asp Gly Val Glu Thr Asn
             25                  30                  35

att ttg gaa cct ttc ctc agt tcc gaa cat ggt ttc agc gtt tcc ctc   259
Ile Leu Glu Pro Phe Leu Ser Ser Glu His Gly Phe Ser Val Ser Leu
         40                  45                  50

gcg gga acc ctg gtg act gtt tac ggt gtt gcc gtg gcg atc gca gca   307
Ala Gly Thr Leu Val Thr Val Tyr Gly Val Ala Val Ala Ile Ala Ala
     55                  60                  65
```

```
ttc ttc gcg gcg gca ctt tcg gac ctg tgg ggt cca cga aaa gtg atg   355
Phe Phe Ala Ala Ala Leu Ser Asp Leu Trp Gly Pro Arg Lys Val Met
 70                  75                  80                  85

atc ctc ggt gct tca atc tgg atc gtc ttt gag ctg atc ttc ctc acc   403
Ile Leu Gly Ala Ser Ile Trp Ile Val Phe Glu Leu Ile Phe Leu Thr
                90                  95                 100

gtg gca ctg acc acc gac cat act tgg ttg atc ttc ctt gct tat ggt   451
Val Ala Leu Thr Thr Asp His Thr Trp Leu Ile Phe Leu Ala Tyr Gly
            105                 110                 115

ctc cgc ggc ttt ggt tat cca ttc ttc gcc tac gga ttc ttg gtg tgg   499
Leu Arg Gly Phe Gly Tyr Pro Phe Phe Ala Tyr Gly Phe Leu Val Trp
        120                 125                 130

atc acc gca act gcc tca cct aag caa ttg ggt acc ggt gtg ggt tgg   547
Ile Thr Ala Thr Ala Ser Pro Lys Gln Leu Gly Thr Gly Val Gly Trp
    135                 140                 145

ttc tac gtt gcc ttc tct gca ggt ctt cct acc ttg ggt gcg ctg gtt   595
Phe Tyr Val Ala Phe Ser Ala Gly Leu Pro Thr Leu Gly Ala Leu Val
150                 155                 160                 165

gcc acc att tcc atg cag tac gtg aac ttg acc ttc tat gaa acg ttg   643
Ala Thr Ile Ser Met Gln Tyr Val Asn Leu Thr Phe Tyr Glu Thr Leu
                170                 175                 180

tgg gtt tcc ctc gtg ctg gtg gtc atc gga tcg ctc atc gca ctg ctg   691
Trp Val Ser Leu Val Leu Val Val Ile Gly Ser Leu Ile Ala Leu Leu
            185                 190                 195

gga gtg aag gaa cgt cgc gga cgc cac cca ctg gtt gcc aac ccc gac   739
Gly Val Lys Glu Arg Arg Gly Arg His Pro Leu Val Ala Asn Pro Asp
        200                 205                 210

gat gtg aag caa aca ctt ggc cag ggc ttc aaa ctt ctg cgc aat gat   787
Asp Val Lys Gln Thr Leu Gly Gln Gly Phe Lys Leu Leu Arg Asn Asp
    215                 220                 225

cga cgt gca cgt ttt gtc acc tac atc cgc acc atc aac tcc att ccg   835
Arg Arg Ala Arg Phe Val Thr Tyr Ile Arg Thr Ile Asn Ser Ile Pro
230                 235                 240                 245

acc tac gcg atg gct gtg ttc ttc cca tca ttt ttc act gac gat ctg   883
Thr Tyr Ala Met Ala Val Phe Phe Pro Ser Phe Phe Thr Asp Asp Leu
                250                 255                 260

aag tgg cag cta agc tgg ttc ctc atc ctc acc act gta att tac gca   931
Lys Trp Gln Leu Ser Trp Phe Leu Ile Leu Thr Thr Val Ile Tyr Ala
            265                 270                 275

gtc aac ctg ccg ttc aat cct ttc ttc ggt agc ttc ggc gac cgc cac   979
Val Asn Leu Pro Phe Asn Pro Phe Phe Gly Ser Phe Gly Asp Arg His
        280                 285                 290

ggt tgg gca cga act gtg ttc tgg ggc gga tca atc ggt ggc gca gtc   1027
Gly Trp Ala Arg Thr Val Phe Trp Gly Gly Ser Ile Gly Gly Ala Val
    295                 300                 305
```

```
acc ctc gcg ttg gtt tac ttc att ccg atg ttc ggc gtt cag gct ggc   1075
Thr Leu Ala Leu Val Tyr Phe Ile Pro Met Phe Gly Val Gln Ala Gly
310                 315                 320                 325

atg tcc aac ggt gtc gtt ttc gga atc acc atc gca gcc ggc gca ctc   1123
Met Ser Asn Gly Val Val Phe Gly Ile Thr Ile Ala Ala Gly Ala Leu
                330                 335                 340

ttt ggt gtg tcc ctc gcg ggc ttc gtg cca ctt tcc gca atc gct gtc   1171
Phe Gly Val Ser Leu Ala Gly Phe Val Pro Leu Ser Ala Ile Ala Val
            345                 350                 355

tcc ctt gat ccc aag cac ccc ggc gca gcg atg gcc aca tac aac ctc   1219
Ser Leu Asp Pro Lys His Pro Gly Ala Ala Met Ala Thr Tyr Asn Leu
        360                 365                 370

ggc gtt ggt ggc gct gta gct gtg gga ccg ctc ctg gtt gca gtc ttc   1267
Gly Val Gly Gly Ala Val Ala Val Gly Pro Leu Leu Val Ala Val Phe
    375                 380                 385

cac cca ctg att ggt cca acc gga ttg atc ctg gtc atg atc gcc ctc   1315
His Pro Leu Ile Gly Pro Thr Gly Leu Ile Leu Val Met Ile Ala Leu
390                 395                 400                 405

tac ctg ctc tcc ggt tgg atg act ctt caa ctt cgc ggc acc caa cca   1363
Tyr Leu Leu Ser Gly Trp Met Thr Leu Gln Leu Arg Gly Thr Gln Pro
                410                 415                 420

gga ttc gac gga gtg cca gca ctt gct gaa gac gcc cac atc gaa gac   1411
Gly Phe Asp Gly Val Pro Ala Leu Ala Glu Asp Ala His Ile Glu Asp
            425                 430                 435

ctt gca gat gta aac gca aac gcc taactgtttt tcgagctaaa ccc         1458
Leu Ala Asp Val Asn Ala Asn Ala
        440                 445
```

<210> 72
<211> 445
<212> PRT
<213> Corynebacterium glutamicum

<400> 72

```
Met Ser Val Gln Gln Ser Gly Leu Leu Glu Arg Leu Gly Ile Pro Arg
  1               5                  10                  15

Pro Leu Ile Phe Gly Phe Ile Gly Leu Thr Ile Phe Met Ile Gly Asp
             20                  25                  30

Gly Val Glu Thr Asn Ile Leu Glu Pro Phe Leu Ser Ser Glu His Gly
         35                  40                  45

Phe Ser Val Ser Leu Ala Gly Thr Leu Val Thr Val Tyr Gly Val Ala
     50                  55                  60

Val Ala Ile Ala Ala Phe Phe Ala Ala Ala Leu Ser Asp Leu Trp Gly
 65                  70                  75                  80

Pro Arg Lys Val Met Ile Leu Gly Ala Ser Ile Trp Ile Val Phe Glu
                 85                  90                  95
```

```
Leu Ile Phe Leu Thr Val Ala Leu Thr Thr Asp His Thr Trp Leu Ile
            100                 105                 110

Phe Leu Ala Tyr Gly Leu Arg Gly Phe Gly Tyr Pro Phe Phe Ala Tyr
        115                 120                 125

Gly Phe Leu Val Trp Ile Thr Ala Thr Ala Ser Pro Lys Gln Leu Gly
    130                 135                 140

Thr Gly Val Gly Trp Phe Tyr Val Ala Phe Ser Ala Gly Leu Pro Thr
145                 150                 155                 160

Leu Gly Ala Leu Val Ala Thr Ile Ser Met Gln Tyr Val Asn Leu Thr
                165                 170                 175

Phe Tyr Glu Thr Leu Trp Val Ser Leu Val Leu Val Val Ile Gly Ser
            180                 185                 190

Leu Ile Ala Leu Leu Gly Val Lys Glu Arg Arg Gly Arg His Pro Leu
        195                 200                 205

Val Ala Asn Pro Asp Asp Val Lys Gln Thr Leu Gly Gln Gly Phe Lys
    210                 215                 220

Leu Leu Arg Asn Asp Arg Arg Ala Arg Phe Val Thr Tyr Ile Arg Thr
225                 230                 235                 240

Ile Asn Ser Ile Pro Thr Tyr Ala Met Ala Val Phe Phe Pro Ser Phe
                245                 250                 255

Phe Thr Asp Asp Leu Lys Trp Gln Leu Ser Trp Phe Leu Ile Leu Thr
            260                 265                 270

Thr Val Ile Tyr Ala Val Asn Leu Pro Phe Asn Pro Phe Phe Gly Ser
        275                 280                 285

Phe Gly Asp Arg His Gly Trp Ala Arg Thr Val Phe Trp Gly Gly Ser
    290                 295                 300

Ile Gly Gly Ala Val Thr Leu Ala Leu Val Tyr Phe Ile Pro Met Phe
305                 310                 315                 320

Gly Val Gln Ala Gly Met Ser Asn Gly Val Val Phe Gly Ile Thr Ile
                325                 330                 335

Ala Ala Gly Ala Leu Phe Gly Val Ser Leu Ala Gly Phe Val Pro Leu
            340                 345                 350

Ser Ala Ile Ala Val Ser Leu Asp Pro Lys His Pro Gly Ala Ala Met
        355                 360                 365

Ala Thr Tyr Asn Leu Gly Val Gly Gly Ala Val Ala Val Gly Pro Leu
    370                 375                 380

Leu Val Ala Val Phe His Pro Leu Ile Gly Pro Thr Gly Leu Ile Leu
385                 390                 395                 400

Val Met Ile Ala Leu Tyr Leu Leu Ser Gly Trp Met Thr Leu Gln Leu
                405                 410                 415

Arg Gly Thr Gln Pro Gly Phe Asp Gly Val Pro Ala Leu Ala Glu Asp
```

```
            420                 425                 430

Ala His Ile Glu Asp Leu Ala Asp Val Asn Ala Asn Ala
        435                 440                 445


<210> 73
<211> 873
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(850)
<223> RXN00056

<400> 73
atatgaattt aataatagat tccgaacgaa atcggtgtta gcgtctgtgc tgaaacaatc 60

taatcgcgtt tcaggacacc tacatgatca ggagctcttt ttg tta aac aga gtc   115
                                          Leu Leu Asn Arg Val
                                            1               5

agt cgt att gca ggc gct tct gca atc aca cta tgc atc ggc tta acc   163
Ser Arg Ile Ala Gly Ala Ser Ala Ile Thr Leu Cys Ile Gly Leu Thr
                10                  15                  20

aca ata cta agc cct act tcc act gca caa agc ctc gaa cag atc acc   211
Thr Ile Leu Ser Pro Thr Ser Thr Ala Gln Ser Leu Glu Gln Ile Thr
            25                  30                  35

cct tta cct gaa tct gca atc gac ctc aac gcc gag att cac gta aac   259
Pro Leu Pro Glu Ser Ala Ile Asp Leu Asn Ala Glu Ile His Val Asn
        40                  45                  50

aca agc gac att tca gct gaa cag atc ctt ggt gct caa gat gaa atc   307
Thr Ser Asp Ile Ser Ala Glu Gln Ile Leu Gly Ala Gln Asp Glu Ile
    55                  60                  65

aca act atg tac gat tct cat gac ccc tac gag tac ttc gat acc ctc   355
Thr Thr Met Tyr Asp Ser His Asp Pro Tyr Glu Tyr Phe Asp Thr Leu
70                  75                  80                  85

acc gac atc gaa cag cgt tca ata ata gca gcg ctt aaa cgg gat ccg   403
Thr Asp Ile Glu Gln Arg Ser Ile Ile Ala Ala Leu Lys Arg Asp Pro
                90                  95                  100

agt tca ctc caa caa cgc caa gaa acc cgt ctc gcg gca cag tcc gac   451
Ser Ser Leu Gln Gln Arg Gln Glu Thr Arg Leu Ala Ala Gln Ser Asp
            105                 110                 115

ccc tac aaa att tac ata tca ggc ctc gaa atg ctt tca tgc atc aat   499
Pro Tyr Lys Ile Tyr Ile Ser Gly Leu Glu Met Leu Ser Cys Ile Asn
        120                 125                 130

cta gtt gat gtt gta tca tgc ggg att gca aac caa gca gca acc aaa   547
Leu Val Asp Val Val Ser Cys Gly Ile Ala Asn Gln Ala Ala Thr Lys
    135                 140                 145

gca aat aat gag gct gtc gca cga tac cca ggc gat tcc ctt cgc aac   595
Ala Asn Asn Glu Ala Val Ala Arg Tyr Pro Gly Asp Ser Leu Arg Asn
```

```
150                 155                 160                 165

ggc aaa ggc gat gca ttt cgg cat tgc tca tgg aac gct ctg atg acg   643
Gly Lys Gly Asp Ala Phe Arg His Cys Ser Trp Asn Ala Leu Met Thr
                170                 175                 180

ata cga atc ggg agc aat gga gct gaa aga att gca aca aac cac gag   691
Ile Arg Ile Gly Ser Asn Gly Ala Glu Arg Ile Ala Thr Asn His Glu
            185                 190                 195

aca atc ggg gac ggt ccg gcc gat gaa aat gca atg gac cta ttc aat   739
Thr Ile Gly Asp Gly Pro Ala Asp Glu Asn Ala Met Asp Leu Phe Asn
        200                 205                 210

aat gca caa ggc cga cag atc gga gcc gga ttc att aat agt aag gat   787
Asn Ala Gln Gly Arg Gln Ile Gly Ala Gly Phe Ile Asn Ser Lys Asp
    215                 220                 225

gaa act agc gcg ctc gcg ata tgc gcg ctg tgg aca aat ctc ggt aga   835
Glu Thr Ser Ala Leu Ala Ile Cys Ala Leu Trp Thr Asn Leu Gly Arg
230                 235                 240                 245

cta aaa act cta aaa taagcaaggt gccctctgat gct                    873
Leu Lys Thr Leu Lys
                250
```

<210> 74
<211> 250
<212> PRT
<213> Corynebacterium glutamicum

<400> 74

```
Leu Leu Asn Arg Val Ser Arg Ile Ala Gly Ala Ser Ala Ile Thr Leu
  1               5                  10                  15

Cys Ile Gly Leu Thr Thr Ile Leu Ser Pro Thr Ser Thr Ala Gln Ser
             20                  25                  30

Leu Glu Gln Ile Thr Pro Leu Pro Glu Ser Ala Ile Asp Leu Asn Ala
         35                  40                  45

Glu Ile His Val Asn Thr Ser Asp Ile Ser Ala Glu Gln Ile Leu Gly
     50                  55                  60

Ala Gln Asp Glu Ile Thr Thr Met Tyr Asp Ser His Asp Pro Tyr Glu
 65                  70                  75                  80

Tyr Phe Asp Thr Leu Thr Asp Ile Glu Gln Arg Ser Ile Ile Ala Ala
                 85                  90                  95

Leu Lys Arg Asp Pro Ser Ser Leu Gln Gln Arg Gln Glu Thr Arg Leu
            100                 105                 110

Ala Ala Gln Ser Asp Pro Tyr Lys Ile Tyr Ile Ser Gly Leu Glu Met
        115                 120                 125

Leu Ser Cys Ile Asn Leu Val Asp Val Val Ser Cys Gly Ile Ala Asn
    130                 135                 140

Gln Ala Ala Thr Lys Ala Asn Asn Glu Ala Val Ala Arg Tyr Pro Gly
```

```
145                 150                 155                 160

Asp Ser Leu Arg Asn Gly Lys Gly Asp Ala Phe Arg His Cys Ser Trp
                165                 170                 175

Asn Ala Leu Met Thr Ile Arg Ile Gly Ser Asn Gly Ala Glu Arg Ile
            180                 185                 190

Ala Thr Asn His Glu Thr Ile Gly Asp Gly Pro Ala Asp Glu Asn Ala
        195                 200                 205

Met Asp Leu Phe Asn Asn Ala Gln Gly Arg Gln Ile Gly Ala Gly Phe
    210                 215                 220

Ile Asn Ser Lys Asp Glu Thr Ser Ala Leu Ala Ile Cys Ala Leu Trp
225                 230                 235                 240

Thr Asn Leu Gly Arg Leu Lys Thr Leu Lys
                245                 250
```

<210> 75
<211> 873
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(850)
<223> FRXA00056

<400> 75

```
atatgaattt aataatagat tccgaacgaa atcggtgtta gcgtctgtgc tgaaacaatc 60

taatcgcgtt tcaggacacc tacatgatca ggagctcttt ttg tta aac aga gtc   115
                                              Leu Leu Asn Arg Val
                                                1               5

agt cgt att gca ggc gct tct gca atc aca cta tgc atc ggc tta acc   163
Ser Arg Ile Ala Gly Ala Ser Ala Ile Thr Leu Cys Ile Gly Leu Thr
                  10                  15                  20

aca ata cta agc cct act tcc act gca caa agc ctc gaa cag atc acc   211
Thr Ile Leu Ser Pro Thr Ser Thr Ala Gln Ser Leu Glu Gln Ile Thr
              25                  30                  35

cct tta cct gaa tct gca atc gac ctc aac gcc gag att cac gta aac   259
Pro Leu Pro Glu Ser Ala Ile Asp Leu Asn Ala Glu Ile His Val Asn
          40                  45                  50

aca agc gac att tca gct gaa cag atc ctt ggt gct caa gat gaa atc   307
Thr Ser Asp Ile Ser Ala Glu Gln Ile Leu Gly Ala Gln Asp Glu Ile
      55                  60                  65

aca act atg tac gat tct cat gac ccc tac gag tac ttc gat acc ctc   355
Thr Thr Met Tyr Asp Ser His Asp Pro Tyr Glu Tyr Phe Asp Thr Leu
  70                  75                  80                  85

acc gac atc gaa cag cgt tca ata ata gca gcg ctt aaa cgg gat ccg   403
Thr Asp Ile Glu Gln Arg Ser Ile Ile Ala Ala Leu Lys Arg Asp Pro
                  90                  95                 100
```

```
agt tca ctc caa caa cgc caa gaa acc cgt ctc gcg gca cag tcc gac   451
Ser Ser Leu Gln Gln Arg Gln Glu Thr Arg Leu Ala Ala Gln Ser Asp
            105                 110                 115

ccc tac aaa att tac ata tca ggc ctc gaa atg ctt tca tgc atc aat   499
Pro Tyr Lys Ile Tyr Ile Ser Gly Leu Glu Met Leu Ser Cys Ile Asn
        120                 125                 130

cta gtt gat gtt gta tca tgc ggg att gca aac caa gca gca acc aaa   547
Leu Val Asp Val Val Ser Cys Gly Ile Ala Asn Gln Ala Ala Thr Lys
    135                 140                 145

gca aat aat gag gct gtc gca cga tac cca ggc gat tcc ctt cgc aac   595
Ala Asn Asn Glu Ala Val Ala Arg Tyr Pro Gly Asp Ser Leu Arg Asn
150                 155                 160                 165

ggc aaa ggc gat gca ttt cgg cat tgc tca tgg aac gct ctg atg acg   643
Gly Lys Gly Asp Ala Phe Arg His Cys Ser Trp Asn Ala Leu Met Thr
                170                 175                 180

ata cga atc ggg agc aat gga gct gaa aga att gca aca aac cac gag   691
Ile Arg Ile Gly Ser Asn Gly Ala Glu Arg Ile Ala Thr Asn His Glu
            185                 190                 195

aca atc ggg gac ggt ccg gcc gat gaa aat gca atg gac cta ttc aat   739
Thr Ile Gly Asp Gly Pro Ala Asp Glu Asn Ala Met Asp Leu Phe Asn
        200                 205                 210

aat gca caa ggc cga cag atc gga gcc gga ttc att aat agt aag gat   787
Asn Ala Gln Gly Arg Gln Ile Gly Ala Gly Phe Ile Asn Ser Lys Asp
    215                 220                 225

gaa act agc gcg ctc gcg ata tgc gcg ctg tgg aca aat ctc ggt aga   835
Glu Thr Ser Ala Leu Ala Ile Cys Ala Leu Trp Thr Asn Leu Gly Arg
230                 235                 240                 245

cta aaa act cta aaa taagcaaggt gccctctgat gct                    873
Leu Lys Thr Leu Lys
                250
```

<210> 76
<211> 250
<212> PRT
<213> Corynebacterium glutamicum

<400> 76

```
Leu Leu Asn Arg Val Ser Arg Ile Ala Gly Ala Ser Ala Ile Thr Leu
  1               5                  10                  15

Cys Ile Gly Leu Thr Thr Ile Leu Ser Pro Thr Ser Thr Ala Gln Ser
             20                  25                  30

Leu Glu Gln Ile Thr Pro Leu Pro Glu Ser Ala Ile Asp Leu Asn Ala
         35                  40                  45

Glu Ile His Val Asn Thr Ser Asp Ile Ser Ala Glu Gln Ile Leu Gly
     50                  55                  60

Ala Gln Asp Glu Ile Thr Thr Met Tyr Asp Ser His Asp Pro Tyr Glu
```

```
 65                  70                  75                  80

Tyr Phe Asp Thr Leu Thr Asp Ile Glu Gln Arg Ser Ile Ile Ala Ala
                85                  90                  95

Leu Lys Arg Asp Pro Ser Ser Leu Gln Gln Arg Gln Glu Thr Arg Leu
            100                 105                 110

Ala Ala Gln Ser Asp Pro Tyr Lys Ile Tyr Ile Ser Gly Leu Glu Met
        115                 120                 125

Leu Ser Cys Ile Asn Leu Val Asp Val Val Ser Cys Gly Ile Ala Asn
    130                 135                 140

Gln Ala Ala Thr Lys Ala Asn Asn Glu Ala Val Ala Arg Tyr Pro Gly
145                 150                 155                 160

Asp Ser Leu Arg Asn Gly Lys Gly Asp Ala Phe Arg His Cys Ser Trp
                165                 170                 175

Asn Ala Leu Met Thr Ile Arg Ile Gly Ser Asn Gly Ala Glu Arg Ile
            180                 185                 190

Ala Thr Asn His Glu Thr Ile Gly Asp Gly Pro Ala Asp Glu Asn Ala
        195                 200                 205

Met Asp Leu Phe Asn Asn Ala Gln Gly Arg Gln Ile Gly Ala Gly Phe
    210                 215                 220

Ile Asn Ser Lys Asp Glu Thr Ser Ala Leu Ala Ile Cys Ala Leu Trp
225                 230                 235                 240

Thr Asn Leu Gly Arg Leu Lys Thr Leu Lys
                245                 250
```

<210> 77
<211> 609
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(586)
<223> RXN00067

<400> 77
ggaatcccgc atgttgggct ccagttgggg actgactctg tttttgatca ttttgacgcc 60

aatcattatt ttcctcactt tcagctaaaa ggaccatgca atg gta gac gct cag 115
                                              Met Val Asp Ala Gln
                                                1   5

cgc ccc aaa gca ggc atc ttc ggt agc cac aca gaa gaa aca tgg gtg 163
Arg Pro Lys Ala Gly Ile Phe Gly Ser His Thr Glu Glu Thr Trp Val
            10   15   20

tgg ctc ggt aat gaa ctt ttc gac gag tcc ggc gag gtc atc gcc gac 211
Trp Leu Gly Asn Glu Leu Phe Asp Glu Ser Gly Glu Val Ile Ala Asp
        25   30   35

```
gtt cgc tcc gac gtc ctc tac gtg gat cgc gaa cga cta ctc atc gaa   259
Val Arg Ser Asp Val Leu Tyr Val Asp Arg Glu Arg Leu Leu Ile Glu
         40                  45                  50

tcc acc ccc ggc acc atg cgt ttt cgt tgc cgc gca aca ctg tcc ggg   307
Ser Thr Pro Gly Thr Met Arg Phe Arg Cys Arg Ala Thr Leu Ser Gly
     55                  60                  65

ggt gag gtc tat acg atg act cag aat tct ttc act gtg ggg gat ctc   355
Gly Glu Val Tyr Thr Met Thr Gln Asn Ser Phe Thr Val Gly Asp Leu
 70                  75                  80                  85

act gcg gtg tgc ggg cgc cgg acg tat tca cta aaa agg gtg tcg ccg   403
Thr Ala Val Cys Gly Arg Arg Thr Tyr Ser Leu Lys Arg Val Ser Pro
                 90                  95                 100

tgg cgt aaa gaa cgc ctg atc acc aac aat ggg gtg gaa gtg gcg cgg   451
Trp Arg Lys Glu Arg Leu Ile Thr Asn Asn Gly Val Glu Val Ala Arg
            105                 110                 115

ctt cgc ccg atg acc agc ggt aaa gtc gaa ttc att gtg ggc acc gcg   499
Leu Arg Pro Met Thr Ser Gly Lys Val Glu Phe Ile Val Gly Thr Ala
        120                 125                 130

ggc agc gag gcg ttg ccg ttc gtc gac gca gta ttt ttg agc tgg gcg   547
Gly Ser Glu Ala Leu Pro Phe Val Asp Ala Val Phe Leu Ser Trp Ala
    135                 140                 145

tgc gtc ctg gtg gat tcg gcc gtg cgc cgg ccg aaa att taaaagcttt    596
Cys Val Leu Val Asp Ser Ala Val Arg Arg Pro Lys Ile
150                 155                 160

ttgcttatcg acg                                                   609


<210> 78
<211> 162
<212> PRT
<213> Corynebacterium glutamicum

<400> 78
Met Val Asp Ala Gln Arg Pro Lys Ala Gly Ile Phe Gly Ser His Thr
  1               5                  10                  15

Glu Glu Thr Trp Val Trp Leu Gly Asn Glu Leu Phe Asp Glu Ser Gly
             20                  25                  30

Glu Val Ile Ala Asp Val Arg Ser Asp Val Leu Tyr Val Asp Arg Glu
         35                  40                  45

Arg Leu Leu Ile Glu Ser Thr Pro Gly Thr Met Arg Phe Arg Cys Arg
     50                  55                  60

Ala Thr Leu Ser Gly Gly Glu Val Tyr Thr Met Thr Gln Asn Ser Phe
 65                  70                  75                  80

Thr Val Gly Asp Leu Thr Ala Val Cys Gly Arg Arg Thr Tyr Ser Leu
                 85                  90                  95

Lys Arg Val Ser Pro Trp Arg Lys Glu Arg Leu Ile Thr Asn Asn Gly
            100                 105                 110
```

```
Val Glu Val Ala Arg Leu Arg Pro Met Thr Ser Gly Lys Val Glu Phe
        115                 120                 125

Ile Val Gly Thr Ala Gly Ser Glu Ala Leu Pro Phe Val Asp Ala Val
    130                 135                 140

Phe Leu Ser Trp Ala Cys Val Leu Val Asp Ser Ala Val Arg Arg Pro
145                 150                 155                 160

Lys Ile
```

<210> 79
<211> 609
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(586)
<223> FRXA00067

<400> 79

```
ggaatcccgc atgttgggct ccagttgggg actgactctg tttttgatca ttttgacgcc 60

aatcattatt ttcctcactt tcagctaaaa ggaccatgca atg gta gac gct cag   115
                                           Met Val Asp Ala Gln
                                             1               5

cgc ccc aaa gca ggc atc ttc ggt agc cac aca gaa gaa aca tgg gtg   163
Arg Pro Lys Ala Gly Ile Phe Gly Ser His Thr Glu Glu Thr Trp Val
                10                  15                  20

tgg ctc ggt aat gaa ctt ttc gac gag tcc ggc gag gtc atc gcc gac   211
Trp Leu Gly Asn Glu Leu Phe Asp Glu Ser Gly Glu Val Ile Ala Asp
            25                  30                  35

gtt cgc tcc gac gtc ctc tac gtg gat cgc gaa cga cta ctc atc gaa   259
Val Arg Ser Asp Val Leu Tyr Val Asp Arg Glu Arg Leu Leu Ile Glu
        40                  45                  50

tcc acc ccc ggc acc atg cgt ttt cgt tgc cgc gca aca ctg tcc ggg   307
Ser Thr Pro Gly Thr Met Arg Phe Arg Cys Arg Ala Thr Leu Ser Gly
    55                  60                  65

ggt gag gtc tat acg atg act cag aat tct ttc act gtg ggg gat ctc   355
Gly Glu Val Tyr Thr Met Thr Gln Asn Ser Phe Thr Val Gly Asp Leu
70                  75                  80                  85

act gcg gtg tgc ggg cgc cgg acg tat tca cta aaa agg gtg tcg ccg   403
Thr Ala Val Cys Gly Arg Arg Thr Tyr Ser Leu Lys Arg Val Ser Pro
                90                  95                  100

tgg cgt aaa gaa cgc ctg atc acc aac aat ggg gtg gaa gtg gcg cgg   451
Trp Arg Lys Glu Arg Leu Ile Thr Asn Asn Gly Val Glu Val Ala Arg
            105                 110                 115

ctt cgc ccg atg acc agc ggt aaa gtc gaa ttc att gtg ggc acc gcg   499
Leu Arg Pro Met Thr Ser Gly Lys Val Glu Phe Ile Val Gly Thr Ala
```

```
        120                 125                 130

ggc agc gag gcg ttg ccg ttc gtc gac gca gta ttt ttg agc tgg gcg   547
Gly Ser Glu Ala Leu Pro Phe Val Asp Ala Val Phe Leu Ser Trp Ala
    135                 140                 145

tgc gtc ctg gtg gat tcg gcc gtg cgc cgg ccg aaa att taaaagcttt   596
Cys Val Leu Val Asp Ser Ala Val Arg Arg Pro Lys Ile
150                 155                 160

ttgcttatcg acg                                                  609


<210> 80
<211> 162
<212> PRT
<213> Corynebacterium glutamicum

<400> 80
Met Val Asp Ala Gln Arg Pro Lys Ala Gly Ile Phe Gly Ser His Thr
  1               5                  10                  15

Glu Glu Thr Trp Val Trp Leu Gly Asn Glu Leu Phe Asp Glu Ser Gly
             20                  25                  30

Glu Val Ile Ala Asp Val Arg Ser Asp Val Leu Tyr Val Asp Arg Glu
         35                  40                  45

Arg Leu Leu Ile Glu Ser Thr Pro Gly Thr Met Arg Phe Arg Cys Arg
     50                  55                  60

Ala Thr Leu Ser Gly Gly Glu Val Tyr Thr Met Thr Gln Asn Ser Phe
 65                  70                  75                  80

Thr Val Gly Asp Leu Thr Ala Val Cys Gly Arg Arg Thr Tyr Ser Leu
                 85                  90                  95

Lys Arg Val Ser Pro Trp Arg Lys Glu Arg Leu Ile Thr Asn Asn Gly
            100                 105                 110

Val Glu Val Ala Arg Leu Arg Pro Met Thr Ser Gly Lys Val Glu Phe
        115                 120                 125

Ile Val Gly Thr Ala Gly Ser Glu Ala Leu Pro Phe Val Asp Ala Val
    130                 135                 140

Phe Leu Ser Trp Ala Cys Val Leu Val Asp Ser Ala Val Arg Arg Pro
145                 150                 155                 160

Lys Ile


<210> 81
<211> 1485
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1462)
```

<223> RXN00077

<400> 81

```
ctaaattgtt ttaacgcgtg aagcagtccc cgcccgattt attcgaggcg gggactttcg 60

ctttccggga taaaaattgc aacgcactac actgagcagt atg aat gat gag aat   115
                                          Met Asn Asp Glu Asn
                                            1               5

att caa agc tcc aac tat cag cca ttc ccg agt ttt gac gat tgg aaa   163
Ile Gln Ser Ser Asn Tyr Gln Pro Phe Pro Ser Phe Asp Asp Trp Lys
                 10                  15                  20

cag atc gag gtg tcg ctc tta gat gtc atc gaa tcc tca cgc cat ttt   211
Gln Ile Glu Val Ser Leu Leu Asp Val Ile Glu Ser Ser Arg His Phe
             25                  30                  35

tct gat ttg aaa gat agc act gat cgt tct gcg tta gat gct gcg cta   259
Ser Asp Leu Lys Asp Ser Thr Asp Arg Ser Ala Leu Asp Ala Ala Leu
         40                  45                  50

gag aga gca aaa aga gct gcc gca gtt gat acc aat gcc ata gaa gga   307
Glu Arg Ala Lys Arg Ala Ala Ala Val Asp Thr Asn Ala Ile Glu Gly
     55                  60                  65

atc ttc caa act gat cgc ggt ttt acc cat aca gtt gca acg cag gta   355
Ile Phe Gln Thr Asp Arg Gly Phe Thr His Thr Val Ala Thr Gln Val
 70                  75                  80                  85

ggg gct tgg gag caa caa atg gcg atg aaa ggc aaa cat gtt aag cct   403
Gly Ala Trp Glu Gln Gln Met Ala Met Lys Gly Lys His Val Lys Pro
                 90                  95                 100

gcg ttt gac gat act cta gaa ggc ttt gag tat gtt ctc gat gca gta   451
Ala Phe Asp Asp Thr Leu Glu Gly Phe Glu Tyr Val Leu Asp Ala Val
            105                 110                 115

act ggt aga act cca atc tct cag caa tgg att aga aat ttg cac gcc   499
Thr Gly Arg Thr Pro Ile Ser Gln Gln Trp Ile Arg Asn Leu His Ala
        120                 125                 130

gtc att ctg cgg agc caa gaa agc cac gag gtt ttt aca gcc gtt gga   547
Val Ile Leu Arg Ser Gln Glu Ser His Glu Val Phe Thr Ala Val Gly
    135                 140                 145

gtc caa aat cag gcg ctt cag aaa ggc gag tat aaa act cag cca aat   595
Val Gln Asn Gln Ala Leu Gln Lys Gly Glu Tyr Lys Thr Gln Pro Asn
150                 155                 160                 165

agt cca cag cgc tca gat gga tct gta cat gca tac gcc cca gtt gaa   643
Ser Pro Gln Arg Ser Asp Gly Ser Val His Ala Tyr Ala Pro Val Glu
                170                 175                 180

gat act cct gct gaa atg gct aga ttt att tca gaa ctt gaa tct aag   691
Asp Thr Pro Ala Glu Met Ala Arg Phe Ile Ser Glu Leu Glu Ser Lys
            185                 190                 195

gaa ttc tta gca gcc gag aag gtt att caa gct gcc tat gcc cac tat   739
Glu Phe Leu Ala Ala Glu Lys Val Ile Gln Ala Ala Tyr Ala His Tyr
        200                 205                 210
```

```
gct ttc gta tgt att cat cct ttt gca gat ggg aat gga cga gtt gca   787
Ala Phe Val Cys Ile His Pro Phe Ala Asp Gly Asn Gly Arg Val Ala
    215                 220                 225

cga gcc ttg gct agt gtt ttt cta tac aaa gat cct ggt gtc cct ctc   835
Arg Ala Leu Ala Ser Val Phe Leu Tyr Lys Asp Pro Gly Val Pro Leu
230                 235                 240                 245

gta atc tac caa gat caa cgc aga gat tac atc cat gct cta gaa gca   883
Val Ile Tyr Gln Asp Gln Arg Arg Asp Tyr Ile His Ala Leu Glu Ala
                250                 255                 260

gcg gac aag aat aac ccg ctc ctg ctg att aga ttc ttt gct gaa cga   931
Ala Asp Lys Asn Asn Pro Leu Leu Leu Ile Arg Phe Phe Ala Glu Arg
            265                 270                 275

gtg acc gat act att aac tct att atc gtt gat ctc act acc ccg atc   979
Val Thr Asp Thr Ile Asn Ser Ile Ile Val Asp Leu Thr Thr Pro Ile
        280                 285                 290

gcg ggt aaa tct ggt tcg gct aag ctt tcg gat gcg cta cgc ccc act   1027
Ala Gly Lys Ser Gly Ser Ala Lys Leu Ser Asp Ala Leu Arg Pro Thr
    295                 300                 305

cgc gta tta cca gaa tta cat gat gct gca cat agg ctc caa gaa agt   1075
Arg Val Leu Pro Glu Leu His Asp Ala Ala His Arg Leu Gln Glu Ser
310                 315                 320                 325

tta ttt aca gaa atc cga tct cga ttg gat gaa gaa gga aaa agg aat   1123
Leu Phe Thr Glu Ile Arg Ser Arg Leu Asp Glu Glu Gly Lys Arg Asn
                330                 335                 340

ggg ttg gag ttt cta ctt caa cgg att ttt atc ggt tcc cca ttc aat   1171
Gly Leu Glu Phe Leu Leu Gln Arg Ile Phe Ile Gly Ser Pro Phe Asn
            345                 350                 355

ctg cca gag ggc tat aac gct ttc cct gat agc tat tgt ctg acc tta   1219
Leu Pro Glu Gly Tyr Asn Ala Phe Pro Asp Ser Tyr Cys Leu Thr Leu
        360                 365                 370

gct ttc aat agc aac tct cca aaa caa atc ttc cac ccg cta tcc ata   1267
Ala Phe Asn Ser Asn Ser Pro Lys Gln Ile Phe His Pro Leu Ser Ile
    375                 380                 385

gta ata gca gct cga gat ggg aaa aga gcg agc agc gac ctc gtg gca   1315
Val Ile Ala Ala Arg Asp Gly Lys Arg Ala Ser Ser Asp Leu Val Ala
390                 395                 400                 405

gct act tct att gga tac aac ttt cac gct tac gga cgt gaa gtc gag   1363
Ala Thr Ser Ile Gly Tyr Asn Phe His Ala Tyr Gly Arg Glu Val Glu
                410                 415                 420

cct gtt gtt act gaa agc ttt cga gaa cgt gtg aaa att tac gcc gac   1411
Pro Val Val Thr Glu Ser Phe Arg Glu Arg Val Lys Ile Tyr Ala Asp
            425                 430                 435

ggg att gta gat cac ttc tta acc gaa ctg gct aaa aag ttt caa cag   1459
Gly Ile Val Asp His Phe Leu Thr Glu Leu Ala Lys Lys Phe Gln Gln
        440                 445                 450

aat taattagcct atctcggctt tcg                                    1485
```

Asn

<210> 82
<211> 454
<212> PRT
<213> Corynebacterium glutamicum

<400> 82

```
Met Asn Asp Glu Asn Ile Gln Ser Ser Asn Tyr Gln Pro Phe Pro Ser
  1               5                  10                  15

Phe Asp Asp Trp Lys Gln Ile Glu Val Ser Leu Leu Asp Val Ile Glu
             20                  25                  30

Ser Ser Arg His Phe Ser Asp Leu Lys Asp Ser Thr Asp Arg Ser Ala
         35                  40                  45

Leu Asp Ala Ala Leu Glu Arg Ala Lys Arg Ala Ala Ala Val Asp Thr
     50                  55                  60

Asn Ala Ile Glu Gly Ile Phe Gln Thr Asp Arg Gly Phe Thr His Thr
 65                  70                  75                  80

Val Ala Thr Gln Val Gly Ala Trp Glu Gln Gln Met Ala Met Lys Gly
                 85                  90                  95

Lys His Val Lys Pro Ala Phe Asp Asp Thr Leu Glu Gly Phe Glu Tyr
            100                 105                 110

Val Leu Asp Ala Val Thr Gly Arg Thr Pro Ile Ser Gln Gln Trp Ile
        115                 120                 125

Arg Asn Leu His Ala Val Ile Leu Arg Ser Gln Glu Ser His Glu Val
    130                 135                 140

Phe Thr Ala Val Gly Val Gln Asn Gln Ala Leu Gln Lys Gly Glu Tyr
145                 150                 155                 160

Lys Thr Gln Pro Asn Ser Pro Gln Arg Ser Asp Gly Ser Val His Ala
                165                 170                 175

Tyr Ala Pro Val Glu Asp Thr Pro Ala Glu Met Ala Arg Phe Ile Ser
            180                 185                 190

Glu Leu Glu Ser Lys Glu Phe Leu Ala Ala Glu Lys Val Ile Gln Ala
        195                 200                 205

Ala Tyr Ala His Tyr Ala Phe Val Cys Ile His Pro Phe Ala Asp Gly
    210                 215                 220

Asn Gly Arg Val Ala Arg Ala Leu Ala Ser Val Phe Leu Tyr Lys Asp
225                 230                 235                 240

Pro Gly Val Pro Leu Val Ile Tyr Gln Asp Gln Arg Arg Asp Tyr Ile
                245                 250                 255

His Ala Leu Glu Ala Ala Asp Lys Asn Asn Pro Leu Leu Leu Ile Arg
            260                 265                 270
```

```
Phe Phe Ala Glu Arg Val Thr Asp Thr Ile Asn Ser Ile Ile Val Asp
        275                 280                 285

Leu Thr Thr Pro Ile Ala Gly Lys Ser Gly Ser Ala Lys Leu Ser Asp
    290                 295                 300

Ala Leu Arg Pro Thr Arg Val Leu Pro Glu Leu His Asp Ala Ala His
305                 310                 315                 320

Arg Leu Gln Glu Ser Leu Phe Thr Glu Ile Arg Ser Arg Leu Asp Glu
                325                 330                 335

Glu Gly Lys Arg Asn Gly Leu Glu Phe Leu Leu Gln Arg Ile Phe Ile
            340                 345                 350

Gly Ser Pro Phe Asn Leu Pro Glu Gly Tyr Asn Ala Phe Pro Asp Ser
        355                 360                 365

Tyr Cys Leu Thr Leu Ala Phe Asn Ser Asn Ser Pro Lys Gln Ile Phe
    370                 375                 380

His Pro Leu Ser Ile Val Ile Ala Ala Arg Asp Gly Lys Arg Ala Ser
385                 390                 395                 400

Ser Asp Leu Val Ala Ala Thr Ser Ile Gly Tyr Asn Phe His Ala Tyr
                405                 410                 415

Gly Arg Glu Val Glu Pro Val Val Thr Glu Ser Phe Arg Glu Arg Val
            420                 425                 430

Lys Ile Tyr Ala Asp Gly Ile Val Asp His Phe Leu Thr Glu Leu Ala
        435                 440                 445

Lys Lys Phe Gln Gln Asn
    450
```

<210> 83
<211> 1485
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1462)
<223> FRXA00077

<400> 83
ctaaattgtt ttaacgcgtg aagcagtccc cgcccgattt attcgaggcg gggactttcg 60

ctttccggga taaaaattgc aacgcactac actgagcagt atg aat gat gag aat 115
                                              Met Asn Asp Glu Asn
                                                1   5

att caa agc tcc aac tat cag cca ttc ccg agt ttt gac gat tgg aaa 163
Ile Gln Ser Ser Asn Tyr Gln Pro Phe Pro Ser Phe Asp Asp Trp Lys
                10   15   20

cag atc gag gtg tcg ctc tta gat gtc atc gaa tcc tca cgc cat ttt 211
Gln Ile Glu Val Ser Leu Leu Asp Val Ile Glu Ser Ser Arg His Phe
            25   30   35

```
tct gat ttg aaa gat agc act gat cgt tct gcg tta gat gct gcg cta   259
Ser Asp Leu Lys Asp Ser Thr Asp Arg Ser Ala Leu Asp Ala Ala Leu
         40                  45                  50

gag aga gca aaa aga gct gcc gca gtt gat acc aat gcc ata gaa gga   307
Glu Arg Ala Lys Arg Ala Ala Ala Val Asp Thr Asn Ala Ile Glu Gly
     55                  60                  65

atc ttc caa act gat cgc ggt ttt acc cat aca gtt gca acg cag gta   355
Ile Phe Gln Thr Asp Arg Gly Phe Thr His Thr Val Ala Thr Gln Val
 70                  75                  80                  85

ggg gct tgg gag caa caa atg gcg atg aaa ggc aaa cat gtt aag cct   403
Gly Ala Trp Glu Gln Gln Met Ala Met Lys Gly Lys His Val Lys Pro
                 90                  95                 100

gcg ttt gac gat act cta gaa ggc ttt gag tat gtt ctc gat gca gta   451
Ala Phe Asp Asp Thr Leu Glu Gly Phe Glu Tyr Val Leu Asp Ala Val
            105                 110                 115

act ggt aga act cca atc tct cag caa tgg att aga aat ttg cac gcc   499
Thr Gly Arg Thr Pro Ile Ser Gln Gln Trp Ile Arg Asn Leu His Ala
        120                 125                 130

gtc att ctg cgg agc caa gaa agc cac gag gtt ttt aca gcc gtt gga   547
Val Ile Leu Arg Ser Gln Glu Ser His Glu Val Phe Thr Ala Val Gly
    135                 140                 145

gtc caa aat cag gcg ctt cag aaa ggc gag tat aaa act cag cca aat   595
Val Gln Asn Gln Ala Leu Gln Lys Gly Glu Tyr Lys Thr Gln Pro Asn
150                 155                 160                 165

agt cca cag cgc tca gat gga tct gta cat gca tac gcc cca gtt gaa   643
Ser Pro Gln Arg Ser Asp Gly Ser Val His Ala Tyr Ala Pro Val Glu
                170                 175                 180

gat act cct gct gaa atg gct aga ttt att tca gaa ctt gaa tct aag   691
Asp Thr Pro Ala Glu Met Ala Arg Phe Ile Ser Glu Leu Glu Ser Lys
            185                 190                 195

gaa ttc tta gca gcc gag aag gtt att caa gct gcc tat gcc cac tat   739
Glu Phe Leu Ala Ala Glu Lys Val Ile Gln Ala Ala Tyr Ala His Tyr
        200                 205                 210

gct ttc gta tgt att cat cct ttt gca gat ggg aat gga cga gtt gca   787
Ala Phe Val Cys Ile His Pro Phe Ala Asp Gly Asn Gly Arg Val Ala
    215                 220                 225

cga gcc ttg gct agt gtt ttt cta tac aaa gat cct ggt gtc cct ctc   835
Arg Ala Leu Ala Ser Val Phe Leu Tyr Lys Asp Pro Gly Val Pro Leu
230                 235                 240                 245

gta atc tac caa gat caa cgc aga gat tac atc cat gct cta gaa gca   883
Val Ile Tyr Gln Asp Gln Arg Arg Asp Tyr Ile His Ala Leu Glu Ala
                250                 255                 260

gcg gac aag aat aac ccg ctc ctg ctg att aga ttc ttt gct gaa cga   931
Ala Asp Lys Asn Asn Pro Leu Leu Leu Ile Arg Phe Phe Ala Glu Arg
            265                 270                 275
```

```
gtg acc gat act att aac tct att atc gtt gat ctc act acc ccg atc   979
Val Thr Asp Thr Ile Asn Ser Ile Ile Val Asp Leu Thr Thr Pro Ile
        280                 285                 290

gcg ggt aaa tct ggt tcg gct aag ctt tcg gat gcg cta cgc ccc act   1027
Ala Gly Lys Ser Gly Ser Ala Lys Leu Ser Asp Ala Leu Arg Pro Thr
    295                 300                 305

cgc gta tta cca gaa tta cat gat gct gca cat agg ctc caa gaa agt   1075
Arg Val Leu Pro Glu Leu His Asp Ala Ala His Arg Leu Gln Glu Ser
310                 315                 320                 325

tta ttt aca gaa atc cga tct cga ttg gat gaa gaa gga aaa agg aat   1123
Leu Phe Thr Glu Ile Arg Ser Arg Leu Asp Glu Glu Gly Lys Arg Asn
                330                 335                 340

ggg ttg gag ttt cta ctt caa cgg att ttt atc ggt tcc cca ttc aat   1171
Gly Leu Glu Phe Leu Leu Gln Arg Ile Phe Ile Gly Ser Pro Phe Asn
            345                 350                 355

ctg cca gag ggc tat aac gct ttc cct gat agc tat tgt ctg acc tta   1219
Leu Pro Glu Gly Tyr Asn Ala Phe Pro Asp Ser Tyr Cys Leu Thr Leu
        360                 365                 370

gct ttc aat agc aac tct cca aaa caa atc ttc cac ccg cta tcc ata   1267
Ala Phe Asn Ser Asn Ser Pro Lys Gln Ile Phe His Pro Leu Ser Ile
    375                 380                 385

gta ata gca gct cga gat ggg aaa aga gcg agc agc gac ctc gtg gca   1315
Val Ile Ala Ala Arg Asp Gly Lys Arg Ala Ser Ser Asp Leu Val Ala
390                 395                 400                 405

gct act tct att gga tac aac ttt cac gct tac gga cgt gaa gtc gag   1363
Ala Thr Ser Ile Gly Tyr Asn Phe His Ala Tyr Gly Arg Glu Val Glu
                410                 415                 420

cct gtt gtt act gaa agc ttt cga gaa cgt gtg aaa att tac gcc gac   1411
Pro Val Val Thr Glu Ser Phe Arg Glu Arg Val Lys Ile Tyr Ala Asp
            425                 430                 435

ggg att gta gat cac ttc tta acc gaa ctg gct aaa aag ttt caa cag   1459
Gly Ile Val Asp His Phe Leu Thr Glu Leu Ala Lys Lys Phe Gln Gln
        440                 445                 450

aat taattagcct atctcggctt tcg                                    1485
Asn
```

<210> 84
<211> 454
<212> PRT
<213> Corynebacterium glutamicum

<400> 84

```
Met Asn Asp Glu Asn Ile Gln Ser Ser Asn Tyr Gln Pro Phe Pro Ser
  1               5                  10                  15

Phe Asp Asp Trp Lys Gln Ile Glu Val Ser Leu Leu Asp Val Ile Glu
             20                  25                  30
```

```
Ser Ser Arg His Phe Ser Asp Leu Lys Asp Ser Thr Asp Arg Ser Ala
         35                  40                  45

Leu Asp Ala Ala Leu Glu Arg Ala Lys Arg Ala Ala Ala Val Asp Thr
     50                  55                  60

Asn Ala Ile Glu Gly Ile Phe Gln Thr Asp Arg Gly Phe Thr His Thr
 65                  70                  75                  80

Val Ala Thr Gln Val Gly Ala Trp Glu Gln Gln Met Ala Met Lys Gly
                 85                  90                  95

Lys His Val Lys Pro Ala Phe Asp Asp Thr Leu Glu Gly Phe Glu Tyr
            100                 105                 110

Val Leu Asp Ala Val Thr Gly Arg Thr Pro Ile Ser Gln Gln Trp Ile
        115                 120                 125

Arg Asn Leu His Ala Val Ile Leu Arg Ser Gln Glu Ser His Glu Val
    130                 135                 140

Phe Thr Ala Val Gly Val Gln Asn Gln Ala Leu Gln Lys Gly Glu Tyr
145                 150                 155                 160

Lys Thr Gln Pro Asn Ser Pro Gln Arg Ser Asp Gly Ser Val His Ala
                165                 170                 175

Tyr Ala Pro Val Glu Asp Thr Pro Ala Glu Met Ala Arg Phe Ile Ser
            180                 185                 190

Glu Leu Glu Ser Lys Glu Phe Leu Ala Ala Glu Lys Val Ile Gln Ala
        195                 200                 205

Ala Tyr Ala His Tyr Ala Phe Val Cys Ile His Pro Phe Ala Asp Gly
    210                 215                 220

Asn Gly Arg Val Ala Arg Ala Leu Ala Ser Val Phe Leu Tyr Lys Asp
225                 230                 235                 240

Pro Gly Val Pro Leu Val Ile Tyr Gln Asp Gln Arg Arg Asp Tyr Ile
                245                 250                 255

His Ala Leu Glu Ala Ala Asp Lys Asn Asn Pro Leu Leu Leu Ile Arg
            260                 265                 270

Phe Phe Ala Glu Arg Val Thr Asp Thr Ile Asn Ser Ile Ile Val Asp
        275                 280                 285

Leu Thr Thr Pro Ile Ala Gly Lys Ser Gly Ser Ala Lys Leu Ser Asp
    290                 295                 300

Ala Leu Arg Pro Thr Arg Val Leu Pro Glu Leu His Asp Ala Ala His
305                 310                 315                 320

Arg Leu Gln Glu Ser Leu Phe Thr Glu Ile Arg Ser Arg Leu Asp Glu
                325                 330                 335

Glu Gly Lys Arg Asn Gly Leu Glu Phe Leu Leu Gln Arg Ile Phe Ile
            340                 345                 350

Gly Ser Pro Phe Asn Leu Pro Glu Gly Tyr Asn Ala Phe Pro Asp Ser
```

```
        355                 360                 365

Tyr Cys Leu Thr Leu Ala Phe Asn Ser Asn Ser Pro Lys Gln Ile Phe
    370                 375                 380

His Pro Leu Ser Ile Val Ile Ala Ala Arg Asp Gly Lys Arg Ala Ser
385                 390                 395                 400

Ser Asp Leu Val Ala Ala Thr Ser Ile Gly Tyr Asn Phe His Ala Tyr
                405                 410                 415

Gly Arg Glu Val Glu Pro Val Val Thr Glu Ser Phe Arg Glu Arg Val
            420                 425                 430

Lys Ile Tyr Ala Asp Gly Ile Val Asp His Phe Leu Thr Glu Leu Ala
        435                 440                 445

Lys Lys Phe Gln Gln Asn
    450
```

<210> 85
<211> 1653
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1630)
<223> RXN00080

<400> 85

```
atgttcttgt ttccctcatg atgagctccg tggtctacct cgcattcgat gtgggcttgg 60

gacttaatct tccttccgga cttttgggtg gtggctttta atg gat att ttg tcc   115
                                            Met Asp Ile Leu Ser
                                              1               5

ctc ttg atg gaa ggt ttc gcc ggc gcg cta acg ccg atg aac ctc ctc   163
Leu Leu Met Glu Gly Phe Ala Gly Ala Leu Thr Pro Met Asn Leu Leu
                  10                  15                  20

tgg gtg att gtc ggc tgt ttg ctc ggc acc gcg gtt ggc gtc atg cct   211
Trp Val Ile Val Gly Cys Leu Leu Gly Thr Ala Val Gly Val Met Pro
              25                  30                  35

ggt ctt gga tcc tcc atg gct gtg gcg ctg ctg ctg cca atg acc ttc   259
Gly Leu Gly Ser Ser Met Ala Val Ala Leu Leu Leu Pro Met Thr Phe
          40                  45                  50

gcg ctt gat cca act gcc gcg ttc att atg ttc tct ggc gta tat ttc   307
Ala Leu Asp Pro Thr Ala Ala Phe Ile Met Phe Ser Gly Val Tyr Phe
      55                  60                  65

ggt ggt ctc ttc ggt gac tcc acg atg gca att ttg atg aac acc cca   355
Gly Gly Leu Phe Gly Asp Ser Thr Met Ala Ile Leu Met Asn Thr Pro
  70                  75                  80                  85

ggt cag gca tcg gca atc gcc tca aca ttc gag ggc cac cgc atg gct   403
Gly Gln Ala Ser Ala Ile Ala Ser Thr Phe Glu Gly His Arg Met Ala
                  90                  95                 100
```

```
ctt aac ggc cgt gcg cca cag gct ctg gct acc gca gcg atc ggt gcc   451
Leu Asn Gly Arg Ala Pro Gln Ala Leu Ala Thr Ala Ala Ile Gly Ala
            105                 110                 115

ttc atc ggc ggt atc gtc tcc tcc ttc atc gtg gtc ttc ctc gca cca   499
Phe Ile Gly Gly Ile Val Ser Ser Phe Ile Val Val Phe Leu Ala Pro
        120                 125                 130

acc ctg gcg gaa ctg tcc acc gca ttc ggc ccc gcc gag tac ttc gca   547
Thr Leu Ala Glu Leu Ser Thr Ala Phe Gly Pro Ala Glu Tyr Phe Ala
    135                 140                 145

ctg gca ctc ttc gcg ttc gtc gcc acc tcc tcc gtg gtg tcc gac tcc   595
Leu Ala Leu Phe Ala Phe Val Ala Thr Ser Ser Val Val Ser Asp Ser
150                 155                 160                 165

gtg ttt aag gga ctt gcg tcc ctc att ttc ggc ctc ggc att gcg acc   643
Val Phe Lys Gly Leu Ala Ser Leu Ile Phe Gly Leu Gly Ile Ala Thr
                170                 175                 180

atc ggc atc gat tcg gtc acc ggc atc gag cgc ttc acg ctc ggg gca   691
Ile Gly Ile Asp Ser Val Thr Gly Ile Glu Arg Phe Thr Leu Gly Ala
            185                 190                 195

ccg cag ctt ttc gac gga att tcc ctc gtt act gtt acc gtc gcg att   739
Pro Gln Leu Phe Asp Gly Ile Ser Leu Val Thr Val Thr Val Ala Ile
        200                 205                 210

ttg gca ctg gga gaa gtg ttt tac att gca gcc cgc gca cgc cgt gac   787
Leu Ala Leu Gly Glu Val Phe Tyr Ile Ala Ala Arg Ala Arg Arg Asp
    215                 220                 225

aaa gca aat ctg gag acg cgc tct gca ggc cgt ccg tgg ctt acc gga   835
Lys Ala Asn Leu Glu Thr Arg Ser Ala Gly Arg Pro Trp Leu Thr Gly
230                 235                 240                 245

acg gaa ttc aaa gaa gcc gct cca gcc tgg gca cgc gga acc atc att   883
Thr Glu Phe Lys Glu Ala Ala Pro Ala Trp Ala Arg Gly Thr Ile Ile
                250                 255                 260

ggt ctg cct ttc ggt gtg atc cct gtt ggt gga tct gaa gtt cca acc   931
Gly Leu Pro Phe Gly Val Ile Pro Val Gly Gly Ser Glu Val Pro Thr
            265                 270                 275

ttc ttg gct tac tcc acc gag cgc gca ttg gat aaa cga cgc aaa gat   979
Phe Leu Ala Tyr Ser Thr Glu Arg Ala Leu Asp Lys Arg Arg Lys Asp
        280                 285                 290

ccg cag ttc ggc gat aaa ggt gca atc cga gga ctc gct gct cct gaa   1027
Pro Gln Phe Gly Asp Lys Gly Ala Ile Arg Gly Leu Ala Ala Pro Glu
    295                 300                 305

gct gca ggt aac gcc acc aca ggc atg gcg atg ggc gct ctt ctt gcc   1075
Ala Ala Gly Asn Ala Thr Thr Gly Met Ala Met Gly Ala Leu Leu Ala
310                 315                 320                 325

ctg ggt ctc cca gtc tct gca act gcg gcc atc atg ttg gca gcg ttc   1123
Leu Gly Leu Pro Val Ser Ala Thr Ala Ala Ile Met Leu Ala Ala Phe
                330                 335                 340
```

```
cgc cag tac gga atc cag ccc gga cca cta ctc ttc gat cgc aac cct   1171
Arg Gln Tyr Gly Ile Gln Pro Gly Pro Leu Leu Phe Asp Arg Asn Pro
            345                 350                 355

gaa ctt gtc tgg gca ctt ctt gcc agc ttc ttc atc gcg atg atc gtc   1219
Glu Leu Val Trp Ala Leu Leu Ala Ser Phe Phe Ile Ala Met Ile Val
        360                 365                 370

ctg ctg ttc atc aac ctg ccg ttc gca cag ctg tgg gca aag ctc ctg   1267
Leu Leu Phe Ile Asn Leu Pro Phe Ala Gln Leu Trp Ala Lys Leu Leu
    375                 380                 385

ctc att cca aac cac tac ctc tac tcc ggc atc gca ttg ttc tgt ggc   1315
Leu Ile Pro Asn His Tyr Leu Tyr Ser Gly Ile Ala Leu Phe Cys Gly
390                 395                 400                 405

ctg ggc att tac gcc acc tcc ggc gca gtg ttc gac ctg ctc atg ctg   1363
Leu Gly Ile Tyr Ala Thr Ser Gly Ala Val Phe Asp Leu Leu Met Leu
                410                 415                 420

ctc ggc atc ggt gtc gtg gct ttg atc atg cgt cgc tac ggt tac ccg   1411
Leu Gly Ile Gly Val Val Ala Leu Ile Met Arg Arg Tyr Gly Tyr Pro
            425                 430                 435

ctg gca ccg ctg atg atc ggt atg gtt ctt gga cct ttg gct gaa acc   1459
Leu Ala Pro Leu Met Ile Gly Met Val Leu Gly Pro Leu Ala Glu Thr
        440                 445                 450

tcc ctc cgc gac gca cta ctg tcc tcg gtt ggc gat ttc tcc atc ctc   1507
Ser Leu Arg Asp Ala Leu Leu Ser Ser Val Gly Asp Phe Ser Ile Leu
    455                 460                 465

gtc tcc agc ccc atc acc tgg tct ctc tac gca gtg ctc gcc atc ttc   1555
Val Ser Ser Pro Ile Thr Trp Ser Leu Tyr Ala Val Leu Ala Ile Phe
470                 475                 480                 485

atc gcg gtc agt gtc atc act gca atc cgc ggt cgt cgc aag cac ctg   1603
Ile Ala Val Ser Val Ile Thr Ala Ile Arg Gly Arg Arg Lys His Leu
                490                 495                 500

act tct cag ctc gaa acc atc gac gct taaagtcccc gtatagaaac         1650
Thr Ser Gln Leu Glu Thr Ile Asp Ala
            505                 510

agg                                                              1653


<210> 86
<211> 510
<212> PRT
<213> Corynebacterium glutamicum

<400> 86
Met Asp Ile Leu Ser Leu Leu Met Glu Gly Phe Ala Gly Ala Leu Thr
  1               5                  10                  15

Pro Met Asn Leu Leu Trp Val Ile Val Gly Cys Leu Leu Gly Thr Ala
            20                  25                  30

Val Gly Val Met Pro Gly Leu Gly Ser Ser Met Ala Val Ala Leu Leu
        35                  40                  45
```

Leu Pro Met Thr Phe Ala Leu Asp Pro Thr Ala Ala Phe Ile Met Phe
50 55 60

Ser Gly Val Tyr Phe Gly Gly Leu Phe Gly Asp Ser Thr Met Ala Ile
65 70 75 80

Leu Met Asn Thr Pro Gly Gln Ala Ser Ala Ile Ala Ser Thr Phe Glu
85 90 95

Gly His Arg Met Ala Leu Asn Gly Arg Ala Pro Gln Ala Leu Ala Thr
100 105 110

Ala Ala Ile Gly Ala Phe Ile Gly Gly Ile Val Ser Ser Phe Ile Val
115 120 125

Val Phe Leu Ala Pro Thr Leu Ala Glu Leu Ser Thr Ala Phe Gly Pro
130 135 140

Ala Glu Tyr Phe Ala Leu Ala Leu Phe Ala Phe Val Ala Thr Ser Ser
145 150 155 160

Val Val Ser Asp Ser Val Phe Lys Gly Leu Ala Ser Leu Ile Phe Gly
165 170 175

Leu Gly Ile Ala Thr Ile Gly Ile Asp Ser Val Thr Gly Ile Glu Arg
180 185 190

Phe Thr Leu Gly Ala Pro Gln Leu Phe Asp Gly Ile Ser Leu Val Thr
195 200 205

Val Thr Val Ala Ile Leu Ala Leu Gly Glu Val Phe Tyr Ile Ala Ala
210 215 220

Arg Ala Arg Arg Asp Lys Ala Asn Leu Glu Thr Arg Ser Ala Gly Arg
225 230 235 240

Pro Trp Leu Thr Gly Thr Glu Phe Lys Glu Ala Ala Pro Ala Trp Ala
245 250 255

Arg Gly Thr Ile Ile Gly Leu Pro Phe Gly Val Ile Pro Val Gly Gly
260 265 270

Ser Glu Val Pro Thr Phe Leu Ala Tyr Ser Thr Glu Arg Ala Leu Asp
275 280 285

Lys Arg Arg Lys Asp Pro Gln Phe Gly Asp Lys Gly Ala Ile Arg Gly
290 295 300

Leu Ala Ala Pro Glu Ala Ala Gly Asn Ala Thr Thr Gly Met Ala Met
305 310 315 320

Gly Ala Leu Leu Ala Leu Gly Leu Pro Val Ser Ala Thr Ala Ala Ile
325 330 335

Met Leu Ala Ala Phe Arg Gln Tyr Gly Ile Gln Pro Gly Pro Leu Leu
340 345 350

Phe Asp Arg Asn Pro Glu Leu Val Trp Ala Leu Leu Ala Ser Phe Phe
355 360 365

```
Ile Ala Met Ile Val Leu Leu Phe Ile Asn Leu Pro Phe Ala Gln Leu
    370                 375                 380

Trp Ala Lys Leu Leu Leu Ile Pro Asn His Tyr Leu Tyr Ser Gly Ile
385                 390                 395                 400

Ala Leu Phe Cys Gly Leu Gly Ile Tyr Ala Thr Ser Gly Ala Val Phe
                405                 410                 415

Asp Leu Leu Met Leu Leu Gly Ile Gly Val Val Ala Leu Ile Met Arg
            420                 425                 430

Arg Tyr Gly Tyr Pro Leu Ala Pro Leu Met Ile Gly Met Val Leu Gly
        435                 440                 445

Pro Leu Ala Glu Thr Ser Leu Arg Asp Ala Leu Leu Ser Ser Val Gly
    450                 455                 460

Asp Phe Ser Ile Leu Val Ser Ser Pro Ile Thr Trp Ser Leu Tyr Ala
465                 470                 475                 480

Val Leu Ala Ile Phe Ile Ala Val Ser Val Ile Thr Ala Ile Arg Gly
                485                 490                 495

Arg Arg Lys His Leu Thr Ser Gln Leu Glu Thr Ile Asp Ala
            500                 505                 510


<210> 87
<211> 543
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(520)
<223> FRXA00080

<400> 87
ttggcagcgt tccgccagta cggaatccag cccggaccac tactcttcga tcgcaaccct 60

gaacttgtct gggcacttct tgccagcttc tttcatcgcg atg atc gtc ctg ctg   115
                                              Met Ile Val Leu Leu
                                                1               5

ttc atc aac ctg ccg ttc gca cag ctg tgg gca aag ctc ctg ctc att   163
Phe Ile Asn Leu Pro Phe Ala Gln Leu Trp Ala Lys Leu Leu Leu Ile
                10                  15                  20

cca aac cac tac ctc tac tcc ggc atc gca ttg ttc tgt ggc ctg ggc   211
Pro Asn His Tyr Leu Tyr Ser Gly Ile Ala Leu Phe Cys Gly Leu Gly
            25                  30                  35

att tac gcc acc tcc ggc gca gtg ttc gac ctg ctc atg ctg ctc ggc   259
Ile Tyr Ala Thr Ser Gly Ala Val Phe Asp Leu Leu Met Leu Leu Gly
        40                  45                  50

atc ggt gtc gtg gct ttg atc atg cgt cgc tac ggt tac ccg ctg gca   307
Ile Gly Val Val Ala Leu Ile Met Arg Arg Tyr Gly Tyr Pro Leu Ala
    55                  60                  65
```

```
ccg ctg atg atc ggt atg gtt ctt gga cct ttg gct gaa acc tcc ctc   355
Pro Leu Met Ile Gly Met Val Leu Gly Pro Leu Ala Glu Thr Ser Leu
 70                  75                  80                  85

cgc gac gca cta ctg tcc tcg gtt ggc gat ttc tcc atc ctc gtc tcc   403
Arg Asp Ala Leu Leu Ser Ser Val Gly Asp Phe Ser Ile Leu Val Ser
                90                  95                 100

agc ccc atc acc tgg tct ctc tac gca gtg ctc gcc atc ttc atc gcg   451
Ser Pro Ile Thr Trp Ser Leu Tyr Ala Val Leu Ala Ile Phe Ile Ala
            105                 110                 115

gtc agt gtc atc act gca atc cgc ggt cgt cgc aag cac ctg act tct   499
Val Ser Val Ile Thr Ala Ile Arg Gly Arg Arg Lys His Leu Thr Ser
        120                 125                 130

cag ctc gaa acc atc gac gct taaagtcccc gtatagaaac agg             543
Gln Leu Glu Thr Ile Asp Ala
    135                 140
```

<210> 88
<211> 140
<212> PRT
<213> Corynebacterium glutamicum

<400> 88

```
Met Ile Val Leu Leu Phe Ile Asn Leu Pro Phe Ala Gln Leu Trp Ala
  1               5                  10                  15

Lys Leu Leu Leu Ile Pro Asn His Tyr Leu Tyr Ser Gly Ile Ala Leu
             20                  25                  30

Phe Cys Gly Leu Gly Ile Tyr Ala Thr Ser Gly Ala Val Phe Asp Leu
         35                  40                  45

Leu Met Leu Leu Gly Ile Gly Val Val Ala Leu Ile Met Arg Arg Tyr
     50                  55                  60

Gly Tyr Pro Leu Ala Pro Leu Met Ile Gly Met Val Leu Gly Pro Leu
 65                  70                  75                  80

Ala Glu Thr Ser Leu Arg Asp Ala Leu Leu Ser Ser Val Gly Asp Phe
                 85                  90                  95

Ser Ile Leu Val Ser Ser Pro Ile Thr Trp Ser Leu Tyr Ala Val Leu
            100                 105                 110

Ala Ile Phe Ile Ala Val Ser Val Ile Thr Ala Ile Arg Gly Arg Arg
        115                 120                 125

Lys His Leu Thr Ser Gln Leu Glu Thr Ile Asp Ala
    130                 135                 140
```

<210> 89
<211> 651
<212> DNA
<213> Corynebacterium glutamicum

<220>

<221> CDS
<222> (101)..(628)
<223> RXN00087

<400> 89
tcgtcagtca acaaacgttt tcccacccgg aggtctcccc gtgtctaccg aaatccacaa 60

cgccccaccc aaggccccaa cttggcttgg ctgggtgctc atg atc ggc gga ata 115
Met Ile Gly Gly Ile
1 5

atc ggc ctc att ttg tcg gtg atc atc atg gcc gaa aaa ctt gcc atc 163
Ile Gly Leu Ile Leu Ser Val Ile Ile Met Ala Glu Lys Leu Ala Ile
10 15 20

ctc gag gat ccc ggt cac atc acc agc tgc gat ttc aat gca gtc cta 211
Leu Glu Asp Pro Gly His Ile Thr Ser Cys Asp Phe Asn Ala Val Leu
25 30 35

gct tgt ggc gat gtc atg cgt tcc ggc caa gct aac gcg ttc ggc atc 259
Ala Cys Gly Asp Val Met Arg Ser Gly Gln Ala Asn Ala Phe Gly Ile
40 45 50

ccg aat ccg ctc atc ggc atc gcc ggt ttc gcc gct gtc gcc atc atc 307
Pro Asn Pro Leu Ile Gly Ile Ala Gly Phe Ala Ala Val Ala Ile Ile
55 60 65

ggc gcc ggc atc ctc gcg ggc ggc ggg ttc cgc ggt tgg ttc tgg ttc 355
Gly Ala Gly Ile Leu Ala Gly Gly Gly Phe Arg Gly Trp Phe Trp Phe
70 75 80 85

ggc gcc cag gcc gga ctc act ttt gcc atg atg ttc tgc cac tgg ctc 403
Gly Ala Gln Ala Gly Leu Thr Phe Ala Met Met Phe Cys His Trp Leu
90 95 100

gcc tac caa tcc atg tcc gtc atc cgc gcg ctc tgc cct tac tgc atg 451
Ala Tyr Gln Ser Met Ser Val Ile Arg Ala Leu Cys Pro Tyr Cys Met
105 110 115

ggc gtg tgg acc gta tcg atc atc atg ttc gtg ctg gtc act gca tgg 499
Gly Val Trp Thr Val Ser Ile Ile Met Phe Val Leu Val Thr Ala Trp
120 125 130

aat gtg aaa act ttc agc ggc tcc gac agc acg ttc gtc aac gca ctg 547
Asn Val Lys Thr Phe Ser Gly Ser Asp Ser Thr Phe Val Asn Ala Leu
135 140 145

tac aaa tac aag tgg gtc atc gcg atc gtc tgg ctg ctg ctc atc gca 595
Tyr Lys Tyr Lys Trp Val Ile Ala Ile Val Trp Leu Leu Leu Ile Ala
150 155 160 165

gcc gca gct gtg tgg tca ttc cgc tac atg ttc taggcattta aggctttcag 648
Ala Ala Ala Val Trp Ser Phe Arg Tyr Met Phe
170 175

gcc 651

<210> 90
<211> 176
<212> PRT

<213> Corynebacterium glutamicum

<400> 90
Met Ile Gly Gly Ile Ile Gly Leu Ile Leu Ser Val Ile Ile Met Ala
1 5 10 15

Glu Lys Leu Ala Ile Leu Glu Asp Pro Gly His Ile Thr Ser Cys Asp
20 25 30

Phe Asn Ala Val Leu Ala Cys Gly Asp Val Met Arg Ser Gly Gln Ala
35 40 45

Asn Ala Phe Gly Ile Pro Asn Pro Leu Ile Gly Ile Ala Gly Phe Ala
50 55 60

Ala Val Ala Ile Ile Gly Ala Gly Ile Leu Ala Gly Gly Gly Phe Arg
65 70 75 80

Gly Trp Phe Trp Phe Gly Ala Gln Ala Gly Leu Thr Phe Ala Met Met
85 90 95

Phe Cys His Trp Leu Ala Tyr Gln Ser Met Ser Val Ile Arg Ala Leu
100 105 110

Cys Pro Tyr Cys Met Gly Val Trp Thr Val Ser Ile Ile Met Phe Val
115 120 125

Leu Val Thr Ala Trp Asn Val Lys Thr Phe Ser Gly Ser Asp Ser Thr
130 135 140

Phe Val Asn Ala Leu Tyr Lys Tyr Lys Trp Val Ile Ala Ile Val Trp
145 150 155 160

Leu Leu Leu Ile Ala Ala Ala Ala Val Trp Ser Phe Arg Tyr Met Phe
165 170 175

<210> 91
<211> 651
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(628)
<223> FRXA00087

<400> 91
tcgtcagtca acaaacgttt tcccacccgg aggtctcccc gtgtctaccg aaatccacaa 60

cgccccaccc aaggccccaa cttggcttgg ctgggtgctc atg atc ggc gga ata 115
Met Ile Gly Gly Ile
1 5

atc ggc ctc att ttg tcg gtg atc atc atg gcc gaa aaa ctt gcc atc 163
Ile Gly Leu Ile Leu Ser Val Ile Ile Met Ala Glu Lys Leu Ala Ile
10 15 20

```
ctc gag gat ccc ggt cac atc acc agc tgc gat ttc aat gca gtc cta   211
Leu Glu Asp Pro Gly His Ile Thr Ser Cys Asp Phe Asn Ala Val Leu
            25                  30                  35

gct tgt ggc gat gtc atg cgt tcc ggc caa gct aac gcg ttc ggc atc   259
Ala Cys Gly Asp Val Met Arg Ser Gly Gln Ala Asn Ala Phe Gly Ile
        40                  45                  50

ccg aat ccg ctc atc ggc atc gcc ggt ttc gcc gct gtc gcc atc atc   307
Pro Asn Pro Leu Ile Gly Ile Ala Gly Phe Ala Ala Val Ala Ile Ile
    55                  60                  65

ggc gcc ggc atc ctc gcg ggc ggc ggg ttc cgc ggt tgg ttc tgg ttc   355
Gly Ala Gly Ile Leu Ala Gly Gly Gly Phe Arg Gly Trp Phe Trp Phe
70                  75                  80                  85

ggc gcc cag gcc gga ctc act ttt gcc atg atg ttc tgc cac tgg ctc   403
Gly Ala Gln Ala Gly Leu Thr Phe Ala Met Met Phe Cys His Trp Leu
                90                  95                  100

gcc tac caa tcc atg tcc gtc atc cgc gcg ctc tgc cct tac tgc atg   451
Ala Tyr Gln Ser Met Ser Val Ile Arg Ala Leu Cys Pro Tyr Cys Met
            105                 110                 115

ggc gtg tgg acc gta tcg atc atc atg ttc gtg ctg gtc act gca tgg   499
Gly Val Trp Thr Val Ser Ile Ile Met Phe Val Leu Val Thr Ala Trp
        120                 125                 130

aat gtg aaa act ttc agc ggc tcc gac agc acg ttc gtc aac gca ctg   547
Asn Val Lys Thr Phe Ser Gly Ser Asp Ser Thr Phe Val Asn Ala Leu
    135                 140                 145

tac aaa tac aag tgg gtc atc gcg atc gtc tgg ctg ctg ctc atc gca   595
Tyr Lys Tyr Lys Trp Val Ile Ala Ile Val Trp Leu Leu Leu Ile Ala
150                 155                 160                 165

gcc gca gct gtg tgg tca ttc cgc tac atg ttc taggcattta aggctttcag 648
Ala Ala Ala Val Trp Ser Phe Arg Tyr Met Phe
                170                 175

gcc                                                               651
```

Sequence Listing

<210> 92
<211> 176
<212> PRT
<213> Corynebacterium glutamicum

<400> 92

```
Met Ile Gly Gly Ile Ile Gly Leu Ile Leu Ser Val Ile Ile Met Ala
  1               5                  10                  15

Glu Lys Leu Ala Ile Leu Glu Asp Pro Gly His Ile Thr Ser Cys Asp
            20                  25                  30

Phe Asn Ala Val Leu Ala Cys Gly Asp Val Met Arg Ser Gly Gln Ala
        35                  40                  45

Asn Ala Phe Gly Ile Pro Asn Pro Leu Ile Gly Ile Ala Gly Phe Ala
    50                  55                  60
```

```
Ala Val Ala Ile Ile Gly Ala Gly Ile Leu Ala Gly Gly Gly Phe Arg
 65                  70                  75                  80

Gly Trp Phe Trp Phe Gly Ala Gln Ala Gly Leu Thr Phe Ala Met Met
                 85                  90                  95

Phe Cys His Trp Leu Ala Tyr Gln Ser Met Ser Val Ile Arg Ala Leu
            100                 105                 110

Cys Pro Tyr Cys Met Gly Val Trp Thr Val Ser Ile Ile Met Phe Val
        115                 120                 125

Leu Val Thr Ala Trp Asn Val Lys Thr Phe Ser Gly Ser Asp Ser Thr
    130                 135                 140

Phe Val Asn Ala Leu Tyr Lys Tyr Lys Trp Val Ile Ala Ile Val Trp
145                 150                 155                 160

Leu Leu Leu Ile Ala Ala Ala Ala Val Trp Ser Phe Arg Tyr Met Phe
                165                 170                 175
```

Page 136 of 144 - 2009-12-29 09:44:44

<210> 93
<211> 426
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(403)
<223> RXN00096

<400> 93
ggggaacctg gggtaaaagg agaagtattc attaccccaa taacctacta ggtggggtgg 60

```
acacgcatag tcgacagcca gacgtggcag aatagtgtgc atg act aat gca ggt   115
                                        Met Thr Asn Ala Gly
                                          1               5

gac aac ttc gag atc agg atg cct tct ggc acg gat gac cca ttg tcc   163
Asp Asn Phe Glu Ile Arg Met Pro Ser Gly Thr Asp Asp Pro Leu Ser
                 10                  15                  20

gat gcg gag atc caa aag tat cgc gag gag atc aac cgc ttg gac cgc   211
Asp Ala Glu Ile Gln Lys Tyr Arg Glu Glu Ile Asn Arg Leu Asp Arg
             25                  30                  35

gaa atc ctc gat gcg gtg aaa cgc cgc acg aag att tcc caa acc atc   259
Glu Ile Leu Asp Ala Val Lys Arg Arg Thr Lys Ile Ser Gln Thr Ile
         40                  45                  50

gga aaa aca cgc atg agc tcg ggc gga aca cgt ctc gtg cac acc cga   307
Gly Lys Thr Arg Met Ser Ser Gly Gly Thr Arg Leu Val His Thr Arg
     55                  60                  65

gaa gta gca atc atc aac caa ttc cgt gaa gag atc ggc gag gaa ggc   355
Glu Val Ala Ile Ile Asn Gln Phe Arg Glu Glu Ile Gly Glu Glu Gly
 70                  75                  80                  85
```

cct gcc ctc gct gga att ttg ctg cgc atg gga cgc gga aaa ctc gga 403
Pro Ala Leu Ala Gly Ile Leu Leu Arg Met Gly Arg Gly Lys Leu Gly
90 95 100

taagttatcc acaggtagaa aaa 426

<210> 94
<211> 101
<212> PRT
<213> Corynebacterium glutamicum

<400> 94
Met Thr Asn Ala Gly Asp Asn Phe Glu Ile Arg Met Pro Ser Gly Thr
1 5 10 15

Asp Asp Pro Leu Ser Asp Ala Glu Ile Gln Lys Tyr Arg Glu Glu Ile
20 25 30

Asn Arg Leu Asp Arg Glu Ile Leu Asp Ala Val Lys Arg Arg Thr Lys
35 40 45

Ile Ser Gln Thr Ile Gly Lys Thr Arg Met Ser Ser Gly Gly Thr Arg
50 55 60

Leu Val His Thr Arg Glu Val Ala Ile Ile Asn Gln Phe Arg Glu Glu
65 70 75 80

Ile Gly Glu Glu Gly Pro Ala Leu Ala Gly Ile Leu Leu Arg Met Gly
85 90 95

Arg Gly Lys Leu Gly
100

<210> 95
<211> 426
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(403)
<223> FRXA00096

<400> 95
ggggaacctg gggtaaaagg agaagtattc attaccccaa taacctacta ggtggggtgg 60

acacgcatag tcgacagcca gacgtggcag aatagtgtgc atg act aat gca ggt 115
Met Thr Asn Ala Gly
1 5

gac aac ttc gag atc agg atg cct tct ggc acg gat gac cca ttg tcc 163
Asp Asn Phe Glu Ile Arg Met Pro Ser Gly Thr Asp Asp Pro Leu Ser
10 15 20

gat gcg gag atc caa aag tat cgc gag gag atc aac cgc ttg gac cgc 211
Asp Ala Glu Ile Gln Lys Tyr Arg Glu Glu Ile Asn Arg Leu Asp Arg
25 30 35

```
gaa atc ctc gat gcg gtg aaa cgc cgc acg aag att tcc caa acc atc   259
Glu Ile Leu Asp Ala Val Lys Arg Arg Thr Lys Ile Ser Gln Thr Ile
         40                  45                  50

gga aaa aca cgc atg agc tcg ggc gga aca cgt ctc gtg cac acc cga   307
Gly Lys Thr Arg Met Ser Ser Gly Gly Thr Arg Leu Val His Thr Arg
     55                  60                  65

gaa gta gca atc atc aac cag ttc cgt gaa gag atc ggc gag gaa ggc   355
Glu Val Ala Ile Ile Asn Gln Phe Arg Glu Glu Ile Gly Glu Glu Gly
 70                  75                  80                  85

cct gcc ctc gct gga att ttg ctg cgc atg gga cgc gga aaa ctc gga   403
Pro Ala Leu Ala Gly Ile Leu Leu Arg Met Gly Arg Gly Lys Leu Gly
                 90                  95                 100

taagttatcc acaggtagaa aaa                                        426
```

<210> 96
<211> 101
<212> PRT
<213> Corynebacterium glutamicum

<400> 96

```
Met Thr Asn Ala Gly Asp Asn Phe Glu Ile Arg Met Pro Ser Gly Thr
  1               5                  10                  15

Asp Asp Pro Leu Ser Asp Ala Glu Ile Gln Lys Tyr Arg Glu Glu Ile
             20                  25                  30

Asn Arg Leu Asp Arg Glu Ile Leu Asp Ala Val Lys Arg Arg Thr Lys
         35                  40                  45

Ile Ser Gln Thr Ile Gly Lys Thr Arg Met Ser Ser Gly Gly Thr Arg
     50                  55                  60

Leu Val His Thr Arg Glu Val Ala Ile Ile Asn Gln Phe Arg Glu Glu
 65                  70                  75                  80

Ile Gly Glu Glu Gly Pro Ala Leu Ala Gly Ile Leu Leu Arg Met Gly
                 85                  90                  95

Arg Gly Lys Leu Gly
             100
```

<210> 97
<211> 1299
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1276)
<223> RXN00097

<400> 97

```
tcagggtttt agccgttgat gggcagagtt atccacaggt ttttagcgag ctggtttccg 60

acgaagaaaa tagtggatag gttacagggc agaatcccga atg gag gtg cct tcc   115
```

```
                                                  Met Glu Val Pro Ser
                                                    1               5

ttg ttt acc aac ttc ttc gca gtc aac aac cca gac agt ccg ccc gca   163
Leu Phe Thr Asn Phe Phe Ala Val Asn Asn Pro Asp Ser Pro Pro Ala
                  10                  15                  20

cga caa aaa acc aaa ctc aga gaa ctg gaa cac cgc ttc tgg caa gaa   211
Arg Gln Lys Thr Lys Leu Arg Glu Leu Glu His Arg Phe Trp Gln Glu
              25                  30                  35

cac ctg cca ggc gac gac gat gac cat tcc acc gca atc tcc agc ctc   259
His Leu Pro Gly Asp Asp Asp Asp His Ser Thr Ala Ile Ser Ser Leu
          40                  45                  50

gcc atc gtc aca ggt cta aca aaa gcg cag gtc tcc cgc ata tcc atc   307
Ala Ile Val Thr Gly Leu Thr Lys Ala Gln Val Ser Arg Ile Ser Ile
      55                  60                  65

gcg ttt gcc acg ctc gcc gac ttg ccc gaa ctc aaa gcc ctg caa caa   355
Ala Phe Ala Thr Leu Ala Asp Leu Pro Glu Leu Lys Ala Leu Gln Gln
  70                  75                  80                  85

aag ctg tac cac ctc gac ctc tcc cga ctg atc acc att agc aac gaa   403
Lys Leu Tyr His Leu Asp Leu Ser Arg Leu Ile Thr Ile Ser Asn Glu
                  90                  95                 100

ctc gcc ggc atc aac ccc gac aac ctc gcc ggc gcc gac gca atc ctc   451
Leu Ala Gly Ile Asn Pro Asp Asn Leu Ala Gly Ala Asp Ala Ile Leu
              105                 110                 115

acc gaa tac ctc acc gcc acc agc ccc aac cag att ctg cca agc ccg   499
Thr Glu Tyr Leu Thr Ala Thr Ser Pro Asn Gln Ile Leu Pro Ser Pro
          120                 125                 130

gcg tcc ata gga cgc aag ata aaa gaa ata aga gat ttg ctt gac gac   547
Ala Ser Ile Gly Arg Lys Ile Lys Glu Ile Arg Asp Leu Leu Asp Asp
      135                 140                 145

gca aga gcc acc ggt tcg cgc ggt acc caa gac gac agc tct ttc gga   595
Ala Arg Ala Thr Gly Ser Arg Gly Thr Gln Asp Asp Ser Ser Phe Gly
150                 155                 160                 165

gtg acc ttc tcc cca gac gga acc gcc gaa atc gga gcc tcc gtc gat   643
Val Thr Phe Ser Pro Asp Gly Thr Ala Glu Ile Gly Ala Ser Val Asp
                  170                 175                 180

gct gtg gac ggg cac atc atc aac gac gcc gtc acc caa cac gcg aag   691
Ala Val Asp Gly His Ile Ile Asn Asp Ala Val Thr Gln His Ala Lys
              185                 190                 195

aaa aac gac ctc acc tac ggc gaa gct ttc agc gac atc ctt cgg aac   739
Lys Asn Asp Leu Thr Tyr Gly Glu Ala Phe Ser Asp Ile Leu Arg Asn
          200                 205                 210

aat atc caa gtc aag gta gtc ctc aac ttg tac acc gcc aaa gac ctc   787
Asn Ile Gln Val Lys Val Val Leu Asn Leu Tyr Thr Ala Lys Asp Leu
      215                 220                 225

gcc aac gcc cca gtg tgg gcc agc gga atc ggc tgg ttg gat gcc aag   835
Ala Asn Ala Pro Val Trp Ala Ser Gly Ile Gly Trp Leu Asp Ala Lys
```

```
230                 235                 240                 245

act gga aca ttc tgg tca gag aaa gcc aac aaa gaa caa gac atg gat   883
Thr Gly Thr Phe Trp Ser Glu Lys Ala Asn Lys Glu Gln Asp Met Asp
                250                 255                 260

gcg gct gcc aaa atc agc acc gac aaa cac gat cct cca cca gcg ttg   931
Ala Ala Ala Lys Ile Ser Thr Asp Lys His Asp Pro Pro Pro Ala Leu
            265                 270                 275

cgt gac gca ctc att ggt cgt gat ggc acc tgc cga ttc cct ggc tgt   979
Arg Asp Ala Leu Ile Gly Arg Asp Gly Thr Cys Arg Phe Pro Gly Cys
        280                 285                 290

tca gtc cca gcg ctc aaa acc caa gcc gac cac cgc atc ccc tac gaa   1027
Ser Val Pro Ala Leu Lys Thr Gln Ala Asp His Arg Ile Pro Tyr Glu
    295                 300                 305

gaa ggc gga gaa act tgc cta ggc gga atc ggc tgc ctc tgt caa cac   1075
Glu Gly Gly Glu Thr Cys Leu Gly Gly Ile Gly Cys Leu Cys Gln His
310                 315                 320                 325

cac cac aac atg aaa acc gac ggc cga gtc acc tac ctt ctc gat ccc   1123
His His Asn Met Lys Thr Asp Gly Arg Val Thr Tyr Leu Leu Asp Pro
                330                 335                 340

ttc tcc ggc atc atc gtc tgg ctc atg gga gac gga aca tgg gca gtg   1171
Phe Ser Gly Ile Ile Val Trp Leu Met Gly Asp Gly Thr Trp Ala Val
            345                 350                 355

tca gaa ccc aac ggg ccg ctc aat ccc aaa aat gcg aga tgg gcg caa   1219
Ser Glu Pro Asn Gly Pro Leu Asn Pro Lys Asn Ala Arg Trp Ala Gln
        360                 365                 370

aca gtc gcc caa cac cgg gca cgc cac cac aag cgt tgg gtt aag gag   1267
Thr Val Ala Gln His Arg Ala Arg His His Lys Arg Trp Val Lys Glu
    375                 380                 385

gac gcc aag tagccggatg gccacgtcga aaa                            1299
Asp Ala Lys
390
```

<210> 98
<211> 392
<212> PRT
<213> Corynebacterium glutamicum

<400> 98

```
Met Glu Val Pro Ser Leu Phe Thr Asn Phe Phe Ala Val Asn Asn Pro
  1               5                  10                  15

Asp Ser Pro Pro Ala Arg Gln Lys Thr Lys Leu Arg Glu Leu Glu His
             20                  25                  30

Arg Phe Trp Gln Glu His Leu Pro Gly Asp Asp Asp His Ser Thr
         35                  40                  45

Ala Ile Ser Ser Leu Ala Ile Val Thr Gly Leu Thr Lys Ala Gln Val
     50                  55                  60
```

```
Ser Arg Ile Ser Ile Ala Phe Ala Thr Leu Ala Asp Leu Pro Glu Leu
 65                  70                  75                  80

Lys Ala Leu Gln Gln Lys Leu Tyr His Leu Asp Leu Ser Arg Leu Ile
                85                  90                  95

Thr Ile Ser Asn Glu Leu Ala Gly Ile Asn Pro Asp Asn Leu Ala Gly
            100                 105                 110

Ala Asp Ala Ile Leu Thr Glu Tyr Leu Thr Ala Thr Ser Pro Asn Gln
        115                 120                 125

Ile Leu Pro Ser Pro Ala Ser Ile Gly Arg Lys Ile Lys Glu Ile Arg
    130                 135                 140

Asp Leu Leu Asp Asp Ala Arg Ala Thr Gly Ser Arg Gly Thr Gln Asp
145                 150                 155                 160

Asp Ser Ser Phe Gly Val Thr Phe Ser Pro Asp Gly Thr Ala Glu Ile
                165                 170                 175

Gly Ala Ser Val Asp Ala Val Asp Gly His Ile Ile Asn Asp Ala Val
            180                 185                 190

Thr Gln His Ala Lys Lys Asn Asp Leu Thr Tyr Gly Glu Ala Phe Ser
        195                 200                 205

Asp Ile Leu Arg Asn Asn Ile Gln Val Lys Val Val Leu Asn Leu Tyr
    210                 215                 220

Thr Ala Lys Asp Leu Ala Asn Ala Pro Val Trp Ala Ser Gly Ile Gly
225                 230                 235                 240

Trp Leu Asp Ala Lys Thr Gly Thr Phe Trp Ser Glu Lys Ala Asn Lys
                245                 250                 255

Glu Gln Asp Met Asp Ala Ala Ala Lys Ile Ser Thr Asp Lys His Asp
            260                 265                 270

Pro Pro Pro Ala Leu Arg Asp Ala Leu Ile Gly Arg Asp Gly Thr Cys
        275                 280                 285

Arg Phe Pro Gly Cys Ser Val Pro Ala Leu Lys Thr Gln Ala Asp His
    290                 295                 300

Arg Ile Pro Tyr Glu Glu Gly Gly Glu Thr Cys Leu Gly Gly Ile Gly
305                 310                 315                 320

Cys Leu Cys Gln His His His Asn Met Lys Thr Asp Gly Arg Val Thr
                325                 330                 335

Tyr Leu Leu Asp Pro Phe Ser Gly Ile Ile Val Trp Leu Met Gly Asp
            340                 345                 350

Gly Thr Trp Ala Val Ser Glu Pro Asn Gly Pro Leu Asn Pro Lys Asn
        355                 360                 365

Ala Arg Trp Ala Gln Thr Val Ala Gln His Arg Ala Arg His His Lys
    370                 375                 380

Arg Trp Val Lys Glu Asp Ala Lys
```

385 390

<210> 99
<211> 1284
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1261)
<223> FRXA00097

<400> 99
ttgatgggca gagttatcca caggttttta gcgagctggt ttccgacgaa gaaaatagtg 60

gataggttac agggcagaat cccgaatgga ggtgccttcc ttg ttt acc aac ttc 115
Leu Phe Thr Asn Phe
1 5

ttc gca gtc aac aac cca gac agt ccg ccc gca cga caa aaa acc aaa 163
Phe Ala Val Asn Asn Pro Asp Ser Pro Pro Ala Arg Gln Lys Thr Lys
10 15 20

ctc aga gaa ctg gaa cac cgc ttc tgg caa gaa cac ctg cca ggc gac 211
Leu Arg Glu Leu Glu His Arg Phe Trp Gln Glu His Leu Pro Gly Asp
25 30 35

gac gat gac cat tcc acc gca atc tcc agc ctc gcc atc gtc aca ggt 259
Asp Asp Asp His Ser Thr Ala Ile Ser Ser Leu Ala Ile Val Thr Gly
40 45 50

cta aca aaa gcg cag gtc tcc cgc ata tcc atc gcg ttt gcc acg ctc 307
Leu Thr Lys Ala Gln Val Ser Arg Ile Ser Ile Ala Phe Ala Thr Leu
55 60 65

gcc gac ttg ccc gaa ctc aaa gcc ctg caa caa aag ctg tac cac ctc 355
Ala Asp Leu Pro Glu Leu Lys Ala Leu Gln Gln Lys Leu Tyr His Leu
70 75 80 85

gac ctc tcc cga ctg atc acc att agc aac gaa ctc gcc ggc atc aac 403
Asp Leu Ser Arg Leu Ile Thr Ile Ser Asn Glu Leu Ala Gly Ile Asn
90 95 100

ccc gac aac ctc gcc ggc gcc gac gca atc ctc acc gaa tac ctc acc 451
Pro Asp Asn Leu Ala Gly Ala Asp Ala Ile Leu Thr Glu Tyr Leu Thr
105 110 115

gcc acc agc ccc aac cag att ctg cca agc ccg gcg tcc ata gga cgc 499
Ala Thr Ser Pro Asn Gln Ile Leu Pro Ser Pro Ala Ser Ile Gly Arg
120 125 130

aag ata aaa gaa ata aga gat ttg ctt gac gac gca aga gcc acc ggt 547
Lys Ile Lys Glu Ile Arg Asp Leu Leu Asp Asp Ala Arg Ala Thr Gly
135 140 145

tcg cgc ggt acc caa gac gac agc tct ttc gga gtg acc ttc tcc cca 595
Ser Arg Gly Thr Gln Asp Asp Ser Ser Phe Gly Val Thr Phe Ser Pro
150 155 160 165

gac gga acc gcc gaa atc gga gcc tcc gtc gat gct gtg gac ggg cac 643

```
Asp Gly Thr Ala Glu Ile Gly Ala Ser Val Asp Ala Val Asp Gly His
                170                 175                 180

atc atc aac gac gcc gtc acc caa cac gcg aag aaa aac gac ctc acc   691
Ile Ile Asn Asp Ala Val Thr Gln His Ala Lys Lys Asn Asp Leu Thr
            185                 190                 195

tac ggc gaa gct ttc agc gac atc ctt cgg aac aat atc caa gtc aag   739
Tyr Gly Glu Ala Phe Ser Asp Ile Leu Arg Asn Asn Ile Gln Val Lys
        200                 205                 210

gta gtc ctc aac ttg tac acc gcc aaa gac ctc gcc aac gcc cca gtg   787
Val Val Leu Asn Leu Tyr Thr Ala Lys Asp Leu Ala Asn Ala Pro Val
    215                 220                 225

tgg gcc agc gga atc ggc tgg ttg gat gcc aag act gga aca ttc tgg   835
Trp Ala Ser Gly Ile Gly Trp Leu Asp Ala Lys Thr Gly Thr Phe Trp
230                 235                 240                 245

tca gag aaa gcc aac aaa gaa caa gac atg gat gcg gct gcc aaa atc   883
Ser Glu Lys Ala Asn Lys Glu Gln Asp Met Asp Ala Ala Ala Lys Ile
                250                 255                 260

agc acc gac aaa cac gat cct cca cca gcg ttg cgt gac gca ctc att   931
Ser Thr Asp Lys His Asp Pro Pro Pro Ala Leu Arg Asp Ala Leu Ile
            265                 270                 275

ggt cgt gat ggc acc tgc cga ttc cct ggc tgt tca gtc cca gcg ctc   979
Gly Arg Asp Gly Thr Cys Arg Phe Pro Gly Cys Ser Val Pro Ala Leu
        280                 285                 290

aaa acc caa gcc gac cac cgc atc ccc tac gaa gaa ggc gga gaa act  1027
Lys Thr Gln Ala Asp His Arg Ile Pro Tyr Glu Glu Gly Gly Glu Thr
    295                 300                 305

tgc cta ggc gga atc ggc tgc ctc tgt caa cac cac cac aac atg aaa  1075
Cys Leu Gly Gly Ile Gly Cys Leu Cys Gln His His His Asn Met Lys
310                 315                 320                 325

acc gac ggc cga gtc acc tac ctt ctc gat ccc ttc tcc ggc atc atc  1123
Thr Asp Gly Arg Val Thr Tyr Leu Leu Asp Pro Phe Ser Gly Ile Ile
                330                 335                 340

gtc tgg ctc atg gga gac gga aca tgg gca gtg tca gaa ccc aac ggg  1171
Val Trp Leu Met Gly Asp Gly Thr Trp Ala Val Ser Glu Pro Asn Gly
            345                 350                 355

ccg ctc aat ccc aaa aat gcg aga tgg gcg caa aca gtc gcc caa cac  1219
Pro Leu Asn Pro Lys Asn Ala Arg Trp Ala Gln Thr Val Ala Gln His
        360                 365                 370

cgg gca cgc cac cac aag cgt tgg gtt aag gag gac gcc aag          1261
Arg Ala Arg His His Lys Arg Trp Val Lys Glu Asp Ala Lys
    375                 380                 385

tagccggatg gccacgtcga aaa                                       1284
```

<210> 100
<211> 387
<212> PRT

<213> Corynebacterium glutamicum

<400> 100

```
Leu Phe Thr Asn Phe Phe Ala Val Asn Asn Pro Asp Ser Pro Pro Ala
 1               5                  10                  15

Arg Gln Lys Thr Lys Leu Arg Glu Leu Glu His Arg Phe Trp Gln Glu
            20                  25                  30

His Leu Pro Gly Asp Asp Asp Asp His Ser Thr Ala Ile Ser Ser Leu
        35                  40                  45

Ala Ile Val Thr Gly Leu Thr Lys Ala Gln Val Ser Arg Ile Ser Ile
    50                  55                  60

Ala Phe Ala Thr Leu Ala Asp Leu Pro Glu Leu Lys Ala Leu Gln Gln
65                  70                  75                  80

Lys Leu Tyr His Leu Asp Leu Ser Arg Leu Ile Thr Ile Ser Asn Glu
                85                  90                  95

Leu Ala Gly Ile Asn Pro Asp Asn Leu Ala Gly Ala Asp Ala Ile Leu
            100                 105                 110

Thr Glu Tyr Leu Thr Ala Thr Ser Pro Asn Gln Ile Leu Pro Ser Pro
        115                 120                 125

Ala Ser Ile Gly Arg Lys Ile Lys Glu Ile Arg Asp Leu Leu Asp Asp
    130                 135                 140

Ala Arg Ala Thr Gly Ser Arg Gly Thr Gln Asp Asp Ser Ser Phe Gly
145                 150                 155                 160

Val Thr Phe Ser Pro Asp Gly Thr Ala Glu Ile Gly Ala Ser Val Asp
                165                 170                 175

Ala Val Asp Gly His Ile Ile Asn Asp Ala Val Thr Gln His Ala Lys
            180                 185                 190

Lys Asn Asp Leu Thr Tyr Gly Glu Ala Phe Ser Asp Ile Leu Arg Asn
        195                 200                 205

Asn Ile Gln Val Lys Val Val Leu Asn Leu Tyr Thr Ala Lys Asp Leu
    210                 215                 220

Ala Asn Ala Pro Val Trp Ala Ser Gly Ile Gly Trp Leu Asp Ala Lys
225                 230                 235                 240

Thr Gly Thr Phe Trp Ser Glu Lys Ala Asn Lys Glu Gln Asp Met Asp
                245                 250                 255

Ala Ala Ala Lys Ile Ser Thr Asp Lys His Asp Pro Pro Pro Ala Leu
            260                 265                 270

Arg Asp Ala Leu Ile Gly Arg Asp Gly Thr Cys Arg Phe Pro Gly Cys
        275                 280                 285

Ser Val Pro Ala Leu Lys Thr Gln Ala Asp His Arg Ile Pro Tyr Glu
    290                 295                 300

Glu Gly Gly Glu Thr Cys Leu Gly Gly Ile Gly Cys Leu Cys Gln His
```

```
305                 310                 315                 320

His His Asn Met Lys Thr Asp Gly Arg Val Thr Tyr Leu Leu Asp Pro
                325                 330                 335

Phe Ser Gly Ile Ile Val Trp Leu Met Gly Asp Gly Thr Trp Ala Val
            340                 345                 350

Ser Glu Pro Asn Gly Pro Leu Asn Pro Lys Asn Ala Arg Trp Ala Gln
        355                 360                 365

Thr Val Ala Gln His Arg Ala Arg His His Lys Arg Trp Val Lys Glu
    370                 375                 380

Asp Ala Lys
385
```

<210> 101
<211> 612
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(589)
<223> RXN00114

<400> 101

```
tgcattccct aacgggaatg cagctttttg tgttcctagt gcaaatcgaa atctcatgtg 60

atttacttaa aacctaatta aatctactat cggagatctc atg aaa ctt ctc aag   115
                                            Met Lys Leu Leu Lys
                                              1               5

ttt gct gca gca gga acc ttc gca cta gcc ctg gct ggc tgc aca cag   163
Phe Ala Ala Ala Gly Thr Phe Ala Leu Ala Leu Ala Gly Cys Thr Gln
                10                  15                  20

act gag tct ctc gta gca aca atc gaa tct gca acc tct gca gca cag   211
Thr Glu Ser Leu Val Ala Thr Ile Glu Ser Ala Thr Ser Ala Ala Gln
            25                  30                  35

gca tcc gga aac gac gta gaa gga gac caa acc tcc gcg ttc gaa ctc   259
Ala Ser Gly Asn Asp Val Glu Gly Asp Gln Thr Ser Ala Phe Glu Leu
        40                  45                  50

tcc gtt ggc gaa tgc ttc aac gac acc tac gaa gaa gaa atc tcc gaa   307
Ser Val Gly Glu Cys Phe Asn Asp Thr Tyr Glu Glu Glu Ile Ser Glu
    55                  60                  65

gta ccc atc gtc gac tgc gca gaa cct cac gac aac gag atc tac tac   355
Val Pro Ile Val Asp Cys Ala Glu Pro His Asp Asn Glu Ile Tyr Tyr
70                  75                  80                  85

ctc tac gac atc gaa ggc gac gac ttc cca acc gac atc acc acc aca   403
Leu Tyr Asp Ile Glu Gly Asp Asp Phe Pro Thr Asp Ile Thr Thr Thr
                90                  95                  100

ggc tac gaa ggc tgc ctc cca aca ttt gaa ggc ttc gta gga gct cct   451
Gly Tyr Glu Gly Cys Leu Pro Thr Phe Glu Gly Phe Val Gly Ala Pro
```

```
            105                 110                 115

tac gaa acc tcc atc tac gag gtc tac cca atg acc cca acc ttt ggc   499
Tyr Glu Thr Ser Ile Tyr Glu Val Tyr Pro Met Thr Pro Thr Phe Gly
        120                 125                 130

tcc tgg aca aac ggc gac cgc gag gta gtg tgc tcc gtg tac ttg gcc   547
Ser Trp Thr Asn Gly Asp Arg Glu Val Val Cys Ser Val Tyr Leu Ala
    135                 140                 145

acc ggt gag cag atg acc gga acc gca gca gga acc gcg cag           589
Thr Gly Glu Gln Met Thr Gly Thr Ala Ala Gly Thr Ala Gln
150                 155                 160

tagattttgg atagggaatt ttg                                        612


<210> 102
<211> 163
<212> PRT
<213> Corynebacterium glutamicum

<400> 102
Met Lys Leu Leu Lys Phe Ala Ala Ala Gly Thr Phe Ala Leu Ala Leu
  1               5                  10                  15

Ala Gly Cys Thr Gln Thr Glu Ser Leu Val Ala Thr Ile Glu Ser Ala
             20                  25                  30

Thr Ser Ala Ala Gln Ala Ser Gly Asn Asp Val Glu Gly Asp Gln Thr
         35                  40                  45

Ser Ala Phe Glu Leu Ser Val Gly Glu Cys Phe Asn Asp Thr Tyr Glu
     50                  55                  60

Glu Glu Ile Ser Glu Val Pro Ile Val Asp Cys Ala Glu Pro His Asp
 65                  70                  75                  80

Asn Glu Ile Tyr Tyr Leu Tyr Asp Ile Glu Gly Asp Asp Phe Pro Thr
                 85                  90                  95

Asp Ile Thr Thr Thr Gly Tyr Glu Gly Cys Leu Pro Thr Phe Glu Gly
            100                 105                 110

Phe Val Gly Ala Pro Tyr Glu Thr Ser Ile Tyr Glu Val Tyr Pro Met
        115                 120                 125

Thr Pro Thr Phe Gly Ser Trp Thr Asn Gly Asp Arg Glu Val Val Cys
    130                 135                 140

Ser Val Tyr Leu Ala Thr Gly Glu Gln Met Thr Gly Thr Ala Ala Gly
145                 150                 155                 160

Thr Ala Gln


<210> 103
<211> 612
<212> DNA
<213> Corynebacterium glutamicum
```

EFS Web 2.2.0.6 Feb 27, 2008 10:44:27 AM

<220>
<221> CDS
<222> (101)..(589)
<223> FRXA00114

<400> 103
tgcattccct aacgggaatg cagctttttg tgttcctagt gcaaatcgaa atctcatgtg 60

atttacttaa aacctaatta aatctactat cggagatctc atg aaa ctt ctc aag 115
Met Lys Leu Leu Lys
1 5

ttt gct gca gca gga acc ttc gca cta gcc ctg gct ggc tgc aca cag 163
Phe Ala Ala Ala Gly Thr Phe Ala Leu Ala Leu Ala Gly Cys Thr Gln
10 15 20

act gag tct ctc gta gca aca atc gaa tct gca acc tct gca gca cag 211
Thr Glu Ser Leu Val Ala Thr Ile Glu Ser Ala Thr Ser Ala Ala Gln
25 30 35

gca tcc gga aac gac gta gaa gga gac caa acc tcc gcg ttc gaa ctc 259
Ala Ser Gly Asn Asp Val Glu Gly Asp Gln Thr Ser Ala Phe Glu Leu
40 45 50

tcc gtt ggc gaa tgc ttc aac gac acc tac gaa gaa gaa atc tcc gaa 307
Ser Val Gly Glu Cys Phe Asn Asp Thr Tyr Glu Glu Glu Ile Ser Glu
55 60 65

gta ccc atc gtc gac tgc gca gaa cct cac gac aac gag atc tac tac 355
Val Pro Ile Val Asp Cys Ala Glu Pro His Asp Asn Glu Ile Tyr Tyr
70 75 80 85

ctc tac gac atc gaa ggc gac gac ttc cca acc gac atc acc acc aca 403
Leu Tyr Asp Ile Glu Gly Asp Asp Phe Pro Thr Asp Ile Thr Thr Thr
90 95 100

ggc tac gaa ggc tgc ctc cca aca ttt gaa ggc ttc gta gga gct cct 451
Gly Tyr Glu Gly Cys Leu Pro Thr Phe Glu Gly Phe Val Gly Ala Pro
105 110 115

tac gaa acc tcc atc tac gag gtc tac cca atg acc cca acc ttt ggc 499
Tyr Glu Thr Ser Ile Tyr Glu Val Tyr Pro Met Thr Pro Thr Phe Gly
120 125 130

tcc tgg aca aac ggc gac cgc gag gta gtg tgc tcc gtg tac ttg gcc 547
Ser Trp Thr Asn Gly Asp Arg Glu Val Val Cys Ser Val Tyr Leu Ala
135 140 145

acc ggt gag cag atg acc gga acc gca gca gga acc gcg cag 589
Thr Gly Glu Gln Met Thr Gly Thr Ala Ala Gly Thr Ala Gln
150 155 160

tagattttgg atagggaatt ttg 612

<210> 104
<211> 163
<212> PRT
<213> Corynebacterium glutamicum

<400> 104
Met Lys Leu Leu Lys Phe Ala Ala Ala Gly Thr Phe Ala Leu Ala Leu
1 5 10 15

Ala Gly Cys Thr Gln Thr Glu Ser Leu Val Ala Thr Ile Glu Ser Ala
20 25 30

Thr Ser Ala Ala Gln Ala Ser Gly Asn Asp Val Glu Gly Asp Gln Thr
35 40 45

Ser Ala Phe Glu Leu Ser Val Gly Glu Cys Phe Asn Asp Thr Tyr Glu
50 55 60

Glu Glu Ile Ser Glu Val Pro Ile Val Asp Cys Ala Glu Pro His Asp
65 70 75 80

Asn Glu Ile Tyr Tyr Leu Tyr Asp Ile Glu Gly Asp Asp Phe Pro Thr
85 90 95

Asp Ile Thr Thr Thr Gly Tyr Glu Gly Cys Leu Pro Thr Phe Glu Gly
100 105 110

Phe Val Gly Ala Pro Tyr Glu Thr Ser Ile Tyr Glu Val Tyr Pro Met
115 120 125

Thr Pro Thr Phe Gly Ser Trp Thr Asn Gly Asp Arg Glu Val Val Cys
130 135 140

Ser Val Tyr Leu Ala Thr Gly Glu Gln Met Thr Gly Thr Ala Ala Gly
145 150 155 160

Thr Ala Gln

<210> 105
<211> 963
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(940)
<223> RXN00120

<400> 105
acaaactctt aatttaatga gacgtaagta gttgatagtt aggggaaata ctcccaaatc 60

ctcacaggaa acgctctgaa ttctttcaaa aaaatgtttc atg ctt att ggc atg 115
Met Leu Ile Gly Met
1 5

agc aat caa aca gtc aat caa gca gtg tcg tca ggg gtg aaa gca tcc 163
Ser Asn Gln Thr Val Asn Gln Ala Val Ser Ser Gly Val Lys Ala Ser
10 15 20

ccg cac agg ttc aat cgt ttt gaa atc aaa tac ttg att aca gag caa 211
Pro His Arg Phe Asn Arg Phe Glu Ile Lys Tyr Leu Ile Thr Glu Gln
25 30 35

gat gta cct gca ctc cgc gag cag ttg gca acg agg atg agc acg gat 259

```
Asp Val Pro Ala Leu Arg Glu Gln Leu Ala Thr Arg Met Ser Thr Asp
         40                  45                  50

ccg ctt tcc cca ccc gga ggc tac cga gtg gaa tcc ctt tac ttc gat   307
Pro Leu Ser Pro Pro Gly Gly Tyr Arg Val Glu Ser Leu Tyr Phe Asp
     55                  60                  65

tca gcc gat tta cgg tgc tac acc gaa aag atc gag ggt ctg aaa ttc   355
Ser Ala Asp Leu Arg Cys Tyr Thr Glu Lys Ile Glu Gly Leu Lys Phe
 70                  75                  80                  85

cga agg aaa cta cgg atc cgt acc tac ggt gat gga gtg ctc act cca   403
Arg Arg Lys Leu Arg Ile Arg Thr Tyr Gly Asp Gly Val Leu Thr Pro
                 90                  95                 100

gaa tcc acc gtg tcg gta gag atc aag cag cgg gtt aac aaa gta act   451
Glu Ser Thr Val Ser Val Glu Ile Lys Gln Arg Val Asn Lys Val Thr
            105                 110                 115

caa aag cgt cgg ctg gat ttg ccc ttt ata tat gcg ctc gcc ctg ggc   499
Gln Lys Arg Arg Leu Asp Leu Pro Phe Ile Tyr Ala Leu Ala Leu Gly
        120                 125                 130

gat agc acg ggc gcc gcg gta ggc gag cag gtg gac gtc gag aag ctt   547
Asp Ser Thr Gly Ala Ala Val Gly Glu Gln Val Asp Val Glu Lys Leu
    135                 140                 145

ctt gaa atc tct ccg gaa aac cag cac gct ttg att cac gaa atg gcg   595
Leu Glu Ile Ser Pro Glu Asn Gln His Ala Leu Ile His Glu Met Ala
150                 155                 160                 165

tcg ttt gct aaa aat tat cgg ctg cga ccc atc gcc acc acg aag tat   643
Ser Phe Ala Lys Asn Tyr Arg Leu Arg Pro Ile Ala Thr Thr Lys Tyr
                170                 175                 180

cac cgc gag gca ttc gtc ggc gct gat gcg gag gaa agt tcg cga gtc   691
His Arg Glu Ala Phe Val Gly Ala Asp Ala Glu Glu Ser Ser Arg Val
            185                 190                 195

acc att gac cac ggt gtt tca ggc cgt gat cgt gat ttt ctg ctt ggc   739
Thr Ile Asp His Gly Val Ser Gly Arg Asp Arg Asp Phe Leu Leu Gly
        200                 205                 210

caa gac ctt gaa gac cgc cca acg gtg gcg caa gga ttg gca gtc gtg   787
Gln Asp Leu Glu Asp Arg Pro Thr Val Ala Gln Gly Leu Ala Val Val
    215                 220                 225

gaa atc aaa tgc gat gaa cgc gtg ccg ttt tgg ctc act gat atg act   835
Glu Ile Lys Cys Asp Glu Arg Val Pro Phe Trp Leu Thr Asp Met Thr
230                 235                 240                 245

gct caa ctg gaa atg tcc gtg att cgg atg tcc aaa tac tgc gaa acc   883
Ala Gln Leu Glu Met Ser Val Ile Arg Met Ser Lys Tyr Cys Glu Thr
                250                 255                 260

atc gaa gcg ttt cac aac cgt ccg gca tca gct ttc ggc gct gtc gac   931
Ile Glu Ala Phe His Asn Arg Pro Ala Ser Ala Phe Gly Ala Val Asp
            265                 270                 275

ccc atc ttc taaacaagaa aggcccctcc aat                            963
Pro Ile Phe
```

280

<210> 106
<211> 280
<212> PRT
<213> Corynebacterium glutamicum

<400> 106
Met Leu Ile Gly Met Ser Asn Gln Thr Val Asn Gln Ala Val Ser Ser
1 5 10 15

Gly Val Lys Ala Ser Pro His Arg Phe Asn Arg Phe Glu Ile Lys Tyr
20 25 30

Leu Ile Thr Glu Gln Asp Val Pro Ala Leu Arg Glu Gln Leu Ala Thr
35 40 45

Arg Met Ser Thr Asp Pro Leu Ser Pro Pro Gly Gly Tyr Arg Val Glu
50 55 60

Ser Leu Tyr Phe Asp Ser Ala Asp Leu Arg Cys Tyr Thr Glu Lys Ile
65 70 75 80

Glu Gly Leu Lys Phe Arg Arg Lys Leu Arg Ile Arg Thr Tyr Gly Asp
85 90 95

Gly Val Leu Thr Pro Glu Ser Thr Val Ser Val Glu Ile Lys Gln Arg
100 105 110

Val Asn Lys Val Thr Gln Lys Arg Arg Leu Asp Leu Pro Phe Ile Tyr
115 120 125

Ala Leu Ala Leu Gly Asp Ser Thr Gly Ala Ala Val Gly Glu Gln Val
130 135 140

Asp Val Glu Lys Leu Leu Glu Ile Ser Pro Glu Asn Gln His Ala Leu
145 150 155 160

Ile His Glu Met Ala Ser Phe Ala Lys Asn Tyr Arg Leu Arg Pro Ile
165 170 175

Ala Thr Thr Lys Tyr His Arg Glu Ala Phe Val Gly Ala Asp Ala Glu
180 185 190

Glu Ser Ser Arg Val Thr Ile Asp His Gly Val Ser Gly Arg Asp Arg
195 200 205

Asp Phe Leu Leu Gly Gln Asp Leu Glu Asp Arg Pro Thr Val Ala Gln
210 215 220

Gly Leu Ala Val Val Glu Ile Lys Cys Asp Glu Arg Val Pro Phe Trp
225 230 235 240

Leu Thr Asp Met Thr Ala Gln Leu Glu Met Ser Val Ile Arg Met Ser
245 250 255

Lys Tyr Cys Glu Thr Ile Glu Ala Phe His Asn Arg Pro Ala Ser Ala
260 265 270

Phe Gly Ala Val Asp Pro Ile Phe

275 280

<210> 107
<211> 777
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(754)
<223> FRXA00120

<400> 107
aatcaaatac ttgattacag agcaagatgt acctgcactc cgcgagcagt tggcaacgag 60

gatgagcacg gatccgcttt ccccacccgg aggctaccga gtg gaa tcc ctt tac 115
Val Glu Ser Leu Tyr
1 5

ttc gat tca gcc gat tta cgg tgc tac acc gaa aag atc gag ggt ctg 163
Phe Asp Ser Ala Asp Leu Arg Cys Tyr Thr Glu Lys Ile Glu Gly Leu
10 15 20

aaa ttc cga agg aaa cta cgg atc cgt acc tac ggt gat gga gtg ctc 211
Lys Phe Arg Arg Lys Leu Arg Ile Arg Thr Tyr Gly Asp Gly Val Leu
25 30 35

act cca gaa tcc acc gtg tcg gta gag atc aag cag cgg gtt aac aaa 259
Thr Pro Glu Ser Thr Val Ser Val Glu Ile Lys Gln Arg Val Asn Lys
40 45 50

gta act caa aag cgt cgg ctg gat ttg ccc ttt ata tat gcg ctc gcc 307
Val Thr Gln Lys Arg Arg Leu Asp Leu Pro Phe Ile Tyr Ala Leu Ala
55 60 65

ctg ggc gat agc acg ggc gcc gcg gta ggc gag cag gtg gac gtc gag 355
Leu Gly Asp Ser Thr Gly Ala Ala Val Gly Glu Gln Val Asp Val Glu
70 75 80 85

aag ctt ctt gaa atc tct ccg gaa aac cag cac gct ttg att cac gaa 403
Lys Leu Leu Glu Ile Ser Pro Glu Asn Gln His Ala Leu Ile His Glu
90 95 100

atg gcg tcg ttt gct aaa aat tat cgg ctg cga ccc atc gcc acc acg 451
Met Ala Ser Phe Ala Lys Asn Tyr Arg Leu Arg Pro Ile Ala Thr Thr
105 110 115

aag tat cac cgc gag gca ttc gtc ggc gct gat gcg gag gaa agt tcg 499
Lys Tyr His Arg Glu Ala Phe Val Gly Ala Asp Ala Glu Glu Ser Ser
120 125 130

cga gtc acc att gac cac ggt gtt tca ggc cgt gat cgt gat ttt ctg 547
Arg Val Thr Ile Asp His Gly Val Ser Gly Arg Asp Arg Asp Phe Leu
135 140 145

ctt ggc caa gac ctt gaa gac cgc cca acg gtg gcg caa gga ttg gca 595
Leu Gly Gln Asp Leu Glu Asp Arg Pro Thr Val Ala Gln Gly Leu Ala
150 155 160 165

gtc gtg gaa atc aaa tgc gat gaa cgc gtg ccg ttt tgg ctc act gat 643

```
Val Val Glu Ile Lys Cys Asp Glu Arg Val Pro Phe Trp Leu Thr Asp
                170                 175                 180

atg act gct caa ctg gaa atg tcc gtg att cgg atg tcc aaa tac tgc   691
Met Thr Ala Gln Leu Glu Met Ser Val Ile Arg Met Ser Lys Tyr Cys
            185                 190                 195

gaa acc atc gaa gcg ttt cac aac cgt ccg gca tca gct ttc ggc gct   739
Glu Thr Ile Glu Ala Phe His Asn Arg Pro Ala Ser Ala Phe Gly Ala
        200                 205                 210

gtc gac ccc atc ttc taaacaagaa aggcccctcc aat                    777
Val Asp Pro Ile Phe
    215
```

<210> 108
<211> 218
<212> PRT
<213> Corynebacterium glutamicum

<400> 108

```
Val Glu Ser Leu Tyr Phe Asp Ser Ala Asp Leu Arg Cys Tyr Thr Glu
  1               5                  10                  15

Lys Ile Glu Gly Leu Lys Phe Arg Arg Lys Leu Arg Ile Arg Thr Tyr
             20                  25                  30

Gly Asp Gly Val Leu Thr Pro Glu Ser Thr Val Ser Val Glu Ile Lys
         35                  40                  45

Gln Arg Val Asn Lys Val Thr Gln Lys Arg Arg Leu Asp Leu Pro Phe
     50                  55                  60

Ile Tyr Ala Leu Ala Leu Gly Asp Ser Thr Gly Ala Ala Val Gly Glu
 65                  70                  75                  80

Gln Val Asp Val Glu Lys Leu Leu Glu Ile Ser Pro Glu Asn Gln His
                 85                  90                  95

Ala Leu Ile His Glu Met Ala Ser Phe Ala Lys Asn Tyr Arg Leu Arg
            100                 105                 110

Pro Ile Ala Thr Thr Lys Tyr His Arg Glu Ala Phe Val Gly Ala Asp
        115                 120                 125

Ala Glu Glu Ser Ser Arg Val Thr Ile Asp His Gly Val Ser Gly Arg
    130                 135                 140

Asp Arg Asp Phe Leu Leu Gly Gln Asp Leu Glu Asp Arg Pro Thr Val
145                 150                 155                 160

Ala Gln Gly Leu Ala Val Val Glu Ile Lys Cys Asp Glu Arg Val Pro
                165                 170                 175

Phe Trp Leu Thr Asp Met Thr Ala Gln Leu Glu Met Ser Val Ile Arg
            180                 185                 190

Met Ser Lys Tyr Cys Glu Thr Ile Glu Ala Phe His Asn Arg Pro Ala
        195                 200                 205
```

Ser Ala Phe Gly Ala Val Asp Pro Ile Phe
210 215

<210> 109
<211> 1827
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1804)
<223> RXN00128

<400> 109
ccattttccg tttggtcttg cctaaagaac cgcatggaaa ttatcgtgaa gcaccgatcc 60

cgttgatcgc tccagagaca ccgtgggaag gggagcagca gtg agt aaa att tcg 115
Val Ser Lys Ile Ser
1 5

acg aaa ctg aag gcc ctc acc gcg gtg ctg tct gtg acc act ctg gtg 163
Thr Lys Leu Lys Ala Leu Thr Ala Val Leu Ser Val Thr Thr Leu Val
10 15 20

gct ggg tgt tcc acg ctt ccg cag aac acg gat ccg caa gtg ctg cgc 211
Ala Gly Cys Ser Thr Leu Pro Gln Asn Thr Asp Pro Gln Val Leu Arg
25 30 35

tca ttt tcc ggg tcc caa agc aca caa gag ata gca ggg ccg acc ccg 259
Ser Phe Ser Gly Ser Gln Ser Thr Gln Glu Ile Ala Gly Pro Thr Pro
40 45 50

aat caa gat ccg gat ttg ttg atc cgc ggc ttc ttc agc gca ggt gcg 307
Asn Gln Asp Pro Asp Leu Leu Ile Arg Gly Phe Phe Ser Ala Gly Ala
55 60 65

tat ccg act cag cag tat gaa gcg gcg aag gcg tat ctg acg gaa ggg 355
Tyr Pro Thr Gln Gln Tyr Glu Ala Ala Lys Ala Tyr Leu Thr Glu Gly
70 75 80 85

acg cgc agc acg tgg aat ccg gct gcg tcg act cgt att ttg gat cgc 403
Thr Arg Ser Thr Trp Asn Pro Ala Ala Ser Thr Arg Ile Leu Asp Arg
90 95 100

att gat ctg aac act ctg cca ggt tcg acg aat gcg gaa cga acg att 451
Ile Asp Leu Asn Thr Leu Pro Gly Ser Thr Asn Ala Glu Arg Thr Ile
105 110 115

gcg atc cgt gga acg cag gtc gga acg ttg ctc agc ggt ggc gtg tat 499
Ala Ile Arg Gly Thr Gln Val Gly Thr Leu Leu Ser Gly Gly Val Tyr
120 125 130

cag ccg gag aat gcg gag ttt gaa gct gag atc acg atg cgt cgg gaa 547
Gln Pro Glu Asn Ala Glu Phe Glu Ala Glu Ile Thr Met Arg Arg Glu
135 140 145

gat ggg gag tgg cgt atc gat gct ttg ccg gac ggg att tta tta gag 595
Asp Gly Glu Trp Arg Ile Asp Ala Leu Pro Asp Gly Ile Leu Leu Glu
150 155 160 165

```
aga aac gat ctg cgg aac cat tac act ccg cac gat gtg tat ttc ttt   643
Arg Asn Asp Leu Arg Asn His Tyr Thr Pro His Asp Val Tyr Phe Phe
                170                 175                 180

gat cct tct ggc cag gtg ttg gtg ggg gat cgg cgt tgg ttg ttc aat   691
Asp Pro Ser Gly Gln Val Leu Val Gly Asp Arg Arg Trp Leu Phe Asn
            185                 190                 195

gag tcg cag tcg atg tcc acg gtg ctg atg gcc ctt ctg gtt aat ggt   739
Glu Ser Gln Ser Met Ser Thr Val Leu Met Ala Leu Leu Val Asn Gly
        200                 205                 210

cct tcg ccg gca att tct cct ggt gtg gtc aat cag ctg tcc acg gat   787
Pro Ser Pro Ala Ile Ser Pro Gly Val Val Asn Gln Leu Ser Thr Asp
    215                 220                 225

gcg tcg ttc gtg ggg ttc aat gat ggg gag tat cag ttc act ggt ttg   835
Ala Ser Phe Val Gly Phe Asn Asp Gly Glu Tyr Gln Phe Thr Gly Leu
230                 235                 240                 245

gga aat ttg gat gat gat gcg cgt ttg cgt ttc gcc gcc cag gcc gtg   883
Gly Asn Leu Asp Asp Asp Ala Arg Leu Arg Phe Ala Ala Gln Ala Val
                250                 255                 260

tgg acg ttg gcg cat gct gat gtc gca ggc ccc tac act ttg gtc gct   931
Trp Thr Leu Ala His Ala Asp Val Ala Gly Pro Tyr Thr Leu Val Ala
            265                 270                 275

gac ggc gcg ccg ttg ctg tcg gag ttc cca acg ctc acc acc gat gac   979
Asp Gly Ala Pro Leu Leu Ser Glu Phe Pro Thr Leu Thr Thr Asp Asp
        280                 285                 290

ctc gcc gaa tac aac cca gag gct tac acc aac acg gtg tcc acg ttg   1027
Leu Ala Glu Tyr Asn Pro Glu Ala Tyr Thr Asn Thr Val Ser Thr Leu
    295                 300                 305

ttt gcg ttg cag gat gga tcg ttg tcg agg gtc agt tcc ggc aat gtg   1075
Phe Ala Leu Gln Asp Gly Ser Leu Ser Arg Val Ser Ser Gly Asn Val
310                 315                 320                 325

agt cca cta cag ggc att tgg agc ggt gga gat atc gat tct gca gcg   1123
Ser Pro Leu Gln Gly Ile Trp Ser Gly Gly Asp Ile Asp Ser Ala Ala
                330                 335                 340

att tcc tcc tcc gcc aat gtg gtg gca gcg gta cgc cac gaa aac aac   1171
Ile Ser Ser Ser Ala Asn Val Val Ala Ala Val Arg His Glu Asn Asn
            345                 350                 355

gag gca gtg ctt act gtt ggc tcc atg gaa ggc gtg act tca gat gcg   1219
Glu Ala Val Leu Thr Val Gly Ser Met Glu Gly Val Thr Ser Asp Ala
        360                 365                 370

ttg agg agt gaa acg atc act cgt ccc acc ttt gaa tac gcg tcg agt   1267
Leu Arg Ser Glu Thr Ile Thr Arg Pro Thr Phe Glu Tyr Ala Ser Ser
    375                 380                 385

ggg ttg tgg gct gtg gtg gat ggg gag acg cct gtc cga gtc gca cga   1315
Gly Leu Trp Ala Val Val Asp Gly Glu Thr Pro Val Arg Val Ala Arg
390                 395                 400                 405

tcg gca aca acc ggt gag ctc gtc cag acg gag gcg gag att gtg ctg   1363
```

```
Ser Ala Thr Thr Gly Glu Leu Val Gln Thr Glu Ala Glu Ile Val Leu
                410                 415                 420

cca agg gat gtg acg ggt ccg atc tct gaa ttc caa ctg tca cga act   1411
Pro Arg Asp Val Thr Gly Pro Ile Ser Glu Phe Gln Leu Ser Arg Thr
            425                 430                 435

ggg gtc cgg gcc gcc atg atc att gaa ggc aag gtg tac gtg ggc gtc   1459
Gly Val Arg Ala Ala Met Ile Ile Glu Gly Lys Val Tyr Val Gly Val
        440                 445                 450

gta acg cgt cct ggt ccg ggc gag cgg cgc gtg aca aat atc acg gag   1507
Val Thr Arg Pro Gly Pro Gly Glu Arg Arg Val Thr Asn Ile Thr Glu
    455                 460                 465

gtg gcg ccg agc ttg ggc gag gcg gcg ctg tcg atc aac tgg cgc cca   1555
Val Ala Pro Ser Leu Gly Glu Ala Ala Leu Ser Ile Asn Trp Arg Pro
470                 475                 480                 485

gac ggc att ttg ctt gtg ggc acg tca att cca gag acg ccg ctg tgg   1603
Asp Gly Ile Leu Leu Val Gly Thr Ser Ile Pro Glu Thr Pro Leu Trp
                490                 495                 500

cgc gtc gag cag gac gga tcg gcg att tcg tcg atg ccg agc ggg aat   1651
Arg Val Glu Gln Asp Gly Ser Ala Ile Ser Ser Met Pro Ser Gly Asn
            505                 510                 515

ctc agc gcg ccg gtg gtg gcg gtg gca agt tcc gcg acg acg gtc tac   1699
Leu Ser Ala Pro Val Val Ala Val Ala Ser Ser Ala Thr Thr Val Tyr
        520                 525                 530

gtc act gat tcg cat gcg atg ctt cag ctg ccg act gcc gat aat gat   1747
Val Thr Asp Ser His Ala Met Leu Gln Leu Pro Thr Ala Asp Asn Asp
    535                 540                 545

att tgg cgc gag gtg ccc ggt ttg ctg ggc acg cgt gcg gcg ccg gtg   1795
Ile Trp Arg Glu Val Pro Gly Leu Leu Gly Thr Arg Ala Ala Pro Val
550                 555                 560                 565

gtt gcg tac tgatggagct gttcttcccg cgc                            1827
Val Ala Tyr
```

<210> 110
<211> 568
<212> PRT
<213> Corynebacterium glutamicum

<400> 110

```
Val Ser Lys Ile Ser Thr Lys Leu Lys Ala Leu Thr Ala Val Leu Ser
  1               5                  10                  15

Val Thr Thr Leu Val Ala Gly Cys Ser Thr Leu Pro Gln Asn Thr Asp
             20                  25                  30

Pro Gln Val Leu Arg Ser Phe Ser Gly Ser Gln Ser Thr Gln Glu Ile
         35                  40                  45

Ala Gly Pro Thr Pro Asn Gln Asp Pro Asp Leu Leu Ile Arg Gly Phe
     50                  55                  60
```

```
Phe Ser Ala Gly Ala Tyr Pro Thr Gln Gln Tyr Glu Ala Ala Lys Ala
 65                  70                  75                  80

Tyr Leu Thr Glu Gly Thr Arg Ser Thr Trp Asn Pro Ala Ala Ser Thr
                85                  90                  95

Arg Ile Leu Asp Arg Ile Asp Leu Asn Thr Leu Pro Gly Ser Thr Asn
            100                 105                 110

Ala Glu Arg Thr Ile Ala Ile Arg Gly Thr Gln Val Gly Thr Leu Leu
        115                 120                 125

Ser Gly Gly Val Tyr Gln Pro Glu Asn Ala Glu Phe Glu Ala Glu Ile
    130                 135                 140

Thr Met Arg Arg Glu Asp Gly Glu Trp Arg Ile Asp Ala Leu Pro Asp
145                 150                 155                 160

Gly Ile Leu Leu Glu Arg Asn Asp Leu Arg Asn His Tyr Thr Pro His
                165                 170                 175

Asp Val Tyr Phe Phe Asp Pro Ser Gly Gln Val Leu Val Gly Asp Arg
            180                 185                 190

Arg Trp Leu Phe Asn Glu Ser Gln Ser Met Ser Thr Val Leu Met Ala
        195                 200                 205

Leu Leu Val Asn Gly Pro Ser Pro Ala Ile Ser Pro Gly Val Val Asn
    210                 215                 220

Gln Leu Ser Thr Asp Ala Ser Phe Val Gly Phe Asn Asp Gly Glu Tyr
225                 230                 235                 240

Gln Phe Thr Gly Leu Gly Asn Leu Asp Asp Asp Ala Arg Leu Arg Phe
                245                 250                 255

Ala Ala Gln Ala Val Trp Thr Leu Ala His Ala Asp Val Ala Gly Pro
            260                 265                 270

Tyr Thr Leu Val Ala Asp Gly Ala Pro Leu Leu Ser Glu Phe Pro Thr
        275                 280                 285

Leu Thr Thr Asp Asp Leu Ala Glu Tyr Asn Pro Glu Ala Tyr Thr Asn
    290                 295                 300

Thr Val Ser Thr Leu Phe Ala Leu Gln Asp Gly Ser Leu Ser Arg Val
305                 310                 315                 320

Ser Ser Gly Asn Val Ser Pro Leu Gln Gly Ile Trp Ser Gly Gly Asp
                325                 330                 335

Ile Asp Ser Ala Ala Ile Ser Ser Ser Ala Asn Val Val Ala Ala Val
            340                 345                 350

Arg His Glu Asn Asn Glu Ala Val Leu Thr Val Gly Ser Met Glu Gly
        355                 360                 365

Val Thr Ser Asp Ala Leu Arg Ser Glu Thr Ile Thr Arg Pro Thr Phe
    370                 375                 380
```

```
Glu Tyr Ala Ser Ser Gly Leu Trp Ala Val Val Asp Gly Glu Thr Pro
385                 390                 395                 400

Val Arg Val Ala Arg Ser Ala Thr Thr Gly Glu Leu Val Gln Thr Glu
                405                 410                 415

Ala Glu Ile Val Leu Pro Arg Asp Val Thr Gly Pro Ile Ser Glu Phe
            420                 425                 430

Gln Leu Ser Arg Thr Gly Val Arg Ala Ala Met Ile Ile Glu Gly Lys
        435                 440                 445

Val Tyr Val Gly Val Val Thr Arg Pro Gly Pro Gly Glu Arg Arg Val
    450                 455                 460

Thr Asn Ile Thr Glu Val Ala Pro Ser Leu Gly Glu Ala Ala Leu Ser
465                 470                 475                 480

Ile Asn Trp Arg Pro Asp Gly Ile Leu Leu Val Gly Thr Ser Ile Pro
                485                 490                 495

Glu Thr Pro Leu Trp Arg Val Glu Gln Asp Gly Ser Ala Ile Ser Ser
            500                 505                 510

Met Pro Ser Gly Asn Leu Ser Ala Pro Val Val Ala Val Ala Ser Ser
        515                 520                 525

Ala Thr Thr Val Tyr Val Thr Asp Ser His Ala Met Leu Gln Leu Pro
    530                 535                 540

Thr Ala Asp Asn Asp Ile Trp Arg Glu Val Pro Gly Leu Leu Gly Thr
545                 550                 555                 560

Arg Ala Ala Pro Val Val Ala Tyr
                565
```

Copyright © 2004 Genome Therapeutics Corp.

```
<210> 111
<211> 1827
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1804)
<223> FRXA00128

<400> 111
ccattttccg tttggtcttg cctaaagaac cgcatggaaa ttatcgtgaa gcaccgatcc 60

cgttgatcgc tccagagaca ccgtgggaag gggagcagca gtg agt aaa att tcg   115
                                              Val Ser Lys Ile Ser
                                                1               5

acg aaa ctg aag gcc ctc acc gcg gtg ctg tct gtg acc act ctg gtg   163
Thr Lys Leu Lys Ala Leu Thr Ala Val Leu Ser Val Thr Thr Leu Val
                10                  15                  20

gct ggg tgt tcc acg ctt ccg cag aac acg gat ccg caa gtg ctg cgc   211
Ala Gly Cys Ser Thr Leu Pro Gln Asn Thr Asp Pro Gln Val Leu Arg
            25                  30                  35
```

```
tca ttt tcc ggg tcc caa agc aca caa gag ata gca ggg ccg acc ccg   259
Ser Phe Ser Gly Ser Gln Ser Thr Gln Glu Ile Ala Gly Pro Thr Pro
         40                  45                  50

aat caa gat ccg gat ttg ttg atc cgc ggc ttc ttc agc gca ggt gcg   307
Asn Gln Asp Pro Asp Leu Leu Ile Arg Gly Phe Phe Ser Ala Gly Ala
     55                  60                  65

tat ccg act cag cag tat gaa gcg gcg aag gcg tat ctg acg gaa ggg   355
Tyr Pro Thr Gln Gln Tyr Glu Ala Ala Lys Ala Tyr Leu Thr Glu Gly
 70                  75                  80                  85

acg cgc agc acg tgg aat ccg gct gcg tcg act cgt att ttg gat cgc   403
Thr Arg Ser Thr Trp Asn Pro Ala Ala Ser Thr Arg Ile Leu Asp Arg
                 90                  95                 100

att gat ctg aac act ctg cca ggt tcg acg aat gcg gaa cga acg att   451
Ile Asp Leu Asn Thr Leu Pro Gly Ser Thr Asn Ala Glu Arg Thr Ile
            105                 110                 115

gcg atc cgt gga acg cag gtc gga acg ttg ctc agc ggt ggc gtg tat   499
Ala Ile Arg Gly Thr Gln Val Gly Thr Leu Leu Ser Gly Gly Val Tyr
        120                 125                 130

cag ccg gag aat gcg gag ttt gaa gct gag atc acg atg cgt cgg gaa   547
Gln Pro Glu Asn Ala Glu Phe Glu Ala Glu Ile Thr Met Arg Arg Glu
    135                 140                 145

gat ggg gag tgg cgt atc gat gct ttg ccg gac ggg att tta tta gag   595
Asp Gly Glu Trp Arg Ile Asp Ala Leu Pro Asp Gly Ile Leu Leu Glu
150                 155                 160                 165

aga aac gat ctg cgg aac cat tac act ccg cac gat gtg tat ttc ttt   643
Arg Asn Asp Leu Arg Asn His Tyr Thr Pro His Asp Val Tyr Phe Phe
                170                 175                 180

gat cct tct ggc cag gtg ttg gtg ggg gat cgg cgt tgg ttg ttc aat   691
Asp Pro Ser Gly Gln Val Leu Val Gly Asp Arg Arg Trp Leu Phe Asn
            185                 190                 195

gag tcg cag tcg atg tcc acg gtg ctg atg gcc ctt ctg gtt aat ggt   739
Glu Ser Gln Ser Met Ser Thr Val Leu Met Ala Leu Leu Val Asn Gly
        200                 205                 210

cct tcg ccg gca att tct cct ggt gtg gtc aat cag ctg tcc acg gat   787
Pro Ser Pro Ala Ile Ser Pro Gly Val Val Asn Gln Leu Ser Thr Asp
    215                 220                 225

gcg tcg ttc gtg ggg ttc aat gat ggg gag tat cag ttc act ggt ttg   835
Ala Ser Phe Val Gly Phe Asn Asp Gly Glu Tyr Gln Phe Thr Gly Leu
230                 235                 240                 245

gga aat ttg gat gat gat gcg cgt ttg cgt ttc gcc gcc cag gcc gtg   883
Gly Asn Leu Asp Asp Asp Ala Arg Leu Arg Phe Ala Ala Gln Ala Val
                250                 255                 260

tgg acg ttg gcg cat gct gat gtc gca ggc ccc tac act ttg gtc gct   931
Trp Thr Leu Ala His Ala Asp Val Ala Gly Pro Tyr Thr Leu Val Ala
            265                 270                 275
```

```
gac ggc gcg ccg ttg ctg tcg gag ttc cca acg ctc acc acc gat gac   979
Asp Gly Ala Pro Leu Leu Ser Glu Phe Pro Thr Leu Thr Thr Asp Asp
        280                 285                 290

ctc gcc gaa tac aac cca gag gct tac acc aac acg gtg tcc acg ttg   1027
Leu Ala Glu Tyr Asn Pro Glu Ala Tyr Thr Asn Thr Val Ser Thr Leu
    295                 300                 305

ttt gcg ttg cag gat gga tcg ttg tcg agg gtc agt tcc ggc aat gtg   1075
Phe Ala Leu Gln Asp Gly Ser Leu Ser Arg Val Ser Ser Gly Asn Val
310                 315                 320                 325

agt cca cta cag ggc att tgg agc ggt gga gat atc gat tct gca gcg   1123
Ser Pro Leu Gln Gly Ile Trp Ser Gly Gly Asp Ile Asp Ser Ala Ala
                330                 335                 340

att tcc tcc tcc gcc aat gtg gtg gca gcg gta cgc cac gaa aac aac   1171
Ile Ser Ser Ser Ala Asn Val Val Ala Ala Val Arg His Glu Asn Asn
            345                 350                 355

gag gca gtg ctt act gtt ggc tcc atg gaa ggc gtg act tca gat gcg   1219
Glu Ala Val Leu Thr Val Gly Ser Met Glu Gly Val Thr Ser Asp Ala
        360                 365                 370

ttg agg agt gaa acg atc act cgt ccc acc ttt gaa tac gcg tcg agt   1267
Leu Arg Ser Glu Thr Ile Thr Arg Pro Thr Phe Glu Tyr Ala Ser Ser
    375                 380                 385

ggg ttg tgg gct gtg gtg gat ggg gag acg cct gtc cga gtc gca cga   1315
Gly Leu Trp Ala Val Val Asp Gly Glu Thr Pro Val Arg Val Ala Arg
390                 395                 400                 405

tcg gca aca acc ggt gag ctc gtc cag acg gag gcg gag att gtg ctg   1363
Ser Ala Thr Thr Gly Glu Leu Val Gln Thr Glu Ala Glu Ile Val Leu
                410                 415                 420

cca agg gat gtg acg ggt ccg atc tct gaa ttc caa ctg tca cga act   1411
Pro Arg Asp Val Thr Gly Pro Ile Ser Glu Phe Gln Leu Ser Arg Thr
            425                 430                 435

ggg gtc cgg gcc gcc atg atc att gaa ggc aag gtg tac gtg ggc gtc   1459
Gly Val Arg Ala Ala Met Ile Ile Glu Gly Lys Val Tyr Val Gly Val
        440                 445                 450

gta acg cgt cct ggt ccg ggc gag cgg cgc gtg aca aat atc acg gag   1507
Val Thr Arg Pro Gly Pro Gly Glu Arg Arg Val Thr Asn Ile Thr Glu
    455                 460                 465

gtg gcg ccg agc ttg ggc gag gcg gcg ctg tcg atc aac tgg cgc cca   1555
Val Ala Pro Ser Leu Gly Glu Ala Ala Leu Ser Ile Asn Trp Arg Pro
470                 475                 480                 485

gac ggc att ttg ctt gtg ggc acg tca att cca gag acg ccg ctg tgg   1603
Asp Gly Ile Leu Leu Val Gly Thr Ser Ile Pro Glu Thr Pro Leu Trp
                490                 495                 500

cgc gtc gag cag gac gga tcg gcg att tcg tcg atg ccg agc ggg aat   1651
Arg Val Glu Gln Asp Gly Ser Ala Ile Ser Ser Met Pro Ser Gly Asn
            505                 510                 515

ctc agc gcg ccg gtg gtg gcg gtg gca agt tcc gcg acg acg gtc tac   1699
```

```
Leu Ser Ala Pro Val Val Ala Val Ala Ser Ser Ala Thr Thr Val Tyr
        520                 525                 530

gtc act gat tcg cat gcg atg ctt cag ctg ccg act gcc gat aat gat   1747
Val Thr Asp Ser His Ala Met Leu Gln Leu Pro Thr Ala Asp Asn Asp
    535                 540                 545

att tgg cgc gag gtg ccc ggt ttg ctg ggc acg cgt gcg gcg ccg gtg   1795
Ile Trp Arg Glu Val Pro Gly Leu Leu Gly Thr Arg Ala Ala Pro Val
550                 555                 560                 565

gtt gcg tac tgatggagct gttcttcccg cgc                             1827
Val Ala Tyr
```

<210> 112
<211> 568
<212> PRT
<213> Corynebacterium glutamicum

<400> 112

```
Val Ser Lys Ile Ser Thr Lys Leu Lys Ala Leu Thr Ala Val Leu Ser
  1               5                  10                  15

Val Thr Thr Leu Val Ala Gly Cys Ser Thr Leu Pro Gln Asn Thr Asp
             20                  25                  30

Pro Gln Val Leu Arg Ser Phe Ser Gly Ser Gln Ser Thr Gln Glu Ile
         35                  40                  45

Ala Gly Pro Thr Pro Asn Gln Asp Pro Asp Leu Leu Ile Arg Gly Phe
     50                  55                  60

Phe Ser Ala Gly Ala Tyr Pro Thr Gln Gln Tyr Glu Ala Ala Lys Ala
 65                  70                  75                  80

Tyr Leu Thr Glu Gly Thr Arg Ser Thr Trp Asn Pro Ala Ala Ser Thr
                 85                  90                  95

Arg Ile Leu Asp Arg Ile Asp Leu Asn Thr Leu Pro Gly Ser Thr Asn
            100                 105                 110

Ala Glu Arg Thr Ile Ala Ile Arg Gly Thr Gln Val Gly Thr Leu Leu
        115                 120                 125

Ser Gly Gly Val Tyr Gln Pro Glu Asn Ala Glu Phe Glu Ala Glu Ile
    130                 135                 140

Thr Met Arg Arg Glu Asp Gly Glu Trp Arg Ile Asp Ala Leu Pro Asp
145                 150                 155                 160

Gly Ile Leu Leu Glu Arg Asn Asp Leu Arg Asn His Tyr Thr Pro His
                165                 170                 175

Asp Val Tyr Phe Phe Asp Pro Ser Gly Gln Val Leu Val Gly Asp Arg
            180                 185                 190

Arg Trp Leu Phe Asn Glu Ser Gln Ser Met Ser Thr Val Leu Met Ala
        195                 200                 205
```

```
Leu Leu Val Asn Gly Pro Ser Pro Ala Ile Ser Pro Gly Val Val Asn
    210                 215                 220

Gln Leu Ser Thr Asp Ala Ser Phe Val Gly Phe Asn Asp Gly Glu Tyr
225                 230                 235                 240

Gln Phe Thr Gly Leu Gly Asn Leu Asp Asp Asp Ala Arg Leu Arg Phe
                245                 250                 255

Ala Ala Gln Ala Val Trp Thr Leu Ala His Ala Asp Val Ala Gly Pro
            260                 265                 270

Tyr Thr Leu Val Ala Asp Gly Ala Pro Leu Leu Ser Glu Phe Pro Thr
        275                 280                 285

Leu Thr Thr Asp Asp Leu Ala Glu Tyr Asn Pro Glu Ala Tyr Thr Asn
    290                 295                 300

Thr Val Ser Thr Leu Phe Ala Leu Gln Asp Gly Ser Leu Ser Arg Val
305                 310                 315                 320

Ser Ser Gly Asn Val Ser Pro Leu Gln Gly Ile Trp Ser Gly Gly Asp
                325                 330                 335

Ile Asp Ser Ala Ala Ile Ser Ser Ser Ala Asn Val Val Ala Ala Val
            340                 345                 350

Arg His Glu Asn Asn Glu Ala Val Leu Thr Val Gly Ser Met Glu Gly
        355                 360                 365

Val Thr Ser Asp Ala Leu Arg Ser Glu Thr Ile Thr Arg Pro Thr Phe
    370                 375                 380

Glu Tyr Ala Ser Ser Gly Leu Trp Ala Val Val Asp Gly Glu Thr Pro
385                 390                 395                 400

Val Arg Val Ala Arg Ser Ala Thr Thr Gly Glu Leu Val Gln Thr Glu
                405                 410                 415

Ala Glu Ile Val Leu Pro Arg Asp Val Thr Gly Pro Ile Ser Glu Phe
            420                 425                 430

Gln Leu Ser Arg Thr Gly Val Arg Ala Ala Met Ile Ile Glu Gly Lys
        435                 440                 445

Val Tyr Val Gly Val Val Thr Arg Pro Gly Pro Gly Glu Arg Arg Val
    450                 455                 460

Thr Asn Ile Thr Glu Val Ala Pro Ser Leu Gly Glu Ala Ala Leu Ser
465                 470                 475                 480

Ile Asn Trp Arg Pro Asp Gly Ile Leu Leu Val Gly Thr Ser Ile Pro
                485                 490                 495

Glu Thr Pro Leu Trp Arg Val Glu Gln Asp Gly Ser Ala Ile Ser Ser
            500                 505                 510

Met Pro Ser Gly Asn Leu Ser Ala Pro Val Val Ala Val Ala Ser Ser
        515                 520                 525

Ala Thr Thr Val Tyr Val Thr Asp Ser His Ala Met Leu Gln Leu Pro
```

```
    530                 535                 540

Thr Ala Asp Asn Asp Ile Trp Arg Glu Val Pro Gly Leu Leu Gly Thr
545                 550                 555                 560

Arg Ala Ala Pro Val Val Ala Tyr
                565


<210> 113
<211> 966
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(943)
<223> RXN00154

<400> 113
tagccagacg gcagtatttt gaagcggtga ataaacgttt gctcgaattt ccatagtgtt 60

agggaagtgt agtgcagtgc tttgactagg gtggtgagct atg agt ttt tca gac   115
                                            Met Ser Phe Ser Asp
                                              1               5

ccc tat gca ggc aat att ttt ggt gga cac tcc cgc aac aag cag ccg   163
Pro Tyr Ala Gly Asn Ile Phe Gly Gly His Ser Arg Asn Lys Gln Pro
                10                  15                  20

gag tat ccc gat gtg ccc gca aaa cca ggc ctt gtg gtg gaa gtt cgt   211
Glu Tyr Pro Asp Val Pro Ala Lys Pro Gly Leu Val Val Glu Val Arg
            25                  30                  35

gga gat ggc ttc gtc ggc gct gtg acc ggt ttt gaa cgc acc tac gat   259
Gly Asp Gly Phe Val Gly Ala Val Thr Gly Phe Glu Arg Thr Tyr Asp
        40                  45                  50

ggt gat ttt gtg cgt ctc gag gac cgc cgc gga cgc gat gcg ctg tac   307
Gly Asp Phe Val Arg Leu Glu Asp Arg Arg Gly Arg Asp Ala Leu Tyr
    55                  60                  65

aag ctg cgc aag ggt gcg ttc atg att gat ggg cag atc gtt aac ctc   355
Lys Leu Arg Lys Gly Ala Phe Met Ile Asp Gly Gln Ile Val Asn Leu
70                  75                  80                  85

acc cgt ttc gtg gaa aaa caa gca cca cgt aaa tct aat tct ggt tcc   403
Thr Arg Phe Val Glu Lys Gln Ala Pro Arg Lys Ser Asn Ser Gly Ser
                90                  95                  100

agg cgt gta gaa aac gcg caa gca aag gtc gcg gcg ccg tca cgc atc   451
Arg Arg Val Glu Asn Ala Gln Ala Lys Val Ala Ala Pro Ser Arg Ile
            105                 110                 115

tgg gta gaa ggc atc cat gac gcc gcc atc gtg gag aaa gtg tgg gga   499
Trp Val Glu Gly Ile His Asp Ala Ala Ile Val Glu Lys Val Trp Gly
        120                 125                 130

cac gac ctt cgc gtt gag ggc gtc gtg gtg gag tac ctg gaa ggt cta   547
His Asp Leu Arg Val Glu Gly Val Val Val Glu Tyr Leu Glu Gly Leu
    135                 140                 145
```

```
gac aac ctg gag gaa cgt ctc gcg gaa ttt cag cct ggg cct gga cga   595
Asp Asn Leu Glu Glu Arg Leu Ala Glu Phe Gln Pro Gly Pro Gly Arg
150                 155                 160                 165

cgc atc gga gtg ctc gct gat cac ctt gtt gag gga tct aaa gaa act   643
Arg Ile Gly Val Leu Ala Asp His Leu Val Glu Gly Ser Lys Glu Thr
                170                 175                 180

cgg atg act aaa tca cta ccc gcg gat gtc gct gtc acc ggc cac ccc   691
Arg Met Thr Lys Ser Leu Pro Ala Asp Val Ala Val Thr Gly His Pro
            185                 190                 195

tac atc gat att tgg gct gct gtg aaa cca gag cgt ttg ggg ctt aag   739
Tyr Ile Asp Ile Trp Ala Ala Val Lys Pro Glu Arg Leu Gly Leu Lys
        200                 205                 210

gcg tgg cct gag gtg cca tac ggg gag gat tgg aaa acc ggc atc tgc   787
Ala Trp Pro Glu Val Pro Tyr Gly Glu Asp Trp Lys Thr Gly Ile Cys
    215                 220                 225

aaa cga gtt ggc tgg tca gac ccc aaa gaa ggc tgg cac cgt gtg tat   835
Lys Arg Val Gly Trp Ser Asp Pro Lys Glu Gly Trp His Arg Val Tyr
230                 235                 240                 245

aac gcc gtg aat tcc ttc cgc gat ttg gac tac acc cta att ggg gca   883
Asn Ala Val Asn Ser Phe Arg Asp Leu Asp Tyr Thr Leu Ile Gly Ala
                250                 255                 260

gtg gaa cgt ttg gtg gat ttt gtg acc aac ctc gat ttg agt aaa gag   931
Val Glu Arg Leu Val Asp Phe Val Thr Asn Leu Asp Leu Ser Lys Glu
            265                 270                 275

gac gtc ctc gcc tgatttttcg ggtgtgtttt tgc                        966
Asp Val Leu Ala
        280
```

<210> 114
<211> 281
<212> PRT
<213> Corynebacterium glutamicum

<400> 114

```
Met Ser Phe Ser Asp Pro Tyr Ala Gly Asn Ile Phe Gly Gly His Ser
  1               5                  10                  15

Arg Asn Lys Gln Pro Glu Tyr Pro Asp Val Pro Ala Lys Pro Gly Leu
             20                  25                  30

Val Val Glu Val Arg Gly Asp Gly Phe Val Gly Ala Val Thr Gly Phe
         35                  40                  45

Glu Arg Thr Tyr Asp Gly Asp Phe Val Arg Leu Glu Asp Arg Arg Gly
     50                  55                  60

Arg Asp Ala Leu Tyr Lys Leu Arg Lys Gly Ala Phe Met Ile Asp Gly
 65                  70                  75                  80

Gln Ile Val Asn Leu Thr Arg Phe Val Glu Lys Gln Ala Pro Arg Lys
                 85                  90                  95
```

```
Ser Asn Ser Gly Ser Arg Arg Val Glu Asn Ala Gln Ala Lys Val Ala
            100                 105                 110

Ala Pro Ser Arg Ile Trp Val Glu Gly Ile His Asp Ala Ala Ile Val
        115                 120                 125

Glu Lys Val Trp Gly His Asp Leu Arg Val Glu Gly Val Val Val Glu
    130                 135                 140

Tyr Leu Glu Gly Leu Asp Asn Leu Glu Glu Arg Leu Ala Glu Phe Gln
145                 150                 155                 160

Pro Gly Pro Gly Arg Arg Ile Gly Val Leu Ala Asp His Leu Val Glu
                165                 170                 175

Gly Ser Lys Glu Thr Arg Met Thr Lys Ser Leu Pro Ala Asp Val Ala
            180                 185                 190

Val Thr Gly His Pro Tyr Ile Asp Ile Trp Ala Ala Val Lys Pro Glu
        195                 200                 205

Arg Leu Gly Leu Lys Ala Trp Pro Glu Val Pro Tyr Gly Glu Asp Trp
    210                 215                 220

Lys Thr Gly Ile Cys Lys Arg Val Gly Trp Ser Asp Pro Lys Glu Gly
225                 230                 235                 240

Trp His Arg Val Tyr Asn Ala Val Asn Ser Phe Arg Asp Leu Asp Tyr
                245                 250                 255

Thr Leu Ile Gly Ala Val Glu Arg Leu Val Asp Phe Val Thr Asn Leu
            260                 265                 270

Asp Leu Ser Lys Glu Asp Val Leu Ala
        275                 280


<210> 115
<211> 966
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(943)
<223> FRXA00154

<400> 115
tagccagacg gcagtatttt gaagcggtga ataaacgttt gctcgaattt ccatagtgtt 60

agggaagtgt agtgcagtgc tttgactagg gtggtgagct atg agt ttt tca gac   115
                                               Met Ser Phe Ser Asp
                                                 1               5

ccc tat gca ggc aat att ttt ggt gga cac tcc cgc aac aag cag ccg   163
Pro Tyr Ala Gly Asn Ile Phe Gly Gly His Ser Arg Asn Lys Gln Pro
                 10                  15                  20

gag tat ccc gat gtg ccc gca aaa cca ggc ctt gtg gtg gaa gtt cgt   211
Glu Tyr Pro Asp Val Pro Ala Lys Pro Gly Leu Val Val Glu Val Arg
```

```
                25                  30                  35

gga gat ggc ttc gtc ggc gct gtg acc ggt ttt gaa cgc acc tac gat   259
Gly Asp Gly Phe Val Gly Ala Val Thr Gly Phe Glu Arg Thr Tyr Asp
        40                  45                  50

ggt gat ttt gtg cgt ctc gag gac cgc cgc gga cgc gat gcg ctg tac   307
Gly Asp Phe Val Arg Leu Glu Asp Arg Arg Gly Arg Asp Ala Leu Tyr
    55                  60                  65

aag ctg cgc aag ggt gcg ttc atg att gat ggg cag atc gtt aac ctc   355
Lys Leu Arg Lys Gly Ala Phe Met Ile Asp Gly Gln Ile Val Asn Leu
70                  75                  80                  85

acc cgt ttc gtg gaa aaa caa gca cca cgt aaa tct aat tct ggt tcc   403
Thr Arg Phe Val Glu Lys Gln Ala Pro Arg Lys Ser Asn Ser Gly Ser
                90                  95                  100

agg cgt gta gaa aac gcg caa gca aag gtc gcg gcg ccg tca cgc atc   451
Arg Arg Val Glu Asn Ala Gln Ala Lys Val Ala Ala Pro Ser Arg Ile
            105                 110                 115

tgg gta gaa ggc atc cat gac gcc gcc atc gtg gag aaa gtg tgg gga   499
Trp Val Glu Gly Ile His Asp Ala Ala Ile Val Glu Lys Val Trp Gly
        120                 125                 130

cac gac ctt cgc gtt gag ggc gtc gtg gtg gag tac ctg gaa ggt cta   547
His Asp Leu Arg Val Glu Gly Val Val Val Glu Tyr Leu Glu Gly Leu
    135                 140                 145

gac aac ctg gag gaa cgt ctc gcg gaa ttt cag cct ggg cct gga cga   595
Asp Asn Leu Glu Glu Arg Leu Ala Glu Phe Gln Pro Gly Pro Gly Arg
150                 155                 160                 165

cgc atc gga gtg ctc gct gat cac ctt gtt gag gga tct aaa gaa act   643
Arg Ile Gly Val Leu Ala Asp His Leu Val Glu Gly Ser Lys Glu Thr
                170                 175                 180

cgg atg act aaa tca cta ccc gcg gat gtc gct gtc acc ggc cac ccc   691
Arg Met Thr Lys Ser Leu Pro Ala Asp Val Ala Val Thr Gly His Pro
            185                 190                 195

tac atc gat att tgg gct gct gtg aaa cca gag cgt ttg ggg ctt aag   739
Tyr Ile Asp Ile Trp Ala Ala Val Lys Pro Glu Arg Leu Gly Leu Lys
        200                 205                 210

gcg tgg cct gag gtg cca tac ggg gag gat tgg aaa acc ggc atc tgc   787
Ala Trp Pro Glu Val Pro Tyr Gly Glu Asp Trp Lys Thr Gly Ile Cys
    215                 220                 225

aaa cga gtt ggc tgg tca gac ccc aaa gaa ggc tgg cac cgt gtg tat   835
Lys Arg Val Gly Trp Ser Asp Pro Lys Glu Gly Trp His Arg Val Tyr
230                 235                 240                 245

aac gcc gtg aat tcc ttc cgc gat ttg gac tac acc cta att ggg gca   883
Asn Ala Val Asn Ser Phe Arg Asp Leu Asp Tyr Thr Leu Ile Gly Ala
                250                 255                 260

gtg gaa cgt ttg gtg gat ttt gtg acc aac ctc gat ttg agt aaa gag   931
Val Glu Arg Leu Val Asp Phe Val Thr Asn Leu Asp Leu Ser Lys Glu
            265                 270                 275
```

gac gtc ctc gcc tgatttttcg ggtgtgtttt tgc 966
Asp Val Leu Ala
280

<210> 116
<211> 281
<212> PRT
<213> Corynebacterium glutamicum

<400> 116
Met Ser Phe Ser Asp Pro Tyr Ala Gly Asn Ile Phe Gly Gly His Ser
1 5 10 15

Arg Asn Lys Gln Pro Glu Tyr Pro Asp Val Pro Ala Lys Pro Gly Leu
20 25 30

Val Val Glu Val Arg Gly Asp Gly Phe Val Gly Ala Val Thr Gly Phe
35 40 45

Glu Arg Thr Tyr Asp Gly Asp Phe Val Arg Leu Glu Asp Arg Arg Gly
50 55 60

Arg Asp Ala Leu Tyr Lys Leu Arg Lys Gly Ala Phe Met Ile Asp Gly
65 70 75 80

Gln Ile Val Asn Leu Thr Arg Phe Val Glu Lys Gln Ala Pro Arg Lys
85 90 95

Ser Asn Ser Gly Ser Arg Arg Val Glu Asn Ala Gln Ala Lys Val Ala
100 105 110

Ala Pro Ser Arg Ile Trp Val Glu Gly Ile His Asp Ala Ala Ile Val
115 120 125

Glu Lys Val Trp Gly His Asp Leu Arg Val Glu Gly Val Val Val Glu
130 135 140

Tyr Leu Glu Gly Leu Asp Asn Leu Glu Glu Arg Leu Ala Glu Phe Gln
145 150 155 160

Pro Gly Pro Gly Arg Arg Ile Gly Val Leu Ala Asp His Leu Val Glu
165 170 175

Gly Ser Lys Glu Thr Arg Met Thr Lys Ser Leu Pro Ala Asp Val Ala
180 185 190

Val Thr Gly His Pro Tyr Ile Asp Ile Trp Ala Ala Val Lys Pro Glu
195 200 205

Arg Leu Gly Leu Lys Ala Trp Pro Glu Val Pro Tyr Gly Glu Asp Trp
210 215 220

Lys Thr Gly Ile Cys Lys Arg Val Gly Trp Ser Asp Pro Lys Glu Gly
225 230 235 240

Trp His Arg Val Tyr Asn Ala Val Asn Ser Phe Arg Asp Leu Asp Tyr
245 250 255

Thr Leu Ile Gly Ala Val Glu Arg Leu Val Asp Phe Val Thr Asn Leu

```
            260                 265                 270

Asp Leu Ser Lys Glu Asp Val Leu Ala
        275                 280


<210> 117
<211> 477
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(454)
<223> RXN00162

<400> 117
ggagacgtcg aaaagcataa acctggaact tttccgggcc cgcgcccgac tgctttgctg 60

aagccctatc ccgctatttt atttttgaag gaagagttgc gtg tct acc acc acc   115
                                        Val Ser Thr Thr Thr
                                          1               5

cca atc cac cct gag cgc aag aaa cgc gtt cgt cag gcc ctc acc atg   163
Pro Ile His Pro Glu Arg Lys Lys Arg Val Arg Gln Ala Leu Thr Met
                10                  15                  20

ttc tcc atc gct gcg tgg gtg act ggt gtg ttt ttg ctg gcg ctg gtg   211
Phe Ser Ile Ala Ala Trp Val Thr Gly Val Phe Leu Leu Ala Leu Val
            25                  30                  35

gcg gag atg atc atg aag tac ata att ggc atg gat ctt cct gag tgg   259
Ala Glu Met Ile Met Lys Tyr Ile Ile Gly Met Asp Leu Pro Glu Trp
        40                  45                  50

gca cga ttc gtt ccg att gca cat gga tgg gtt tac att gtt ttc ttg   307
Ala Arg Phe Val Pro Ile Ala His Gly Trp Val Tyr Ile Val Phe Leu
    55                  60                  65

atg acc acc ctg aac ctg ggt ctg aag gcg cgt tgg aat ccg act cgt   355
Met Thr Thr Leu Asn Leu Gly Leu Lys Ala Arg Trp Asn Pro Thr Arg
70                  75                  80                  85

tgg gtg acc acc gct atc gca ggt gtg gtt ccg ctg ctg tcg ttt ttt   403
Trp Val Thr Thr Ala Ile Ala Gly Val Val Pro Leu Leu Ser Phe Phe
                90                  95                  100

gtt gag cac aac cgc cgc aag gaa gtt act cag aca ttc cag ctg aac   451
Val Glu His Asn Arg Arg Lys Glu Val Thr Gln Thr Phe Gln Leu Asn
            105                 110                 115

tca tagttaaata cacaaaaacc tcc                                    477
Ser



<210> 118
<211> 118
<212> PRT
<213> Corynebacterium glutamicum
```

<400> 118
Val Ser Thr Thr Thr Pro Ile His Pro Glu Arg Lys Lys Arg Val Arg
1 5 10 15

Gln Ala Leu Thr Met Phe Ser Ile Ala Ala Trp Val Thr Gly Val Phe
20 25 30

Leu Leu Ala Leu Val Ala Glu Met Ile Met Lys Tyr Ile Ile Gly Met
35 40 45

Asp Leu Pro Glu Trp Ala Arg Phe Val Pro Ile Ala His Gly Trp Val
50 55 60

Tyr Ile Val Phe Leu Met Thr Thr Leu Asn Leu Gly Leu Lys Ala Arg
65 70 75 80

Trp Asn Pro Thr Arg Trp Val Thr Thr Ala Ile Ala Gly Val Val Pro
85 90 95

Leu Leu Ser Phe Phe Val Glu His Asn Arg Arg Lys Glu Val Thr Gln
100 105 110

Thr Phe Gln Leu Asn Ser
115

<210> 119
<211> 477
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(454)
<223> FRXA00162

<400> 119
ggagacgtcg aaaagcataa acctggaact tttccgggcc cgcgcccgac tgctttgctg 60

aagccctatc ccgctatttt atttttgaag gaagagttgc gtg tct acc acc acc 115
Val Ser Thr Thr Thr
1 5

cca atc cac cct gag cgc aag aaa cgc gtt cgt cag gcc ctc acc atg 163
Pro Ile His Pro Glu Arg Lys Lys Arg Val Arg Gln Ala Leu Thr Met
10 15 20

ttc tcc atc gct gcg tgg gtg act ggt gtg ttt ttg ctg gcg ctg gtg 211
Phe Ser Ile Ala Ala Trp Val Thr Gly Val Phe Leu Leu Ala Leu Val
25 30 35

gcg gag atg atc atg aag tac ata att ggc atg gat ctt cct gag tgg 259
Ala Glu Met Ile Met Lys Tyr Ile Ile Gly Met Asp Leu Pro Glu Trp
40 45 50

gca cga ttc gtt ccg att gca cat gga tgg gtt tac att gtt ttc ttg 307
Ala Arg Phe Val Pro Ile Ala His Gly Trp Val Tyr Ile Val Phe Leu
55 60 65

atg acc acc ctg aac ctg ggt ctg aag gcg cgt tgg aat ccg act cgt 355
Met Thr Thr Leu Asn Leu Gly Leu Lys Ala Arg Trp Asn Pro Thr Arg

```
 70                  75                  80                  85

tgg gtg acc acc gct atc gca ggt gtg gtt ccg ctg ctg tcg ttt ttt   403
Trp Val Thr Thr Ala Ile Ala Gly Val Val Pro Leu Leu Ser Phe Phe
                 90                  95                 100

gtt gag cac aac cgc cgc aag gaa gtt act cag aca ttc cag ctg aac   451
Val Glu His Asn Arg Arg Lys Glu Val Thr Gln Thr Phe Gln Leu Asn
            105                 110                 115

tca tagttaaata cacaaaaacc tcc                                    477
Ser
```

<210> 120
<211> 118
<212> PRT
<213> Corynebacterium glutamicum

<400> 120

```
Val Ser Thr Thr Thr Pro Ile His Pro Glu Arg Lys Lys Arg Val Arg
  1               5                  10                  15

Gln Ala Leu Thr Met Phe Ser Ile Ala Ala Trp Val Thr Gly Val Phe
             20                  25                  30

Leu Leu Ala Leu Val Ala Glu Met Ile Met Lys Tyr Ile Ile Gly Met
         35                  40                  45

Asp Leu Pro Glu Trp Ala Arg Phe Val Pro Ile Ala His Gly Trp Val
     50                  55                  60

Tyr Ile Val Phe Leu Met Thr Thr Leu Asn Leu Gly Leu Lys Ala Arg
 65                  70                  75                  80

Trp Asn Pro Thr Arg Trp Val Thr Thr Ala Ile Ala Gly Val Val Pro
                 85                  90                  95

Leu Leu Ser Phe Phe Val Glu His Asn Arg Arg Lys Glu Val Thr Gln
            100                 105                 110

Thr Phe Gln Leu Asn Ser
        115
```

<210> 121
<211> 621
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(598)
<223> RXN00167

<400> 121

```
ccgacaatcc agtggaactt ccctatcgct gtgatgcatt tttactttca cgttccggta 60

ccctggcagg cagatcttcc aatctttagg agccctcgcc atg tac ctg ttg aat   115
                                               Met Tyr Leu Leu Asn
```

```
                                                    1               5

cca cca gtc act gaa ccc gag atc ctc act gtc aac gag att ccg acc   163
Pro Pro Val Thr Glu Pro Glu Ile Leu Thr Val Asn Glu Ile Pro Thr
                10                  15                  20

gtc gtc gct gtc ttt gac aac cac ccc atg aac gac atg ccc gca gca   211
Val Val Ala Val Phe Asp Asn His Pro Met Asn Asp Met Pro Ala Ala
            25                  30                  35

ttc gat caa acc tac caa gtg ctc ttc ccc acc ttg ggt gcc aag ggc   259
Phe Asp Gln Thr Tyr Gln Val Leu Phe Pro Thr Leu Gly Ala Lys Gly
        40                  45                  50

atc gcg cca att ggc ccc gga ttt gct ctg tac acc tcc gaa cca act   307
Ile Ala Pro Ile Gly Pro Gly Phe Ala Leu Tyr Thr Ser Glu Pro Thr
    55                  60                  65

gac acc gtc agc ttt gaa gtg ggc atc cca gtc agc caa cca ctt gag   355
Asp Thr Val Ser Phe Glu Val Gly Ile Pro Val Ser Gln Pro Leu Glu
70                  75                  80                  85

gga gat gtt tca gcc gcc agc ggc atc gtg ctg aaa aac tca gtg gtc   403
Gly Asp Val Ser Ala Ala Ser Gly Ile Val Leu Lys Asn Ser Val Val
                90                  95                  100

cct gcc gga aaa att gcg cga atc agc cac atc ggc tca ttc gac gga   451
Pro Ala Gly Lys Ile Ala Arg Ile Ser His Ile Gly Ser Phe Asp Gly
            105                 110                 115

ctg agc caa gca tgg ggt tca ttc gtg gaa gct ctt gaa tct gca ggc   499
Leu Ser Gln Ala Trp Gly Ser Phe Val Glu Ala Leu Glu Ser Ala Gly
        120                 125                 130

cat gag atc gat atg ccg tgt tgg gag gta tat gtc acc gag cct tcc   547
His Glu Ile Asp Met Pro Cys Trp Glu Val Tyr Val Thr Glu Pro Ser
    135                 140                 145

ccc gac atg gat ccc gca aca ctc caa act gat cta tac gtc ctg ttg   595
Pro Asp Met Asp Pro Ala Thr Leu Gln Thr Asp Leu Tyr Val Leu Leu
150                 155                 160                 165

aag tagagaagct ttctggtcaa gtt                                    621
Lys
```

<210> 122
<211> 166
<212> PRT
<213> Corynebacterium glutamicum

<400> 122

```
Met Tyr Leu Leu Asn Pro Pro Val Thr Glu Pro Glu Ile Leu Thr Val
  1               5                  10                  15

Asn Glu Ile Pro Thr Val Val Ala Val Phe Asp Asn His Pro Met Asn
            20                  25                  30

Asp Met Pro Ala Ala Phe Asp Gln Thr Tyr Gln Val Leu Phe Pro Thr
        35                  40                  45
```

```
Leu Gly Ala Lys Gly Ile Ala Pro Ile Gly Pro Gly Phe Ala Leu Tyr
     50                  55                  60

Thr Ser Glu Pro Thr Asp Thr Val Ser Phe Glu Val Gly Ile Pro Val
 65                  70                  75                  80

Ser Gln Pro Leu Glu Gly Asp Val Ser Ala Ala Ser Gly Ile Val Leu
                 85                  90                  95

Lys Asn Ser Val Val Pro Ala Gly Lys Ile Ala Arg Ile Ser His Ile
            100                 105                 110

Gly Ser Phe Asp Gly Leu Ser Gln Ala Trp Gly Ser Phe Val Glu Ala
        115                 120                 125

Leu Glu Ser Ala Gly His Glu Ile Asp Met Pro Cys Trp Glu Val Tyr
    130                 135                 140

Val Thr Glu Pro Ser Pro Asp Met Asp Pro Ala Thr Leu Gln Thr Asp
145                 150                 155                 160

Leu Tyr Val Leu Leu Lys
                165
```

Do not delete, alter, or write over this page

<210> 123
<211> 361
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(361)
<223> FRXA00167

<400> 123

```
ccgacaatcc agtggaactt ccctatcgct gtgatgcatt tttactttca cgttccggta 60

ccctggcagg cagatcttcc aatctttagg agccctcgcc atg tac ctg ttg aat   115
                                              Met Tyr Leu Leu Asn
                                                1               5

cca cca gtc act gaa ccc gag atc ctc act gtc aac gag att ccg acc   163
Pro Pro Val Thr Glu Pro Glu Ile Leu Thr Val Asn Glu Ile Pro Thr
                10                  15                  20

gtc gtc gct gtc ttt gac aac cac ccc atg aac gac atg ccc gca gca   211
Val Val Ala Val Phe Asp Asn His Pro Met Asn Asp Met Pro Ala Ala
            25                  30                  35

ttc gat caa acc tac caa gtg ctc ttc ccc acc ttg ggt gcc aag ggc   259
Phe Asp Gln Thr Tyr Gln Val Leu Phe Pro Thr Leu Gly Ala Lys Gly
        40                  45                  50

atc gcg cca att ggc ccc gga ttt gct ctg tac acc tcc gaa cca act   307
Ile Ala Pro Ile Gly Pro Gly Phe Ala Leu Tyr Thr Ser Glu Pro Thr
    55                  60                  65

gac acc gtc agc ttt gaa gtg ggc atg cca gtc agc caa cca ctt gag   355
Asp Thr Val Ser Phe Glu Val Gly Met Pro Val Ser Gln Pro Leu Glu
```

```
 70                  75                  80                  85

gga gag                                                          361
Gly Glu
```

<210> 124
<211> 87
<212> PRT
<213> Corynebacterium glutamicum

<400> 124

```
Met Tyr Leu Leu Asn Pro Pro Val Thr Glu Pro Glu Ile Leu Thr Val
  1               5                  10                  15

Asn Glu Ile Pro Thr Val Val Ala Val Phe Asp Asn His Pro Met Asn
             20                  25                  30

Asp Met Pro Ala Ala Phe Asp Gln Thr Tyr Gln Val Leu Phe Pro Thr
         35                  40                  45

Leu Gly Ala Lys Gly Ile Ala Pro Ile Gly Pro Gly Phe Ala Leu Tyr
     50                  55                  60

Thr Ser Glu Pro Thr Asp Thr Val Ser Phe Glu Val Gly Met Pro Val
 65                  70                  75                  80

Ser Gln Pro Leu Glu Gly Glu
                 85
```

<210> 125
<211> 281
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(258)
<223> RXN00171

<400> 125

```
aaa gat cag cag aag cag att cat aac ttg gca gct gag gta aag cgt   48
Lys Asp Gln Gln Lys Gln Ile His Asn Leu Ala Ala Glu Val Lys Arg
  1               5                  10                  15

ctt cgt gag cgt gac gat gca cga gat cag cag cta gga gtg ctt aat   96
Leu Arg Glu Arg Asp Asp Ala Arg Asp Gln Gln Leu Gly Val Leu Asn
             20                  25                  30

gaa gcc atg ttt tca cta cta gga gat gga ctt gac cgt ttt cgt gaa  144
Glu Ala Met Phe Ser Leu Leu Gly Asp Gly Leu Asp Arg Phe Arg Glu
         35                  40                  45

tct ggc gat gag gca tcc ttc aat gct gca ttg aac tat cag gca gtg  192
Ser Gly Asp Glu Ala Ser Phe Asn Ala Ala Leu Asn Tyr Gln Ala Val
     50                  55                  60

gtg gca cca gaa atg ttt aag acc gtg tat ggt gtc gat ccg tct acc  240
Val Ala Pro Glu Met Phe Lys Thr Val Tyr Gly Val Asp Pro Ser Thr
```

```
 65                  70                  75                  80

gga gag cct att ccc act taaagtacaa cacagtcttt tca                 281
Gly Glu Pro Ile Pro Thr
                85


<210> 126
<211> 86
<212> PRT
<213> Corynebacterium glutamicum

<400> 126
Lys Asp Gln Gln Lys Gln Ile His Asn Leu Ala Ala Glu Val Lys Arg
  1               5                  10                  15

Leu Arg Glu Arg Asp Asp Ala Arg Asp Gln Gln Leu Gly Val Leu Asn
            20                  25                  30

Glu Ala Met Phe Ser Leu Leu Gly Asp Gly Leu Asp Arg Phe Arg Glu
        35                  40                  45

Ser Gly Asp Glu Ala Ser Phe Asn Ala Ala Leu Asn Tyr Gln Ala Val
    50                  55                  60

Val Ala Pro Glu Met Phe Lys Thr Val Tyr Gly Val Asp Pro Ser Thr
 65                  70                  75                  80

Gly Glu Pro Ile Pro Thr
                85


<210> 127
<211> 354
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(331)
<223> FRXA00171

<400> 127
cgattaaggt aggggcctta aaaaggggaa taaagaatat tgggcccaga cgaaaactgc  60

tggcgagatc atcaaagatc agcagaagca gattcataac ttg gca gct gag gta    115
                                            Leu Ala Ala Glu Val
                                              1               5

aag cgt ctt cgt gag cgt gac gat gca cga gat cag cag cta gga gtg    163
Lys Arg Leu Arg Glu Arg Asp Asp Ala Arg Asp Gln Gln Leu Gly Val
                10                  15                  20

ctt aat gaa gcc atg ttt tca cta cta gga gat gga ctt gac cgt ttt    211
Leu Asn Glu Ala Met Phe Ser Leu Leu Gly Asp Gly Leu Asp Arg Phe
            25                  30                  35

cgt gaa tct ggc gat gag gca tcc ttc aat gct gca ttg aac tat cag    259
Arg Glu Ser Gly Asp Glu Ala Ser Phe Asn Ala Ala Leu Asn Tyr Gln
        40                  45                  50
```

```
gca gtg gtg gca cca gaa atg ttt aag acc gtg tat ggt gtc gat ccg   307
Ala Val Val Ala Pro Glu Met Phe Lys Thr Val Tyr Gly Val Asp Pro
     55                  60                  65

tct acc gga gag cct att ccc act taaagtacaa cacagtcttt tca        354
Ser Thr Gly Glu Pro Ile Pro Thr
 70                  75


<210> 128
<211> 77
<212> PRT
<213> Corynebacterium glutamicum

<400> 128
Leu Ala Ala Glu Val Lys Arg Leu Arg Glu Arg Asp Asp Ala Arg Asp
  1               5                  10                  15

Gln Gln Leu Gly Val Leu Asn Glu Ala Met Phe Ser Leu Leu Gly Asp
             20                  25                  30

Gly Leu Asp Arg Phe Arg Glu Ser Gly Asp Glu Ala Ser Phe Asn Ala
         35                  40                  45

Ala Leu Asn Tyr Gln Ala Val Val Ala Pro Glu Met Phe Lys Thr Val
     50                  55                  60

Tyr Gly Val Asp Pro Ser Thr Gly Glu Pro Ile Pro Thr
 65                  70                  75


<210> 129
<211> 564
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(541)
<223> RXN00194

<400> 129
aaatatgaga acatagtgag agttaaacca agttctgtag gtgcttgttg cagcgggcgc 60

gaaggcgtac cactgcaact tgcgaataaa ggagtaaaac gtg gct ggt tcc tcc   115
                                          Val Ala Gly Ser Ser
                                            1               5

cac acg att gag cct gag atc tac cgc ggt gta tcc acc ctt gat gag   163
His Thr Ile Glu Pro Glu Ile Tyr Arg Gly Val Ser Thr Leu Asp Glu
                10                  15                  20

cct tcg gct gca tgg gga tgg cac ggt ctc aag cgc aac acc atc caa   211
Pro Ser Ala Ala Trp Gly Trp His Gly Leu Lys Arg Asn Thr Ile Gln
             25                  30                  35

ctc gct ggc tgg att tcc gtt ctg ttc atg ctt gga tac aac ttc ggt   259
Leu Ala Gly Trp Ile Ser Val Leu Phe Met Leu Gly Tyr Asn Phe Gly
         40                  45                  50

aac cac aag ggc cac gtt gaa acc atc tgg ctt ctc gtc atc acc gcc   307
```

```
Asn His Lys Gly His Val Glu Thr Ile Trp Leu Leu Val Ile Thr Ala
     55                  60                  65

ctt ctg gtc atc ggc ctg ctg atc cac ctg ttc gag cca aag ctc ttc   355
Leu Leu Val Ile Gly Leu Leu Ile His Leu Phe Glu Pro Lys Leu Phe
 70                  75                  80                  85

cag gtt cgc acc atc act tcc cgc aac aag cct gtc ggc cac gtc gag   403
Gln Val Arg Thr Ile Thr Ser Arg Asn Lys Pro Val Gly His Val Glu
                90                  95                 100

cca gac tgg acc tac gac cag gca acc ctc acc ggc acc tgg ggt aac   451
Pro Asp Trp Thr Tyr Asp Gln Ala Thr Leu Thr Gly Thr Trp Gly Asn
            105                 110                 115

ctc act gac tcc cag ctt cgc tcc gtc aac atc gag cca agc cgt gtc   499
Leu Thr Asp Ser Gln Leu Arg Ser Val Asn Ile Glu Pro Ser Arg Val
        120                 125                 130

gct cac ctg cgt gct gca gat tct gcg aaa gaa cta gac aac           541
Ala His Leu Arg Ala Ala Asp Ser Ala Lys Glu Leu Asp Asn
    135                 140                 145

tagtttttta aaaagaaaat gcg                                        564


<210> 130
<211> 147
<212> PRT
<213> Corynebacterium glutamicum

<400> 130
Val Ala Gly Ser Ser His Thr Ile Glu Pro Glu Ile Tyr Arg Gly Val
  1               5                  10                  15

Ser Thr Leu Asp Glu Pro Ser Ala Ala Trp Gly Trp His Gly Leu Lys
             20                  25                  30

Arg Asn Thr Ile Gln Leu Ala Gly Trp Ile Ser Val Leu Phe Met Leu
         35                  40                  45

Gly Tyr Asn Phe Gly Asn His Lys Gly His Val Glu Thr Ile Trp Leu
     50                  55                  60

Leu Val Ile Thr Ala Leu Leu Val Ile Gly Leu Leu Ile His Leu Phe
 65                  70                  75                  80

Glu Pro Lys Leu Phe Gln Val Arg Thr Ile Thr Ser Arg Asn Lys Pro
                85                  90                  95

Val Gly His Val Glu Pro Asp Trp Thr Tyr Asp Gln Ala Thr Leu Thr
            100                 105                 110

Gly Thr Trp Gly Asn Leu Thr Asp Ser Gln Leu Arg Ser Val Asn Ile
        115                 120                 125

Glu Pro Ser Arg Val Ala His Leu Arg Ala Ala Asp Ser Ala Lys Glu
    130                 135                 140

Leu Asp Asn
145
```

<210> 131
<211> 385
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(385)
<223> FRXA00194

<400> 131
aaatatgaga acatagtgag agttaaacca agttctgtag gtgcttgttg cagcgggcgc 60

gaaggcgtac cactgcaact tgcgaataaa ggagtaaaac gtg gct ggt tcc tcc 115
Val Ala Gly Ser Ser
1 5

cac acg att gag cct gag atc tac cgc ggt gta tcc acc ctt gat gag 163
His Thr Ile Glu Pro Glu Ile Tyr Arg Gly Val Ser Thr Leu Asp Glu
10 15 20

cct tcg gct gca tgg gga tgg cac ggt ctc aag cgc aac acc atc caa 211
Pro Ser Ala Ala Trp Gly Trp His Gly Leu Lys Arg Asn Thr Ile Gln
25 30 35

ctc gct ggc tgg att tcc gtt ctg ttc atg ctt gga tac aac ttc ggt 259
Leu Ala Gly Trp Ile Ser Val Leu Phe Met Leu Gly Tyr Asn Phe Gly
40 45 50

aac cac aag ggc cac gtt gaa acc atc tgg ctt ctc gtc atc acc gcc 307
Asn His Lys Gly His Val Glu Thr Ile Trp Leu Leu Val Ile Thr Ala
55 60 65

ctt ctg gtc atc ggc ctg ctg atc cac ctg ttc gag cca aaa gct ctt 355
Leu Leu Val Ile Gly Leu Leu Ile His Leu Phe Glu Pro Lys Ala Leu
70 75 80 85

cca ggt tcg cac cat cac ttc tcg caa caa 385
Pro Gly Ser His His His Phe Ser Gln Gln
90 95

<210> 132
<211> 95
<212> PRT
<213> Corynebacterium glutamicum

<400> 132
Val Ala Gly Ser Ser His Thr Ile Glu Pro Glu Ile Tyr Arg Gly Val
1 5 10 15

Ser Thr Leu Asp Glu Pro Ser Ala Ala Trp Gly Trp His Gly Leu Lys
20 25 30

Arg Asn Thr Ile Gln Leu Ala Gly Trp Ile Ser Val Leu Phe Met Leu
35 40 45

Gly Tyr Asn Phe Gly Asn His Lys Gly His Val Glu Thr Ile Trp Leu
50 55 60

```
Leu Val Ile Thr Ala Leu Leu Val Ile Gly Leu Leu Ile His Leu Phe
 65                  70                  75                  80

Glu Pro Lys Ala Leu Pro Gly Ser His His His Phe Ser Gln Gln
                 85                  90                  95


<210> 133
<211> 1335
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1312)
<223> RXN00197

<400> 133
gtcgatgata ttttggcaac cgaatctgag gcacgcgcgc gtgcgaatgc tttgatcaac 60

cggttggcaa ccaacttgta agctaaggag cttccgcctc gtg gca gcc tat ctt   115
                                              Val Ala Ala Tyr Leu
                                                1               5

ctt ggt gtc gta tta ttt ttc ctc ggc atc gca gta acc atc gcg ctt   163
Leu Gly Val Val Leu Phe Phe Leu Gly Ile Ala Val Thr Ile Ala Leu
                10                  15                  20

cac gag tgg ggg cac ttc atc aca gcg cgc att ttc gga atg aaa gtg   211
His Glu Trp Gly His Phe Ile Thr Ala Arg Ile Phe Gly Met Lys Val
            25                  30                  35

cgg cgt ttc ttc atc ggt ttc ggc ccg acg gtg ttt gcc aaa aga cgc   259
Arg Arg Phe Phe Ile Gly Phe Gly Pro Thr Val Phe Ala Lys Arg Arg
        40                  45                  50

ggc gaa acc gtg tac ggc ctt aaa gcg att ccg gtc ggc ggt ttt tgt   307
Gly Glu Thr Val Tyr Gly Leu Lys Ala Ile Pro Val Gly Gly Phe Cys
    55                  60                  65

gac atc gcg ggg atg act gcc caa gat gaa ctt gat ccg gaa gac ctg   355
Asp Ile Ala Gly Met Thr Ala Gln Asp Glu Leu Asp Pro Glu Asp Leu
70                  75                  80                  85

ccg cgc gcc atg tat cta aag ccc tgg tgg cag cgc ata att gtg ctt   403
Pro Arg Ala Met Tyr Leu Lys Pro Trp Trp Gln Arg Ile Ile Val Leu
                90                  95                 100

tcc ggc ggc gtg atc atg aat ctg atc gtc ggc ttt ttg gtg ctt tac   451
Ser Gly Gly Val Ile Met Asn Leu Ile Val Gly Phe Leu Val Leu Tyr
            105                 110                 115

ggc gtg gcg gtg agc tcc gga atc ccg aat ccg gat gtg gat acc acc   499
Gly Val Ala Val Ser Ser Gly Ile Pro Asn Pro Asp Val Asp Thr Thr
        120                 125                 130

gcg aca gtc gac acc gtt cag tgc gtg ccg gaa acc caa att tcc gca   547
Ala Thr Val Asp Thr Val Gln Cys Val Pro Glu Thr Gln Ile Ser Ala
    135                 140                 145
```

```
act gaa ctg tcc tcc tgc gta ggt tca ggc cca gcg ggc gac gcc ggc   595
Thr Glu Leu Ser Ser Cys Val Gly Ser Gly Pro Ala Gly Asp Ala Gly
150                 155                 160                 165

att gag cac ggc gat aag att ttg gcc gtc aac ggc caa gag atg gca   643
Ile Glu His Gly Asp Lys Ile Leu Ala Val Asn Gly Gln Glu Met Ala
                170                 175                 180

agc ttc acc gcc atc cgc gat gcg atc ctc gag ctc cca ggc gaa acg   691
Ser Phe Thr Ala Ile Arg Asp Ala Ile Leu Glu Leu Pro Gly Glu Thr
            185                 190                 195

gca acg ctg acg att gaa cgg gag gga acg ctt ttc gac gtc gac ctc   739
Ala Thr Leu Thr Ile Glu Arg Glu Gly Thr Leu Phe Asp Val Asp Leu
        200                 205                 210

cag gtt gcc tct gtc acc cgt ctc gcc tct gac ggt tca gaa att acc   787
Gln Val Ala Ser Val Thr Arg Leu Ala Ser Asp Gly Ser Glu Ile Thr
    215                 220                 225

gtc ggc gcg gtg ggc atg tcg agc ctt cca ccg acc gat gtg tac aaa   835
Val Gly Ala Val Gly Met Ser Ser Leu Pro Pro Thr Asp Val Tyr Lys
230                 235                 240                 245

aaa tac ggc cca atc gag ggt gtg gga gca act gca cgt ttc acc ggc   883
Lys Tyr Gly Pro Ile Glu Gly Val Gly Ala Thr Ala Arg Phe Thr Gly
                250                 255                 260

gac atg atc agc gcc acg tgg gat ggc ctc aaa gcc ttc ccg gcg aaa   931
Asp Met Ile Ser Ala Thr Trp Asp Gly Leu Lys Ala Phe Pro Ala Lys
            265                 270                 275

atc cca ggg gtc gtc gca tcc atc ttc ggt gca gaa cga gat gta gaa   979
Ile Pro Gly Val Val Ala Ser Ile Phe Gly Ala Glu Arg Asp Val Glu
        280                 285                 290

agc ccc atg agt gtg gtg ggc gcc gta cgc atc ggc ggc gaa ttt gtc   1027
Ser Pro Met Ser Val Val Gly Ala Val Arg Ile Gly Gly Glu Phe Val
    295                 300                 305

gaa cgt tcc atg tgg gac atg ttc atg atg atg ctg gcc agc ctg aac   1075
Glu Arg Ser Met Trp Asp Met Phe Met Met Met Leu Ala Ser Leu Asn
310                 315                 320                 325

ttc ttc ctc gcg ctg ttt aac ctc gtg ccg ctg cca cca ctt gat ggc   1123
Phe Phe Leu Ala Leu Phe Asn Leu Val Pro Leu Pro Pro Leu Asp Gly
                330                 335                 340

gga cac att gcc gtg gtg atc tat gaa aaa atc cgc gac ttc ttc cgc   1171
Gly His Ile Ala Val Val Ile Tyr Glu Lys Ile Arg Asp Phe Phe Arg
            345                 350                 355

aaa ctg cgc gga aaa cca gcg ggc ggc cca gcg gat tac acc aaa cta   1219
Lys Leu Arg Gly Lys Pro Ala Gly Gly Pro Ala Asp Tyr Thr Lys Leu
        360                 365                 370

atg ccc gtc acc gta gct gtc gca gcc ttg ctg atg aca gtg gga ggc   1267
Met Pro Val Thr Val Ala Val Ala Ala Leu Leu Met Thr Val Gly Gly
    375                 380                 385

ctg gtc att gtc gcc gat gtg gtc aat ccc atc cga ctc ttt ggc       1312
```

Leu Val Ile Val Ala Asp Val Val Asn Pro Ile Arg Leu Phe Gly
390 395 400

taacgatacg gaattgaact gcc 1335

<210> 134
<211> 404
<212> PRT
<213> Corynebacterium glutamicum

<400> 134
Val Ala Ala Tyr Leu Leu Gly Val Val Leu Phe Phe Leu Gly Ile Ala
1 5 10 15

Val Thr Ile Ala Leu His Glu Trp Gly His Phe Ile Thr Ala Arg Ile
20 25 30

Phe Gly Met Lys Val Arg Arg Phe Phe Ile Gly Phe Gly Pro Thr Val
35 40 45

Phe Ala Lys Arg Arg Gly Glu Thr Val Tyr Gly Leu Lys Ala Ile Pro
50 55 60

Val Gly Gly Phe Cys Asp Ile Ala Gly Met Thr Ala Gln Asp Glu Leu
65 70 75 80

Asp Pro Glu Asp Leu Pro Arg Ala Met Tyr Leu Lys Pro Trp Trp Gln
85 90 95

Arg Ile Ile Val Leu Ser Gly Gly Val Ile Met Asn Leu Ile Val Gly
100 105 110

Phe Leu Val Leu Tyr Gly Val Ala Val Ser Ser Gly Ile Pro Asn Pro
115 120 125

Asp Val Asp Thr Thr Ala Thr Val Asp Thr Val Gln Cys Val Pro Glu
130 135 140

Thr Gln Ile Ser Ala Thr Glu Leu Ser Ser Cys Val Gly Ser Gly Pro
145 150 155 160

Ala Gly Asp Ala Gly Ile Glu His Gly Asp Lys Ile Leu Ala Val Asn
165 170 175

Gly Gln Glu Met Ala Ser Phe Thr Ala Ile Arg Asp Ala Ile Leu Glu
180 185 190

Leu Pro Gly Glu Thr Ala Thr Leu Thr Ile Glu Arg Glu Gly Thr Leu
195 200 205

Phe Asp Val Asp Leu Gln Val Ala Ser Val Thr Arg Leu Ala Ser Asp
210 215 220

Gly Ser Glu Ile Thr Val Gly Ala Val Gly Met Ser Ser Leu Pro Pro
225 230 235 240

Thr Asp Val Tyr Lys Lys Tyr Gly Pro Ile Glu Gly Val Gly Ala Thr
245 250 255

Ala Arg Phe Thr Gly Asp Met Ile Ser Ala Thr Trp Asp Gly Leu Lys

```
            260                 265                 270

Ala Phe Pro Ala Lys Ile Pro Gly Val Val Ala Ser Ile Phe Gly Ala
        275                 280                 285

Glu Arg Asp Val Glu Ser Pro Met Ser Val Val Gly Ala Val Arg Ile
    290                 295                 300

Gly Gly Glu Phe Val Glu Arg Ser Met Trp Asp Met Phe Met Met Met
305                 310                 315                 320

Leu Ala Ser Leu Asn Phe Phe Leu Ala Leu Phe Asn Leu Val Pro Leu
                325                 330                 335

Pro Pro Leu Asp Gly Gly His Ile Ala Val Val Ile Tyr Glu Lys Ile
            340                 345                 350

Arg Asp Phe Phe Arg Lys Leu Arg Gly Lys Pro Ala Gly Gly Pro Ala
        355                 360                 365

Asp Tyr Thr Lys Leu Met Pro Val Thr Val Ala Val Ala Ala Leu Leu
    370                 375                 380

Met Thr Val Gly Gly Leu Val Ile Val Ala Asp Val Val Asn Pro Ile
385                 390                 395                 400

Arg Leu Phe Gly
```

CURRENT SEQUENCE LISTING

<210> 135
<211> 1111
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1111)
<223> FRXA00197

<400> 135

```
gtcgatgata ttttggcaac cgaatctgag gcacgcgcgc gtgcgaatgc tttgatcaac 60

cggttggcaa ccaacttgta agctaaggag cttccgcctc gtg gca gcc tat ctt   115
                                              Val Ala Ala Tyr Leu
                                                1               5

ctt ggt gtc gta tta ttt ttc ctc ggc atc gca gta acc atc gcg ctt   163
Leu Gly Val Val Leu Phe Phe Leu Gly Ile Ala Val Thr Ile Ala Leu
                10                  15                  20

cac gag tgg ggg cac ttc atc aca gcg cgc att ttc gga atg aaa gtg   211
His Glu Trp Gly His Phe Ile Thr Ala Arg Ile Phe Gly Met Lys Val
            25                  30                  35

cgg cgt ttc ttc atc ggt ttc ggc ccg acg gtg ttt gcc aaa aga cgc   259
Arg Arg Phe Phe Ile Gly Phe Gly Pro Thr Val Phe Ala Lys Arg Arg
        40                  45                  50

ggc gaa acc gtg tac ggc ctt aaa gcg att ccg gtc ggc ggt ttt tgt   307
Gly Glu Thr Val Tyr Gly Leu Lys Ala Ile Pro Val Gly Gly Phe Cys
```

```
     55                  60                  65

gac atc gcg ggg atg act gcc caa gat gaa ctt gat ccg gaa gac ctg   355
Asp Ile Ala Gly Met Thr Ala Gln Asp Glu Leu Asp Pro Glu Asp Leu
 70                  75                  80                  85

ccg cgc gcc atg tat cta aag ccc tgg tgg cag cgc ata att gtg ctt   403
Pro Arg Ala Met Tyr Leu Lys Pro Trp Trp Gln Arg Ile Ile Val Leu
                90                  95                 100

tcc ggc ggc gtg atc atg aat ctg atc gtc ggc ttt ttg gtg ctt tac   451
Ser Gly Gly Val Ile Met Asn Leu Ile Val Gly Phe Leu Val Leu Tyr
            105                 110                 115

ggc gtg gcg gtg agc tcc gga atc ccg aat ccg gat gtg gat acc acc   499
Gly Val Ala Val Ser Ser Gly Ile Pro Asn Pro Asp Val Asp Thr Thr
        120                 125                 130

gcg aca gtc gac acc gtt cag tgc gtg ccg gaa acc caa att tcc gca   547
Ala Thr Val Asp Thr Val Gln Cys Val Pro Glu Thr Gln Ile Ser Ala
    135                 140                 145

act gaa ctg tcc tcc tgc gta ggt tca ggc cca gcg ggc gac gcc ggc   595
Thr Glu Leu Ser Ser Cys Val Gly Ser Gly Pro Ala Gly Asp Ala Gly
150                 155                 160                 165

att gag cac ggc gat aag att ttg gcc gtc aac ggc caa gag atg gca   643
Ile Glu His Gly Asp Lys Ile Leu Ala Val Asn Gly Gln Glu Met Ala
                170                 175                 180

agc ttc acc gcc atc cgc gat gcg atc ctc gag ctc cca ggc gaa acg   691
Ser Phe Thr Ala Ile Arg Asp Ala Ile Leu Glu Leu Pro Gly Glu Thr
            185                 190                 195

gca acg ctg acg att gaa cgg gag gga acg ctt ttc gac gtc gac ctc   739
Ala Thr Leu Thr Ile Glu Arg Glu Gly Thr Leu Phe Asp Val Asp Leu
        200                 205                 210

cag gtt gcc tct gtc acc cgt ctc gcc tct gac ggt tca gaa att acc   787
Gln Val Ala Ser Val Thr Arg Leu Ala Ser Asp Gly Ser Glu Ile Thr
    215                 220                 225

gtc ggc gcg gtg ggc atg tcg agc ctt cca ccg acc gat gtg tac aaa   835
Val Gly Ala Val Gly Met Ser Ser Leu Pro Pro Thr Asp Val Tyr Lys
230                 235                 240                 245

aaa tac ggc cca atc gag ggt gtg gga gca act gca cgt ttc acc ggc   883
Lys Tyr Gly Pro Ile Glu Gly Val Gly Ala Thr Ala Arg Phe Thr Gly
                250                 255                 260

gac atg atc agc gcc acg tgg gat ggc ctc aaa gcc ttc ccg gcg aaa   931
Asp Met Ile Ser Ala Thr Trp Asp Gly Leu Lys Ala Phe Pro Ala Lys
            265                 270                 275

atc cca ggg gtc gtc gca tcc atc ttc ggt gca gaa cga gat gta gaa   979
Ile Pro Gly Val Val Ala Ser Ile Phe Gly Ala Glu Arg Asp Val Glu
        280                 285                 290

agc ccc atg agt gtg gtg ggc gcg tca cgc atc ggc ggc gaa ttt gtc  1027
Ser Pro Met Ser Val Val Gly Ala Ser Arg Ile Gly Gly Glu Phe Val
    295                 300                 305
```

```
gaa cgt tcc atg tgg gac atg ttc atg atg atg ctg gcc agc ctg aac   1075
Glu Arg Ser Met Trp Asp Met Phe Met Met Met Leu Ala Ser Leu Asn
310                 315                 320                 325

ttc ttc ctc gcg ctg ttt aac ctc gtg ccg ctg cca                   1111
Phe Phe Leu Ala Leu Phe Asn Leu Val Pro Leu Pro
                330                 335
```

<210> 136
<211> 337
<212> PRT
<213> Corynebacterium glutamicum

<400> 136

```
Val Ala Ala Tyr Leu Leu Gly Val Val Leu Phe Phe Leu Gly Ile Ala
  1               5                  10                  15

Val Thr Ile Ala Leu His Glu Trp Gly His Phe Ile Thr Ala Arg Ile
             20                  25                  30

Phe Gly Met Lys Val Arg Arg Phe Phe Ile Gly Phe Gly Pro Thr Val
         35                  40                  45

Phe Ala Lys Arg Arg Gly Glu Thr Val Tyr Gly Leu Lys Ala Ile Pro
     50                  55                  60

Val Gly Gly Phe Cys Asp Ile Ala Gly Met Thr Ala Gln Asp Glu Leu
 65                  70                  75                  80

Asp Pro Glu Asp Leu Pro Arg Ala Met Tyr Leu Lys Pro Trp Trp Gln
                 85                  90                  95

Arg Ile Ile Val Leu Ser Gly Gly Val Ile Met Asn Leu Ile Val Gly
            100                 105                 110

Phe Leu Val Leu Tyr Gly Val Ala Val Ser Ser Gly Ile Pro Asn Pro
        115                 120                 125

Asp Val Asp Thr Thr Ala Thr Val Asp Thr Val Gln Cys Val Pro Glu
    130                 135                 140

Thr Gln Ile Ser Ala Thr Glu Leu Ser Ser Cys Val Gly Ser Gly Pro
145                 150                 155                 160

Ala Gly Asp Ala Gly Ile Glu His Gly Asp Lys Ile Leu Ala Val Asn
                165                 170                 175

Gly Gln Glu Met Ala Ser Phe Thr Ala Ile Arg Asp Ala Ile Leu Glu
            180                 185                 190

Leu Pro Gly Glu Thr Ala Thr Leu Thr Ile Glu Arg Glu Gly Thr Leu
        195                 200                 205

Phe Asp Val Asp Leu Gln Val Ala Ser Val Thr Arg Leu Ala Ser Asp
    210                 215                 220

Gly Ser Glu Ile Thr Val Gly Ala Val Gly Met Ser Ser Leu Pro Pro
225                 230                 235                 240
```

```
Thr Asp Val Tyr Lys Lys Tyr Gly Pro Ile Glu Gly Val Gly Ala Thr
                245                 250                 255

Ala Arg Phe Thr Gly Asp Met Ile Ser Ala Thr Trp Asp Gly Leu Lys
            260                 265                 270

Ala Phe Pro Ala Lys Ile Pro Gly Val Val Ala Ser Ile Phe Gly Ala
        275                 280                 285

Glu Arg Asp Val Glu Ser Pro Met Ser Val Val Gly Ala Ser Arg Ile
    290                 295                 300

Gly Gly Glu Phe Val Glu Arg Ser Met Trp Asp Met Phe Met Met Met
305                 310                 315                 320

Leu Ala Ser Leu Asn Phe Phe Leu Ala Leu Phe Asn Leu Val Pro Leu
                325                 330                 335

Pro
```

<210> 137
<211> 1113
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1090)
<223> RXN00216

<400> 137

```
gtgttgctcg cggccaggca gcagtgctgt acctgcctga cgcggatggt gacatcgttc 60

ttggatcagg caccatctgc cacacggagt cttaagaaaa ttg ggc gct tat ggt   115
                                               Leu Gly Ala Tyr Gly
                                                 1               5

tta ggt gag ctt cct gga aaa tcc gcc gcg gaa gcc gcc gac att att   163
Leu Gly Glu Leu Pro Gly Lys Ser Ala Ala Glu Ala Ala Asp Ile Ile
                10                  15                  20

cag ggt gaa acg ggc gat ctt ctc cat att cct cag ctt ccg gcg cga   211
Gln Gly Glu Thr Gly Asp Leu Leu His Ile Pro Gln Leu Pro Ala Arg
            25                  30                  35

ggt ttg ggt gct gat ctg atc ggt cga acc gtc ggt ctg ctg gac atg   259
Gly Leu Gly Ala Asp Leu Ile Gly Arg Thr Val Gly Leu Leu Asp Met
        40                  45                  50

atc aac gtt gat cgc ggg gcc cga tct tgg gtg atg agc aca cgc ccc   307
Ile Asn Val Asp Arg Gly Ala Arg Ser Trp Val Met Ser Thr Arg Pro
    55                  60                  65

agc aga ttg acg cac ctg acc ggc gat ttc ctt gac atg gat ttg gat   355
Ser Arg Leu Thr His Leu Thr Gly Asp Phe Leu Asp Met Asp Leu Asp
70                  75                  80                  85

gcg tgc gag gaa acc tgg gga acg ggc gtc gac aag cta aaa atc caa   403
Ala Cys Glu Glu Thr Trp Gly Thr Gly Val Asp Lys Leu Lys Ile Gln
```

```
                    90                  95                 100

gtt gct ggt ccc tgg act tta ggt gcg cgc att gag ttg gcc aat ggc   451
Val Ala Gly Pro Trp Thr Leu Gly Ala Arg Ile Glu Leu Ala Asn Gly
            105                 110                 115

cat cgc gtt ttg tct gat cgc ggt gcg atg cgt gat ctc acg cag gcg   499
His Arg Val Leu Ser Asp Arg Gly Ala Met Arg Asp Leu Thr Gln Ala
        120                 125                 130

ctg atc gcc ggc atc gat gcg cat gca cgc aag gtt gct ggg cga ttt   547
Leu Ile Ala Gly Ile Asp Ala His Ala Arg Lys Val Ala Gly Arg Phe
    135                 140                 145

cgc gcc gaa gtg cag gtg caa att gat gag ccg gag ctg aaa tcg ctt   595
Arg Ala Glu Val Gln Val Gln Ile Asp Glu Pro Glu Leu Lys Ser Leu
150                 155                 160                 165

atc gac ggc tcc ctc cct ggc act tcc acc ttt gac att att cct gcg   643
Ile Asp Gly Ser Leu Pro Gly Thr Ser Thr Phe Asp Ile Ile Pro Ala
                170                 175                 180

gtg aat gtc gct gat gcc agt gaa cgt ttg cag cag gtc ttt agc tcg   691
Val Asn Val Ala Asp Ala Ser Glu Arg Leu Gln Gln Val Phe Ser Ser
            185                 190                 195

att gag ggg ccg aca tat ctc aac ctc acc ggc cag att cct act tgg   739
Ile Glu Gly Pro Thr Tyr Leu Asn Leu Thr Gly Gln Ile Pro Thr Trp
        200                 205                 210

gat gtg gct cgg ggt gcg ggc gcc gat act gtg cag att tcc atg gat   787
Asp Val Ala Arg Gly Ala Gly Ala Asp Thr Val Gln Ile Ser Met Asp
    215                 220                 225

caa gtc cgt gga aat gaa cat ttg gat ggt ttt ggt gaa acc atc acc   835
Gln Val Arg Gly Asn Glu His Leu Asp Gly Phe Gly Glu Thr Ile Thr
230                 235                 240                 245

agt gga att cgt ctt ggt ttg ggc att acg aca gga aaa gat gtc gta   883
Ser Gly Ile Arg Leu Gly Leu Gly Ile Thr Thr Gly Lys Asp Val Val
                250                 255                 260

gat gaa ctg ctc gag cga ccg cgg caa aag gcc gtt gag gta gca cgc   931
Asp Glu Leu Leu Glu Arg Pro Arg Gln Lys Ala Val Glu Val Ala Arg
            265                 270                 275

ttt ttt gat cgt tta ggt gtg ggc cga aac tat ctc gtg gat gct gtt   979
Phe Phe Asp Arg Leu Gly Val Gly Arg Asn Tyr Leu Val Asp Ala Val
        280                 285                 290

gat att cat ccg ggt gag gat ttg gtg cag ggg acc atc acc gag gcc  1027
Asp Ile His Pro Gly Glu Asp Leu Val Gln Gly Thr Ile Thr Glu Ala
    295                 300                 305

gcg cag gct tat cgc atg gcc cgg gtg atg tcg gag atg ttg tcg aag  1075
Ala Gln Ala Tyr Arg Met Ala Arg Val Met Ser Glu Met Leu Ser Lys
310                 315                 320                 325

gat tca tgc gac ctt taaggcttta ccggcgctgg gtg                   1113
Asp Ser Cys Asp Leu
                330
```

<210> 138
<211> 330
<212> PRT
<213> Corynebacterium glutamicum

<400> 138
Leu Gly Ala Tyr Gly Leu Gly Glu Leu Pro Gly Lys Ser Ala Ala Glu
1 5 10 15

Ala Ala Asp Ile Ile Gln Gly Glu Thr Gly Asp Leu Leu His Ile Pro
20 25 30

Gln Leu Pro Ala Arg Gly Leu Gly Ala Asp Leu Ile Gly Arg Thr Val
35 40 45

Gly Leu Leu Asp Met Ile Asn Val Asp Arg Gly Ala Arg Ser Trp Val
50 55 60

Met Ser Thr Arg Pro Ser Arg Leu Thr His Leu Thr Gly Asp Phe Leu
65 70 75 80

Asp Met Asp Leu Asp Ala Cys Glu Glu Thr Trp Gly Thr Gly Val Asp
85 90 95

Lys Leu Lys Ile Gln Val Ala Gly Pro Trp Thr Leu Gly Ala Arg Ile
100 105 110

Glu Leu Ala Asn Gly His Arg Val Leu Ser Asp Arg Gly Ala Met Arg
115 120 125

Asp Leu Thr Gln Ala Leu Ile Ala Gly Ile Asp Ala His Ala Arg Lys
130 135 140

Val Ala Gly Arg Phe Arg Ala Glu Val Gln Val Gln Ile Asp Glu Pro
145 150 155 160

Glu Leu Lys Ser Leu Ile Asp Gly Ser Leu Pro Gly Thr Ser Thr Phe
165 170 175

Asp Ile Ile Pro Ala Val Asn Val Ala Asp Ala Ser Glu Arg Leu Gln
180 185 190

Gln Val Phe Ser Ser Ile Glu Gly Pro Thr Tyr Leu Asn Leu Thr Gly
195 200 205

Gln Ile Pro Thr Trp Asp Val Ala Arg Gly Ala Gly Ala Asp Thr Val
210 215 220

Gln Ile Ser Met Asp Gln Val Arg Gly Asn Glu His Leu Asp Gly Phe
225 230 235 240

Gly Glu Thr Ile Thr Ser Gly Ile Arg Leu Gly Leu Gly Ile Thr Thr
245 250 255

Gly Lys Asp Val Val Asp Glu Leu Leu Glu Arg Pro Arg Gln Lys Ala
260 265 270

Val Glu Val Ala Arg Phe Phe Asp Arg Leu Gly Val Gly Arg Asn Tyr
275 280 285

```
Leu Val Asp Ala Val Asp Ile His Pro Gly Glu Asp Leu Val Gln Gly
    290                 295                 300

Thr Ile Thr Glu Ala Ala Gln Ala Tyr Arg Met Ala Arg Val Met Ser
305                 310                 315                 320

Glu Met Leu Ser Lys Asp Ser Cys Asp Leu
                325                 330


<210> 139
<211> 1269
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1246)
<223> RXN00222

<400> 139
agggaaaaac taccgtccgc ctggacaaag tcatcgatgt actccgcgtc cttggactcg 60

agctttctgt tggaattcac gatcccctca aggttaatca atg acc ccc act gcc   115
                                        Met Thr Pro Thr Ala
                                          1               5

gat atc tgg ttt aaa gat act ttg gct gct cat ttc aca cgc gac ggc   163
Asp Ile Trp Phe Lys Asp Thr Leu Ala Ala His Phe Thr Arg Asp Gly
                 10                  15                  20

gac cag acc aca ttc tcc tac aca gct gat tac gca ggt cca ccg att   211
Asp Gln Thr Thr Phe Ser Tyr Thr Ala Asp Tyr Ala Gly Pro Pro Ile
            25                  30                  35

gcc acg tcc ctg ccc atc aat tct gaa ccc gtg att acg cgc tct gga   259
Ala Thr Ser Leu Pro Ile Asn Ser Glu Pro Val Ile Thr Arg Ser Gly
        40                  45                  50

gcg atc cca cca ttt ttc gcg gga tta ctc ccc gaa ggt cgt cgc tta   307
Ala Ile Pro Pro Phe Phe Ala Gly Leu Leu Pro Glu Gly Arg Arg Leu
    55                  60                  65

agt tca ctc cgg aga aac att aaa gcc tct gcc gat gat gaa ctt tca   355
Ser Ser Leu Arg Arg Asn Ile Lys Ala Ser Ala Asp Asp Glu Leu Ser
70                  75                  80                  85

ctc ctt cta gca gtg gga gct gat cct gtt ggt gca gtc gct atc ttc   403
Leu Leu Leu Ala Val Gly Ala Asp Pro Val Gly Ala Val Ala Ile Phe
                90                  95                 100

ccc cat ggt gaa aat aca caa cct gca cca ccc aca gtt gat ttt gac   451
Pro His Gly Glu Asn Thr Gln Pro Ala Pro Pro Thr Val Asp Phe Asp
            105                 110                 115

gat gaa ctt gat ttc tcg gct gca cta acc gag tcc ggg att gcg gat   499
Asp Glu Leu Asp Phe Ser Ala Ala Leu Thr Glu Ser Gly Ile Ala Asp
        120                 125                 130

ccc gtt gca ctg gcc ggt gtc caa gac aaa gcc tct gca cgc acc atc   547
```

```
Pro Val Ala Leu Ala Gly Val Gln Asp Lys Ala Ser Ala Arg Thr Ile
    135                 140                 145

gcg gtc ccc gtt gca agc gat gcc atc ttg aaa ctc tcc ccg cct gaa   595
Ala Val Pro Val Ala Ser Asp Ala Ile Leu Lys Leu Ser Pro Pro Glu
150                 155                 160                 165

tac cct tac ttg gtg gaa aac gaa gca gct tgt tac cag ttg ctg acc   643
Tyr Pro Tyr Leu Val Glu Asn Glu Ala Ala Cys Tyr Gln Leu Leu Thr
                170                 175                 180

aaa aat aag ctt cgc att gaa ctg tcc aaa gta gaa gtt ctc cat gac   691
Lys Asn Lys Leu Arg Ile Glu Leu Ser Lys Val Glu Val Leu His Asp
            185                 190                 195

aaa cac ggc agg tcc gga ctc tta gtt cac cgc ttt gac cgc aca ccc   739
Lys His Gly Arg Ser Gly Leu Leu Val His Arg Phe Asp Arg Thr Pro
        200                 205                 210

aaa ggc aaa atc ccc gtc gag gat gca gga cag gtc ttg gga atc tgg   787
Lys Gly Lys Ile Pro Val Glu Asp Ala Gly Gln Val Leu Gly Ile Trp
    215                 220                 225

cct gca gat aaa tac tta gtg agc tac gag gac atc gca caa gcc ctc   835
Pro Ala Asp Lys Tyr Leu Val Ser Tyr Glu Asp Ile Ala Gln Ala Leu
230                 235                 240                 245

act aaa gtg tgc gcc tcc ccc atc ttg gcg atg cgc aat ctc gcc ttc   883
Thr Lys Val Cys Ala Ser Pro Ile Leu Ala Met Arg Asn Leu Ala Phe
                250                 255                 260

caa atc gca gtc gcg tgg ctc agc ggc aat ggt gat ctt cat gcc aag   931
Gln Ile Ala Val Ala Trp Leu Ser Gly Asn Gly Asp Leu His Ala Lys
            265                 270                 275

aac atc tcc att atc aac aaa ggc cgc gga ttt gag atc agc ccc atc   979
Asn Ile Ser Ile Ile Asn Lys Gly Arg Gly Phe Glu Ile Ser Pro Ile
        280                 285                 290

tat gac atc cct gcc acc gca gta tat ggc gac acc acg atg gca tta   1027
Tyr Asp Ile Pro Ala Thr Ala Val Tyr Gly Asp Thr Thr Met Ala Leu
    295                 300                 305

gaa atc cag gga tcc aaa aag gat ctc agc caa aag aaa ttc cta aaa   1075
Glu Ile Gln Gly Ser Lys Lys Asp Leu Ser Gln Lys Lys Phe Leu Lys
310                 315                 320                 325

ttc tgt aca tcc atc gga cta cca gaa aaa aca gcc atg tcg gtt gcg   1123
Phe Cys Thr Ser Ile Gly Leu Pro Glu Lys Thr Ala Met Ser Val Ala
                330                 335                 340

aac gct gca ctg ttg gca aca gaa aat gcc gca gag aca att ctt gct   1171
Asn Ala Ala Leu Leu Ala Thr Glu Asn Ala Ala Glu Thr Ile Leu Ala
            345                 350                 355

tcg gga aat ttt gat aca cgg atg aat cga gat ctg gcc agg gtt ctc   1219
Ser Gly Asn Phe Asp Thr Arg Met Asn Arg Asp Leu Ala Arg Val Leu
        360                 365                 370

aaa cat cga cga agc gca tgg gga gct taattcgcct gtttaagagg         1266
Lys His Arg Arg Ser Ala Trp Gly Ala
```

375 380

tcg 1269

<210> 140
<211> 382
<212> PRT
<213> Corynebacterium glutamicum

<400> 140
Met Thr Pro Thr Ala Asp Ile Trp Phe Lys Asp Thr Leu Ala Ala His
1 5 10 15

Phe Thr Arg Asp Gly Asp Gln Thr Thr Phe Ser Tyr Thr Ala Asp Tyr
20 25 30

Ala Gly Pro Pro Ile Ala Thr Ser Leu Pro Ile Asn Ser Glu Pro Val
35 40 45

Ile Thr Arg Ser Gly Ala Ile Pro Pro Phe Phe Ala Gly Leu Leu Pro
50 55 60

Glu Gly Arg Arg Leu Ser Ser Leu Arg Arg Asn Ile Lys Ala Ser Ala
65 70 75 80

Asp Asp Glu Leu Ser Leu Leu Leu Ala Val Gly Ala Asp Pro Val Gly
85 90 95

Ala Val Ala Ile Phe Pro His Gly Glu Asn Thr Gln Pro Ala Pro Pro
100 105 110

Thr Val Asp Phe Asp Asp Glu Leu Asp Phe Ser Ala Ala Leu Thr Glu
115 120 125

Ser Gly Ile Ala Asp Pro Val Ala Leu Ala Gly Val Gln Asp Lys Ala
130 135 140

Ser Ala Arg Thr Ile Ala Val Pro Val Ala Ser Asp Ala Ile Leu Lys
145 150 155 160

Leu Ser Pro Pro Glu Tyr Pro Tyr Leu Val Glu Asn Glu Ala Ala Cys
165 170 175

Tyr Gln Leu Leu Thr Lys Asn Lys Leu Arg Ile Glu Leu Ser Lys Val
180 185 190

Glu Val Leu His Asp Lys His Gly Arg Ser Gly Leu Leu Val His Arg
195 200 205

Phe Asp Arg Thr Pro Lys Gly Lys Ile Pro Val Glu Asp Ala Gly Gln
210 215 220

Val Leu Gly Ile Trp Pro Ala Asp Lys Tyr Leu Val Ser Tyr Glu Asp
225 230 235 240

Ile Ala Gln Ala Leu Thr Lys Val Cys Ala Ser Pro Ile Leu Ala Met
245 250 255

Arg Asn Leu Ala Phe Gln Ile Ala Val Ala Trp Leu Ser Gly Asn Gly
260 265 270

```
Asp Leu His Ala Lys Asn Ile Ser Ile Ile Asn Lys Gly Arg Gly Phe
        275                 280                 285

Glu Ile Ser Pro Ile Tyr Asp Ile Pro Ala Thr Ala Val Tyr Gly Asp
    290                 295                 300

Thr Thr Met Ala Leu Glu Ile Gln Gly Ser Lys Lys Asp Leu Ser Gln
305                 310                 315                 320

Lys Lys Phe Leu Lys Phe Cys Thr Ser Ile Gly Leu Pro Glu Lys Thr
                325                 330                 335

Ala Met Ser Val Ala Asn Ala Ala Leu Leu Ala Thr Glu Asn Ala Ala
            340                 345                 350

Glu Thr Ile Leu Ala Ser Gly Asn Phe Asp Thr Arg Met Asn Arg Asp
        355                 360                 365

Leu Ala Arg Val Leu Lys His Arg Arg Ser Ala Trp Gly Ala
    370                 375                 380
```

Application as filed - not to be published

<210> 141
<211> 1269
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1246)
<223> FRXA00222

<400> 141

```
agggaaaaac taccgtccgc ctggacaaag tcatcgatgt actccgcgtc cttggactcg 60

agctttctgt tggaattcac gatcccctca aggttaatca atg acc ccc act gcc   115
                                            Met Thr Pro Thr Ala
                                              1               5

gat atc tgg ttt aaa gat act ttg gct gct cat ttc aca cgc gac ggc   163
Asp Ile Trp Phe Lys Asp Thr Leu Ala Ala His Phe Thr Arg Asp Gly
                10                  15                  20

gac cag acc aca ttc tcc tac aca gct gat tac gca ggt cca ccg att   211
Asp Gln Thr Thr Phe Ser Tyr Thr Ala Asp Tyr Ala Gly Pro Pro Ile
            25                  30                  35

gcc acg tcc ctg ccc atc aat tct gaa ccc gtg att acg cgc tct gga   259
Ala Thr Ser Leu Pro Ile Asn Ser Glu Pro Val Ile Thr Arg Ser Gly
        40                  45                  50

gcg atc cca cca ttt ttc gcg gga tta ctc ccc gaa ggt cgt cgc tta   307
Ala Ile Pro Pro Phe Phe Ala Gly Leu Leu Pro Glu Gly Arg Arg Leu
    55                  60                  65

agt tca ctc cgg aga aac att aaa gcc tct gcc gat gat gaa ctt tca   355
Ser Ser Leu Arg Arg Asn Ile Lys Ala Ser Ala Asp Asp Glu Leu Ser
70                  75                  80                  85

ctc ctt cta gca gtg gga gct gat cct gtt ggt gca gtc gct atc ttc   403
```

```
Leu Leu Leu Ala Val Gly Ala Asp Pro Val Gly Ala Val Ala Ile Phe
                 90                  95                 100

ccc cat ggt gaa aat aca caa cct gca cca ccc aca gtt gat ttt gac   451
Pro His Gly Glu Asn Thr Gln Pro Ala Pro Pro Thr Val Asp Phe Asp
            105                 110                 115

gat gaa ctt gat ttc tcg gct gca cta acc gag tcc ggg att gcg gat   499
Asp Glu Leu Asp Phe Ser Ala Ala Leu Thr Glu Ser Gly Ile Ala Asp
        120                 125                 130

ccc gtt gca ctg gcc ggt gtc caa gac aaa gcc tct gca cgc acc atc   547
Pro Val Ala Leu Ala Gly Val Gln Asp Lys Ala Ser Ala Arg Thr Ile
    135                 140                 145

gcg gtc ccc gtt gca agc gat gcc atc ttg aaa ctc tcc ccg cct gaa   595
Ala Val Pro Val Ala Ser Asp Ala Ile Leu Lys Leu Ser Pro Pro Glu
150                 155                 160                 165

tac cct tac ttg gtg gaa aac gaa gca gct tgt tac cag ttg ctg acc   643
Tyr Pro Tyr Leu Val Glu Asn Glu Ala Ala Cys Tyr Gln Leu Leu Thr
                170                 175                 180

aaa aat aag ctt cgc att gaa ctg tcc aaa gta gaa gtt ctc cat gac   691
Lys Asn Lys Leu Arg Ile Glu Leu Ser Lys Val Glu Val Leu His Asp
            185                 190                 195

aaa cac ggc agg tcc gga ctc tta gtt cac cgc ttt gac cgc aca ccc   739
Lys His Gly Arg Ser Gly Leu Leu Val His Arg Phe Asp Arg Thr Pro
        200                 205                 210

aaa ggc aaa atc ccc gtc gag gat gca gga cag gtc ttg gga atc tgg   787
Lys Gly Lys Ile Pro Val Glu Asp Ala Gly Gln Val Leu Gly Ile Trp
    215                 220                 225

cct gca gat aaa tac tta gtg agc tac gag gac atc gca caa gcc ctc   835
Pro Ala Asp Lys Tyr Leu Val Ser Tyr Glu Asp Ile Ala Gln Ala Leu
230                 235                 240                 245

act aaa gtg tgc gcc tcc ccc atc ttg gcg atg cgc aat ctc gcc ttc   883
Thr Lys Val Cys Ala Ser Pro Ile Leu Ala Met Arg Asn Leu Ala Phe
                250                 255                 260

caa atc gca gtc gcg tgg ctc agc ggc aat ggt gat ctt cat gcc aag   931
Gln Ile Ala Val Ala Trp Leu Ser Gly Asn Gly Asp Leu His Ala Lys
            265                 270                 275

aac atc tcc att atc aac aaa ggc cgc gga ttt gag atc agc ccc atc   979
Asn Ile Ser Ile Ile Asn Lys Gly Arg Gly Phe Glu Ile Ser Pro Ile
        280                 285                 290

tat gac atc cct gcc acc gca gta tat ggc gac acc acg atg gca tta   1027
Tyr Asp Ile Pro Ala Thr Ala Val Tyr Gly Asp Thr Thr Met Ala Leu
    295                 300                 305

gaa atc cag gga tcc aaa aag gat ctc agc caa aag aaa ttc cta aaa   1075
Glu Ile Gln Gly Ser Lys Lys Asp Leu Ser Gln Lys Lys Phe Leu Lys
310                 315                 320                 325

ttc tgt aca tcc atc gga cta cca gaa aaa aca gcc atg tcg gtt gcg   1123
Phe Cys Thr Ser Ile Gly Leu Pro Glu Lys Thr Ala Met Ser Val Ala
```

```
                330                 335                 340

aac gct gca ctg ttg gca aca gaa aat gcc gca gag aca att ctt gct   1171
Asn Ala Ala Leu Leu Ala Thr Glu Asn Ala Ala Glu Thr Ile Leu Ala
            345                 350                 355

tcg gga aat ttt gat aca cgg atg aat cga gat ctg gcc agg gtt ctc   1219
Ser Gly Asn Phe Asp Thr Arg Met Asn Arg Asp Leu Ala Arg Val Leu
        360                 365                 370

aaa cat cga cga agc gca tgg gga gct taattcgcct gtttaagagg         1266
Lys His Arg Arg Ser Ala Trp Gly Ala
    375                 380

tcg                                                               1269
```

<210> 142
<211> 382
<212> PRT
<213> Corynebacterium glutamicum

<400> 142

```
Met Thr Pro Thr Ala Asp Ile Trp Phe Lys Asp Thr Leu Ala Ala His
  1               5                  10                  15

Phe Thr Arg Asp Gly Asp Gln Thr Thr Phe Ser Tyr Thr Ala Asp Tyr
             20                  25                  30

Ala Gly Pro Pro Ile Ala Thr Ser Leu Pro Ile Asn Ser Glu Pro Val
         35                  40                  45

Ile Thr Arg Ser Gly Ala Ile Pro Pro Phe Phe Ala Gly Leu Leu Pro
     50                  55                  60

Glu Gly Arg Arg Leu Ser Ser Leu Arg Arg Asn Ile Lys Ala Ser Ala
 65                  70                  75                  80

Asp Asp Glu Leu Ser Leu Leu Leu Ala Val Gly Ala Asp Pro Val Gly
                 85                  90                  95

Ala Val Ala Ile Phe Pro His Gly Glu Asn Thr Gln Pro Ala Pro Pro
            100                 105                 110

Thr Val Asp Phe Asp Asp Glu Leu Asp Phe Ser Ala Ala Leu Thr Glu
        115                 120                 125

Ser Gly Ile Ala Asp Pro Val Ala Leu Ala Gly Val Gln Asp Lys Ala
    130                 135                 140

Ser Ala Arg Thr Ile Ala Val Pro Val Ala Ser Asp Ala Ile Leu Lys
145                 150                 155                 160

Leu Ser Pro Pro Glu Tyr Pro Tyr Leu Val Glu Asn Glu Ala Ala Cys
                165                 170                 175

Tyr Gln Leu Leu Thr Lys Asn Lys Leu Arg Ile Glu Leu Ser Lys Val
            180                 185                 190

Glu Val Leu His Asp Lys His Gly Arg Ser Gly Leu Leu Val His Arg
        195                 200                 205
```

```
Phe Asp Arg Thr Pro Lys Gly Lys Ile Pro Val Glu Asp Ala Gly Gln
    210                 215                 220

Val Leu Gly Ile Trp Pro Ala Asp Lys Tyr Leu Val Ser Tyr Glu Asp
225                 230                 235                 240

Ile Ala Gln Ala Leu Thr Lys Val Cys Ala Ser Pro Ile Leu Ala Met
                245                 250                 255

Arg Asn Leu Ala Phe Gln Ile Ala Val Ala Trp Leu Ser Gly Asn Gly
            260                 265                 270

Asp Leu His Ala Lys Asn Ile Ser Ile Ile Asn Lys Gly Arg Gly Phe
        275                 280                 285

Glu Ile Ser Pro Ile Tyr Asp Ile Pro Ala Thr Ala Val Tyr Gly Asp
    290                 295                 300

Thr Thr Met Ala Leu Glu Ile Gln Gly Ser Lys Lys Asp Leu Ser Gln
305                 310                 315                 320

Lys Lys Phe Leu Lys Phe Cys Thr Ser Ile Gly Leu Pro Glu Lys Thr
                325                 330                 335

Ala Met Ser Val Ala Asn Ala Ala Leu Leu Ala Thr Glu Asn Ala Ala
            340                 345                 350

Glu Thr Ile Leu Ala Ser Gly Asn Phe Asp Thr Arg Met Asn Arg Asp
        355                 360                 365

Leu Ala Arg Val Leu Lys His Arg Arg Ser Ala Trp Gly Ala
    370                 375                 380


<210> 143
<211> 633
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(610)
<223> RXN00232

<400> 143
gctgaaaaaa ctcccatttg gacaatgaac acttgtcaaa atgggagttt tggattttcg 60

caccaccggc agcactcgaa aacgtgttta tacttgaact atg aac gac agg gct   115
                                              Met Asn Asp Arg Ala
                                                1               5

cac caa cga ata ggc gac atc gag cga tcc caa gcc ctc gac cga ctt   163
His Gln Arg Ile Gly Asp Ile Glu Arg Ser Gln Ala Leu Asp Arg Leu
                 10                  15                  20

ggg tca tat ttt gca gac gga tac ctc gac atc gac gaa ttc gat acc   211
Gly Ser Tyr Phe Ala Asp Gly Tyr Leu Asp Ile Asp Glu Phe Asp Thr
             25                  30                  35

cga acc ggc gcc gca gca atc gca cgc aca gcc ggt gaa ata gat gtc   259
```

```
Arg Thr Gly Ala Ala Ala Ile Ala Arg Thr Ala Gly Glu Ile Asp Val
         40                  45                  50

ttg ttc aca gat ctt ccc gaa caa cag gca agc acc gcc gtg aca ccc   307
Leu Phe Thr Asp Leu Pro Glu Gln Gln Ala Ser Thr Ala Val Thr Pro
     55                  60                  65

gtg caa gac gat acc gag aaa gaa tta gac ctg gtc cta cag cga gga   355
Val Gln Asp Asp Thr Glu Lys Glu Leu Asp Leu Val Leu Gln Arg Gly
 70                  75                  80                  85

aag aag ctc aag cag atc gac tcc gcc att tgg gct gtc gtg atg gtc   403
Lys Lys Leu Lys Gln Ile Asp Ser Ala Ile Trp Ala Val Val Met Val
                 90                  95                 100

tcg ttc ttc cta ggc ttg ttt gtt ttc aac gtg cca tat ttc tgg gtt   451
Ser Phe Phe Leu Gly Leu Phe Val Phe Asn Val Pro Tyr Phe Trp Val
            105                 110                 115

gtg ttc atc ctt ggc gga gcg gcc tcc gcg ggt gcg cga ttc ttg ctc   499
Val Phe Ile Leu Gly Gly Ala Ala Ser Ala Gly Ala Arg Phe Leu Leu
        120                 125                 130

aaa gta gat gac gcc gat gaa aaa ctc ttt gag gaa ctc cac agc aag   547
Lys Val Asp Asp Ala Asp Glu Lys Leu Phe Glu Glu Leu His Ser Lys
    135                 140                 145

gaa caa agc gaa cgc gaa gca cgc cta cgc att gcg gca caa cgt cga   595
Glu Gln Ser Glu Arg Glu Ala Arg Leu Arg Ile Ala Ala Gln Arg Arg
150                 155                 160                 165

cgc gag ttg gaa caa tagccacaaa agctatcaag ccc                    633
Arg Glu Leu Glu Gln
                170
```

Sequence Listing Page 193 of 239

<210> 144
<211> 170
<212> PRT
<213> Corynebacterium glutamicum

<400> 144

```
Met Asn Asp Arg Ala His Gln Arg Ile Gly Asp Ile Glu Arg Ser Gln
  1               5                  10                  15

Ala Leu Asp Arg Leu Gly Ser Tyr Phe Ala Asp Gly Tyr Leu Asp Ile
             20                  25                  30

Asp Glu Phe Asp Thr Arg Thr Gly Ala Ala Ala Ile Ala Arg Thr Ala
         35                  40                  45

Gly Glu Ile Asp Val Leu Phe Thr Asp Leu Pro Glu Gln Gln Ala Ser
     50                  55                  60

Thr Ala Val Thr Pro Val Gln Asp Asp Thr Glu Lys Glu Leu Asp Leu
 65                  70                  75                  80

Val Leu Gln Arg Gly Lys Lys Leu Lys Gln Ile Asp Ser Ala Ile Trp
                 85                  90                  95

Ala Val Val Met Val Ser Phe Phe Leu Gly Leu Phe Val Phe Asn Val
```

```
            100                 105                 110

Pro Tyr Phe Trp Val Val Phe Ile Leu Gly Gly Ala Ala Ser Ala Gly
        115                 120                 125

Ala Arg Phe Leu Leu Lys Val Asp Asp Ala Asp Glu Lys Leu Phe Glu
    130                 135                 140

Glu Leu His Ser Lys Glu Gln Ser Glu Arg Glu Ala Arg Leu Arg Ile
145                 150                 155                 160

Ala Ala Gln Arg Arg Arg Glu Leu Glu Gln
                165                 170


<210> 145
<211> 627
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(610)
<223> FRXA00232

<400> 145
gctgaaaaaa ctcccatttg gacaatgaac acttgtcaaa atgggagttt tggattttcg 60

caccaccggc agcactcgaa aacgtgttta tacttgaact atg aac gac agg gct   115
                                          Met Asn Asp Arg Ala
                                            1               5

cac caa cga ata ggc gac atc gag cga tcc caa gcc ctc gac cga ctt   163
His Gln Arg Ile Gly Asp Ile Glu Arg Ser Gln Ala Leu Asp Arg Leu
                10                  15                  20

ggg tca tat ttt gca gac gga tac ctc gac atc gac gaa ttc gat acc   211
Gly Ser Tyr Phe Ala Asp Gly Tyr Leu Asp Ile Asp Glu Phe Asp Thr
            25                  30                  35

cga acc ggc gcc gca gca atc gca cgc aca gcc ggt gaa ata gat gtc   259
Arg Thr Gly Ala Ala Ala Ile Ala Arg Thr Ala Gly Glu Ile Asp Val
        40                  45                  50

ttg ttc aca gat ctt ccc gaa caa cag gca agc acc gcc gtg aca ccc   307
Leu Phe Thr Asp Leu Pro Glu Gln Gln Ala Ser Thr Ala Val Thr Pro
    55                  60                  65

gtg caa gac gat acc gag aaa gaa tta gac ctg gtc cta cag cga gga   355
Val Gln Asp Asp Thr Glu Lys Glu Leu Asp Leu Val Leu Gln Arg Gly
70                  75                  80                  85

aag aag ctc aag cag atc gac tcc gcc att tgg gct gtc gtg atg gtc   403
Lys Lys Leu Lys Gln Ile Asp Ser Ala Ile Trp Ala Val Val Met Val
                90                  95                  100

tcg ttc ttc cta ggc ttg ttt gtt ttc aac gtg cca tat ttc tgg gtt   451
Ser Phe Phe Leu Gly Leu Phe Val Phe Asn Val Pro Tyr Phe Trp Val
            105                 110                 115

gtg ttc atc ctt ggc gga gcg gcc tcc gcg ggt gcg cga ttc ttg ctc   499
```

```
Val Phe Ile Leu Gly Gly Ala Ala Ser Ala Gly Ala Arg Phe Leu Leu
        120                 125                 130

aaa gta gat gac gcc gat gaa aaa ctc ttt gag gaa ctc cac agc aag   547
Lys Val Asp Asp Ala Asp Glu Lys Leu Phe Glu Glu Leu His Ser Lys
    135                 140                 145

gaa caa agc gaa cgc gaa gca cgc cta cgc att gcg gca caa cgt cga   595
Glu Gln Ser Glu Arg Glu Ala Arg Leu Arg Ile Ala Ala Gln Arg Arg
150                 155                 160                 165

cgc gag ttg gaa caa tagccacaaa agctatc                           627
Arg Glu Leu Glu Gln
                170
```

<210> 146
<211> 170
<212> PRT
<213> Corynebacterium glutamicum

<400> 146

```
Met Asn Asp Arg Ala His Gln Arg Ile Gly Asp Ile Glu Arg Ser Gln
  1               5                  10                  15

Ala Leu Asp Arg Leu Gly Ser Tyr Phe Ala Asp Gly Tyr Leu Asp Ile
             20                  25                  30

Asp Glu Phe Asp Thr Arg Thr Gly Ala Ala Ala Ile Ala Arg Thr Ala
         35                  40                  45

Gly Glu Ile Asp Val Leu Phe Thr Asp Leu Pro Glu Gln Gln Ala Ser
     50                  55                  60

Thr Ala Val Thr Pro Val Gln Asp Asp Thr Glu Lys Glu Leu Asp Leu
 65                  70                  75                  80

Val Leu Gln Arg Gly Lys Lys Leu Lys Gln Ile Asp Ser Ala Ile Trp
                 85                  90                  95

Ala Val Val Met Val Ser Phe Phe Leu Gly Leu Phe Val Phe Asn Val
            100                 105                 110

Pro Tyr Phe Trp Val Val Phe Ile Leu Gly Gly Ala Ala Ser Ala Gly
        115                 120                 125

Ala Arg Phe Leu Leu Lys Val Asp Asp Ala Asp Glu Lys Leu Phe Glu
    130                 135                 140

Glu Leu His Ser Lys Glu Gln Ser Glu Arg Glu Ala Arg Leu Arg Ile
145                 150                 155                 160

Ala Ala Gln Arg Arg Arg Glu Leu Glu Gln
                165                 170
```

<210> 147
<211> 849
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(826)
<223> RXN00236

<400> 147
aatgcgagag ttctaaaacg agccggtaac atcgaccccc atgagttcag gggttagaaa 60

agcaatggga tttggatgcg gttcggtttt ggccgtcatc atg gtg atc tca ttt 115
Met Val Ile Ser Phe
1 5

gtt gga tgg gcg ctc agc ttc atg gat gga acg gca cct att cgc caa 163
Val Gly Trp Ala Leu Ser Phe Met Asp Gly Thr Ala Pro Ile Arg Gln
10 15 20

ctc cag caa atc cct gaa gat gtt ccg ccg gcg cgt ggt gta gaa gtt 211
Leu Gln Gln Ile Pro Glu Asp Val Pro Pro Ala Arg Gly Val Glu Val
25 30 35

ccg caa att gat aca gag gca gat gga cgc aca tcc aac cat ttg cgt 259
Pro Gln Ile Asp Thr Glu Ala Asp Gly Arg Thr Ser Asn His Leu Arg
40 45 50

ttt tgg gcg gaa cca att gct caa gat act ggt gtg tcc gct caa gcg 307
Phe Trp Ala Glu Pro Ile Ala Gln Asp Thr Gly Val Ser Ala Gln Ala
55 60 65

att gcg gct tat gga aac gca gag ctc atc gcg agt act gcg tgg cct 355
Ile Ala Ala Tyr Gly Asn Ala Glu Leu Ile Ala Ser Thr Ala Trp Pro
70 75 80 85

ggc tgc aat ctg ggg tgg aat acc ttg gca ggt atc ggc cag gtg gaa 403
Gly Cys Asn Leu Gly Trp Asn Thr Leu Ala Gly Ile Gly Gln Val Glu
90 95 100

acc cgt cac ggt acc tac aac ggc aaa atg ttc ggg ggc agt tcc ctg 451
Thr Arg His Gly Thr Tyr Asn Gly Lys Met Phe Gly Gly Ser Ser Leu
105 110 115

gat gaa aat gga gtt gca acc cct cca atc atc ggc gtt cca ctt gat 499
Asp Glu Asn Gly Val Ala Thr Pro Pro Ile Ile Gly Val Pro Leu Asp
120 125 130

ggt tca ccg ggg ttt gcg gaa att ccc gac act gat ggt ggg gaa tta 547
Gly Ser Pro Gly Phe Ala Glu Ile Pro Asp Thr Asp Gly Gly Glu Leu
135 140 145

gat ggc gat act gaa tat gat cgc gcg gta ggt ccc atg cag ttc att 595
Asp Gly Asp Thr Glu Tyr Asp Arg Ala Val Gly Pro Met Gln Phe Ile
150 155 160 165

ccg gaa acg tgg cga ctt atg gga ttg gat gca aac ggt gat ggg gta 643
Pro Glu Thr Trp Arg Leu Met Gly Leu Asp Ala Asn Gly Asp Gly Val
170 175 180

gcg gac ccc aac caa att gat gac gca gca ttg agt gcc gca aac ctg 691
Ala Asp Pro Asn Gln Ile Asp Asp Ala Ala Leu Ser Ala Ala Asn Leu
185 190 195

ttg tgt tcc aac gat cgt gac ttg tcc act cct gaa gga tgg acc gca 739

```
Leu Cys Ser Asn Asp Arg Asp Leu Ser Thr Pro Glu Gly Trp Thr Ala
        200                 205                 210

gct gtt cat tct tac aac atg tct aat cag tat ttg atg gac gtt cga   787
Ala Val His Ser Tyr Asn Met Ser Asn Gln Tyr Leu Met Asp Val Arg
    215                 220                 225

gat gct gcc gcg tcc tac gct tta cga cag ccg gcg atc taaaacttaa    836
Asp Ala Ala Ala Ser Tyr Ala Leu Arg Gln Pro Ala Ile
230                 235                 240

caagcgcaac ccc                                                   849


<210> 148
<211> 242
<212> PRT
<213> Corynebacterium glutamicum

<400> 148
Met Val Ile Ser Phe Val Gly Trp Ala Leu Ser Phe Met Asp Gly Thr
  1               5                  10                  15

Ala Pro Ile Arg Gln Leu Gln Gln Ile Pro Glu Asp Val Pro Pro Ala
            20                  25                  30

Arg Gly Val Glu Val Pro Gln Ile Asp Thr Glu Ala Asp Gly Arg Thr
        35                  40                  45

Ser Asn His Leu Arg Phe Trp Ala Glu Pro Ile Ala Gln Asp Thr Gly
    50                  55                  60

Val Ser Ala Gln Ala Ile Ala Ala Tyr Gly Asn Ala Glu Leu Ile Ala
65                  70                  75                  80

Ser Thr Ala Trp Pro Gly Cys Asn Leu Gly Trp Asn Thr Leu Ala Gly
                85                  90                  95

Ile Gly Gln Val Glu Thr Arg His Gly Thr Tyr Asn Gly Lys Met Phe
            100                 105                 110

Gly Gly Ser Ser Leu Asp Glu Asn Gly Val Ala Thr Pro Pro Ile Ile
        115                 120                 125

Gly Val Pro Leu Asp Gly Ser Pro Gly Phe Ala Glu Ile Pro Asp Thr
    130                 135                 140

Asp Gly Gly Glu Leu Asp Gly Asp Thr Glu Tyr Asp Arg Ala Val Gly
145                 150                 155                 160

Pro Met Gln Phe Ile Pro Glu Thr Trp Arg Leu Met Gly Leu Asp Ala
                165                 170                 175

Asn Gly Asp Gly Val Ala Asp Pro Asn Gln Ile Asp Asp Ala Ala Leu
            180                 185                 190

Ser Ala Ala Asn Leu Leu Cys Ser Asn Asp Arg Asp Leu Ser Thr Pro
        195                 200                 205

Glu Gly Trp Thr Ala Ala Val His Ser Tyr Asn Met Ser Asn Gln Tyr
    210                 215                 220
```

```
Leu Met Asp Val Arg Asp Ala Ala Ala Ser Tyr Ala Leu Arg Gln Pro
225                 230                 235                 240

Ala Ile



<210> 149
<211> 849
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(826)
<223> FRXA00236

<400> 149
aatgcgagag ttctaaaacg agccggtaac atcgaccccc atgagttcag gggttagaaa 60

agcaatggga tttggatgcg gttcggtttt ggccgtcatc atg gtg atc tca ttt   115
                                          Met Val Ile Ser Phe
                                            1               5

gtt gga tgg gcg ctc agc ttc atg gat gga acg gca cct att cgc caa   163
Val Gly Trp Ala Leu Ser Phe Met Asp Gly Thr Ala Pro Ile Arg Gln
                10                  15                  20

ctc cag caa atc cct gaa gat gtt ccg ccg gcg cgt ggt gta gaa gtt   211
Leu Gln Gln Ile Pro Glu Asp Val Pro Pro Ala Arg Gly Val Glu Val
            25                  30                  35

ccg caa att gat aca gag gca gat gga cgc aca tcc aac cat ttg cgt   259
Pro Gln Ile Asp Thr Glu Ala Asp Gly Arg Thr Ser Asn His Leu Arg
        40                  45                  50

ttt tgg gcg gaa cca att gct caa gat act ggt gtg tcc gct caa gcg   307
Phe Trp Ala Glu Pro Ile Ala Gln Asp Thr Gly Val Ser Ala Gln Ala
    55                  60                  65

att gcg gct tat gga aac gca gag ctc atc gcg agt act gcg tgg cct   355
Ile Ala Ala Tyr Gly Asn Ala Glu Leu Ile Ala Ser Thr Ala Trp Pro
70                  75                  80                  85

ggc tgc aat ctg ggg tgg aat acc ttg gca ggt atc ggc cag gtg gaa   403
Gly Cys Asn Leu Gly Trp Asn Thr Leu Ala Gly Ile Gly Gln Val Glu
                90                  95                  100

acc cgt cac ggt acc tac aac ggc aaa atg ttc ggg ggc agt tcc ctg   451
Thr Arg His Gly Thr Tyr Asn Gly Lys Met Phe Gly Gly Ser Ser Leu
            105                 110                 115

gat gaa aat gga gtt gca acc cct cca atc atc ggc gtt cca ctt gat   499
Asp Glu Asn Gly Val Ala Thr Pro Pro Ile Ile Gly Val Pro Leu Asp
        120                 125                 130

ggt tca ccg ggg ttt gcg gaa att ccc gac act gat ggt ggg gaa tta   547
Gly Ser Pro Gly Phe Ala Glu Ile Pro Asp Thr Asp Gly Gly Glu Leu
    135                 140                 145
```

```
gat ggc gat act gaa tat gat cgc gcg gta ggt ccc atg cag ttc att   595
Asp Gly Asp Thr Glu Tyr Asp Arg Ala Val Gly Pro Met Gln Phe Ile
150                 155                 160                 165

ccg gaa acg tgg cga ctt atg gga ttg gat gca aac ggt gat ggg gta   643
Pro Glu Thr Trp Arg Leu Met Gly Leu Asp Ala Asn Gly Asp Gly Val
                170                 175                 180

gcg gac ccc aac caa att gat gac gca gca ttg agt gcc gca aac ctg   691
Ala Asp Pro Asn Gln Ile Asp Asp Ala Ala Leu Ser Ala Ala Asn Leu
            185                 190                 195

ttg tgt tcc aac gat cgt gac ttg tcc act cct gaa gga tgg acc gca   739
Leu Cys Ser Asn Asp Arg Asp Leu Ser Thr Pro Glu Gly Trp Thr Ala
        200                 205                 210

gct gtt cat tct tac aac atg tct aat cag tat ttg atg gac gtt cga   787
Ala Val His Ser Tyr Asn Met Ser Asn Gln Tyr Leu Met Asp Val Arg
    215                 220                 225

gat gct gcc gcg tcc tac gct tta cga cag ccg gcg atc taaaacttaa    836
Asp Ala Ala Ala Ser Tyr Ala Leu Arg Gln Pro Ala Ile
230                 235                 240

caagcgcaac ccc                                                   849
```

<210> 150
<211> 242
<212> PRT
<213> Corynebacterium glutamicum

<400> 150

```
Met Val Ile Ser Phe Val Gly Trp Ala Leu Ser Phe Met Asp Gly Thr
  1               5                  10                  15

Ala Pro Ile Arg Gln Leu Gln Gln Ile Pro Glu Asp Val Pro Pro Ala
             20                  25                  30

Arg Gly Val Glu Val Pro Gln Ile Asp Thr Glu Ala Asp Gly Arg Thr
         35                  40                  45

Ser Asn His Leu Arg Phe Trp Ala Glu Pro Ile Ala Gln Asp Thr Gly
     50                  55                  60

Val Ser Ala Gln Ala Ile Ala Ala Tyr Gly Asn Ala Glu Leu Ile Ala
 65                  70                  75                  80

Ser Thr Ala Trp Pro Gly Cys Asn Leu Gly Trp Asn Thr Leu Ala Gly
                 85                  90                  95

Ile Gly Gln Val Glu Thr Arg His Gly Thr Tyr Asn Gly Lys Met Phe
            100                 105                 110

Gly Gly Ser Ser Leu Asp Glu Asn Gly Val Ala Thr Pro Pro Ile Ile
        115                 120                 125

Gly Val Pro Leu Asp Gly Ser Pro Gly Phe Ala Glu Ile Pro Asp Thr
    130                 135                 140

Asp Gly Gly Glu Leu Asp Gly Asp Thr Glu Tyr Asp Arg Ala Val Gly
```

```
145                 150                 155                 160

Pro Met Gln Phe Ile Pro Glu Thr Trp Arg Leu Met Gly Leu Asp Ala
                165                 170                 175

Asn Gly Asp Gly Val Ala Asp Pro Asn Gln Ile Asp Asp Ala Ala Leu
            180                 185                 190

Ser Ala Ala Asn Leu Leu Cys Ser Asn Asp Arg Asp Leu Ser Thr Pro
        195                 200                 205

Glu Gly Trp Thr Ala Ala Val His Ser Tyr Asn Met Ser Asn Gln Tyr
    210                 215                 220

Leu Met Asp Val Arg Asp Ala Ala Ala Ser Tyr Ala Leu Arg Gln Pro
225                 230                 235                 240

Ala Ile
```

Application Filed Under 37 CFR 1.53(b)

```
<210> 151
<211> 1401
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1378)
<223> RXN00242

<400> 151
ggatcactat cgctttaaac accgaaacct tcctgctagt tcaccaagat ttttaagttt 60

taccgcaatt tcttgagagc tttgggagga taatggcggt gtg aat gaa tgg cga   115
                                           Val Asn Glu Trp Arg
                                             1               5

aca gtc tcg ctt gta gat tcc acg gcg ctg acc gtg atc atc agt gtg   163
Thr Val Ser Leu Val Asp Ser Thr Ala Leu Thr Val Ile Ile Ser Val
                10                  15                  20

gcc gtg ttt act tct gct gtg gct ctg ctc gga gtt gtg aaa aag cgc   211
Ala Val Phe Thr Ser Ala Val Ala Leu Leu Gly Val Val Lys Lys Arg
            25                  30                  35

tct cgg tgg cgg gtt ctc gga gct ctc atc tcc tca gca gtt ctc acc   259
Ser Arg Trp Arg Val Leu Gly Ala Leu Ile Ser Ser Ala Val Leu Thr
        40                  45                  50

agt ggc gca tgg gtg gtt att gaa aag ctg tgg aag cct ttc ccc gac   307
Ser Gly Ala Trp Val Val Ile Glu Lys Leu Trp Lys Pro Phe Pro Asp
    55                  60                  65

ccc aat ccg tgg acc atc tat ctt tcc gct ggt ttg gcg gtt ttt cct   355
Pro Asn Pro Trp Thr Ile Tyr Leu Ser Ala Gly Leu Ala Val Phe Pro
70                  75                  80                  85

ctg ttg agc atc ttg ttc cgc act ggt cgt aca aga ata ctg atg gct   403
Leu Leu Ser Ile Leu Phe Arg Thr Gly Arg Thr Arg Ile Leu Met Ala
                90                  95                  100
```

```
aca ctc acc gtg att gca ctg gtt aat acg gcc gca gtc atc aat gtc   451
Thr Leu Thr Val Ile Ala Leu Val Asn Thr Ala Ala Val Ile Asn Val
            105                 110                 115

atc tac cag cca tac ccg acg ttg ggt tct ttc aat ccc gtg cca acg   499
Ile Tyr Gln Pro Tyr Pro Thr Leu Gly Ser Phe Asn Pro Val Pro Thr
        120                 125                 130

gct gtg tcc atg tcg tat gca gat ttt gaa tct cag acc act gcc ccg   547
Ala Val Ser Met Ser Tyr Ala Asp Phe Glu Ser Gln Thr Thr Ala Pro
    135                 140                 145

acg atg gat gac cgt gaa gtc ggt gcc ctt gtg cag gtg ccg cta gct   595
Thr Met Asp Asp Arg Glu Val Gly Ala Leu Val Gln Val Pro Leu Ala
150                 155                 160                 165

gga aca aca gat gat tcc acc tcc ggc ttt gat gcg cgc gat gcc tac   643
Gly Thr Thr Asp Asp Ser Thr Ser Gly Phe Asp Ala Arg Asp Ala Tyr
                170                 175                 180

gcc tat att ccg cct gcg tat tgg gat aat cct tcc cta caa ctg cca   691
Ala Tyr Ile Pro Pro Ala Tyr Trp Asp Asn Pro Ser Leu Gln Leu Pro
            185                 190                 195

gtt ttg gtt ctc atg ccc gga aac ccc ggc cag cca gat cag tgg ttt   739
Val Leu Val Leu Met Pro Gly Asn Pro Gly Gln Pro Asp Gln Trp Phe
        200                 205                 210

agc agt gga aat gcc gat caa aca gca gat aat ttc caa gca acc cac   787
Ser Ser Gly Asn Ala Asp Gln Thr Ala Asp Asn Phe Gln Ala Thr His
    215                 220                 225

gat ggc atc agc ccc att gtc atc agc gtg gat ggc aca gga tca ttc   835
Asp Gly Ile Ser Pro Ile Val Ile Ser Val Asp Gly Thr Gly Ser Phe
230                 235                 240                 245

agc gga aac cct gct tgc gtg gat tct gat gcc caa agc gtg atg aca   883
Ser Gly Asn Pro Ala Cys Val Asp Ser Asp Ala Gln Ser Val Met Thr
                250                 255                 260

tat cta tcc cac gat gtc ccc atg ttg atc aaa cag aaa ttc cga gtc   931
Tyr Leu Ser His Asp Val Pro Met Leu Ile Lys Gln Lys Phe Arg Val
            265                 270                 275

aat cag gat cag cgc acc tgg aca att ggt ggt tta agt tac ggc ggc   979
Asn Gln Asp Gln Arg Thr Trp Thr Ile Gly Gly Leu Ser Tyr Gly Gly
        280                 285                 290

acc tgt gct ttg cag atc atg acc aat cac ccc gaa gcg tat ggt tct   1027
Thr Cys Ala Leu Gln Ile Met Thr Asn His Pro Glu Ala Tyr Gly Ser
    295                 300                 305

ttc ctt gac ttc tcg ggc cag gaa gaa cca aca ctt ggc aca cgc cag   1075
Phe Leu Asp Phe Ser Gly Gln Glu Glu Pro Thr Leu Gly Thr Arg Gln
310                 315                 320                 325

caa act gtt gat cag ctt ttc ggc ggc gat gaa gac gca ttc aaa gcc   1123
Gln Thr Val Asp Gln Leu Phe Gly Gly Asp Glu Asp Ala Phe Lys Ala
                330                 335                 340
```

```
gtt aat ccg gaa gat ctg ctc aat caa gca atc agc tca gga gcg cat   1171
Val Asn Pro Glu Asp Leu Leu Asn Gln Ala Ile Ser Ser Gly Ala His
            345                 350                 355

acc tac agc ggg att tcg ggc agg ttt att gct ggt agc aac gat aaa   1219
Thr Tyr Ser Gly Ile Ser Gly Arg Phe Ile Ala Gly Ser Asn Asp Lys
        360                 365                 370

agt gca gtg agc gcg ctg tct cat ctt gat aat ttg agc aat cag gcg   1267
Ser Ala Val Ser Ala Leu Ser His Leu Asp Asn Leu Ser Asn Gln Ala
    375                 380                 385

ggc atg tcc acc acc ttt gat acc gtg gcc ggt gga cat tcc ttc cag   1315
Gly Met Ser Thr Thr Phe Asp Thr Val Ala Gly Gly His Ser Phe Gln
390                 395                 400                 405

gtg tgg cgc gtg gct tta gcg aat act ttt gat tgg gtt gcc aag cgc   1363
Val Trp Arg Val Ala Leu Ala Asn Thr Phe Asp Trp Val Ala Lys Arg
                410                 415                 420

ggc gga ttg cag gtt taacaatgaa agacgcttca cag                    1401
Gly Gly Leu Gln Val
            425
```

<210> 152
<211> 426
<212> PRT
<213> Corynebacterium glutamicum

<400> 152

```
Val Asn Glu Trp Arg Thr Val Ser Leu Val Asp Ser Thr Ala Leu Thr
  1               5                  10                  15

Val Ile Ile Ser Val Ala Val Phe Thr Ser Ala Val Ala Leu Leu Gly
             20                  25                  30

Val Val Lys Lys Arg Ser Arg Trp Arg Val Leu Gly Ala Leu Ile Ser
         35                  40                  45

Ser Ala Val Leu Thr Ser Gly Ala Trp Val Val Ile Glu Lys Leu Trp
     50                  55                  60

Lys Pro Phe Pro Asp Pro Asn Pro Trp Thr Ile Tyr Leu Ser Ala Gly
 65                  70                  75                  80

Leu Ala Val Phe Pro Leu Leu Ser Ile Leu Phe Arg Thr Gly Arg Thr
                 85                  90                  95

Arg Ile Leu Met Ala Thr Leu Thr Val Ile Ala Leu Val Asn Thr Ala
            100                 105                 110

Ala Val Ile Asn Val Ile Tyr Gln Pro Tyr Pro Thr Leu Gly Ser Phe
        115                 120                 125

Asn Pro Val Pro Thr Ala Val Ser Met Ser Tyr Ala Asp Phe Glu Ser
    130                 135                 140

Gln Thr Thr Ala Pro Thr Met Asp Asp Arg Glu Val Gly Ala Leu Val
145                 150                 155                 160
```

```
Gln Val Pro Leu Ala Gly Thr Thr Asp Asp Ser Thr Ser Gly Phe Asp
                165                 170                 175

Ala Arg Asp Ala Tyr Ala Tyr Ile Pro Pro Ala Tyr Trp Asp Asn Pro
            180                 185                 190

Ser Leu Gln Leu Pro Val Leu Val Leu Met Pro Gly Asn Pro Gly Gln
        195                 200                 205

Pro Asp Gln Trp Phe Ser Ser Gly Asn Ala Asp Gln Thr Ala Asp Asn
    210                 215                 220

Phe Gln Ala Thr His Asp Gly Ile Ser Pro Ile Val Ile Ser Val Asp
225                 230                 235                 240

Gly Thr Gly Ser Phe Ser Gly Asn Pro Ala Cys Val Asp Ser Asp Ala
                245                 250                 255

Gln Ser Val Met Thr Tyr Leu Ser His Asp Val Pro Met Leu Ile Lys
            260                 265                 270

Gln Lys Phe Arg Val Asn Gln Asp Gln Arg Thr Trp Thr Ile Gly Gly
        275                 280                 285

Leu Ser Tyr Gly Gly Thr Cys Ala Leu Gln Ile Met Thr Asn His Pro
    290                 295                 300

Glu Ala Tyr Gly Ser Phe Leu Asp Phe Ser Gly Gln Glu Glu Pro Thr
305                 310                 315                 320

Leu Gly Thr Arg Gln Gln Thr Val Asp Gln Leu Phe Gly Gly Asp Glu
                325                 330                 335

Asp Ala Phe Lys Ala Val Asn Pro Glu Asp Leu Leu Asn Gln Ala Ile
            340                 345                 350

Ser Ser Gly Ala His Thr Tyr Ser Gly Ile Ser Gly Arg Phe Ile Ala
        355                 360                 365

Gly Ser Asn Asp Lys Ser Ala Val Ser Ala Leu Ser His Leu Asp Asn
    370                 375                 380

Leu Ser Asn Gln Ala Gly Met Ser Thr Thr Phe Asp Thr Val Ala Gly
385                 390                 395                 400

Gly His Ser Phe Gln Val Trp Arg Val Ala Leu Ala Asn Thr Phe Asp
                405                 410                 415

Trp Val Ala Lys Arg Gly Gly Leu Gln Val
            420                 425
```

<210> 153
<211> 1303
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1303)
<223> FRXA00242

<400> 153
ggatcactat cgctttaaac accgaaacct tcctgctagt tcaccaagat ttttaagttt 60

taccgcaatt tcttgagagc tttgggagga taatggcggt gtg aat gaa tgg cga 115
Val Asn Glu Trp Arg
1 5

aca gtc tcg ctt gta gat tcc acg gcg ctg acc gtg atc atc agt gtg 163
Thr Val Ser Leu Val Asp Ser Thr Ala Leu Thr Val Ile Ile Ser Val
10 15 20

gcc gtg ttt act tct gct gtg gct ctg ctc gga gtt gtg aaa aag cgc 211
Ala Val Phe Thr Ser Ala Val Ala Leu Leu Gly Val Val Lys Lys Arg
25 30 35

tct cgg tgg cgg gtt ctc gga gct ctc atc tcc tca gca gtt ctc acc 259
Ser Arg Trp Arg Val Leu Gly Ala Leu Ile Ser Ser Ala Val Leu Thr
40 45 50

agt ggc gca tgg gtg gtt att gaa aag ctg tgg aag cct ttc ccc gac 307
Ser Gly Ala Trp Val Val Ile Glu Lys Leu Trp Lys Pro Phe Pro Asp
55 60 65

ccc aat ccg tgg acc atc tat ctt tcc gct ggt ttg gcg gtt ttt cct 355
Pro Asn Pro Trp Thr Ile Tyr Leu Ser Ala Gly Leu Ala Val Phe Pro
70 75 80 85

ctg ttg agc atc ttg ttc cgc act ggt cgt aca aga ata ctg atg gct 403
Leu Leu Ser Ile Leu Phe Arg Thr Gly Arg Thr Arg Ile Leu Met Ala
90 95 100

aca ctc acc gtg att gca ctg gtt aat acg gcc gca gtc atc aat gtc 451
Thr Leu Thr Val Ile Ala Leu Val Asn Thr Ala Ala Val Ile Asn Val
105 110 115

atc tac cag cca tac ccg acg ttg ggt tct ttc aat ccc gtg cca acg 499
Ile Tyr Gln Pro Tyr Pro Thr Leu Gly Ser Phe Asn Pro Val Pro Thr
120 125 130

gct gtg tcc atg tcg tat gca gat ttt gaa tct cag acc act gcc ccg 547
Ala Val Ser Met Ser Tyr Ala Asp Phe Glu Ser Gln Thr Thr Ala Pro
135 140 145

acg atg gat gac cgt gaa gtc ggt gcc ctt gtg cag gtg ccg cta gct 595
Thr Met Asp Asp Arg Glu Val Gly Ala Leu Val Gln Val Pro Leu Ala
150 155 160 165

gga aca aca gat gat tcc acc tcc ggc ttt gat gcg cgc gat gcc tac 643
Gly Thr Thr Asp Asp Ser Thr Ser Gly Phe Asp Ala Arg Asp Ala Tyr
170 175 180

gcc tat att ccg cct gcg tat tgg gat aat cct tcc cta caa ctg cca 691
Ala Tyr Ile Pro Pro Ala Tyr Trp Asp Asn Pro Ser Leu Gln Leu Pro
185 190 195

gtt ttg gtt ctc atg ccc gga aac ccc ggc cag cca gat cag tgg ttt 739
Val Leu Val Leu Met Pro Gly Asn Pro Gly Gln Pro Asp Gln Trp Phe
200 205 210

agc agt gga aat gcc gat caa aca gca gat aat ttc caa gca acc cac 787

```
Ser Ser Gly Asn Ala Asp Gln Thr Ala Asp Asn Phe Gln Ala Thr His
    215                 220                 225

gat ggc atc agc ccc att gtc atc agc gtg gat ggc aca gga tca ttc   835
Asp Gly Ile Ser Pro Ile Val Ile Ser Val Asp Gly Thr Gly Ser Phe
230                 235                 240                 245

agc gga aac cct gct tgc gtg gat tct gat gcc caa agc gtg atg aca   883
Ser Gly Asn Pro Ala Cys Val Asp Ser Asp Ala Gln Ser Val Met Thr
                250                 255                 260

tat cta tcc cac gat gtc ccc atg ttg atc aaa cag aaa ttc cga gtc   931
Tyr Leu Ser His Asp Val Pro Met Leu Ile Lys Gln Lys Phe Arg Val
            265                 270                 275

aat cag gat cag cgc acc tgg aca att ggt ggt tta agt tac ggc ggc   979
Asn Gln Asp Gln Arg Thr Trp Thr Ile Gly Gly Leu Ser Tyr Gly Gly
        280                 285                 290

acc tgt gct ttg cag atc atg acc aat cac ccc gaa gcg tat ggt tct   1027
Thr Cys Ala Leu Gln Ile Met Thr Asn His Pro Glu Ala Tyr Gly Ser
    295                 300                 305

ttc ctt gac ttc tcg ggc cag gaa gaa cca aca ctt ggc aca cgc cag   1075
Phe Leu Asp Phe Ser Gly Gln Glu Glu Pro Thr Leu Gly Thr Arg Gln
310                 315                 320                 325

caa act gtt gat cag ctt ttc ggc ggc gat gaa gac gca ttc aaa gcc   1123
Gln Thr Val Asp Gln Leu Phe Gly Gly Asp Glu Asp Ala Phe Lys Ala
                330                 335                 340

gtt aat ccg gaa gat ctg ctc aat caa gca atc agc tca gga gcg cat   1171
Val Asn Pro Glu Asp Leu Leu Asn Gln Ala Ile Ser Ser Gly Ala His
            345                 350                 355

acc tac agc ggg att tcg ggc agg ttt att gct ggt agc aac gat aaa   1219
Thr Tyr Ser Gly Ile Ser Gly Arg Phe Ile Ala Gly Ser Asn Asp Lys
        360                 365                 370

agt gca gtg agc gcg ctg tct cat ctt gat aat ttg agc aat cag gcg   1267
Ser Ala Val Ser Ala Leu Ser His Leu Asp Asn Leu Ser Asn Gln Ala
    375                 380                 385

ggc atg tcc acc acc ttt gat acc gtg gcc ggt gga                   1303
Gly Met Ser Thr Thr Phe Asp Thr Val Ala Gly Gly
390                 395                 400
```

<210> 154
<211> 401
<212> PRT
<213> Corynebacterium glutamicum

<400> 154

```
Val Asn Glu Trp Arg Thr Val Ser Leu Val Asp Ser Thr Ala Leu Thr
  1               5                  10                  15

Val Ile Ile Ser Val Ala Val Phe Thr Ser Ala Val Ala Leu Leu Gly
             20                  25                  30

Val Val Lys Lys Arg Ser Arg Trp Arg Val Leu Gly Ala Leu Ile Ser
```

```
         35                  40                  45

Ser Ala Val Leu Thr Ser Gly Ala Trp Val Val Ile Glu Lys Leu Trp
     50                  55                  60

Lys Pro Phe Pro Asp Pro Asn Pro Trp Thr Ile Tyr Leu Ser Ala Gly
 65                  70                  75                  80

Leu Ala Val Phe Pro Leu Leu Ser Ile Leu Phe Arg Thr Gly Arg Thr
                 85                  90                  95

Arg Ile Leu Met Ala Thr Leu Thr Val Ile Ala Leu Val Asn Thr Ala
            100                 105                 110

Ala Val Ile Asn Val Ile Tyr Gln Pro Tyr Pro Thr Leu Gly Ser Phe
        115                 120                 125

Asn Pro Val Pro Thr Ala Val Ser Met Ser Tyr Ala Asp Phe Glu Ser
    130                 135                 140

Gln Thr Thr Ala Pro Thr Met Asp Asp Arg Glu Val Gly Ala Leu Val
145                 150                 155                 160

Gln Val Pro Leu Ala Gly Thr Thr Asp Asp Ser Thr Ser Gly Phe Asp
                165                 170                 175

Ala Arg Asp Ala Tyr Ala Tyr Ile Pro Pro Ala Tyr Trp Asp Asn Pro
            180                 185                 190

Ser Leu Gln Leu Pro Val Leu Val Leu Met Pro Gly Asn Pro Gly Gln
        195                 200                 205

Pro Asp Gln Trp Phe Ser Ser Gly Asn Ala Asp Gln Thr Ala Asp Asn
    210                 215                 220

Phe Gln Ala Thr His Asp Gly Ile Ser Pro Ile Val Ile Ser Val Asp
225                 230                 235                 240

Gly Thr Gly Ser Phe Ser Gly Asn Pro Ala Cys Val Asp Ser Asp Ala
                245                 250                 255

Gln Ser Val Met Thr Tyr Leu Ser His Asp Val Pro Met Leu Ile Lys
            260                 265                 270

Gln Lys Phe Arg Val Asn Gln Asp Gln Arg Thr Trp Thr Ile Gly Gly
        275                 280                 285

Leu Ser Tyr Gly Gly Thr Cys Ala Leu Gln Ile Met Thr Asn His Pro
    290                 295                 300

Glu Ala Tyr Gly Ser Phe Leu Asp Phe Ser Gly Gln Glu Glu Pro Thr
305                 310                 315                 320

Leu Gly Thr Arg Gln Gln Thr Val Asp Gln Leu Phe Gly Gly Asp Glu
                325                 330                 335

Asp Ala Phe Lys Ala Val Asn Pro Glu Asp Leu Leu Asn Gln Ala Ile
            340                 345                 350

Ser Ser Gly Ala His Thr Tyr Ser Gly Ile Ser Gly Arg Phe Ile Ala
        355                 360                 365
```

```
Gly Ser Asn Asp Lys Ser Ala Val Ser Ala Leu Ser His Leu Asp Asn
    370                 375                 380

Leu Ser Asn Gln Ala Gly Met Ser Thr Thr Phe Asp Thr Val Ala Gly
385                 390                 395                 400

Gly
```

<210> 155
<211> 1050
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1027)
<223> RXN00247

<400> 155

```
aacccctaac tactgacctc gcaccacttg ttgcagcccg ttaccacgct gcattgagcg 60

cactgctggc acatatctaa gaccgctaag gaaatcagct atg cag aca tta atc   115
                                              Met Gln Thr Leu Ile
                                                1               5

ttt atc gcc att gca ggc gtc gca gca cag ctt gtt gat ggc ggc ctc   163
Phe Ile Ala Ile Ala Gly Val Ala Ala Gln Leu Val Asp Gly Gly Leu
                10                  15                  20

ggc atg ggg ttc ggc gtc acc tca acc acc atc ctc atc atg ctc gca   211
Gly Met Gly Phe Gly Val Thr Ser Thr Thr Ile Leu Ile Met Leu Ala
            25                  30                  35

ggt tta ggc cct gcg cag gca tcc gcc gtc gtg cac acc gca gag gtt   259
Gly Leu Gly Pro Ala Gln Ala Ser Ala Val Val His Thr Ala Glu Val
        40                  45                  50

gga acc acc tta gtt tct ggt tta agc cac tgg aaa ttt ggc aac gtg   307
Gly Thr Thr Leu Val Ser Gly Leu Ser His Trp Lys Phe Gly Asn Val
    55                  60                  65

gat tgg aaa gta gtt gtc cgg ctc ggt atc ccc ggc gct atc ggc gca   355
Asp Trp Lys Val Val Val Arg Leu Gly Ile Pro Gly Ala Ile Gly Ala
70                  75                  80                  85

ttt gct ggc gct acc ttc ttg tcc aat att tcc acc gaa gca gca gca   403
Phe Ala Gly Ala Thr Phe Leu Ser Asn Ile Ser Thr Glu Ala Ala Ala
                90                  95                 100

ccg atc acc tcc ctg att ctt gcc ctg atc ggc atg aac cta gtc tgg   451
Pro Ile Thr Ser Leu Ile Leu Ala Leu Ile Gly Met Asn Leu Val Trp
            105                 110                 115

cga ttc agc aag gga cgc atc cgc cgc gac tat tcc gat cgc ccg cac   499
Arg Phe Ser Lys Gly Arg Ile Arg Arg Asp Tyr Ser Asp Arg Pro His
        120                 125                 130

agc agg gga ttc ctc ggc gga ctc ggt att gtc ggt ggt ttc gtt gac   547
```

```
Ser Arg Gly Phe Leu Gly Gly Leu Gly Ile Val Gly Gly Phe Val Asp
    135                 140                 145

gca tcc ggt ggc ggc gga tgg ggt cca gtg acc acc tct acg ctg ctg   595
Ala Ser Gly Gly Gly Gly Trp Gly Pro Val Thr Thr Ser Thr Leu Leu
150                 155                 160                 165

tct ttg gga cgc acc gaa ccc cgc aaa gta gtc ggc acc gtc aac acc   643
Ser Leu Gly Arg Thr Glu Pro Arg Lys Val Val Gly Thr Val Asn Thr
                170                 175                 180

gca gaa ttc tta gtc tcc cta gcc gca aca ttg ggc ttc gtc gtg gga   691
Ala Glu Phe Leu Val Ser Leu Ala Ala Thr Leu Gly Phe Val Val Gly
            185                 190                 195

ctg tgg gat gac cta gta gct aac ctc tct gca gtt ctc gcg ttg ctc   739
Leu Trp Asp Asp Leu Val Ala Asn Leu Ser Ala Val Leu Ala Leu Leu
        200                 205                 210

atc ggc ggc gca atc gca gca cca atc ggc gcc tgg atg atc tct cgc   787
Ile Gly Gly Ala Ile Ala Ala Pro Ile Gly Ala Trp Met Ile Ser Arg
    215                 220                 225

gtt aat gca acc gtc ctc ggt ggc ttc gtg ggc acc ctg att gtc aca   835
Val Asn Ala Thr Val Leu Gly Gly Phe Val Gly Thr Leu Ile Val Thr
230                 235                 240                 245

ctg aac ctg cca aag gtg ctc aac gtg gtt ggc ctt gat ttc atc ccc   883
Leu Asn Leu Pro Lys Val Leu Asn Val Val Gly Leu Asp Phe Ile Pro
                250                 255                 260

acc ggc ctc atc cag gtc acc gtc ctc ctc atc ggc ctg ccg ctg acg   931
Thr Gly Leu Ile Gln Val Thr Val Leu Leu Ile Gly Leu Pro Leu Thr
            265                 270                 275

tac ctc ggc ttc cgc cgc tac cgc aaa aat ctc ctc aac gag acc atc   979
Tyr Leu Gly Phe Arg Arg Tyr Arg Lys Asn Leu Leu Asn Glu Thr Ile
        280                 285                 290

tcc agc gaa gtt gtc tcc gaa cca aag ggc caa aag att aaa agc act   1027
Ser Ser Glu Val Val Ser Glu Pro Lys Gly Gln Lys Ile Lys Ser Thr
    295                 300                 305

taaaacacgc ttttcgacgc cca                                        1050


<210> 156
<211> 309
<212> PRT
<213> Corynebacterium glutamicum

<400> 156
Met Gln Thr Leu Ile Phe Ile Ala Ile Ala Gly Val Ala Ala Gln Leu
  1               5                  10                  15

Val Asp Gly Gly Leu Gly Met Gly Phe Gly Val Thr Ser Thr Thr Ile
             20                  25                  30

Leu Ile Met Leu Ala Gly Leu Gly Pro Ala Gln Ala Ser Ala Val Val
         35                  40                  45
```

```
His Thr Ala Glu Val Gly Thr Thr Leu Val Ser Gly Leu Ser His Trp
     50                  55                  60

Lys Phe Gly Asn Val Asp Trp Lys Val Val Val Arg Leu Gly Ile Pro
 65                  70                  75                  80

Gly Ala Ile Gly Ala Phe Ala Gly Ala Thr Phe Leu Ser Asn Ile Ser
                85                  90                  95

Thr Glu Ala Ala Ala Pro Ile Thr Ser Leu Ile Leu Ala Leu Ile Gly
            100                 105                 110

Met Asn Leu Val Trp Arg Phe Ser Lys Gly Arg Ile Arg Arg Asp Tyr
        115                 120                 125

Ser Asp Arg Pro His Ser Arg Gly Phe Leu Gly Gly Leu Gly Ile Val
    130                 135                 140

Gly Gly Phe Val Asp Ala Ser Gly Gly Gly Gly Trp Gly Pro Val Thr
145                 150                 155                 160

Thr Ser Thr Leu Leu Ser Leu Gly Arg Thr Glu Pro Arg Lys Val Val
                165                 170                 175

Gly Thr Val Asn Thr Ala Glu Phe Leu Val Ser Leu Ala Ala Thr Leu
            180                 185                 190

Gly Phe Val Val Gly Leu Trp Asp Asp Leu Val Ala Asn Leu Ser Ala
        195                 200                 205

Val Leu Ala Leu Leu Ile Gly Gly Ala Ile Ala Ala Pro Ile Gly Ala
    210                 215                 220

Trp Met Ile Ser Arg Val Asn Ala Thr Val Leu Gly Gly Phe Val Gly
225                 230                 235                 240

Thr Leu Ile Val Thr Leu Asn Leu Pro Lys Val Leu Asn Val Val Gly
                245                 250                 255

Leu Asp Phe Ile Pro Thr Gly Leu Ile Gln Val Thr Val Leu Leu Ile
            260                 265                 270

Gly Leu Pro Leu Thr Tyr Leu Gly Phe Arg Arg Tyr Arg Lys Asn Leu
        275                 280                 285

Leu Asn Glu Thr Ile Ser Ser Glu Val Val Ser Glu Pro Lys Gly Gln
    290                 295                 300

Lys Ile Lys Ser Thr
305
```

<210> 157
<211> 1050
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1027)
<223> FRXA00247

<400> 157
aacccctaac tactgacctc gcaccacttg ttgcagcccg ttaccacgct gcattgagcg 60

```
cactgctggc acatatctaa gaccgctaag gaaatcagct atg cag aca tta atc   115
                                            Met Gln Thr Leu Ile
                                              1               5

ttt atc gcc att gca ggc gtc gca gca cag ctt gtt gat ggc ggc ctc   163
Phe Ile Ala Ile Ala Gly Val Ala Ala Gln Leu Val Asp Gly Gly Leu
                 10                  15                  20

ggc atg ggg ttc ggc gtc acc tca acc acc atc ctc atc atg ctc gca   211
Gly Met Gly Phe Gly Val Thr Ser Thr Thr Ile Leu Ile Met Leu Ala
             25                  30                  35

ggt tta ggc cct gcg cag gca tcc gcc gtc gtg cac acc gca gag gtt   259
Gly Leu Gly Pro Ala Gln Ala Ser Ala Val Val His Thr Ala Glu Val
         40                  45                  50

gga acc acc tta gtt tct ggt tta agc cac tgg aaa ttt ggc aac gtg   307
Gly Thr Thr Leu Val Ser Gly Leu Ser His Trp Lys Phe Gly Asn Val
     55                  60                  65

gat tgg aaa gta gtt gtc cgg ctc ggt atc ccc ggc gct atc ggc gca   355
Asp Trp Lys Val Val Val Arg Leu Gly Ile Pro Gly Ala Ile Gly Ala
 70                  75                  80                  85

ttt gct ggc gct acc ttc ttg tcc aat att tcc acc gaa gca gca gca   403
Phe Ala Gly Ala Thr Phe Leu Ser Asn Ile Ser Thr Glu Ala Ala Ala
                 90                  95                 100

ccg atc acc tcc ctg att ctt gcc ctg atc ggc atg aac cta gtc tgg   451
Pro Ile Thr Ser Leu Ile Leu Ala Leu Ile Gly Met Asn Leu Val Trp
            105                 110                 115

cga ttc agc aag gga cgc atc cgc cgc gac tat tcc gat cgc ccg cac   499
Arg Phe Ser Lys Gly Arg Ile Arg Arg Asp Tyr Ser Asp Arg Pro His
        120                 125                 130

agc agg gga ttc ctc ggc gga ctc ggt att gtc ggt ggt ttc gtt gac   547
Ser Arg Gly Phe Leu Gly Gly Leu Gly Ile Val Gly Gly Phe Val Asp
    135                 140                 145

gca tcc ggt ggc ggc gga tgg ggt cca gtg acc acc tct acg ctg ctg   595
Ala Ser Gly Gly Gly Gly Trp Gly Pro Val Thr Thr Ser Thr Leu Leu
150                 155                 160                 165

tct ttg gga cgc acc gaa ccc cgc aaa gta gtc ggc acc gtc aac acc   643
Ser Leu Gly Arg Thr Glu Pro Arg Lys Val Val Gly Thr Val Asn Thr
                170                 175                 180

gca gaa ttc tta gtc tcc cta gcc gca aca ttg ggc ttc gtc gtg gga   691
Ala Glu Phe Leu Val Ser Leu Ala Ala Thr Leu Gly Phe Val Val Gly
            185                 190                 195

ctg tgg gat gac cta gta gct aac ctc tct gca gtt ctc gcg ttg ctc   739
Leu Trp Asp Asp Leu Val Ala Asn Leu Ser Ala Val Leu Ala Leu Leu
        200                 205                 210

atc ggc ggc gca atc gca gca cca atc ggc gcc tgg atg atc tct cgc   787
```

```
Ile Gly Gly Ala Ile Ala Ala Pro Ile Gly Ala Trp Met Ile Ser Arg
    215                 220                 225

gtt aat gca acc gtc ctc ggt ggc ttc gtg ggc acc ctg att gtc aca   835
Val Asn Ala Thr Val Leu Gly Gly Phe Val Gly Thr Leu Ile Val Thr
230                 235                 240                 245

ctg aac ctg cca aag gtg ctc aac gtg gtt ggc ctt gat ttc atc ccc   883
Leu Asn Leu Pro Lys Val Leu Asn Val Val Gly Leu Asp Phe Ile Pro
                250                 255                 260

acc ggc ctc atc cag gtc acc gtc ctc ctc atc ggc ctg ccg ctg acg   931
Thr Gly Leu Ile Gln Val Thr Val Leu Leu Ile Gly Leu Pro Leu Thr
            265                 270                 275

tac ctc ggc ttc cgc cgc tac cgc aaa aat ctc ctc aac gag acc atc   979
Tyr Leu Gly Phe Arg Arg Tyr Arg Lys Asn Leu Leu Asn Glu Thr Ile
        280                 285                 290

tcc agc gaa gtt gtc tcc gaa cca aag ggc caa aag att aaa agc act   1027
Ser Ser Glu Val Val Ser Glu Pro Lys Gly Gln Lys Ile Lys Ser Thr
    295                 300                 305

taaaacacgc ttttcgacgc cca                                        1050


<210> 158
<211> 309
<212> PRT
<213> Corynebacterium glutamicum

<400> 158
Met Gln Thr Leu Ile Phe Ile Ala Ile Ala Gly Val Ala Ala Gln Leu
  1               5                  10                  15

Val Asp Gly Gly Leu Gly Met Gly Phe Gly Val Thr Ser Thr Thr Ile
             20                  25                  30

Leu Ile Met Leu Ala Gly Leu Gly Pro Ala Gln Ala Ser Ala Val Val
         35                  40                  45

His Thr Ala Glu Val Gly Thr Thr Leu Val Ser Gly Leu Ser His Trp
     50                  55                  60

Lys Phe Gly Asn Val Asp Trp Lys Val Val Val Arg Leu Gly Ile Pro
 65                  70                  75                  80

Gly Ala Ile Gly Ala Phe Ala Gly Ala Thr Phe Leu Ser Asn Ile Ser
                 85                  90                  95

Thr Glu Ala Ala Ala Pro Ile Thr Ser Leu Ile Leu Ala Leu Ile Gly
            100                 105                 110

Met Asn Leu Val Trp Arg Phe Ser Lys Gly Arg Ile Arg Arg Asp Tyr
        115                 120                 125

Ser Asp Arg Pro His Ser Arg Gly Phe Leu Gly Gly Leu Gly Ile Val
    130                 135                 140

Gly Gly Phe Val Asp Ala Ser Gly Gly Gly Gly Trp Gly Pro Val Thr
145                 150                 155                 160
```

```
Thr Ser Thr Leu Leu Ser Leu Gly Arg Thr Glu Pro Arg Lys Val Val
                165                 170                 175

Gly Thr Val Asn Thr Ala Glu Phe Leu Val Ser Leu Ala Ala Thr Leu
            180                 185                 190

Gly Phe Val Val Gly Leu Trp Asp Asp Leu Val Ala Asn Leu Ser Ala
        195                 200                 205

Val Leu Ala Leu Leu Ile Gly Gly Ala Ile Ala Ala Pro Ile Gly Ala
    210                 215                 220

Trp Met Ile Ser Arg Val Asn Ala Thr Val Leu Gly Gly Phe Val Gly
225                 230                 235                 240

Thr Leu Ile Val Thr Leu Asn Leu Pro Lys Val Leu Asn Val Val Gly
                245                 250                 255

Leu Asp Phe Ile Pro Thr Gly Leu Ile Gln Val Thr Val Leu Leu Ile
            260                 265                 270

Gly Leu Pro Leu Thr Tyr Leu Gly Phe Arg Arg Tyr Arg Lys Asn Leu
        275                 280                 285

Leu Asn Glu Thr Ile Ser Ser Glu Val Val Ser Glu Pro Lys Gly Gln
    290                 295                 300

Lys Ile Lys Ser Thr
305
```

<210> 159
<211> 894
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(871)
<223> RXN00256

<400> 159

```
aattaatcaa tcagaaaaac atattgaata cttataaatt tctgacatac tcattaatga 60

gatattcgaa gtctttatca aaatgattaa caaaaggagt atg ttt atg tcg cta   115
                                              Met Phe Met Ser Leu
                                                1               5

aaa act cgc cga ata ttc ggc gca ctt gct gtt tcg cta tca atc tct   163
Lys Thr Arg Arg Ile Phe Gly Ala Leu Ala Val Ser Leu Ser Ile Ser
                10                  15                  20

ttc tca gcc att gct aca cct gca gca tcc gca caa gaa cta gtg gtg   211
Phe Ser Ala Ile Ala Thr Pro Ala Ala Ser Ala Gln Glu Leu Val Val
            25                  30                  35

agc aca tca gca gta aac gaa ttt ggt gta gtt acc agt gac atc acg   259
Ser Thr Ser Ala Val Asn Glu Phe Gly Val Val Thr Ser Asp Ile Thr
        40                  45                  50
```

```
gct gag caa att ctt cag gcg caa gat cta atc gct gag atg aaa cag   307
Ala Glu Gln Ile Leu Gln Ala Gln Asp Leu Ile Ala Glu Met Lys Gln
     55                  60                  65

tca gag gac ata tat gag tat ttc ggt gcc ttg tct gac gtt gaa cag   355
Ser Glu Asp Ile Tyr Glu Tyr Phe Gly Ala Leu Ser Asp Val Glu Gln
 70                  75                  80                  85

aga tcc atc att gca gct gta aag gaa aat cca tat ctc att gag aac   403
Arg Ser Ile Ile Ala Ala Val Lys Glu Asn Pro Tyr Leu Ile Glu Asn
                 90                  95                 100

gaa tca ccc cgt atg aga gtc caa agt gaa aca ccc gac gag gaa aca   451
Glu Ser Pro Arg Met Arg Val Gln Ser Glu Thr Pro Asp Glu Glu Thr
            105                 110                 115

cct gat aag aaa aag ccg agc aaa acc tac aag ctc tat atg agc att   499
Pro Asp Lys Lys Lys Pro Ser Lys Thr Tyr Lys Leu Tyr Met Ser Ile
        120                 125                 130

ctc gaa atg atg tca tgt atc aat ctt gtt gat gtt ccg tca tgt gcc   547
Leu Glu Met Met Ser Cys Ile Asn Leu Val Asp Val Pro Ser Cys Ala
    135                 140                 145

caa gcc ctt aaa gcg gca aat ata gct gaa cgc gag gcc aag gcc cgt   595
Gln Ala Leu Lys Ala Ala Asn Ile Ala Glu Arg Glu Ala Lys Ala Arg
150                 155                 160                 165

tac ccc gat tcg gtc act aat ggt aaa ggc gat gcc ctt cgt cat tgt   643
Tyr Pro Asp Ser Val Thr Asn Gly Lys Gly Asp Ala Leu Arg His Cys
                170                 175                 180

gca tgg agc gct ctc atg act att cga atc gga aaa gat gca gcc gaa   691
Ala Trp Ser Ala Leu Met Thr Ile Arg Ile Gly Lys Asp Ala Ala Glu
            185                 190                 195

aga att ggt aac gct cat gaa acc gtt gtg aga ggt gaa ccc gaa gaa   739
Arg Ile Gly Asn Ala His Glu Thr Val Val Arg Gly Glu Pro Glu Glu
        200                 205                 210

aga gaa atg gat ctc atc aat aac gcg ctg ggt aga gac atc ggc gaa   787
Arg Glu Met Asp Leu Ile Asn Asn Ala Leu Gly Arg Asp Ile Gly Glu
    215                 220                 225

aga ttc atc atc aat ggc gat gaa acg ggt gcg ctc agt act tgt gta   835
Arg Phe Ile Ile Asn Gly Asp Glu Thr Gly Ala Leu Ser Thr Cys Val
230                 235                 240                 245

tcc atg gct aat atc ggg cta ctt cat act ctg ttg taaacaaagg        881
Ser Met Ala Asn Ile Gly Leu Leu His Thr Leu Leu
                250                 255

aagtttctat cat                                                   894
```

<210> 160
<211> 257
<212> PRT
<213> Corynebacterium glutamicum

<400> 160

```
Met Phe Met Ser Leu Lys Thr Arg Arg Ile Phe Gly Ala Leu Ala Val
 1               5                  10                  15

Ser Leu Ser Ile Ser Phe Ser Ala Ile Ala Thr Pro Ala Ala Ser Ala
            20                  25                  30

Gln Glu Leu Val Val Ser Thr Ser Ala Val Asn Glu Phe Gly Val Val
        35                  40                  45

Thr Ser Asp Ile Thr Ala Glu Gln Ile Leu Gln Ala Gln Asp Leu Ile
    50                  55                  60

Ala Glu Met Lys Gln Ser Glu Asp Ile Tyr Glu Tyr Phe Gly Ala Leu
65                  70                  75                  80

Ser Asp Val Glu Gln Arg Ser Ile Ile Ala Ala Val Lys Glu Asn Pro
                85                  90                  95

Tyr Leu Ile Glu Asn Glu Ser Pro Arg Met Arg Val Gln Ser Glu Thr
            100                 105                 110

Pro Asp Glu Glu Thr Pro Asp Lys Lys Lys Pro Ser Lys Thr Tyr Lys
        115                 120                 125

Leu Tyr Met Ser Ile Leu Glu Met Met Ser Cys Ile Asn Leu Val Asp
    130                 135                 140

Val Pro Ser Cys Ala Gln Ala Leu Lys Ala Ala Asn Ile Ala Glu Arg
145                 150                 155                 160

Glu Ala Lys Ala Arg Tyr Pro Asp Ser Val Thr Asn Gly Lys Gly Asp
                165                 170                 175

Ala Leu Arg His Cys Ala Trp Ser Ala Leu Met Thr Ile Arg Ile Gly
            180                 185                 190

Lys Asp Ala Ala Glu Arg Ile Gly Asn Ala His Glu Thr Val Val Arg
        195                 200                 205

Gly Glu Pro Glu Glu Arg Glu Met Asp Leu Ile Asn Asn Ala Leu Gly
    210                 215                 220

Arg Asp Ile Gly Glu Arg Phe Ile Ile Asn Gly Asp Glu Thr Gly Ala
225                 230                 235                 240

Leu Ser Thr Cys Val Ser Met Ala Asn Ile Gly Leu Leu His Thr Leu
                245                 250                 255

Leu
```

<210> 161
<211> 894
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(871)
<223> FRXA00256

<400> 161
aattaatcaa tcagaaaaac atattgaata cttataaatt tctgacatac tcattaatga 60

gatattcgaa gtctttatca aaatgattaa caaaaggagt atg ttt atg tcg cta 115
Met Phe Met Ser Leu
1 5

aaa act cgc cga ata ttc ggc gca ctt gct gtt tcg cta tca atc tct 163
Lys Thr Arg Arg Ile Phe Gly Ala Leu Ala Val Ser Leu Ser Ile Ser
10 15 20

ttc tca gcc att gct aca cct gca gca tcc gca caa gaa cta gtg gtg 211
Phe Ser Ala Ile Ala Thr Pro Ala Ala Ser Ala Gln Glu Leu Val Val
25 30 35

agc aca tca gca gta aac gaa ttt ggt gta gtt acc agt gac atc acg 259
Ser Thr Ser Ala Val Asn Glu Phe Gly Val Val Thr Ser Asp Ile Thr
40 45 50

gct gag caa att ctt cag gcg caa gat cta atc gct gag atg aaa cag 307
Ala Glu Gln Ile Leu Gln Ala Gln Asp Leu Ile Ala Glu Met Lys Gln
55 60 65

tca gag gac ata tat gag tat ttc ggt gcc ttg tct gac gtt gaa cag 355
Ser Glu Asp Ile Tyr Glu Tyr Phe Gly Ala Leu Ser Asp Val Glu Gln
70 75 80 85

aga tcc atc att gca gct gta aag gaa aat cca tat ctc att gag aac 403
Arg Ser Ile Ile Ala Ala Val Lys Glu Asn Pro Tyr Leu Ile Glu Asn
90 95 100

gaa tca ccc cgt atg aga gtc caa agt gaa aca ccc gac gag gaa aca 451
Glu Ser Pro Arg Met Arg Val Gln Ser Glu Thr Pro Asp Glu Glu Thr
105 110 115

cct gat aag aaa aag ccg agc aaa acc tac aag ctc tat atg agc att 499
Pro Asp Lys Lys Lys Pro Ser Lys Thr Tyr Lys Leu Tyr Met Ser Ile
120 125 130

ctc gaa atg atg tca tgt atc aat ctt gtt gat gtt ccg tca tgt gcc 547
Leu Glu Met Met Ser Cys Ile Asn Leu Val Asp Val Pro Ser Cys Ala
135 140 145

caa gcc ctt aaa gcg gca aat ata gct gaa cgc gag gcc aag gcc cgt 595
Gln Ala Leu Lys Ala Ala Asn Ile Ala Glu Arg Glu Ala Lys Ala Arg
150 155 160 165

tac ccc gat tcg gtc act aat ggt aaa ggc gat gcc ctt cgt cat tgt 643
Tyr Pro Asp Ser Val Thr Asn Gly Lys Gly Asp Ala Leu Arg His Cys
170 175 180

gca tgg agc gct ctc atg act att cga atc gga aaa gat gca gcc gaa 691
Ala Trp Ser Ala Leu Met Thr Ile Arg Ile Gly Lys Asp Ala Ala Glu
185 190 195

aga att ggt aac gct cat gaa acc gtt gtg aga ggt gaa ccc gaa gaa 739
Arg Ile Gly Asn Ala His Glu Thr Val Val Arg Gly Glu Pro Glu Glu
200 205 210

aga gaa atg gat ctc atc aat aac gcg ctg ggt aga gac atc ggc gaa 787

```
Arg Glu Met Asp Leu Ile Asn Asn Ala Leu Gly Arg Asp Ile Gly Glu
    215                 220                 225

aga ttc atc atc aat ggc gat gaa acg ggt gcg ctc agt act tgt gta   835
Arg Phe Ile Ile Asn Gly Asp Glu Thr Gly Ala Leu Ser Thr Cys Val
230                 235                 240                 245

tcc atg gct aat atc ggg cta ctt cat act ctg ttg taaacaaagg       881
Ser Met Ala Asn Ile Gly Leu Leu His Thr Leu Leu
                250                 255

aagtttctat cat                                                  894


<210> 162
<211> 257
<212> PRT
<213> Corynebacterium glutamicum

<400> 162
Met Phe Met Ser Leu Lys Thr Arg Arg Ile Phe Gly Ala Leu Ala Val
  1               5                  10                  15

Ser Leu Ser Ile Ser Phe Ser Ala Ile Ala Thr Pro Ala Ala Ser Ala
            20                  25                  30

Gln Glu Leu Val Val Ser Thr Ser Ala Val Asn Glu Phe Gly Val Val
         35                  40                  45

Thr Ser Asp Ile Thr Ala Glu Gln Ile Leu Gln Ala Gln Asp Leu Ile
     50                  55                  60

Ala Glu Met Lys Gln Ser Glu Asp Ile Tyr Glu Tyr Phe Gly Ala Leu
 65                  70                  75                  80

Ser Asp Val Glu Gln Arg Ser Ile Ile Ala Ala Val Lys Glu Asn Pro
                85                  90                  95

Tyr Leu Ile Glu Asn Glu Ser Pro Arg Met Arg Val Gln Ser Glu Thr
            100                 105                 110

Pro Asp Glu Glu Thr Pro Asp Lys Lys Lys Pro Ser Lys Thr Tyr Lys
        115                 120                 125

Leu Tyr Met Ser Ile Leu Glu Met Met Ser Cys Ile Asn Leu Val Asp
    130                 135                 140

Val Pro Ser Cys Ala Gln Ala Leu Lys Ala Ala Asn Ile Ala Glu Arg
145                 150                 155                 160

Glu Ala Lys Ala Arg Tyr Pro Asp Ser Val Thr Asn Gly Lys Gly Asp
                165                 170                 175

Ala Leu Arg His Cys Ala Trp Ser Ala Leu Met Thr Ile Arg Ile Gly
            180                 185                 190

Lys Asp Ala Ala Glu Arg Ile Gly Asn Ala His Glu Thr Val Val Arg
        195                 200                 205

Gly Glu Pro Glu Glu Arg Glu Met Asp Leu Ile Asn Asn Ala Leu Gly
    210                 215                 220
```

```
Arg Asp Ile Gly Glu Arg Phe Ile Ile Asn Gly Asp Glu Thr Gly Ala
225                 230                 235                 240

Leu Ser Thr Cys Val Ser Met Ala Asn Ile Gly Leu Leu His Thr Leu
                245                 250                 255

Leu
```

<210> 163
<211> 501
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(478)
<223> RXN00264

<400> 163

```
aaaccggaag ggcccgttta ctccccctact tggcgcagaa atccacatca atccaggtga 60

agcagtcatc tttgatgttg atcccacgtt tgaacacggt ttg ctt gtc gat tcc   115
                                          Leu Leu Val Asp Ser
                                            1               5

ggc gac gtc caa cta gaa ggc gtc acc gtc gag ccc acc cag ctg gcc   163
Gly Asp Val Gln Leu Glu Gly Val Thr Val Glu Pro Thr Gln Leu Ala
                10                  15                  20

tac acc ggc atc aat gaa acc caa ctc cga atc cgt aac atc ggc acc   211
Tyr Thr Gly Ile Asn Glu Thr Gln Leu Arg Ile Arg Asn Ile Gly Thr
            25                  30                  35

aca ccg gcg cgt act gta ctg cta ggt ggc gaa cca ttt acc gaa gac   259
Thr Pro Ala Arg Thr Val Leu Leu Gly Gly Glu Pro Phe Thr Glu Asp
        40                  45                  50

atc gtg atg tgg tgg aac ttc att ggc cgc agc cat gaa gaa att gcc   307
Ile Val Met Trp Trp Asn Phe Ile Gly Arg Ser His Glu Glu Ile Ala
    55                  60                  65

gag tac cgt aaa cag tgg cag gcc gaa gct gat cgt ttt ggt atc acc   355
Glu Tyr Arg Lys Gln Trp Gln Ala Glu Ala Asp Arg Phe Gly Ile Thr
70                  75                  80                  85

cac gga tat atc agc cac cac aaa gat ggg ctc acc agg ctt cca gca   403
His Gly Tyr Ile Ser His His Lys Asp Gly Leu Thr Arg Leu Pro Ala
                90                  95                  100

ccc gag ctt ccc aac gct gct atc aag gca cgt aaa aac cca gca cca   451
Pro Glu Leu Pro Asn Ala Ala Ile Lys Ala Arg Lys Asn Pro Ala Pro
            105                 110                 115

act gca cga cca gaa acg aga att gat taaatgcgct ccgctcacgg         498
Thr Ala Arg Pro Glu Thr Arg Ile Asp
        120                 125

ccc                                                              501
```

<210> 164
<211> 126
<212> PRT
<213> Corynebacterium glutamicum

<400> 164
Leu Leu Val Asp Ser Gly Asp Val Gln Leu Glu Gly Val Thr Val Glu
1 5 10 15

Pro Thr Gln Leu Ala Tyr Thr Gly Ile Asn Glu Thr Gln Leu Arg Ile
20 25 30

Arg Asn Ile Gly Thr Thr Pro Ala Arg Thr Val Leu Leu Gly Gly Glu
35 40 45

Pro Phe Thr Glu Asp Ile Val Met Trp Trp Asn Phe Ile Gly Arg Ser
50 55 60

His Glu Glu Ile Ala Glu Tyr Arg Lys Gln Trp Gln Ala Glu Ala Asp
65 70 75 80

Arg Phe Gly Ile Thr His Gly Tyr Ile Ser His His Lys Asp Gly Leu
85 90 95

Thr Arg Leu Pro Ala Pro Glu Leu Pro Asn Ala Ala Ile Lys Ala Arg
100 105 110

Lys Asn Pro Ala Pro Thr Ala Arg Pro Glu Thr Arg Ile Asp
115 120 125

<210> 165
<211> 501
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(478)
<223> FRXA00264

<400> 165
aaaccggaag ggccsgttta ctcccctact tggcgcagaa atccacatca atccaggtga 60

agcagtcatc tttgatgttg atcccacgtt tgaacacggt ttg ctt gtc gat tcc 115
Leu Leu Val Asp Ser
1 5

ggc gac gtc caa cta gaa ggc gtc acc gtc gag ccc acc cag ctg gcc 163
Gly Asp Val Gln Leu Glu Gly Val Thr Val Glu Pro Thr Gln Leu Ala
10 15 20

tac acc ggc atc aat gaa acc caa ctc cga atc cgt aac atc ggc acc 211
Tyr Thr Gly Ile Asn Glu Thr Gln Leu Arg Ile Arg Asn Ile Gly Thr
25 30 35

aca ccg gcg cgt act gta ctg cta ggt ggc gaa cca ttt acc gaa gac 259
Thr Pro Ala Arg Thr Val Leu Leu Gly Gly Glu Pro Phe Thr Glu Asp
40 45 50

```
atc gtg atg tgg tgg aac ttc att ggc cgc agc cat gaa gaa att gcc   307
Ile Val Met Trp Trp Asn Phe Ile Gly Arg Ser His Glu Glu Ile Ala
     55                  60                  65

gag tac cgt aaa cag tgg cag gcc gaa gct gat cgt ttt ggt atc acc   355
Glu Tyr Arg Lys Gln Trp Gln Ala Glu Ala Asp Arg Phe Gly Ile Thr
 70                  75                  80                  85

cac gga tat atc agc cac cac aaa gat ggg ctc acc agg ctt cca gca   403
His Gly Tyr Ile Ser His His Lys Asp Gly Leu Thr Arg Leu Pro Ala
                 90                  95                 100

ccc gag ctt ccc aac gct gct atc aag gca cgt aaa aac cca gca cca   451
Pro Glu Leu Pro Asn Ala Ala Ile Lys Ala Arg Lys Asn Pro Ala Pro
            105                 110                 115

act gca cga cca gaa acg aga att gat taaatgcgct ccgctcacgg         498
Thr Ala Arg Pro Glu Thr Arg Ile Asp
        120                 125

ccc                                                              501
```

Sequence Listing as filed with the application

<210> 166
<211> 126
<212> PRT
<213> Corynebacterium glutamicum

<400> 166

```
Leu Leu Val Asp Ser Gly Asp Val Gln Leu Glu Gly Val Thr Val Glu
  1               5                  10                  15

Pro Thr Gln Leu Ala Tyr Thr Gly Ile Asn Glu Thr Gln Leu Arg Ile
             20                  25                  30

Arg Asn Ile Gly Thr Thr Pro Ala Arg Thr Val Leu Leu Gly Gly Glu
         35                  40                  45

Pro Phe Thr Glu Asp Ile Val Met Trp Trp Asn Phe Ile Gly Arg Ser
     50                  55                  60

His Glu Glu Ile Ala Glu Tyr Arg Lys Gln Trp Gln Ala Glu Ala Asp
 65                  70                  75                  80

Arg Phe Gly Ile Thr His Gly Tyr Ile Ser His His Lys Asp Gly Leu
                 85                  90                  95

Thr Arg Leu Pro Ala Pro Glu Leu Pro Asn Ala Ala Ile Lys Ala Arg
            100                 105                 110

Lys Asn Pro Ala Pro Thr Ala Arg Pro Glu Thr Arg Ile Asp
        115                 120                 125
```

<210> 167
<211> 441
<212> DNA
<213> Corynebacterium glutamicum

<220>

<221> CDS
<222> (101)..(418)
<223> RXN00267

<400> 167
gtcgtactta tcttttaaag tcatgcctta aaggatacgg agatcactcc ggcttggctt 60

gggtggcggt gttatcaaag tagtcgtagc gttgagaact atg cga aac tct aag 115
Met Arg Asn Ser Lys
1 5

tct ggc ctg gcc ttt tcc gca gct gca cta ttt tgt gtc gtc gcg gta 163
Ser Gly Leu Ala Phe Ser Ala Ala Ala Leu Phe Cys Val Val Ala Val
10 15 20

atc act cgt att gca agt tcc cca tca ttt atc gct att gtg gcg atc 211
Ile Thr Arg Ile Ala Ser Ser Pro Ser Phe Ile Ala Ile Val Ala Ile
25 30 35

atc gtg gct gcg atc gca ctt ttt gtg ggt ctg aac agt cgt gtg gga 259
Ile Val Ala Ala Ile Ala Leu Phe Val Gly Leu Asn Ser Arg Val Gly
40 45 50

aca aag ctt gtt gat cag cca gtg gtg ttc acc cag gaa caa att gat 307
Thr Lys Leu Val Asp Gln Pro Val Val Phe Thr Gln Glu Gln Ile Asp
55 60 65

caa ttg aaa gag ttg aaa tcc cgc gac cag gag gcg gca gcg atc cgt 355
Gln Leu Lys Glu Leu Lys Ser Arg Asp Gln Glu Ala Ala Ala Ile Arg
70 75 80 85

cag gcg cag ctg tgg agt agg gga tcg tcc agc gaa gcg gtc gca gag 403
Gln Ala Gln Leu Trp Ser Arg Gly Ser Ser Ser Glu Ala Val Ala Glu
90 95 100

gct gtg agg aag ctc taagtcgact taagtgcgcg aag 441
Ala Val Arg Lys Leu
105

<210> 168
<211> 106
<212> PRT
<213> Corynebacterium glutamicum

<400> 168
Met Arg Asn Ser Lys Ser Gly Leu Ala Phe Ser Ala Ala Ala Leu Phe
1 5 10 15

Cys Val Val Ala Val Ile Thr Arg Ile Ala Ser Ser Pro Ser Phe Ile
20 25 30

Ala Ile Val Ala Ile Ile Val Ala Ala Ile Ala Leu Phe Val Gly Leu
35 40 45

Asn Ser Arg Val Gly Thr Lys Leu Val Asp Gln Pro Val Val Phe Thr
50 55 60

Gln Glu Gln Ile Asp Gln Leu Lys Glu Leu Lys Ser Arg Asp Gln Glu
65 70 75 80

```
Ala Ala Ala Ile Arg Gln Ala Gln Leu Trp Ser Arg Gly Ser Ser Ser
                85                  90                  95

Glu Ala Val Ala Glu Ala Val Arg Lys Leu
            100                 105


<210> 169
<211> 358
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (66)..(335)
<223> FRXA00267

<400> 169
cgtagcgttg agaactatgc gaaactctaa gtctggcctg gccttttccg cagctgcact 60

attttgtg tct gtc gcg gta atc act cgt att gca agt tcc cca tca ttt  110
     Val Ser Val Ala Val Ile Thr Arg Ile Ala Ser Ser Pro Ser Phe
       1               5                  10                  15

atc gct att gtg gcg atc atc gtg gct gcg atc gca ctt ttt gtg ggt   158
Ile Ala Ile Val Ala Ile Ile Val Ala Ala Ile Ala Leu Phe Val Gly
                20                  25                  30

ctg aac agt cgt gtg gga aca aag ctt gtt gat cag cca gtg gtg ttc   206
Leu Asn Ser Arg Val Gly Thr Lys Leu Val Asp Gln Pro Val Val Phe
            35                  40                  45

acc cag gaa caa att gat caa ttg aaa gag ttg aaa tcc cgc gac cag   254
Thr Gln Glu Gln Ile Asp Gln Leu Lys Glu Leu Lys Ser Arg Asp Gln
         50                  55                  60

gag gcg gca gcg atc cgt cag gcg cag ctg tgg agt agg gga tcg tcc   302
Glu Ala Ala Ala Ile Arg Gln Ala Gln Leu Trp Ser Arg Gly Ser Ser
     65                  70                  75

agc gaa gcg gtc gca gag gct gtg agg aag ctc taagtcgact taagtgcgcg 355
Ser Glu Ala Val Ala Glu Ala Val Arg Lys Leu
 80                  85                  90

aag                                                               358


<210> 170
<211> 90
<212> PRT
<213> Corynebacterium glutamicum

<400> 170
Val Ser Val Ala Val Ile Thr Arg Ile Ala Ser Ser Pro Ser Phe Ile
  1               5                  10                  15

Ala Ile Val Ala Ile Ile Val Ala Ala Ile Ala Leu Phe Val Gly Leu
            20                  25                  30

Asn Ser Arg Val Gly Thr Lys Leu Val Asp Gln Pro Val Val Phe Thr
         35                  40                  45
```

```
Gln Glu Gln Ile Asp Gln Leu Lys Glu Leu Lys Ser Arg Asp Gln Glu
     50                  55                  60

Ala Ala Ala Ile Arg Gln Ala Gln Leu Trp Ser Arg Gly Ser Ser Ser
 65                  70                  75                  80

Glu Ala Val Ala Glu Ala Val Arg Lys Leu
                 85                  90


<210> 171
<211> 1113
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1090)
<223> RXN00271

<400> 171
tagtttaaat catgagacat ttcacatatg gttctttatc cgagacatgt gttgacgctg 60

tctgcccctt tttgaaaata acactttaag gagatgtgcc atg ttt tct tcc cgt   115
                                          Met Phe Ser Ser Arg
                                            1               5

tcg aag gta ctc gca agc atc ttt act gtt ggc gcc ttg gcg ttg gct   163
Ser Lys Val Leu Ala Ser Ile Phe Thr Val Gly Ala Leu Ala Leu Ala
                10                  15                  20

tcg tgc tca agc gat tcc agt gac agc tcc acc tcc act gat gct gca   211
Ser Cys Ser Ser Asp Ser Ser Asp Ser Ser Thr Ser Thr Asp Ala Ala
            25                  30                  35

ggt ggc gac tct tac cga gtt ggc atc aac cag ctt gtt cag cac cct   259
Gly Gly Asp Ser Tyr Arg Val Gly Ile Asn Gln Leu Val Gln His Pro
        40                  45                  50

gca ctt gat gca gcg acc act ggt ttc aag gaa gct ttt gaa gag gca   307
Ala Leu Asp Ala Ala Thr Thr Gly Phe Lys Glu Ala Phe Glu Glu Ala
    55                  60                  65

ggc gtt gac gtc acc ttt gat gag caa aac gct aac ggc gag cag ggc   355
Gly Val Asp Val Thr Phe Asp Glu Gln Asn Ala Asn Gly Glu Gln Gly
70                  75                  80                  85

act gca ctg act att tct cag cag ttc gct tct gac aat ttg gat ctc   403
Thr Ala Leu Thr Ile Ser Gln Gln Phe Ala Ser Asp Asn Leu Asp Leu
                90                  95                 100

gtg ttg gct gtt gca act cca gca gca cag gca act gcg cag aat atc   451
Val Leu Ala Val Ala Thr Pro Ala Ala Gln Ala Thr Ala Gln Asn Ile
            105                 110                 115

act gat atc cca gtc ctg ttc acc gca gtt acc gat gca gtg tcg gca   499
Thr Asp Ile Pro Val Leu Phe Thr Ala Val Thr Asp Ala Val Ser Ala
        120                 125                 130

gag ctg gtg gat tct aat gaa gca cct ggc gga aac gtc acc ggt act   547
```

```
Glu Leu Val Asp Ser Asn Glu Ala Pro Gly Gly Asn Val Thr Gly Thr
    135                 140                 145

tct gat atc gca ccg att gag cag cag ttg gag ctt ttg cag cag ctg   595
Ser Asp Ile Ala Pro Ile Glu Gln Gln Leu Glu Leu Leu Gln Gln Leu
150                 155                 160                 165

gtt cct gac gca aag tcc atc ggc atc gtc tac gcg tct ggt gag gtc   643
Val Pro Asp Ala Lys Ser Ile Gly Ile Val Tyr Ala Ser Gly Glu Val
                170                 175                 180

aac tct cag gtg cag gtc gat gag gtc acc aag gct gct gag cca ctg   691
Asn Ser Gln Val Gln Val Asp Glu Val Thr Lys Ala Ala Glu Pro Leu
            185                 190                 195

ggg ctg tcc gtt aat act cag act gtc act acc gtg aac gag att cag   739
Gly Leu Ser Val Asn Thr Gln Thr Val Thr Thr Val Asn Glu Ile Gln
        200                 205                 210

cag gct gtt gaa gct ctc ggc gat gtt gat gtc atc tac gtt cca act   787
Gln Ala Val Glu Ala Leu Gly Asp Val Asp Val Ile Tyr Val Pro Thr
    215                 220                 225

gac aac atg gtt gtt tcc ggt att tct tct ctg gtt cag gtt gct gag   835
Asp Asn Met Val Val Ser Gly Ile Ser Ser Leu Val Gln Val Ala Glu
230                 235                 240                 245

cag aag cag atc cct gtg atc ggc gct gag tcc ggc act gtt gag ggt   883
Gln Lys Gln Ile Pro Val Ile Gly Ala Glu Ser Gly Thr Val Glu Gly
                250                 255                 260

ggc gca ctg gca acc ctg ggt atc gat tac acc gag ctt ggc cgc cag   931
Gly Ala Leu Ala Thr Leu Gly Ile Asp Tyr Thr Glu Leu Gly Arg Gln
            265                 270                 275

act ggt gag atg gct ctg cgt att ctg cag gac ggc gaa gac cca gca   979
Thr Gly Glu Met Ala Leu Arg Ile Leu Gln Asp Gly Glu Asp Pro Ala
        280                 285                 290

acc atg cct gtg gag act gca act gag ttc acc tac gtg atc aac gaa   1027
Thr Met Pro Val Glu Thr Ala Thr Glu Phe Thr Tyr Val Ile Asn Glu
    295                 300                 305

gat gca gca gag cgc cag ggc gtg gag atc cct caa gag att ttg gat   1075
Asp Ala Ala Glu Arg Gln Gly Val Glu Ile Pro Gln Glu Ile Leu Asp
310                 315                 320                 325

aag gcc gaa cgc gta tgatcggcgc ttttgagttc gga                    1113
Lys Ala Glu Arg Val
                330
```

<210> 172
<211> 330
<212> PRT
<213> Corynebacterium glutamicum

<400> 172

```
Met Phe Ser Ser Arg Ser Lys Val Leu Ala Ser Ile Phe Thr Val Gly
  1               5                  10                  15
```

```
Ala Leu Ala Leu Ala Ser Cys Ser Ser Asp Ser Ser Asp Ser Ser Thr
            20                  25                  30

Ser Thr Asp Ala Ala Gly Gly Asp Ser Tyr Arg Val Gly Ile Asn Gln
        35                  40                  45

Leu Val Gln His Pro Ala Leu Asp Ala Ala Thr Thr Gly Phe Lys Glu
    50                  55                  60

Ala Phe Glu Glu Ala Gly Val Asp Val Thr Phe Asp Glu Gln Asn Ala
65                  70                  75                  80

Asn Gly Glu Gln Gly Thr Ala Leu Thr Ile Ser Gln Gln Phe Ala Ser
                85                  90                  95

Asp Asn Leu Asp Leu Val Leu Ala Val Ala Thr Pro Ala Ala Gln Ala
            100                 105                 110

Thr Ala Gln Asn Ile Thr Asp Ile Pro Val Leu Phe Thr Ala Val Thr
        115                 120                 125

Asp Ala Val Ser Ala Glu Leu Val Asp Ser Asn Glu Ala Pro Gly Gly
    130                 135                 140

Asn Val Thr Gly Thr Ser Asp Ile Ala Pro Ile Glu Gln Gln Leu Glu
145                 150                 155                 160

Leu Leu Gln Gln Leu Val Pro Asp Ala Lys Ser Ile Gly Ile Val Tyr
                165                 170                 175

Ala Ser Gly Glu Val Asn Ser Gln Val Gln Val Asp Glu Val Thr Lys
            180                 185                 190

Ala Ala Glu Pro Leu Gly Leu Ser Val Asn Thr Gln Thr Val Thr Thr
        195                 200                 205

Val Asn Glu Ile Gln Gln Ala Val Glu Ala Leu Gly Asp Val Asp Val
    210                 215                 220

Ile Tyr Val Pro Thr Asp Asn Met Val Val Ser Gly Ile Ser Ser Leu
225                 230                 235                 240

Val Gln Val Ala Glu Gln Lys Gln Ile Pro Val Ile Gly Ala Glu Ser
                245                 250                 255

Gly Thr Val Glu Gly Gly Ala Leu Ala Thr Leu Gly Ile Asp Tyr Thr
            260                 265                 270

Glu Leu Gly Arg Gln Thr Gly Glu Met Ala Leu Arg Ile Leu Gln Asp
        275                 280                 285

Gly Glu Asp Pro Ala Thr Met Pro Val Glu Thr Ala Thr Glu Phe Thr
    290                 295                 300

Tyr Val Ile Asn Glu Asp Ala Ala Glu Arg Gln Gly Val Glu Ile Pro
305                 310                 315                 320

Gln Glu Ile Leu Asp Lys Ala Glu Arg Val
                325                 330
```

<210> 173
<211> 1113
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1090)
<223> FRXA00271

<400> 173
tagtttaaat catgagacat ttcacatatg gttctttatc cgagacatgt gttgacgctg 60

tctgcccctt tttgaaaata acactttaag gagatgtgcc atg ttt tct tcc cgt 115
Met Phe Ser Ser Arg
1 5

tcg aag gta ctc gca agc atc ttt act gtt ggc gcc ttg gcg ttg gct 163
Ser Lys Val Leu Ala Ser Ile Phe Thr Val Gly Ala Leu Ala Leu Ala
10 15 20

tcg tgc tca agc gat tcc agt gac agc tcc acc tcc act gat gct gca 211
Ser Cys Ser Ser Asp Ser Ser Asp Ser Ser Thr Ser Thr Asp Ala Ala
25 30 35

ggt ggc gac tct tac cga gtt ggc atc aac cag ctt gtt cag cac cct 259
Gly Gly Asp Ser Tyr Arg Val Gly Ile Asn Gln Leu Val Gln His Pro
40 45 50

gca ctt gat gca gcg acc act ggt ttc aag gaa gct ttt gaa gag gca 307
Ala Leu Asp Ala Ala Thr Thr Gly Phe Lys Glu Ala Phe Glu Glu Ala
55 60 65

ggc gtt gac gtc acc ttt gat gag caa aac gct aac ggc gag cag ggc 355
Gly Val Asp Val Thr Phe Asp Glu Gln Asn Ala Asn Gly Glu Gln Gly
70 75 80 85

act gca ctg act att tct cag cag ttc gct tct gac aat ttg gat ctc 403
Thr Ala Leu Thr Ile Ser Gln Gln Phe Ala Ser Asp Asn Leu Asp Leu
90 95 100

gtg ttg gct gtt gca act cca gca gca cag gca act gcg cag aat atc 451
Val Leu Ala Val Ala Thr Pro Ala Ala Gln Ala Thr Ala Gln Asn Ile
105 110 115

act gat atc cca gtc ctg ttc acc gca gtt acc gat gca gtg tcg gca 499
Thr Asp Ile Pro Val Leu Phe Thr Ala Val Thr Asp Ala Val Ser Ala
120 125 130

gag ctg gtg gat tct aat gaa gca cct ggc gga aac gtc acc ggt act 547
Glu Leu Val Asp Ser Asn Glu Ala Pro Gly Gly Asn Val Thr Gly Thr
135 140 145

tct gat atc gca ccg att gag cag cag ttg gag ctt ttg cag cag ctg 595
Ser Asp Ile Ala Pro Ile Glu Gln Gln Leu Glu Leu Leu Gln Gln Leu
150 155 160 165

gtt cct gac gca aag tcc atc ggc atc gtc tac gcg tct ggt gag gtc 643
Val Pro Asp Ala Lys Ser Ile Gly Ile Val Tyr Ala Ser Gly Glu Val
170 175 180

```
aac tct cag gtg cag gtc gat gag gtc acc aag gct gct gag cca ctg   691
Asn Ser Gln Val Gln Val Asp Glu Val Thr Lys Ala Ala Glu Pro Leu
            185                 190                 195

ggg ctg tcc gtt aat act cag act gtc act acc gtg aac gag att cag   739
Gly Leu Ser Val Asn Thr Gln Thr Val Thr Thr Val Asn Glu Ile Gln
        200                 205                 210

cag gct gtt gaa gct ctc ggc gat gtt gat gtc atc tac gtt cca act   787
Gln Ala Val Glu Ala Leu Gly Asp Val Asp Val Ile Tyr Val Pro Thr
    215                 220                 225

gac aac atg gtt gtt tcc ggt att tct tct ctg gtt cag gtt gct gag   835
Asp Asn Met Val Val Ser Gly Ile Ser Ser Leu Val Gln Val Ala Glu
230                 235                 240                 245

cag aag cag atc cct gtg atc ggc gct gag tcc ggc act gtt gag ggt   883
Gln Lys Gln Ile Pro Val Ile Gly Ala Glu Ser Gly Thr Val Glu Gly
                250                 255                 260

ggc gca ctg gca acc ctg ggt atc gat tac acc gag ctt ggc cgc cag   931
Gly Ala Leu Ala Thr Leu Gly Ile Asp Tyr Thr Glu Leu Gly Arg Gln
            265                 270                 275

act ggt gag atg gct ctg cgt att ctg cag gac ggc gaa gac cca gca   979
Thr Gly Glu Met Ala Leu Arg Ile Leu Gln Asp Gly Glu Asp Pro Ala
        280                 285                 290

acc atg cct gtg gag act gca act gag ttc acc tac gtg atc aac gaa   1027
Thr Met Pro Val Glu Thr Ala Thr Glu Phe Thr Tyr Val Ile Asn Glu
    295                 300                 305

gat gca gca gag cgc cag ggc gtg gag atc cct caa gag att ttg gat   1075
Asp Ala Ala Glu Arg Gln Gly Val Glu Ile Pro Gln Glu Ile Leu Asp
310                 315                 320                 325

aag gcc gaa cgc gta tgatcggcgc ttttgagttc gga                    1113
Lys Ala Glu Arg Val
                330
```

<210> 174
<211> 330
<212> PRT
<213> Corynebacterium glutamicum

<400> 174

```
Met Phe Ser Ser Arg Ser Lys Val Leu Ala Ser Ile Phe Thr Val Gly
  1               5                  10                  15

Ala Leu Ala Leu Ala Ser Cys Ser Ser Asp Ser Ser Asp Ser Ser Thr
             20                  25                  30

Ser Thr Asp Ala Ala Gly Gly Asp Ser Tyr Arg Val Gly Ile Asn Gln
         35                  40                  45

Leu Val Gln His Pro Ala Leu Asp Ala Ala Thr Thr Gly Phe Lys Glu
     50                  55                  60

Ala Phe Glu Glu Ala Gly Val Asp Val Thr Phe Asp Glu Gln Asn Ala
 65                  70                  75                  80
```

```
Asn Gly Glu Gln Gly Thr Ala Leu Thr Ile Ser Gln Gln Phe Ala Ser
                85                  90                  95

Asp Asn Leu Asp Leu Val Leu Ala Val Ala Thr Pro Ala Ala Gln Ala
            100                 105                 110

Thr Ala Gln Asn Ile Thr Asp Ile Pro Val Leu Phe Thr Ala Val Thr
        115                 120                 125

Asp Ala Val Ser Ala Glu Leu Val Asp Ser Asn Glu Ala Pro Gly Gly
    130                 135                 140

Asn Val Thr Gly Thr Ser Asp Ile Ala Pro Ile Glu Gln Gln Leu Glu
145                 150                 155                 160

Leu Leu Gln Gln Leu Val Pro Asp Ala Lys Ser Ile Gly Ile Val Tyr
                165                 170                 175

Ala Ser Gly Glu Val Asn Ser Gln Val Gln Val Asp Glu Val Thr Lys
            180                 185                 190

Ala Ala Glu Pro Leu Gly Leu Ser Val Asn Thr Gln Thr Val Thr Thr
        195                 200                 205

Val Asn Glu Ile Gln Gln Ala Val Glu Ala Leu Gly Asp Val Asp Val
    210                 215                 220

Ile Tyr Val Pro Thr Asp Asn Met Val Val Ser Gly Ile Ser Ser Leu
225                 230                 235                 240

Val Gln Val Ala Glu Gln Lys Gln Ile Pro Val Ile Gly Ala Glu Ser
                245                 250                 255

Gly Thr Val Glu Gly Gly Ala Leu Ala Thr Leu Gly Ile Asp Tyr Thr
            260                 265                 270

Glu Leu Gly Arg Gln Thr Gly Glu Met Ala Leu Arg Ile Leu Gln Asp
        275                 280                 285

Gly Glu Asp Pro Ala Thr Met Pro Val Glu Thr Ala Thr Glu Phe Thr
    290                 295                 300

Tyr Val Ile Asn Glu Asp Ala Ala Glu Arg Gln Gly Val Glu Ile Pro
305                 310                 315                 320

Gln Glu Ile Leu Asp Lys Ala Glu Arg Val
                325                 330
```

<210> 175
<211> 495
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(472)
<223> RXN00272

<400> 175

```
accgatgcac cagccaccaa cgcgtccaaa tcaatatcag cctggcccac aaggtggaat 60

tccagtgggt ggccatctgc cacaaccagg tgcagggcac atg ccg gaa cca gaa   115
                                             Met Pro Glu Pro Glu
                                               1               5

acc tcc acg atg ggc tcc atc caa aag tcc ggt gaa tgg ctc gtt cct   163
Thr Ser Thr Met Gly Ser Ile Gln Lys Ser Gly Glu Trp Leu Val Pro
                 10                  15                  20

gca tat tcg gca tac aag ctc aac ggt gct gac ctt ttc tta gat atc   211
Ala Tyr Ser Ala Tyr Lys Leu Asn Gly Ala Asp Leu Phe Leu Asp Ile
             25                  30                  35

cgc cat gcc acc gcg gct gct cct gtc att acc ttt gat gtc aac atg   259
Arg His Ala Thr Ala Ala Ala Pro Val Ile Thr Phe Asp Val Asn Met
         40                  45                  50

acc atg ggt tct atg acg ctg att gtt cca ccg ggt gtg tat gtg gaa   307
Thr Met Gly Ser Met Thr Leu Ile Val Pro Pro Gly Val Tyr Val Glu
     55                  60                  65

gtg cag atg gct tcc aag aac tgg tcg gat ttc aag gtt caa aca acc   355
Val Gln Met Ala Ser Lys Asn Trp Ser Asp Phe Lys Val Gln Thr Thr
 70                  75                  80                  85

aat cct ctc ccc ggt gct ccc cga gtg ttc atc act ggt gtt gca cgc   403
Asn Pro Leu Pro Gly Ala Pro Arg Val Phe Ile Thr Gly Val Ala Arg
                 90                  95                 100

gca tca ggg ttg aag gtt ttc acc aag cat cct cat gag cct ttt ggg   451
Ala Ser Gly Leu Lys Val Phe Thr Lys His Pro His Glu Pro Phe Gly
            105                 110                 115

ttc tgg cag aaa atg ttt gag tagcctcggg ccacgcccga acc            495
Phe Trp Gln Lys Met Phe Glu
        120


<210> 176
<211> 124
<212> PRT
<213> Corynebacterium glutamicum

<400> 176
Met Pro Glu Pro Glu Thr Ser Thr Met Gly Ser Ile Gln Lys Ser Gly
  1               5                  10                  15

Glu Trp Leu Val Pro Ala Tyr Ser Ala Tyr Lys Leu Asn Gly Ala Asp
             20                  25                  30

Leu Phe Leu Asp Ile Arg His Ala Thr Ala Ala Ala Pro Val Ile Thr
         35                  40                  45

Phe Asp Val Asn Met Thr Met Gly Ser Met Thr Leu Ile Val Pro Pro
     50                  55                  60

Gly Val Tyr Val Glu Val Gln Met Ala Ser Lys Asn Trp Ser Asp Phe
 65                  70                  75                  80

Lys Val Gln Thr Thr Asn Pro Leu Pro Gly Ala Pro Arg Val Phe Ile
```

```
                85                  90                  95

Thr Gly Val Ala Arg Ala Ser Gly Leu Lys Val Phe Thr Lys His Pro
            100                 105                 110

His Glu Pro Phe Gly Phe Trp Gln Lys Met Phe Glu
        115                 120


<210> 177
<211> 495
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(472)
<223> FRXA00272

<400> 177
accgatgcac cagccaccaa cgcgtccaaa tcaatatcag cctggcccac aaggtggaat 60

tccagtgggt ggccatctgc cacaaccagg tgcagggcac atg ccg gaa cca gaa   115
                                              Met Pro Glu Pro Glu
                                                1               5

acc tcc acg atg ggc tcc atc caa aag tcc ggt gaa tgg ctc gtt cct   163
Thr Ser Thr Met Gly Ser Ile Gln Lys Ser Gly Glu Trp Leu Val Pro
                10                  15                  20

gca tat tcg gca tac aag ctc aac ggt gct gac ctt ttc tta gat atc   211
Ala Tyr Ser Ala Tyr Lys Leu Asn Gly Ala Asp Leu Phe Leu Asp Ile
            25                  30                  35

cgc cat gcc acc gcg gct gct cct gtc att acc ttt gat gtc aac atg   259
Arg His Ala Thr Ala Ala Ala Pro Val Ile Thr Phe Asp Val Asn Met
        40                  45                  50

acc atg ggt tct atg acg ctg att gtt cca ccg ggt gtg tat gtg gaa   307
Thr Met Gly Ser Met Thr Leu Ile Val Pro Pro Gly Val Tyr Val Glu
    55                  60                  65

gtg cag atg gct tcc aag aac tgg tcg gat ttc aag gtt caa aca acc   355
Val Gln Met Ala Ser Lys Asn Trp Ser Asp Phe Lys Val Gln Thr Thr
70                  75                  80                  85

aat cct ctc ccc ggt gct ccc cga gtg ttc atc act ggt gtt gca cgc   403
Asn Pro Leu Pro Gly Ala Pro Arg Val Phe Ile Thr Gly Val Ala Arg
                90                  95                  100

gca tca ggg ttg aag gtt ttc acc aag cat cct cat gag cct ttt ggg   451
Ala Ser Gly Leu Lys Val Phe Thr Lys His Pro His Glu Pro Phe Gly
            105                 110                 115

ttc tgg cag aaa atg ttt gag tagcctcggg ccacgcccga acc            495
Phe Trp Gln Lys Met Phe Glu
        120


<210> 178
<211> 124
```

<212> PRT
<213> Corynebacterium glutamicum

<400> 178
Met Pro Glu Pro Glu Thr Ser Thr Met Gly Ser Ile Gln Lys Ser Gly
1 5 10 15

Glu Trp Leu Val Pro Ala Tyr Ser Ala Tyr Lys Leu Asn Gly Ala Asp
20 25 30

Leu Phe Leu Asp Ile Arg His Ala Thr Ala Ala Ala Pro Val Ile Thr
35 40 45

Phe Asp Val Asn Met Thr Met Gly Ser Met Thr Leu Ile Val Pro Pro
50 55 60

Gly Val Tyr Val Glu Val Gln Met Ala Ser Lys Asn Trp Ser Asp Phe
65 70 75 80

Lys Val Gln Thr Thr Asn Pro Leu Pro Gly Ala Pro Arg Val Phe Ile
85 90 95

Thr Gly Val Ala Arg Ala Ser Gly Leu Lys Val Phe Thr Lys His Pro
100 105 110

His Glu Pro Phe Gly Phe Trp Gln Lys Met Phe Glu
115 120

<210> 179
<211> 1155
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1132)
<223> RXN00283

<400> 179
gcgttggcat tggcgttttt agcgcgctat gacgccctca tcatggcctt cgtagccatg 60

tggactgtcg gatttatgac atggcgcgca cgataccgcc gtg gct tcc gcg acc 115
Val Ala Ser Ala Thr
1 5

gca tcg gat tcg cac ttg tcg aca tgc tgc tcc tcg tct ggc cga tcg 163
Ala Ser Asp Ser His Leu Ser Thr Cys Cys Ser Ser Ser Gly Arg Ser
10 15 20

gct tcg cct tcg tcg cct gga ctg gcg cca agc tgg ctc act acc ggc 211
Ala Ser Pro Ser Ser Pro Gly Leu Ala Pro Ser Trp Leu Thr Thr Gly
25 30 35

gaa ctc ttt gcc caa ttc acc tcc aca gac ggc aac gct gcg atc atc 259
Glu Leu Phe Ala Gln Phe Thr Ser Thr Asp Gly Asn Ala Ala Ile Ile
40 45 50

gca gca tcc ggc ggc ggc gcc ata ggg ccc caa gcg ctt ttc gac gcc 307
Ala Ala Ser Gly Gly Gly Ala Ile Gly Pro Gln Ala Leu Phe Asp Ala
55 60 65

```
tcc gtc cgc acc ttc ctc atc tcc cca gct ctc cta ctc gtc gca gta   355
Ser Val Arg Thr Phe Leu Ile Ser Pro Ala Leu Leu Leu Val Ala Val
 70                  75                  80                  85

gtt gca gtc ttt ttt gct tat cga cgc cgc gac ccc gaa ccc atc atc   403
Val Ala Val Phe Phe Ala Tyr Arg Arg Arg Asp Pro Glu Pro Ile Ile
                90                  95                 100

ccc tta gct ctc atc ggc tct gtg gtg ttc ttc caa atc att acc tac   451
Pro Leu Ala Leu Ile Gly Ser Val Val Phe Phe Gln Ile Ile Thr Tyr
            105                 110                 115

tca ctt gga tct acc ttc ggc ctg ctg cgc ttt ttc ctc acc gcc ctg   499
Ser Leu Gly Ser Thr Phe Gly Leu Leu Arg Phe Phe Leu Thr Ala Leu
        120                 125                 130

ccg ctc acc att atc ttg ctg ttc caa att atc ccg ccc cgc cac cga   547
Pro Leu Thr Ile Ile Leu Leu Phe Gln Ile Ile Pro Pro Arg His Arg
    135                 140                 145

ttc ccc tca ctg cga cca ggt gcg tgc tac cgc gat cgc gtc acc ggc   595
Phe Pro Ser Leu Arg Pro Gly Ala Cys Tyr Arg Asp Arg Val Thr Gly
150                 155                 160                 165

aag tac gtg ccc aaa aca atc acc ggt gtt tta gtt ctc gcg atc ttc   643
Lys Tyr Val Pro Lys Thr Ile Thr Gly Val Leu Val Leu Ala Ile Phe
                170                 175                 180

ggc ggc acc ggc atc acc ctg tac ggc atg agc agt gct aac tgg gcg   691
Gly Gly Thr Gly Ile Thr Leu Tyr Gly Met Ser Ser Ala Asn Trp Ala
            185                 190                 195

ccc cag gaa tat gcc atc caa gaa cta gtt ttc aac atg gga tcg cca   739
Pro Gln Glu Tyr Ala Ile Gln Glu Leu Val Phe Asn Met Gly Ser Pro
        200                 205                 210

tcg cag gac gcc gtc cac acc ctg aac acc ttc tcc act gaa atg gat   787
Ser Gln Asp Ala Val His Thr Leu Asn Thr Phe Ser Thr Glu Met Asp
    215                 220                 225

gtc gcc gat ttc gtc gac tcc cta aac ctt gga gac ggc gaa gtc ctt   835
Val Ala Asp Phe Val Asp Ser Leu Asn Leu Gly Asp Gly Glu Val Leu
230                 235                 240                 245

ctc tcc acc acc tac ggc ttc gcc gtc ctc acc gca tca aac aac caa   883
Leu Ser Thr Thr Tyr Gly Phe Ala Val Leu Thr Ala Ser Asn Asn Gln
                250                 255                 260

aag caa ttc atc atc ccc tcc gac gaa gac ttc atc acc acc ctc aac   931
Lys Gln Phe Ile Ile Pro Ser Asp Glu Asp Phe Ile Thr Thr Leu Asn
            265                 270                 275

gaa ccc gct gag cac ggc gtt aag tac atc ctc gcc ctc cca cgc gaa   979
Glu Pro Ala Glu His Gly Val Lys Tyr Ile Leu Ala Leu Pro Arg Glu
        280                 285                 290

ggt cgc ggc gcc acc gac ccg atc aac ctg cgc tac cca gac atg tat   1027
Gly Arg Gly Ala Thr Asp Pro Ile Asn Leu Arg Tyr Pro Asp Met Tyr
    295                 300                 305
```

```
gaa acc ggc agc cac atc gcc acg atg gaa atc gaa ttc atc aat caa   1075
Glu Thr Gly Ser His Ile Ala Thr Met Glu Ile Glu Phe Ile Asn Gln
310                 315                 320                 325

ggc caa gga caa cca aat tgg cgc ctc tat cgg gtg ctc acc aca cct   1123
Gly Gln Gly Gln Pro Asn Trp Arg Leu Tyr Arg Val Leu Thr Thr Pro
                330                 335                 340

gaa cag tcg tagactcttt gtaactaccg ttg                             1155
Glu Gln Ser
```

<210> 180
<211> 344
<212> PRT
<213> Corynebacterium glutamicum

<400> 180

```
Val Ala Ser Ala Thr Ala Ser Asp Ser His Leu Ser Thr Cys Cys Ser
  1               5                  10                  15

Ser Ser Gly Arg Ser Ala Ser Pro Ser Ser Pro Gly Leu Ala Pro Ser
             20                  25                  30

Trp Leu Thr Thr Gly Glu Leu Phe Ala Gln Phe Thr Ser Thr Asp Gly
         35                  40                  45

Asn Ala Ala Ile Ile Ala Ala Ser Gly Gly Gly Ala Ile Gly Pro Gln
     50                  55                  60

Ala Leu Phe Asp Ala Ser Val Arg Thr Phe Leu Ile Ser Pro Ala Leu
 65                  70                  75                  80

Leu Leu Val Ala Val Val Ala Val Phe Phe Ala Tyr Arg Arg Arg Asp
                 85                  90                  95

Pro Glu Pro Ile Ile Pro Leu Ala Leu Ile Gly Ser Val Val Phe Phe
            100                 105                 110

Gln Ile Ile Thr Tyr Ser Leu Gly Ser Thr Phe Gly Leu Leu Arg Phe
        115                 120                 125

Phe Leu Thr Ala Leu Pro Leu Thr Ile Ile Leu Leu Phe Gln Ile Ile
    130                 135                 140

Pro Pro Arg His Arg Phe Pro Ser Leu Arg Pro Gly Ala Cys Tyr Arg
145                 150                 155                 160

Asp Arg Val Thr Gly Lys Tyr Val Pro Lys Thr Ile Thr Gly Val Leu
                165                 170                 175

Val Leu Ala Ile Phe Gly Gly Thr Gly Ile Thr Leu Tyr Gly Met Ser
            180                 185                 190

Ser Ala Asn Trp Ala Pro Gln Glu Tyr Ala Ile Gln Glu Leu Val Phe
        195                 200                 205

Asn Met Gly Ser Pro Ser Gln Asp Ala Val His Thr Leu Asn Thr Phe
    210                 215                 220
```

```
Ser Thr Glu Met Asp Val Ala Asp Phe Val Asp Ser Leu Asn Leu Gly
225                 230                 235                 240

Asp Gly Glu Val Leu Leu Ser Thr Thr Tyr Gly Phe Ala Val Leu Thr
                245                 250                 255

Ala Ser Asn Asn Gln Lys Gln Phe Ile Ile Pro Ser Asp Glu Asp Phe
            260                 265                 270

Ile Thr Thr Leu Asn Glu Pro Ala Glu His Gly Val Lys Tyr Ile Leu
        275                 280                 285

Ala Leu Pro Arg Glu Gly Arg Gly Ala Thr Asp Pro Ile Asn Leu Arg
    290                 295                 300

Tyr Pro Asp Met Tyr Glu Thr Gly Ser His Ile Ala Thr Met Glu Ile
305                 310                 315                 320

Glu Phe Ile Asn Gln Gly Gln Gly Gln Pro Asn Trp Arg Leu Tyr Arg
                325                 330                 335

Val Leu Thr Thr Pro Glu Gln Ser
            340
```

Sequence Listing as filed with the application

<210> 181
<211> 1251
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1228)
<223> FRXA00283

<400> 181

```
gaagctccgt tcatttacgc cactctctgg gcggtgcgca ggctgattcg gtggagttct 60

acggaaaacg tccacagacc tcattacctg tggttttgcg ttg gca ttg gcg ttt   115
                                              Leu Ala Leu Ala Phe
                                                1               5

tta gcg cgc tat gac gcc ctc atc atg gcc ttc gta gcc atg tgg act   163
Leu Ala Arg Tyr Asp Ala Leu Ile Met Ala Phe Val Ala Met Trp Thr
                10                  15                  20

gtc gga ttt atg aca tgg cgc gca cga tac cgc cgt ggc ttc cgc gac   211
Val Gly Phe Met Thr Trp Arg Ala Arg Tyr Arg Arg Gly Phe Arg Asp
            25                  30                  35

cgc atc gga ttc gca ctt gtc gac atg ctg ctc ctc gtc tgg ccg atc   259
Arg Ile Gly Phe Ala Leu Val Asp Met Leu Leu Leu Val Trp Pro Ile
        40                  45                  50

ggc ttc gcc ttc gtc gcc tgg act ggc gcc agc tgg ctc act acc ggc   307
Gly Phe Ala Phe Val Ala Trp Thr Gly Ala Ser Trp Leu Thr Thr Gly
    55                  60                  65

gaa ctc ttt gcc caa ttc acc tcc aca gac ggc aac gct gcg atc atc   355
Glu Leu Phe Ala Gln Phe Thr Ser Thr Asp Gly Asn Ala Ala Ile Ile
70                  75                  80                  85
```

```
gca gca tcc ggc ggc ggc gcc ata ggg ccc caa gcg ctt ttc gac gcc   403
Ala Ala Ser Gly Gly Gly Ala Ile Gly Pro Gln Ala Leu Phe Asp Ala
                 90                  95                 100

tcc gtc cgc acc ttc ctc atc tcc cca gct ctc cta ctc gtc gca gta   451
Ser Val Arg Thr Phe Leu Ile Ser Pro Ala Leu Leu Leu Val Ala Val
            105                 110                 115

gtt gca gtc ttt ttt gct tat cga cgc cgc gac ccc gaa ccc atc atc   499
Val Ala Val Phe Phe Ala Tyr Arg Arg Arg Asp Pro Glu Pro Ile Ile
        120                 125                 130

ccc tta gct ctc atc ggc tct gtg gtg ttc ttc caa atc att acc tac   547
Pro Leu Ala Leu Ile Gly Ser Val Val Phe Phe Gln Ile Ile Thr Tyr
    135                 140                 145

tca ctt gga tct acc ttc ggc ctg ctg cgc ttt ttc ctc acc gcc ctg   595
Ser Leu Gly Ser Thr Phe Gly Leu Leu Arg Phe Phe Leu Thr Ala Leu
150                 155                 160                 165

ccg ctc acc att atc ttg ctg ttc caa att atc ccg ccc cgc cac cga   643
Pro Leu Thr Ile Ile Leu Leu Phe Gln Ile Ile Pro Pro Arg His Arg
                170                 175                 180

ttc ccc tca ctg cga cca ggt gcg tgc tac cgc gat cgc gtc acc ggc   691
Phe Pro Ser Leu Arg Pro Gly Ala Cys Tyr Arg Asp Arg Val Thr Gly
            185                 190                 195

aag tac gtg ccc aaa aca atc acc ggt gtt tta gtt ctc gcg atc ttc   739
Lys Tyr Val Pro Lys Thr Ile Thr Gly Val Leu Val Leu Ala Ile Phe
        200                 205                 210

ggc ggc acc ggc atc acc ctg tac ggc atg agc agt gct aac tgg gcg   787
Gly Gly Thr Gly Ile Thr Leu Tyr Gly Met Ser Ser Ala Asn Trp Ala
    215                 220                 225

ccc cag gaa tat gcc atc caa gaa cta gtt ttc aac atg gga tcg cca   835
Pro Gln Glu Tyr Ala Ile Gln Glu Leu Val Phe Asn Met Gly Ser Pro
230                 235                 240                 245

tcg cag gac gcc gtc cac acc ctg aac acc ttc tcc act gaa atg gat   883
Ser Gln Asp Ala Val His Thr Leu Asn Thr Phe Ser Thr Glu Met Asp
                250                 255                 260

gtc gcc gat ttc gtc gac tcc cta aac ctt gga gac ggc gaa gtc ctt   931
Val Ala Asp Phe Val Asp Ser Leu Asn Leu Gly Asp Gly Glu Val Leu
            265                 270                 275

ctc tcc acc acc tac ggc ttc gcc gtc ctc acc gca tca aac aac caa   979
Leu Ser Thr Thr Tyr Gly Phe Ala Val Leu Thr Ala Ser Asn Asn Gln
        280                 285                 290

aag caa ttc atc atc ccc tcc gac gaa gac ttc atc acc acc ctc aac   1027
Lys Gln Phe Ile Ile Pro Ser Asp Glu Asp Phe Ile Thr Thr Leu Asn
    295                 300                 305

gaa ccc gct gag cac ggc gtt aag tac atc ctc gcc ctc cca cgc gaa   1075
Glu Pro Ala Glu His Gly Val Lys Tyr Ile Leu Ala Leu Pro Arg Glu
310                 315                 320                 325
```

```
ggt cgc ggc gcc acc gac ccg atc aac ctg cgc tac cca gac atg tat   1123
Gly Arg Gly Ala Thr Asp Pro Ile Asn Leu Arg Tyr Pro Asp Met Tyr
                330                 335                 340

gaa acc ggc agc cac atc gcc acg atg gaa atc gaa ttc atc aat caa   1171
Glu Thr Gly Ser His Ile Ala Thr Met Glu Ile Glu Phe Ile Asn Gln
            345                 350                 355

ggc caa gga caa cca aat tgg cgc ctc tat cgg gtg ctc acc aca cct   1219
Gly Gln Gly Gln Pro Asn Trp Arg Leu Tyr Arg Val Leu Thr Thr Pro
        360                 365                 370

gaa cag tcg tagactcttt gtaactaccg ttg                             1251
Glu Gln Ser
    375
```

<210> 182
<211> 376
<212> PRT
<213> Corynebacterium glutamicum

<400> 182

```
Leu Ala Leu Ala Phe Leu Ala Arg Tyr Asp Ala Leu Ile Met Ala Phe
  1               5                  10                  15

Val Ala Met Trp Thr Val Gly Phe Met Thr Trp Arg Ala Arg Tyr Arg
             20                  25                  30

Arg Gly Phe Arg Asp Arg Ile Gly Phe Ala Leu Val Asp Met Leu Leu
         35                  40                  45

Leu Val Trp Pro Ile Gly Phe Ala Phe Val Ala Trp Thr Gly Ala Ser
     50                  55                  60

Trp Leu Thr Thr Gly Glu Leu Phe Ala Gln Phe Thr Ser Thr Asp Gly
 65                  70                  75                  80

Asn Ala Ala Ile Ile Ala Ala Ser Gly Gly Gly Ala Ile Gly Pro Gln
                 85                  90                  95

Ala Leu Phe Asp Ala Ser Val Arg Thr Phe Leu Ile Ser Pro Ala Leu
            100                 105                 110

Leu Leu Val Ala Val Val Ala Val Phe Phe Ala Tyr Arg Arg Arg Asp
        115                 120                 125

Pro Glu Pro Ile Ile Pro Leu Ala Leu Ile Gly Ser Val Val Phe Phe
    130                 135                 140

Gln Ile Ile Thr Tyr Ser Leu Gly Ser Thr Phe Gly Leu Leu Arg Phe
145                 150                 155                 160

Phe Leu Thr Ala Leu Pro Leu Thr Ile Ile Leu Leu Phe Gln Ile Ile
                165                 170                 175

Pro Pro Arg His Arg Phe Pro Ser Leu Arg Pro Gly Ala Cys Tyr Arg
            180                 185                 190

Asp Arg Val Thr Gly Lys Tyr Val Pro Lys Thr Ile Thr Gly Val Leu
        195                 200                 205
```

```
Val Leu Ala Ile Phe Gly Gly Thr Gly Ile Thr Leu Tyr Gly Met Ser
    210                 215                 220

Ser Ala Asn Trp Ala Pro Gln Glu Tyr Ala Ile Gln Glu Leu Val Phe
225                 230                 235                 240

Asn Met Gly Ser Pro Ser Gln Asp Ala Val His Thr Leu Asn Thr Phe
                245                 250                 255

Ser Thr Glu Met Asp Val Ala Asp Phe Val Asp Ser Leu Asn Leu Gly
            260                 265                 270

Asp Gly Glu Val Leu Leu Ser Thr Thr Tyr Gly Phe Ala Val Leu Thr
        275                 280                 285

Ala Ser Asn Asn Gln Lys Gln Phe Ile Ile Pro Ser Asp Glu Asp Phe
    290                 295                 300

Ile Thr Thr Leu Asn Glu Pro Ala Glu His Gly Val Lys Tyr Ile Leu
305                 310                 315                 320

Ala Leu Pro Arg Glu Gly Arg Gly Ala Thr Asp Pro Ile Asn Leu Arg
                325                 330                 335

Tyr Pro Asp Met Tyr Glu Thr Gly Ser His Ile Ala Thr Met Glu Ile
            340                 345                 350

Glu Phe Ile Asn Gln Gly Gln Gly Gln Pro Asn Trp Arg Leu Tyr Arg
        355                 360                 365

Val Leu Thr Thr Pro Glu Gln Ser
    370                 375


<210> 183
<211> 459
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(436)
<223> RXN00334

<400> 183
ataagccccg catgggatat gagaaaagga atgcacgatg agtattgaat ttccgttagg 60

taatccagcg cctgcacagt ggttttctgg cgaggtccat atg gcc aag ctt gat   115
                                               Met Ala Lys Leu Asp
                                                 1               5

gac aac gtg cag att gag act gtg aac gtg tct ttt gag gca ggc ggt   163
Asp Asn Val Gln Ile Glu Thr Val Asn Val Ser Phe Glu Ala Gly Gly
                10                  15                  20

cgc acc aat tgg cac act cac cca gtc ggt caa aac ata att gtg ctg   211
Arg Thr Asn Trp His Thr His Pro Val Gly Gln Asn Ile Ile Val Leu
            25                  30                  35

tcg ggc ttg ggc att tat gag gcg gag ggg gag cct gct cga ctc ctg   259
```

```
Ser Gly Leu Gly Ile Tyr Glu Ala Glu Gly Glu Pro Ala Arg Leu Leu
        40                  45                  50

gag cct ggc gat gtt gtt ttc gca gcc gcc ggg gtt cgc cac tgg cac   307
Glu Pro Gly Asp Val Val Phe Ala Ala Ala Gly Val Arg His Trp His
     55                  60                  65

ggc gcc gtg tct ggt gca ccg atg ttc cac gtg gtg gtt aac ctc aaa   355
Gly Ala Val Ser Gly Ala Pro Met Phe His Val Val Val Asn Leu Lys
 70                  75                  80                  85

ggc atc gac ggc gag acc gtc gat tgg gag gag ccg gtc gac gag gag   403
Gly Ile Asp Gly Glu Thr Val Asp Trp Glu Glu Pro Val Asp Glu Glu
                90                  95                 100

cac tac cgc agc gtg agc gcg gag cta caa aga taaaaatgct tttcgacgtc 456
His Tyr Arg Ser Val Ser Ala Glu Leu Gln Arg
            105                 110

cac                                                               459
```

Untranslated Sequence Listing

<210> 184
<211> 112
<212> PRT
<213> Corynebacterium glutamicum

<400> 184

```
Met Ala Lys Leu Asp Asp Asn Val Gln Ile Glu Thr Val Asn Val Ser
  1               5                  10                  15

Phe Glu Ala Gly Gly Arg Thr Asn Trp His Thr His Pro Val Gly Gln
             20                  25                  30

Asn Ile Ile Val Leu Ser Gly Leu Gly Ile Tyr Glu Ala Glu Gly Glu
         35                  40                  45

Pro Ala Arg Leu Leu Glu Pro Gly Asp Val Val Phe Ala Ala Ala Gly
     50                  55                  60

Val Arg His Trp His Gly Ala Val Ser Gly Ala Pro Met Phe His Val
 65                  70                  75                  80

Val Val Asn Leu Lys Gly Ile Asp Gly Glu Thr Val Asp Trp Glu Glu
                 85                  90                  95

Pro Val Asp Glu Glu His Tyr Arg Ser Val Ser Ala Glu Leu Gln Arg
            100                 105                 110
```

<210> 185
<211> 459
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(436)

<223> FRXA00334

<400> 185
ataagccccg catgggatat gagaaaagga atgcacgatg agtattgaat ttccgttagg 60

taatccagcg cctgcacagt ggttttctgg cgaggtccat atg gcc aag ctt gat 115
Met Ala Lys Leu Asp
1 5

gac aac gtg cag att gag act gtg aac gtg tct ttt gag gca ggc ggt 163
Asp Asn Val Gln Ile Glu Thr Val Asn Val Ser Phe Glu Ala Gly Gly
10 15 20

cgc acc aat tgg cac act cac cca gtc ggt caa aac ata att gtg ctg 211
Arg Thr Asn Trp His Thr His Pro Val Gly Gln Asn Ile Ile Val Leu
25 30 35

tcg ggc ttg ggc att tat gag gcg gag ggg gag cct gct cga ctc ctg 259
Ser Gly Leu Gly Ile Tyr Glu Ala Glu Gly Glu Pro Ala Arg Leu Leu
40 45 50

gag cct ggc gat gtt gtt ttc gca gcc gcc ggg gtt cgc cac tgg cac 307
Glu Pro Gly Asp Val Val Phe Ala Ala Ala Gly Val Arg His Trp His
55 60 65

ggc gcc gtg tct ggt gca ccg atg ttc cac gtg gtg gtt aac ctc aaa 355
Gly Ala Val Ser Gly Ala Pro Met Phe His Val Val Val Asn Leu Lys
70 75 80 85

ggc atc gac ggc gag acc gtc gat tgg gag gag ccg gtc gac gag gag 403
Gly Ile Asp Gly Glu Thr Val Asp Trp Glu Glu Pro Val Asp Glu Glu
90 95 100

cac tac cgc agc gtg agc gcg gag cta caa aga taaaaatgct tttcgacgtc 456
His Tyr Arg Ser Val Ser Ala Glu Leu Gln Arg
105 110

cac 459

<210> 186
<211> 112
<212> PRT
<213> Corynebacterium glutamicum

<400> 186
Met Ala Lys Leu Asp Asp Asn Val Gln Ile Glu Thr Val Asn Val Ser
1 5 10 15

Phe Glu Ala Gly Gly Arg Thr Asn Trp His Thr His Pro Val Gly Gln
20 25 30

Asn Ile Ile Val Leu Ser Gly Leu Gly Ile Tyr Glu Ala Glu Gly Glu
35 40 45

Pro Ala Arg Leu Leu Glu Pro Gly Asp Val Val Phe Ala Ala Ala Gly
50 55 60

Val Arg His Trp His Gly Ala Val Ser Gly Ala Pro Met Phe His Val
65 70 75 80

```
Val Val Asn Leu Lys Gly Ile Asp Gly Glu Thr Val Asp Trp Glu Glu
                85                  90                  95

Pro Val Asp Glu Glu His Tyr Arg Ser Val Ser Ala Glu Leu Gln Arg
            100                 105                 110
```

<210> 187
<211> 1263
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1240)
<223> RXN00338

<400> 187

```
tcttagaagg cgtagtcaca ccattaacct tgccagaatt tttcaaggct tggctagact 60

tgggaaacga acatgcggta ccaaccaggg gagttaatgc gtg agt gat gta acc   115
                                            Val Ser Asp Val Thr
                                              1               5

gtt ggc gat att cgc cgc att ttg gat gag gct tat ccg ccg gcg ttg   163
Val Gly Asp Ile Arg Arg Ile Leu Asp Glu Ala Tyr Pro Pro Ala Leu
                10                  15                  20

gcg gaa agc tgg gac aaa gtg ggg ctg atc tgc ggt gat cca aca gag   211
Ala Glu Ser Trp Asp Lys Val Gly Leu Ile Cys Gly Asp Pro Thr Glu
            25                  30                  35

tcg gtg aag cgt gtc ggt tta gca ctc gat tgc acc cag gca gtg gcc   259
Ser Val Lys Arg Val Gly Leu Ala Leu Asp Cys Thr Gln Ala Val Ala
        40                  45                  50

gac aag gct gtg gac atg ggt ttg gac atg ctg atc att cac cac cca   307
Asp Lys Ala Val Asp Met Gly Leu Asp Met Leu Ile Ile His His Pro
    55                  60                  65

ttg ctg ctg cgt ggg gtg acg tct gtt gct gcg gat gag cca aaa ggc   355
Leu Leu Leu Arg Gly Val Thr Ser Val Ala Ala Asp Glu Pro Lys Gly
70                  75                  80                  85

aag gtc att cac acc cta att cgc ggc ggg gtg gca ctg ttt tcc gcg   403
Lys Val Ile His Thr Leu Ile Arg Gly Gly Val Ala Leu Phe Ser Ala
                90                  95                  100

cac act aat gcg gat tcc gcg cgc cca ggt gtc aac gat aaa ctc gcc   451
His Thr Asn Ala Asp Ser Ala Arg Pro Gly Val Asn Asp Lys Leu Ala
            105                 110                 115

gag ctc gtc ggc atc acg gcc ggg cga ccc atc gcg aca cgg ctt tta   499
Glu Leu Val Gly Ile Thr Ala Gly Arg Pro Ile Ala Thr Arg Leu Leu
        120                 125                 130

ggc ggc atg gac aaa tgg ggc gtg cac gtt ctg ccc aag gat gca gcg   547
Gly Gly Met Asp Lys Trp Gly Val His Val Leu Pro Lys Asp Ala Ala
```

```
    135                 140                 145

tac cta aag aag atg ctt ttc gac gca ggt gcc ggt gcg atc ggc gac   595
Tyr Leu Lys Lys Met Leu Phe Asp Ala Gly Ala Gly Ala Ile Gly Asp
150                 155                 160                 165

tac cga gag tgt gcc ttt gag atc gaa gga acc ggg cag ttt agg ccc   643
Tyr Arg Glu Cys Ala Phe Glu Ile Glu Gly Thr Gly Gln Phe Arg Pro
                170                 175                 180

gtg gag ggg gcg aat ccg gca gag ggg gac gtc gat aag ctt ttt aaa   691
Val Glu Gly Ala Asn Pro Ala Glu Gly Asp Val Asp Lys Leu Phe Lys
            185                 190                 195

tcc ctt gag ctg cgc atc gag ttt gtt gca ccg cgc aac ctg cgc gcc   739
Ser Leu Glu Leu Arg Ile Glu Phe Val Ala Pro Arg Asn Leu Arg Ala
        200                 205                 210

cgg ctc acg tcg gtg ctg cgg gag gct cat ccg tat gag gag cct gcc   787
Arg Leu Thr Ser Val Leu Arg Glu Ala His Pro Tyr Glu Glu Pro Ala
    215                 220                 225

ttc gat att gtt gaa atg cac agc gct gag agt tta gaa aat gcg acc   835
Phe Asp Ile Val Glu Met His Ser Ala Glu Ser Leu Glu Asn Ala Thr
230                 235                 240                 245

gga ttg ggt cgt gtg ggt gaa ttg ccg gag ccg atg cgc ctc gcg gat   883
Gly Leu Gly Arg Val Gly Glu Leu Pro Glu Pro Met Arg Leu Ala Asp
                250                 255                 260

ttc gtg caa caa gtg gcc aac aac ctg cct gtc acc gaa tgg ggc gtg   931
Phe Val Gln Gln Val Ala Asn Asn Leu Pro Val Thr Glu Trp Gly Val
            265                 270                 275

cgc gct acc ggc gat cct gaa caa atg gtg tcc cgt gtg gcg gtt tca   979
Arg Ala Thr Gly Asp Pro Glu Gln Met Val Ser Arg Val Ala Val Ser
        280                 285                 290

tca ggg tcg ggt gac agt ttc tta aac gat gtg att aag ctc gga gtg   1027
Ser Gly Ser Gly Asp Ser Phe Leu Asn Asp Val Ile Lys Leu Gly Val
    295                 300                 305

gac gtt tat gtc act tct gat ctg cgc cac cat cca gtt gat gaa tat   1075
Asp Val Tyr Val Thr Ser Asp Leu Arg His His Pro Val Asp Glu Tyr
310                 315                 320                 325

ctc cga gaa ggt ggc cct gca gta atc gat act gca cac tgg gcc agc   1123
Leu Arg Glu Gly Gly Pro Ala Val Ile Asp Thr Ala His Trp Ala Ser
                330                 335                 340

gaa ttt cca tgg act tcc caa gcc caa gaa att ttg cag gac aaa gcc   1171
Glu Phe Pro Trp Thr Ser Gln Ala Gln Glu Ile Leu Gln Asp Lys Ala
            345                 350                 355

cca cag gtt gaa gtt gat gtg att tcg atc cgc aca gac ccc tgg acc   1219
Pro Gln Val Glu Val Asp Val Ile Ser Ile Arg Thr Asp Pro Trp Thr
        360                 365                 370

atg tct gcg cga gca gtg aac taaattcttg agaactaaaa aag             1263
Met Ser Ala Arg Ala Val Asn
    375                 380
```

<210> 188
<211> 380
<212> PRT
<213> Corynebacterium glutamicum

<400> 188
Val Ser Asp Val Thr Val Gly Asp Ile Arg Arg Ile Leu Asp Glu Ala
1 5 10 15

Tyr Pro Pro Ala Leu Ala Glu Ser Trp Asp Lys Val Gly Leu Ile Cys
20 25 30

Gly Asp Pro Thr Glu Ser Val Lys Arg Val Gly Leu Ala Leu Asp Cys
35 40 45

Thr Gln Ala Val Ala Asp Lys Ala Val Asp Met Gly Leu Asp Met Leu
50 55 60

Ile Ile His His Pro Leu Leu Leu Arg Gly Val Thr Ser Val Ala Ala
65 70 75 80

Asp Glu Pro Lys Gly Lys Val Ile His Thr Leu Ile Arg Gly Gly Val
85 90 95

Ala Leu Phe Ser Ala His Thr Asn Ala Asp Ser Ala Arg Pro Gly Val
100 105 110

Asn Asp Lys Leu Ala Glu Leu Val Gly Ile Thr Ala Gly Arg Pro Ile
115 120 125

Ala Thr Arg Leu Leu Gly Gly Met Asp Lys Trp Gly Val His Val Leu
130 135 140

Pro Lys Asp Ala Ala Tyr Leu Lys Lys Met Leu Phe Asp Ala Gly Ala
145 150 155 160

Gly Ala Ile Gly Asp Tyr Arg Glu Cys Ala Phe Glu Ile Glu Gly Thr
165 170 175

Gly Gln Phe Arg Pro Val Glu Gly Ala Asn Pro Ala Glu Gly Asp Val
180 185 190

Asp Lys Leu Phe Lys Ser Leu Glu Leu Arg Ile Glu Phe Val Ala Pro
195 200 205

Arg Asn Leu Arg Ala Arg Leu Thr Ser Val Leu Arg Glu Ala His Pro
210 215 220

Tyr Glu Glu Pro Ala Phe Asp Ile Val Glu Met His Ser Ala Glu Ser
225 230 235 240

Leu Glu Asn Ala Thr Gly Leu Gly Arg Val Gly Glu Leu Pro Glu Pro
245 250 255

Met Arg Leu Ala Asp Phe Val Gln Gln Val Ala Asn Asn Leu Pro Val
260 265 270

Thr Glu Trp Gly Val Arg Ala Thr Gly Asp Pro Glu Gln Met Val Ser
275 280 285

```
Arg Val Ala Val Ser Ser Gly Ser Gly Asp Ser Phe Leu Asn Asp Val
    290                 295                 300

Ile Lys Leu Gly Val Asp Val Tyr Val Thr Ser Asp Leu Arg His His
305                 310                 315                 320

Pro Val Asp Glu Tyr Leu Arg Glu Gly Gly Pro Ala Val Ile Asp Thr
                325                 330                 335

Ala His Trp Ala Ser Glu Phe Pro Trp Thr Ser Gln Ala Gln Glu Ile
            340                 345                 350

Leu Gln Asp Lys Ala Pro Gln Val Glu Val Asp Val Ile Ser Ile Arg
        355                 360                 365

Thr Asp Pro Trp Thr Met Ser Ala Arg Ala Val Asn
    370                 375                 380


<210> 189
<211> 806
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(783)
<223> FRXA00338

<400> 189
gtc ggc atc acg gcc ggg cga ccc atc gcg aca cgg ctt tta ggc ggc   48
Val Gly Ile Thr Ala Gly Arg Pro Ile Ala Thr Arg Leu Leu Gly Gly
  1               5                  10                  15

atg gac aaa tgg ggc gtg cac gtt ctg ccc aag gat gca gcg tac cta   96
Met Asp Lys Trp Gly Val His Val Leu Pro Lys Asp Ala Ala Tyr Leu
             20                  25                  30

aag aag atg ctt ttc gac gca ggt gcc ggt gcg atc ggc gac tac cga  144
Lys Lys Met Leu Phe Asp Ala Gly Ala Gly Ala Ile Gly Asp Tyr Arg
         35                  40                  45

gag tgt gcc ttt gag atc gaa gga acc ggg cag ttt agg ccc gtg gag  192
Glu Cys Ala Phe Glu Ile Glu Gly Thr Gly Gln Phe Arg Pro Val Glu
     50                  55                  60

ggg gcg aat ccg gca gag ggg gac gtc gat aag ctt ttt aaa tcc ctt  240
Gly Ala Asn Pro Ala Glu Gly Asp Val Asp Lys Leu Phe Lys Ser Leu
 65                  70                  75                  80

gag ctg cgc atc gag ttt gtt gca ccg cgc aac ctg cgc gcc cgg ctc  288
Glu Leu Arg Ile Glu Phe Val Ala Pro Arg Asn Leu Arg Ala Arg Leu
                 85                  90                  95

acg tcg gtg ctg cgg gag gct cat ccg tat gag gag cct gcc ttc gat  336
Thr Ser Val Leu Arg Glu Ala His Pro Tyr Glu Glu Pro Ala Phe Asp
            100                 105                 110

att gtt gaa atg cac agc gct gag agt tta gaa aat gcg acc gga ttg  384
Ile Val Glu Met His Ser Ala Glu Ser Leu Glu Asn Ala Thr Gly Leu
```

```
        115                 120                 125

ggt cgt gtg ggt gaa ttg ccg gag ccg atg cgc ctc gcg gat ttc gtg   432
Gly Arg Val Gly Glu Leu Pro Glu Pro Met Arg Leu Ala Asp Phe Val
    130                 135                 140

caa caa gtg gcc aac aac ctg cct gtc acc gaa tgg ggc gtg cgc gct   480
Gln Gln Val Ala Asn Asn Leu Pro Val Thr Glu Trp Gly Val Arg Ala
145                 150                 155                 160

acc ggc gat cct gaa caa atg gtg tcc cgt gtg gcg gtt tca tca ggg   528
Thr Gly Asp Pro Glu Gln Met Val Ser Arg Val Ala Val Ser Ser Gly
                165                 170                 175

tcg ggt gac agt ttc tta aac gat gtg att aag ctc gga gtg gac gtt   576
Ser Gly Asp Ser Phe Leu Asn Asp Val Ile Lys Leu Gly Val Asp Val
            180                 185                 190

tat gtc act tct gat ctg cgc cac cat cca gtt gat gaa tat ctc cga   624
Tyr Val Thr Ser Asp Leu Arg His His Pro Val Asp Glu Tyr Leu Arg
        195                 200                 205

gaa ggt ggc cct gca gta atc gat act gca cac tgg gcc agc gaa ttt   672
Glu Gly Gly Pro Ala Val Ile Asp Thr Ala His Trp Ala Ser Glu Phe
    210                 215                 220

cca tgg act tcc caa gcc caa gaa att ttg cag gac aaa gcc cca cag   720
Pro Trp Thr Ser Gln Ala Gln Glu Ile Leu Gln Asp Lys Ala Pro Gln
225                 230                 235                 240

gtt gaa gtt gat gtg att tcg atc cgc aca gac ccc tgg acc atg tct   768
Val Glu Val Asp Val Ile Ser Ile Arg Thr Asp Pro Trp Thr Met Ser
                245                 250                 255

gcg cga gca gtg aac taaattcttg agaactaaaa aag                    806
Ala Arg Ala Val Asn
            260
```

Application Number 10/599,760 Amendment Dated March 30, 2009

<210> 190
<211> 261
<212> PRT
<213> Corynebacterium glutamicum

<400> 190

```
Val Gly Ile Thr Ala Gly Arg Pro Ile Ala Thr Arg Leu Leu Gly Gly
  1               5                  10                  15

Met Asp Lys Trp Gly Val His Val Leu Pro Lys Asp Ala Ala Tyr Leu
             20                  25                  30

Lys Lys Met Leu Phe Asp Ala Gly Ala Gly Ala Ile Gly Asp Tyr Arg
         35                  40                  45

Glu Cys Ala Phe Glu Ile Glu Gly Thr Gly Gln Phe Arg Pro Val Glu
     50                  55                  60

Gly Ala Asn Pro Ala Glu Gly Asp Val Asp Lys Leu Phe Lys Ser Leu
 65                  70                  75                  80

Glu Leu Arg Ile Glu Phe Val Ala Pro Arg Asn Leu Arg Ala Arg Leu
```

```
                85                  90                  95

Thr Ser Val Leu Arg Glu Ala His Pro Tyr Glu Glu Pro Ala Phe Asp
            100                 105                 110

Ile Val Glu Met His Ser Ala Glu Ser Leu Glu Asn Ala Thr Gly Leu
        115                 120                 125

Gly Arg Val Gly Glu Leu Pro Glu Pro Met Arg Leu Ala Asp Phe Val
    130                 135                 140

Gln Gln Val Ala Asn Asn Leu Pro Val Thr Glu Trp Gly Val Arg Ala
145                 150                 155                 160

Thr Gly Asp Pro Glu Gln Met Val Ser Arg Val Ala Val Ser Ser Gly
                165                 170                 175

Ser Gly Asp Ser Phe Leu Asn Asp Val Ile Lys Leu Gly Val Asp Val
            180                 185                 190

Tyr Val Thr Ser Asp Leu Arg His His Pro Val Asp Glu Tyr Leu Arg
        195                 200                 205

Glu Gly Gly Pro Ala Val Ile Asp Thr Ala His Trp Ala Ser Glu Phe
    210                 215                 220

Pro Trp Thr Ser Gln Ala Gln Glu Ile Leu Gln Asp Lys Ala Pro Gln
225                 230                 235                 240

Val Glu Val Asp Val Ile Ser Ile Arg Thr Asp Pro Trp Thr Met Ser
                245                 250                 255

Ala Arg Ala Val Asn
            260
```

Application Filed with the Chinese Patent Office on 2006-12-29

<210> 191
<211> 310
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(310)
<223> FRXA00318

<400> 191
tcttagaagg cgtagtcaca ccattaacct tgccagaatt tttcaaggct tggcttgact 60

```
tgggaaacga acatgcggta ccaaccaggg gaggtaatgc gtg agt gat gta acc   115
                                               Val Ser Asp Val Thr
                                                 1               5

gtt ggc gat att ctc cgc att ttg gat gag gct tat ccg ccg gcg ttg   163
Val Gly Asp Ile Leu Arg Ile Leu Asp Glu Ala Tyr Pro Pro Ala Leu
                 10                  15                  20

gcg gaa agc tgg gac aaa gtg gtg ctg atc tgc gtt gat cca aca gag   211
Ala Glu Ser Trp Asp Lys Val Val Leu Ile Cys Val Asp Pro Thr Glu
             25                  30                  35
```

```
tcg gtg aag cgt gtt ggt tta gca ctc gat tgc acc cag gca ctg gcc   259
Ser Val Lys Arg Val Gly Leu Ala Leu Asp Cys Thr Gln Ala Leu Ala
         40                  45                  50

gac aag gct gtg gac atg ggt ttg gac atg ctg atc att cac cac cca   307
Asp Lys Ala Val Asp Met Gly Leu Asp Met Leu Ile Ile His His Pro
     55                  60                  65

tta                                                               310
Leu
 70


<210> 192
<211> 70
<212> PRT
<213> Corynebacterium glutamicum

<400> 192
Val Ser Asp Val Thr Val Gly Asp Ile Leu Arg Ile Leu Asp Glu Ala
  1               5                  10                  15

Tyr Pro Pro Ala Leu Ala Glu Ser Trp Asp Lys Val Val Leu Ile Cys
             20                  25                  30

Val Asp Pro Thr Glu Ser Val Lys Arg Val Gly Leu Ala Leu Asp Cys
         35                  40                  45

Thr Gln Ala Leu Ala Asp Lys Ala Val Asp Met Gly Leu Asp Met Leu
     50                  55                  60

Ile Ile His His Pro Leu
 65                  70


<210> 193
<211> 552
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(529)
<223> RXN00342

<400> 193
cggtaatgtg caattcggat atatcaatag ccccgcggtt tcatgttgaa tccatgtaat 60

cgaaaaacac atcggggccc acacgaggag gattattaaa gtg gcc gac gct ccg   115
                                              Val Ala Asp Ala Pro
                                                1               5

ggc gca gtc aag caa ggt gcc cag gat tat gct caa cta ctc ggc att   163
Gly Ala Val Lys Gln Gly Ala Gln Asp Tyr Ala Gln Leu Leu Gly Ile
                10                  15                  20

caa tcg ggt cat atc gtt caa gaa att gga tgg gat gaa gat tcc gac   211
Gln Ser Gly His Ile Val Gln Glu Ile Gly Trp Asp Glu Asp Ser Asp
            25                  30                  35

acg ctg atc agc gag tcc atc gaa gat gca atc ggt gag gaa cta ctc   259
```

```
Thr Leu Ile Ser Glu Ser Ile Glu Asp Ala Ile Gly Glu Glu Leu Leu
         40                  45                  50

gat gaa gaa acc gac gag ctg tgc gat gtc gtg ctg ctc tgg tgg cgc   307
Asp Glu Glu Thr Asp Glu Leu Cys Asp Val Val Leu Leu Trp Trp Arg
     55                  60                  65

gag gat gac ggc gat ctc gtc gac gga ctt gtg gat tcc atc cgc tcc   355
Glu Asp Asp Gly Asp Leu Val Asp Gly Leu Val Asp Ser Ile Arg Ser
 70                  75                  80                  85

ctc gct gag aat ggt cgt atc tgg gtg ttg act cct ggc att ggt aaa   403
Leu Ala Glu Asn Gly Arg Ile Trp Val Leu Thr Pro Gly Ile Gly Lys
                90                  95                 100

gaa gga gcc ctg gct cct gga gtt atc tct gaa tca gct caa ctg gca   451
Glu Gly Ala Leu Ala Pro Gly Val Ile Ser Glu Ser Ala Gln Leu Ala
            105                 110                 115

ggt ctc gtg cag acc aag gca gaa cgt ctc ggt aat tgg caa ggt tct   499
Gly Leu Val Gln Thr Lys Ala Glu Arg Leu Gly Asn Trp Gln Gly Ser
        120                 125                 130

tgc ctc gtc cag cgt gga aac aag aag cct taacaatcgc taatttccac     549
Cys Leu Val Gln Arg Gly Asn Lys Lys Pro
    135                 140

ggc                                                               552


<210> 194
<211> 143
<212> PRT
<213> Corynebacterium glutamicum

<400> 194
Val Ala Asp Ala Pro Gly Ala Val Lys Gln Gly Ala Gln Asp Tyr Ala
  1               5                  10                  15

Gln Leu Leu Gly Ile Gln Ser Gly His Ile Val Gln Glu Ile Gly Trp
             20                  25                  30

Asp Glu Asp Ser Asp Thr Leu Ile Ser Glu Ser Ile Glu Asp Ala Ile
         35                  40                  45

Gly Glu Glu Leu Leu Asp Glu Glu Thr Asp Glu Leu Cys Asp Val Val
     50                  55                  60

Leu Leu Trp Trp Arg Glu Asp Asp Gly Asp Leu Val Asp Gly Leu Val
 65                  70                  75                  80

Asp Ser Ile Arg Ser Leu Ala Glu Asn Gly Arg Ile Trp Val Leu Thr
                 85                  90                  95

Pro Gly Ile Gly Lys Glu Gly Ala Leu Ala Pro Gly Val Ile Ser Glu
            100                 105                 110

Ser Ala Gln Leu Ala Gly Leu Val Gln Thr Lys Ala Glu Arg Leu Gly
        115                 120                 125

Asn Trp Gln Gly Ser Cys Leu Val Gln Arg Gly Asn Lys Lys Pro
```

130 135 140

<210> 195
<211> 524
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (73)..(501)
<223> FRXA00342

<400> 195
tagccccgcg gtttcatgtt gaatccatgt aatcgaaaac acatcggggc ccacacgagg 60

agaattatta aagtg gcc gac gct ccg ggc gca gtc aag caa ggt gcc cag 111
Val Ala Asp Ala Pro Gly Ala Val Lys Gln Gly Ala Gln
1 5 10

gat tat gct caa cta ctc ggc att caa tcg ggt cat atc gtt caa gaa 159
Asp Tyr Ala Gln Leu Leu Gly Ile Gln Ser Gly His Ile Val Gln Glu
15 20 25

att gga tgg gat gaa gat tcc gac acg ctg atc agc gag tcc atc gaa 207
Ile Gly Trp Asp Glu Asp Ser Asp Thr Leu Ile Ser Glu Ser Ile Glu
30 35 40 45

gat gca atc ggt gag gaa cta ctc gat gaa gaa acc gac gag ctg tgc 255
Asp Ala Ile Gly Glu Glu Leu Leu Asp Glu Glu Thr Asp Glu Leu Cys
50 55 60

gat gtc gtg ctg ctc tgg tgg cgc gag gat gac ggc gat ctc gtc gac 303
Asp Val Val Leu Leu Trp Trp Arg Glu Asp Asp Gly Asp Leu Val Asp
65 70 75

gga ctt gtg gat tcc atc cgc tcc ctc gct gag aat ggt cgt atc tgg 351
Gly Leu Val Asp Ser Ile Arg Ser Leu Ala Glu Asn Gly Arg Ile Trp
80 85 90

gtg ttg act cct ggc att ggt aaa gaa gga gcc ctg gct cct gga gtt 399
Val Leu Thr Pro Gly Ile Gly Lys Glu Gly Ala Leu Ala Pro Gly Val
95 100 105

atc tct gaa tca gct caa ctg gca ggt ctc gtg cag acc aag gca gaa 447
Ile Ser Glu Ser Ala Gln Leu Ala Gly Leu Val Gln Thr Lys Ala Glu
110 115 120 125

cgt ctc ggt aat tgg caa ggt tct tgc ctc gtc cag cgt gga aac aag 495
Arg Leu Gly Asn Trp Gln Gly Ser Cys Leu Val Gln Arg Gly Asn Lys
130 135 140

aag cct taacaatcgc taatttccac ggc 524
Lys Pro

<210> 196
<211> 143
<212> PRT
<213> Corynebacterium glutamicum

<400> 196
Val Ala Asp Ala Pro Gly Ala Val Lys Gln Gly Ala Gln Asp Tyr Ala
1 5 10 15

Gln Leu Leu Gly Ile Gln Ser Gly His Ile Val Gln Glu Ile Gly Trp
20 25 30

Asp Glu Asp Ser Asp Thr Leu Ile Ser Glu Ser Ile Glu Asp Ala Ile
35 40 45

Gly Glu Glu Leu Leu Asp Glu Glu Thr Asp Glu Leu Cys Asp Val Val
50 55 60

Leu Leu Trp Trp Arg Glu Asp Asp Gly Asp Leu Val Asp Gly Leu Val
65 70 75 80

Asp Ser Ile Arg Ser Leu Ala Glu Asn Gly Arg Ile Trp Val Leu Thr
85 90 95

Pro Gly Ile Gly Lys Glu Gly Ala Leu Ala Pro Gly Val Ile Ser Glu
100 105 110

Ser Ala Gln Leu Ala Gly Leu Val Gln Thr Lys Ala Glu Arg Leu Gly
115 120 125

Asn Trp Gln Gly Ser Cys Leu Val Gln Arg Gly Asn Lys Lys Pro
130 135 140

<210> 197
<211> 1002
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(979)
<223> RXN00344

<400> 197
cggcacggtt ggcgatgtca tgcagtccga aaaactcagc gaactctaca acgcacccgt 60

cacggtggct cgcatcaacg acagaatcgt ggtggtttaa gtg gat cta tcc acc 115
Val Asp Leu Ser Thr
1 5

tgg ctt tcc gac acc caa tat ctc atc agc gtc gat ttc gtc cag cac 163
Trp Leu Ser Asp Thr Gln Tyr Leu Ile Ser Val Asp Phe Val Gln His
10 15 20

gca ctc atc gcc tcc gcg ctg ttg ggc ctg ctc tcc ggt gtg atc gcg 211
Ala Leu Ile Ala Ser Ala Leu Leu Gly Leu Leu Ser Gly Val Ile Ala
25 30 35

ccg ctc atc gtg gtg cgc caa cag tcc ttc gca gtc cac ggc acc gcc 259
Pro Leu Ile Val Val Arg Gln Gln Ser Phe Ala Val His Gly Thr Ala
40 45 50

gaa ctc gcc ctc atg gga gcc gcc gcc gcg ctg ctc ttc gga ttg aat 307
Glu Leu Ala Leu Met Gly Ala Ala Ala Ala Leu Leu Phe Gly Leu Asn

```
     55                  60                  65

gta ggc ggc ggt gca gtg atc ggt tcc gtg gtc gcc gcg atc cta ctg   355
Val Gly Gly Gly Ala Val Ile Gly Ser Val Val Ala Ala Ile Leu Leu
 70                  75                  80                  85

gca tta ctc ggc atg aaa caa caa gat tcc gcc gtc ggt gcc gtg atg   403
Ala Leu Leu Gly Met Lys Gln Gln Asp Ser Ala Val Gly Ala Val Met
                90                  95                 100

agt ttc gga ctc ggt ctg tcc gtg ctg ttc att cac ctc tac ccc ggc   451
Ser Phe Gly Leu Gly Leu Ser Val Leu Phe Ile His Leu Tyr Pro Gly
            105                 110                 115

cga agc tcc acc gcg ttc tcc ctg ctc aca ggg caa atc gtt ggt gtt   499
Arg Ser Ser Thr Ala Phe Ser Leu Leu Thr Gly Gln Ile Val Gly Val
        120                 125                 130

tcc tca tca tcg ctg tgg atc ctt gtg gca gtc acc gtg atc gtg gtt   547
Ser Ser Ser Ser Leu Trp Ile Leu Val Ala Val Thr Val Ile Val Val
    135                 140                 145

agc gcc gtg gtg att ttc tgg cgc ccg ctg ctt ttc gcc agc gcc gat   595
Ser Ala Val Val Ile Phe Trp Arg Pro Leu Leu Phe Ala Ser Ala Asp
150                 155                 160                 165

ccg atc atg gcg cag gcc tcc gga gta aac gtc cga ttc atc gcc gtt   643
Pro Ile Met Ala Gln Ala Ser Gly Val Asn Val Arg Phe Ile Ala Val
                170                 175                 180

gcc ttc gca gtt ctg gtt ggc ctc acc acg tcc cag tcc gtg cag att   691
Ala Phe Ala Val Leu Val Gly Leu Thr Thr Ser Gln Ser Val Gln Ile
            185                 190                 195

gtc ggt gcg ctg ctg gtc atg gca ttg ctg atc act ccc ggc gcg gcc   739
Val Gly Ala Leu Leu Val Met Ala Leu Leu Ile Thr Pro Gly Ala Ala
        200                 205                 210

gct gtg gcg gtg acc gcc aat cca gtg aaa gcc gtg gtg ctg gca gtc   787
Ala Val Ala Val Thr Ala Asn Pro Val Lys Ala Val Val Leu Ala Val
    215                 220                 225

atc ttc gcg gaa gta tcg gct gtc ggt ggc ctg cta ttg tcg cta gcg   835
Ile Phe Ala Glu Val Ser Ala Val Gly Gly Leu Leu Leu Ser Leu Ala
230                 235                 240                 245

cct ggt ttg ccg gtg agt gtt ttt gtc acc acc atc tct ttt gtg att   883
Pro Gly Leu Pro Val Ser Val Phe Val Thr Thr Ile Ser Phe Val Ile
                250                 255                 260

tac ctg gtc tgc cgc ctg atc ggt tgg ctc cgc ggc cgt gga gct cag   931
Tyr Leu Val Cys Arg Leu Ile Gly Trp Leu Arg Gly Arg Gly Ala Gln
            265                 270                 275

cgt gac gaa gat gct tat cga cgc cgc cag cac gat cac cac cct cac   979
Arg Asp Glu Asp Ala Tyr Arg Arg Arg Gln His Asp His His Pro His
        280                 285                 290

taggcgtttc gaagtcctat ttc                                        1002
```

<210> 198
<211> 293
<212> PRT
<213> Corynebacterium glutamicum

<400> 198
Val Asp Leu Ser Thr Trp Leu Ser Asp Thr Gln Tyr Leu Ile Ser Val
1 5 10 15

Asp Phe Val Gln His Ala Leu Ile Ala Ser Ala Leu Leu Gly Leu Leu
20 25 30

Ser Gly Val Ile Ala Pro Leu Ile Val Val Arg Gln Gln Ser Phe Ala
35 40 45

Val His Gly Thr Ala Glu Leu Ala Leu Met Gly Ala Ala Ala Ala Leu
50 55 60

Leu Phe Gly Leu Asn Val Gly Gly Gly Ala Val Ile Gly Ser Val Val
65 70 75 80

Ala Ala Ile Leu Leu Ala Leu Leu Gly Met Lys Gln Gln Asp Ser Ala
85 90 95

Val Gly Ala Val Met Ser Phe Gly Leu Gly Leu Ser Val Leu Phe Ile
100 105 110

His Leu Tyr Pro Gly Arg Ser Ser Thr Ala Phe Ser Leu Leu Thr Gly
115 120 125

Gln Ile Val Gly Val Ser Ser Ser Ser Leu Trp Ile Leu Val Ala Val
130 135 140

Thr Val Ile Val Val Ser Ala Val Val Ile Phe Trp Arg Pro Leu Leu
145 150 155 160

Phe Ala Ser Ala Asp Pro Ile Met Ala Gln Ala Ser Gly Val Asn Val
165 170 175

Arg Phe Ile Ala Val Ala Phe Ala Val Leu Val Gly Leu Thr Thr Ser
180 185 190

Gln Ser Val Gln Ile Val Gly Ala Leu Leu Val Met Ala Leu Leu Ile
195 200 205

Thr Pro Gly Ala Ala Ala Val Ala Val Thr Ala Asn Pro Val Lys Ala
210 215 220

Val Val Leu Ala Val Ile Phe Ala Glu Val Ser Ala Val Gly Gly Leu
225 230 235 240

Leu Leu Ser Leu Ala Pro Gly Leu Pro Val Ser Val Phe Val Thr Thr
245 250 255

Ile Ser Phe Val Ile Tyr Leu Val Cys Arg Leu Ile Gly Trp Leu Arg
260 265 270

Gly Arg Gly Ala Gln Arg Asp Glu Asp Ala Tyr Arg Arg Arg Gln His
275 280 285

Asp His His Pro His

290

<210> 199
<211> 594
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(579)
<223> FRXA00344

<400> 199

```
atg agt ttc gga ctc ggt ctg tcc gtg ctg ttc att cac ctc tac ccc   48
Met Ser Phe Gly Leu Gly Leu Ser Val Leu Phe Ile His Leu Tyr Pro
  1               5                  10                  15

ggc cga agc tcc acc gcg ttc tcc ctg ctc aca ggg caa atc gtt ggt   96
Gly Arg Ser Ser Thr Ala Phe Ser Leu Leu Thr Gly Gln Ile Val Gly
            20                  25                  30

gtt tcc tca tca tcg ctg tgg atc ctt gtg gca gtc acc gtg atc gtg   144
Val Ser Ser Ser Ser Leu Trp Ile Leu Val Ala Val Thr Val Ile Val
        35                  40                  45

gtt agc gcc gtg gtg att ttc tgg cgc ccg ctg ctt ttc gcc agc gcc   192
Val Ser Ala Val Val Ile Phe Trp Arg Pro Leu Leu Phe Ala Ser Ala
    50                  55                  60

gat ccg atc atg gcg cag gcc tcc gga gta aac gtc cga ttc atc gcc   240
Asp Pro Ile Met Ala Gln Ala Ser Gly Val Asn Val Arg Phe Ile Ala
65                  70                  75                  80

gtt gcc ttc gca gtt ctg gtt ggc ctc acc acg tcc cag tcc gtg cag   288
Val Ala Phe Ala Val Leu Val Gly Leu Thr Thr Ser Gln Ser Val Gln
                85                  90                  95

att gtc ggt gcg ctg ctg gtc atg gca ttg ctg atc act ccc ggc gcg   336
Ile Val Gly Ala Leu Leu Val Met Ala Leu Leu Ile Thr Pro Gly Ala
            100                 105                 110

gcc gct gtg gcg gtg acc gcc aat cca gtg aaa gcc gtg gtg ctg gca   384
Ala Ala Val Ala Val Thr Ala Asn Pro Val Lys Ala Val Val Leu Ala
        115                 120                 125

gtc atc ttc gcg gaa gta tcg gct gtc ggt ggc ctg cta ttg tcg cta   432
Val Ile Phe Ala Glu Val Ser Ala Val Gly Gly Leu Leu Leu Ser Leu
    130                 135                 140

gcg cct ggt ttg ccg gtg agt gtt ttt gtc acc acc atc tct ttt gtg   480
Ala Pro Gly Leu Pro Val Ser Val Phe Val Thr Thr Ile Ser Phe Val
145                 150                 155                 160

att tac ctg gtc tgc cgc ctg atc ggt tgg ctc cgc ggc cgt gga gct   528
Ile Tyr Leu Val Cys Arg Leu Ile Gly Trp Leu Arg Gly Arg Gly Ala
                165                 170                 175

cag cgt gac gaa gat gct tat cga cgc cgc cag cac gat cac cac cct   576
Gln Arg Asp Glu Asp Ala Tyr Arg Arg Arg Gln His Asp His His Pro
            180                 185                 190
```

cac taggcgtttc gaagt 594
His

<210> 200
<211> 193
<212> PRT
<213> Corynebacterium glutamicum

<400> 200
Met Ser Phe Gly Leu Gly Leu Ser Val Leu Phe Ile His Leu Tyr Pro
1 5 10 15

Gly Arg Ser Ser Thr Ala Phe Ser Leu Leu Thr Gly Gln Ile Val Gly
20 25 30

Val Ser Ser Ser Ser Leu Trp Ile Leu Val Ala Val Thr Val Ile Val
35 40 45

Val Ser Ala Val Val Ile Phe Trp Arg Pro Leu Leu Phe Ala Ser Ala
50 55 60

Asp Pro Ile Met Ala Gln Ala Ser Gly Val Asn Val Arg Phe Ile Ala
65 70 75 80

Val Ala Phe Ala Val Leu Val Gly Leu Thr Thr Ser Gln Ser Val Gln
85 90 95

Ile Val Gly Ala Leu Leu Val Met Ala Leu Leu Ile Thr Pro Gly Ala
100 105 110

Ala Ala Val Ala Val Thr Ala Asn Pro Val Lys Ala Val Val Leu Ala
115 120 125

Val Ile Phe Ala Glu Val Ser Ala Val Gly Gly Leu Leu Leu Ser Leu
130 135 140

Ala Pro Gly Leu Pro Val Ser Val Phe Val Thr Thr Ile Ser Phe Val
145 150 155 160

Ile Tyr Leu Val Cys Arg Leu Ile Gly Trp Leu Arg Gly Arg Gly Ala
165 170 175

Gln Arg Asp Glu Asp Ala Tyr Arg Arg Arg Gln His Asp His His Pro
180 185 190

His

<210> 201
<211> 816
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(793)
<223> RXN00353

<400> 201
ctttcatcag gaccgaaagc gaacgtttcg tattgttgag ccttttggtt ccaccacgga 60

tgcgctgatc tattttcatg gctcccagca gtcaggatct gtg ggg cgc agc ttc 115
Val Gly Arg Ser Phe
1 5

acc aac agg act ttt gat ccg ttg ccg ttc atg gtg gtt tat ccg gat 163
Thr Asn Arg Thr Phe Asp Pro Leu Pro Phe Met Val Val Tyr Pro Asp
10 15 20

ggg gtg gat cag cat tgg aat gat gcg cgg ttg ggt ttg gat gaa aat 211
Gly Val Asp Gln His Trp Asn Asp Ala Arg Leu Gly Leu Asp Glu Asn
25 30 35

acc cgc cat tta ggc att gat gat gtg ggg ttc ttt gta aaa ctc gcc 259
Thr Arg His Leu Gly Ile Asp Asp Val Gly Phe Phe Val Lys Leu Ala
40 45 50

acg cac ttg ggc aac acg tat ggc atc aag agg atc ttt att gtt ggc 307
Thr His Leu Gly Asn Thr Tyr Gly Ile Lys Arg Ile Phe Ile Val Gly
55 60 65

tat tcc aac ggt ggg cag atg gtg ttg cgg ctc atg cat gag gtt ccc 355
Tyr Ser Asn Gly Gly Gln Met Val Leu Arg Leu Met His Glu Val Pro
70 75 80 85

aag atg ctc agt ggc gct gca acc att gca tcc aac atg cca gtt gca 403
Lys Met Leu Ser Gly Ala Ala Thr Ile Ala Ser Asn Met Pro Val Ala
90 95 100

gag aat acg ctg ccg cag gtg aaa acc ttc aag aca cat ccg gtg cct 451
Glu Asn Thr Leu Pro Gln Val Lys Thr Phe Lys Thr His Pro Val Pro
105 110 115

tat ttg gcg atg gct gga act gcc gat act ttt tca ccg tat gag ggt 499
Tyr Leu Ala Met Ala Gly Thr Ala Asp Thr Phe Ser Pro Tyr Glu Gly
120 125 130

ggc gat gcc ggt att ggt cgc gaa cac cgc cgt ggc gtg ggc atg tcc 547
Gly Asp Ala Gly Ile Gly Arg Glu His Arg Arg Gly Val Gly Met Ser
135 140 145

gcc ttt gat tca gct gcc tat att gcc gcc cga aac gga ctg acc gaa 595
Ala Phe Asp Ser Ala Ala Tyr Ile Ala Ala Arg Asn Gly Leu Thr Glu
150 155 160 165

cac cgc cac gac gtg att gat gat gtg gtg tcg atc gat acc tgg gat 643
His Arg His Asp Val Ile Asp Asp Val Val Ser Ile Asp Thr Trp Asp
170 175 180

gga gaa aat ccc gtt gag ttt tgg aca ctc aac ggg atc ggc cac ttg 691
Gly Glu Asn Pro Val Glu Phe Trp Thr Leu Asn Gly Ile Gly His Leu
185 190 195

gta cca agt ggg aaa act tat cca gaa ttt cta ggc ccc tca acc aca 739
Val Pro Ser Gly Lys Thr Tyr Pro Glu Phe Leu Gly Pro Ser Thr Thr
200 205 210

tca gtg ata gcg gct gag gag att ggg aag ttc ttt gat ggg gtc agg 787

Ser Val Ile Ala Ala Glu Glu Ile Gly Lys Phe Phe Asp Gly Val Arg
215 220 225

cgt cga taagctcaag ctttaaaaac gca 816
Arg Arg
230

<210> 202
<211> 231
<212> PRT
<213> Corynebacterium glutamicum

<400> 202
Val Gly Arg Ser Phe Thr Asn Arg Thr Phe Asp Pro Leu Pro Phe Met
1 5 10 15

Val Val Tyr Pro Asp Gly Val Asp Gln His Trp Asn Asp Ala Arg Leu
20 25 30

Gly Leu Asp Glu Asn Thr Arg His Leu Gly Ile Asp Asp Val Gly Phe
35 40 45

Phe Val Lys Leu Ala Thr His Leu Gly Asn Thr Tyr Gly Ile Lys Arg
50 55 60

Ile Phe Ile Val Gly Tyr Ser Asn Gly Gly Gln Met Val Leu Arg Leu
65 70 75 80

Met His Glu Val Pro Lys Met Leu Ser Gly Ala Ala Thr Ile Ala Ser
85 90 95

Asn Met Pro Val Ala Glu Asn Thr Leu Pro Gln Val Lys Thr Phe Lys
100 105 110

Thr His Pro Val Pro Tyr Leu Ala Met Ala Gly Thr Ala Asp Thr Phe
115 120 125

Ser Pro Tyr Glu Gly Gly Asp Ala Gly Ile Gly Arg Glu His Arg Arg
130 135 140

Gly Val Gly Met Ser Ala Phe Asp Ser Ala Ala Tyr Ile Ala Ala Arg
145 150 155 160

Asn Gly Leu Thr Glu His Arg His Asp Val Ile Asp Asp Val Val Ser
165 170 175

Ile Asp Thr Trp Asp Gly Glu Asn Pro Val Glu Phe Trp Thr Leu Asn
180 185 190

Gly Ile Gly His Leu Val Pro Ser Gly Lys Thr Tyr Pro Glu Phe Leu
195 200 205

Gly Pro Ser Thr Thr Ser Val Ile Ala Ala Glu Glu Ile Gly Lys Phe
210 215 220

Phe Asp Gly Val Arg Arg Arg
225 230

<210> 203

<211> 816
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(793)
<223> FRXA00353

<400> 203
ctttcatcag gaccgaaagc gaacgtttcg tattgttgag ccttttggtt ccaccacgga 60

```
tgcgctgatc tattttcatg gctcccagca gtcaggatct gtg ggg cgc agc ttc   115
                                            Val Gly Arg Ser Phe
                                              1               5

acc aac agg act ttt gat ccg ttg ccg ttc atg gtg gtt tat ccg gat   163
Thr Asn Arg Thr Phe Asp Pro Leu Pro Phe Met Val Val Tyr Pro Asp
                 10                  15                  20

ggg gtg gat cag cat tgg aat gat gcg cgg ttg ggt ttg gat gaa aat   211
Gly Val Asp Gln His Trp Asn Asp Ala Arg Leu Gly Leu Asp Glu Asn
             25                  30                  35

acc cgc cat tta ggc att gat gat gtg ggg ttc ttt gta aaa ctc gcc   259
Thr Arg His Leu Gly Ile Asp Asp Val Gly Phe Phe Val Lys Leu Ala
         40                  45                  50

acg cac ttg ggc aac acg tat ggc atc aag agg atc ttt att gtt ggc   307
Thr His Leu Gly Asn Thr Tyr Gly Ile Lys Arg Ile Phe Ile Val Gly
     55                  60                  65

tat tcc aac ggt ggg cag atg gtg ttg cgg ctc atg cat gag gtt ccc   355
Tyr Ser Asn Gly Gly Gln Met Val Leu Arg Leu Met His Glu Val Pro
 70                  75                  80                  85

aag atg ctc agt ggc gct gca acc att gca tcc aac atg cca gtt gca   403
Lys Met Leu Ser Gly Ala Ala Thr Ile Ala Ser Asn Met Pro Val Ala
                 90                  95                 100

gag aat acg ctg ccg cag gtg aaa acc ttc aag aca cat ccg gtg cct   451
Glu Asn Thr Leu Pro Gln Val Lys Thr Phe Lys Thr His Pro Val Pro
             105                 110                 115

tat ttg gcg atg gct gga act gcc gat act ttt tca ccg tat gag ggt   499
Tyr Leu Ala Met Ala Gly Thr Ala Asp Thr Phe Ser Pro Tyr Glu Gly
         120                 125                 130

ggc gat gcc ggt att ggt cgc gaa cac cgc cgt ggc gtg ggc atg tcc   547
Gly Asp Ala Gly Ile Gly Arg Glu His Arg Arg Gly Val Gly Met Ser
     135                 140                 145

gcc ttt gat tca gct gcc tat att gcc gcc cga aac gga ctg acc gaa   595
Ala Phe Asp Ser Ala Ala Tyr Ile Ala Ala Arg Asn Gly Leu Thr Glu
150                 155                 160                 165

cac cgc cac gac gtg att gat gat gtg gtg tcg atc gat acc tgg gat   643
His Arg His Asp Val Ile Asp Asp Val Val Ser Ile Asp Thr Trp Asp
                170                 175                 180

gga gaa aat ccc gtt gag ttt tgg aca ctc aac ggg atc ggc cac ttg   691
```

```
Gly Glu Asn Pro Val Glu Phe Trp Thr Leu Asn Gly Ile Gly His Leu
            185                 190                 195

gta cca agt ggg aaa act tat cca gaa ttt cta ggc ccc tca acc aca   739
Val Pro Ser Gly Lys Thr Tyr Pro Glu Phe Leu Gly Pro Ser Thr Thr
        200                 205                 210

tca gtg ata gcg gct gag gag att ggg aag ttc ttt gat ggg gtc agg   787
Ser Val Ile Ala Ala Glu Glu Ile Gly Lys Phe Phe Asp Gly Val Arg
    215                 220                 225

cgt cga taagctcaag ctttaaaaac gca                                816
Arg Arg
230
```

<210> 204
<211> 231
<212> PRT
<213> Corynebacterium glutamicum

<400> 204

```
Val Gly Arg Ser Phe Thr Asn Arg Thr Phe Asp Pro Leu Pro Phe Met
  1               5                  10                  15

Val Val Tyr Pro Asp Gly Val Asp Gln His Trp Asn Asp Ala Arg Leu
             20                  25                  30

Gly Leu Asp Glu Asn Thr Arg His Leu Gly Ile Asp Asp Val Gly Phe
         35                  40                  45

Phe Val Lys Leu Ala Thr His Leu Gly Asn Thr Tyr Gly Ile Lys Arg
     50                  55                  60

Ile Phe Ile Val Gly Tyr Ser Asn Gly Gly Gln Met Val Leu Arg Leu
 65                  70                  75                  80

Met His Glu Val Pro Lys Met Leu Ser Gly Ala Ala Thr Ile Ala Ser
                 85                  90                  95

Asn Met Pro Val Ala Glu Asn Thr Leu Pro Gln Val Lys Thr Phe Lys
            100                 105                 110

Thr His Pro Val Pro Tyr Leu Ala Met Ala Gly Thr Ala Asp Thr Phe
        115                 120                 125

Ser Pro Tyr Glu Gly Gly Asp Ala Gly Ile Gly Arg Glu His Arg Arg
    130                 135                 140

Gly Val Gly Met Ser Ala Phe Asp Ser Ala Ala Tyr Ile Ala Ala Arg
145                 150                 155                 160

Asn Gly Leu Thr Glu His Arg His Asp Val Ile Asp Asp Val Val Ser
                165                 170                 175

Ile Asp Thr Trp Asp Gly Glu Asn Pro Val Glu Phe Trp Thr Leu Asn
            180                 185                 190

Gly Ile Gly His Leu Val Pro Ser Gly Lys Thr Tyr Pro Glu Phe Leu
        195                 200                 205
```

```
Gly Pro Ser Thr Thr Ser Val Ile Ala Ala Glu Glu Ile Gly Lys Phe
    210                 215                 220

Phe Asp Gly Val Arg Arg Arg
225                 230


<210> 205
<211> 936
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(913)
<223> RXN00354

<400> 205
ggcttgtcgg taaggctgca gggtagcggg agtttccttc agattggaag ttctttaatt 60

ttctcgatta tgtacctcat ttacgcgtaa agtttggggc atg gga aag tta ctt   115
                                            Met Gly Lys Leu Leu
                                              1               5


ttc gta gac atc ggt ggc aca ctg ctg gat tac tca aat gaa gtt ccg   163
Phe Val Asp Ile Gly Gly Thr Leu Leu Asp Tyr Ser Asn Glu Val Pro
                 10                  15                  20

cgt tcg gcc gtt gac gcg atc cgt aag gca cgc gcc aaa gga cac cgc   211
Arg Ser Ala Val Asp Ala Ile Arg Lys Ala Arg Ala Lys Gly His Arg
             25                  30                  35

gtg tac ttg agc tct ggt cga agc agc gct gag gtg act tct cag ttg   259
Val Tyr Leu Ser Ser Gly Arg Ser Ser Ala Glu Val Thr Ser Gln Leu
         40                  45                  50

tgg gat atc gga gtg gat ggc ctc att ggc gca aat ggt gga tat gtg   307
Trp Asp Ile Gly Val Asp Gly Leu Ile Gly Ala Asn Gly Gly Tyr Val
     55                  60                  65

gaa agc gca cag gag tct gtg ttc cac cgc cgt ttg tcg ggt gag gag   355
Glu Ser Ala Gln Glu Ser Val Phe His Arg Arg Leu Ser Gly Glu Glu
 70                  75                  80                  85

acc cgc cac att gtg gag tgg ctc tac aac cgt ggt ttg gag ttt tat   403
Thr Arg His Ile Val Glu Trp Leu Tyr Asn Arg Gly Leu Glu Phe Tyr
                 90                  95                 100

ctc gag tcc aac aac ggt ttg tat gca agc cgt ggt ttc cgt gag gct   451
Leu Glu Ser Asn Asn Gly Leu Tyr Ala Ser Arg Gly Phe Arg Glu Ala
             105                 110                 115

tct aag cca gtg ctg tct cgc ctt tcg gag aag acc gac gtg aca gtc   499
Ser Lys Pro Val Leu Ser Arg Leu Ser Glu Lys Thr Asp Val Thr Val
         120                 125                 130

gat agc atg tac ccg gat atg ttc tgg ggc gcg agc ctt gat cgt gac   547
Asp Ser Met Tyr Pro Asp Met Phe Trp Gly Ala Ser Leu Asp Arg Asp
     135                 140                 145

gat gtg aac aag atc agt tac atc ttc aat tct cag gaa gat ttg gac   595
```

```
Asp Val Asn Lys Ile Ser Tyr Ile Phe Asn Ser Gln Glu Asp Leu Asp
150                 155                 160                 165

gca gcg cgt gag gcg ttc cct aac ctg gag cac acc acg tgg ggt ggt   643
Ala Ala Arg Glu Ala Phe Pro Asn Leu Glu His Thr Thr Trp Gly Gly
                170                 175                 180

cag acg ggt gcg ttg ttc ggc acg atc ggt gtg tct gtc aac aag aag   691
Gln Thr Gly Ala Leu Phe Gly Thr Ile Gly Val Ser Val Asn Lys Lys
            185                 190                 195

atc ggc gtg gat cgc ctg ctg aag tac ctg aac gca gat cgc gca aac   739
Ile Gly Val Asp Arg Leu Leu Lys Tyr Leu Asn Ala Asp Arg Ala Asn
        200                 205                 210

acc att gcg ttc ggc gac agc gat gag gat ctc tcc cta ttt gag gcg   787
Thr Ile Ala Phe Gly Asp Ser Asp Glu Asp Leu Ser Leu Phe Glu Ala
    215                 220                 225

agc gct tac ggc gtc gcg atg ggc gag gcc acc gaa tcg ctc aag gct   835
Ser Ala Tyr Gly Val Ala Met Gly Glu Ala Thr Glu Ser Leu Lys Ala
230                 235                 240                 245

gct gct gac ctg gtc acg gat gct gtt ggg cag gac ggc ttg cgc aat   883
Ala Ala Asp Leu Val Thr Asp Ala Val Gly Gln Asp Gly Leu Arg Asn
                250                 255                 260

gcg ttt tta aag ctt gag ctt atc gac gcc tgaccccatc aaagaacttc     933
Ala Phe Leu Lys Leu Glu Leu Ile Asp Ala
            265                 270

cca                                                              936


<210> 206
<211> 271
<212> PRT
<213> Corynebacterium glutamicum

<400> 206
Met Gly Lys Leu Leu Phe Val Asp Ile Gly Gly Thr Leu Leu Asp Tyr
  1               5                  10                  15

Ser Asn Glu Val Pro Arg Ser Ala Val Asp Ala Ile Arg Lys Ala Arg
             20                  25                  30

Ala Lys Gly His Arg Val Tyr Leu Ser Ser Gly Arg Ser Ser Ala Glu
         35                  40                  45

Val Thr Ser Gln Leu Trp Asp Ile Gly Val Asp Gly Leu Ile Gly Ala
     50                  55                  60

Asn Gly Gly Tyr Val Glu Ser Ala Gln Glu Ser Val Phe His Arg Arg
 65                  70                  75                  80

Leu Ser Gly Glu Glu Thr Arg His Ile Val Glu Trp Leu Tyr Asn Arg
                 85                  90                  95

Gly Leu Glu Phe Tyr Leu Glu Ser Asn Asn Gly Leu Tyr Ala Ser Arg
            100                 105                 110
```

```
Gly Phe Arg Glu Ala Ser Lys Pro Val Leu Ser Arg Leu Ser Glu Lys
        115                 120                 125

Thr Asp Val Thr Val Asp Ser Met Tyr Pro Asp Met Phe Trp Gly Ala
    130                 135                 140

Ser Leu Asp Arg Asp Asp Val Asn Lys Ile Ser Tyr Ile Phe Asn Ser
145                 150                 155                 160

Gln Glu Asp Leu Asp Ala Ala Arg Glu Ala Phe Pro Asn Leu Glu His
                165                 170                 175

Thr Thr Trp Gly Gly Gln Thr Gly Ala Leu Phe Gly Thr Ile Gly Val
            180                 185                 190

Ser Val Asn Lys Lys Ile Gly Val Asp Arg Leu Leu Lys Tyr Leu Asn
        195                 200                 205

Ala Asp Arg Ala Asn Thr Ile Ala Phe Gly Asp Ser Asp Glu Asp Leu
    210                 215                 220

Ser Leu Phe Glu Ala Ser Ala Tyr Gly Val Ala Met Gly Glu Ala Thr
225                 230                 235                 240

Glu Ser Leu Lys Ala Ala Ala Asp Leu Val Thr Asp Ala Val Gly Gln
                245                 250                 255

Asp Gly Leu Arg Asn Ala Phe Leu Lys Leu Glu Leu Ile Asp Ala
            260                 265                 270


<210> 207
<211> 1470
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1447)
<223> RXN00362

<400> 207
cacttttggg gtgaaaattc cacgaagtta atgccgcttt aagtcaattc aatcacatgt 60

aacatgctac ggtttttttcg gtcacttaaa ggaggcgctt atg gga atc att gct   115
                                              Met Gly Ile Ile Ala
                                                1               5

ctg ctc gtt ttt atc gca att gcc gtg ata ttg aat gtg ttt ttg aaa   163
Leu Leu Val Phe Ile Ala Ile Ala Val Ile Leu Asn Val Phe Leu Lys
                  10                  15                  20

cga gat att tca gaa gca ttg cta gtt gga tta gta gga act gcg ctt   211
Arg Asp Ile Ser Glu Ala Leu Leu Val Gly Leu Val Gly Thr Ala Leu
              25                  30                  35

gtc ggc ggt gta aat gca ccg aca tta ctg att gat gct gta gtg gat   259
Val Gly Gly Val Asn Ala Pro Thr Leu Leu Ile Asp Ala Val Val Asp
          40                  45                  50

gct gct cag tcg gaa gtt act ttc gca ggt atg gcc ttt gtt ttc atg   307
```

```
Ala Ala Gln Ser Glu Val Thr Phe Ala Gly Met Ala Phe Val Phe Met
     55                  60                  65

ggc atc gtt gtg caa tca act gga ttg att gat cga tta atc gca atc   355
Gly Ile Val Val Gln Ser Thr Gly Leu Ile Asp Arg Leu Ile Ala Ile
 70                  75                  80                  85

ctt aac tcg att ttt ggt cgg ctt cga ggt ggc gca ggt tat gtt tcc   403
Leu Asn Ser Ile Phe Gly Arg Leu Arg Gly Gly Ala Gly Tyr Val Ser
                 90                  95                 100

act ctt gga tct gcg ctc att gga ctc atc gct gga tca acg gct gga   451
Thr Leu Gly Ser Ala Leu Ile Gly Leu Ile Ala Gly Ser Thr Ala Gly
            105                 110                 115

aac tcc gcg acg gtt ggc tca gtg acg atc cct tgg atg aaa aag acg   499
Asn Ser Ala Thr Val Gly Ser Val Thr Ile Pro Trp Met Lys Lys Thr
        120                 125                 130

gga tgg act gct gaa agg tcc gca acg tta gtc gcg ggc aac tct ggc   547
Gly Trp Thr Ala Glu Arg Ser Ala Thr Leu Val Ala Gly Asn Ser Gly
    135                 140                 145

ctt ggt gtt gcg ttg cct ccc aat tca aca atg ttc atc att ttg gca   595
Leu Gly Val Ala Leu Pro Pro Asn Ser Thr Met Phe Ile Ile Leu Ala
150                 155                 160                 165

ttg cca gct gca gca gct tct tcg gcc tct cag gtg tac att gct ttg   643
Leu Pro Ala Ala Ala Ala Ser Ser Ala Ser Gln Val Tyr Ile Ala Leu
                170                 175                 180

gct tgt ggt ggt gcg tat gca gtg ctc tac cgc tta gcg gtc gtc ttt   691
Ala Cys Gly Gly Ala Tyr Ala Val Leu Tyr Arg Leu Ala Val Val Phe
            185                 190                 195

tac tgg aca cgt aaa gat aaa att cct gcc acc cct gat gat caa cgg   739
Tyr Trp Thr Arg Lys Asp Lys Ile Pro Ala Thr Pro Asp Asp Gln Arg
        200                 205                 210

gtg tca ttc ggt gag gca atg aag act gga tgg cgt tca ccg ttg atc   787
Val Ser Phe Gly Glu Ala Met Lys Thr Gly Trp Arg Ser Pro Leu Ile
    215                 220                 225

ttc ctt gga att ttg atc ccc gta atc ctc aca atc ggc cca ttg tct   835
Phe Leu Gly Ile Leu Ile Pro Val Ile Leu Thr Ile Gly Pro Leu Ser
230                 235                 240                 245

gaa tgg tta aag aca cat gga gtt ggg gag tct ggt gtt aaa tcg atg   883
Glu Trp Leu Lys Thr His Gly Val Gly Glu Ser Gly Val Lys Ser Met
                250                 255                 260

tcg atc atc gtg tgg gtg cca att ctg att acg gca att gct ctg att   931
Ser Ile Ile Val Trp Val Pro Ile Leu Ile Thr Ala Ile Ala Leu Ile
            265                 270                 275

gaa ggg cgt aaa cga att gct aac aac atg gca cac ttt agg gtt cag   979
Glu Gly Arg Lys Arg Ile Ala Asn Asn Met Ala His Phe Arg Val Gln
        280                 285                 290

atc tcc aag gac ttg cca caa ttt gcc acc gta gga att tcg ttg ttt  1027
Ile Ser Lys Asp Leu Pro Gln Phe Ala Thr Val Gly Ile Ser Leu Phe
```

```
    295                 300                 305

tct gcg ctt gca gca gcg aac atc atg gaa gaa ctg ggt gtt ggc ccg   1075
Ser Ala Leu Ala Ala Ala Asn Ile Met Glu Glu Leu Gly Val Gly Pro
310                 315                 320                 325

cag ttg tct aac tgg ctt gat tcc atg gac cta cct aag tct gtc atg   1123
Gln Leu Ser Asn Trp Leu Asp Ser Met Asp Leu Pro Lys Ser Val Met
                330                 335                 340

gtg atc att gtc tgc atc atg tgc att gtg gtg gca acg cca ctg tcg   1171
Val Ile Ile Val Cys Ile Met Cys Ile Val Val Ala Thr Pro Leu Ser
            345                 350                 355

tca aca gca acc gcg gct gcg att ggt gct ccc gct gtc gct gcg ttg   1219
Ser Thr Ala Thr Ala Ala Ala Ile Gly Ala Pro Ala Val Ala Ala Leu
        360                 365                 370

gct gcg gta ggt att gat cca act gtg gcg atc gta gtg atc ttg ctg   1267
Ala Ala Val Gly Ile Asp Pro Thr Val Ala Ile Val Val Ile Leu Leu
    375                 380                 385

tgc act tcc act gaa ggt gca tcc ccg ccg gtg ggc gcg ccg att tac   1315
Cys Thr Ser Thr Glu Gly Ala Ser Pro Pro Val Gly Ala Pro Ile Tyr
390                 395                 400                 405

ctt tct gct gcg atc gcc gat gca aac cca acg aaa atg ttc gta cca   1363
Leu Ser Ala Ala Ile Ala Asp Ala Asn Pro Thr Lys Met Phe Val Pro
                410                 415                 420

ctg att acg tac ttt gtt gtc ccc atg att ctg ctt gct tgg cta gtt   1411
Leu Ile Thr Tyr Phe Val Val Pro Met Ile Leu Leu Ala Trp Leu Val
            425                 430                 435

gga atg gga ttc tta cca gtg att gtt cct acg ggt taaaggggta        1457
Gly Met Gly Phe Leu Pro Val Ile Val Pro Thr Gly
        440                 445

aaaatgaact caa                                                   1470
```

<210> 208
<211> 449
<212> PRT
<213> Corynebacterium glutamicum

<400> 208

```
Met Gly Ile Ile Ala Leu Leu Val Phe Ile Ala Ile Ala Val Ile Leu
  1               5                  10                  15

Asn Val Phe Leu Lys Arg Asp Ile Ser Glu Ala Leu Leu Val Gly Leu
             20                  25                  30

Val Gly Thr Ala Leu Val Gly Gly Val Asn Ala Pro Thr Leu Leu Ile
         35                  40                  45

Asp Ala Val Val Asp Ala Ala Gln Ser Glu Val Thr Phe Ala Gly Met
     50                  55                  60

Ala Phe Val Phe Met Gly Ile Val Val Gln Ser Thr Gly Leu Ile Asp
 65                  70                  75                  80
```

```
Arg Leu Ile Ala Ile Leu Asn Ser Ile Phe Gly Arg Leu Arg Gly Gly
                85                  90                  95

Ala Gly Tyr Val Ser Thr Leu Gly Ser Ala Leu Ile Gly Leu Ile Ala
            100                 105                 110

Gly Ser Thr Ala Gly Asn Ser Ala Thr Val Gly Ser Val Thr Ile Pro
        115                 120                 125

Trp Met Lys Lys Thr Gly Trp Thr Ala Glu Arg Ser Ala Thr Leu Val
    130                 135                 140

Ala Gly Asn Ser Gly Leu Gly Val Ala Leu Pro Pro Asn Ser Thr Met
145                 150                 155                 160

Phe Ile Ile Leu Ala Leu Pro Ala Ala Ala Ala Ser Ser Ala Ser Gln
                165                 170                 175

Val Tyr Ile Ala Leu Ala Cys Gly Gly Ala Tyr Ala Val Leu Tyr Arg
            180                 185                 190

Leu Ala Val Val Phe Tyr Trp Thr Arg Lys Asp Lys Ile Pro Ala Thr
        195                 200                 205

Pro Asp Asp Gln Arg Val Ser Phe Gly Glu Ala Met Lys Thr Gly Trp
    210                 215                 220

Arg Ser Pro Leu Ile Phe Leu Gly Ile Leu Ile Pro Val Ile Leu Thr
225                 230                 235                 240

Ile Gly Pro Leu Ser Glu Trp Leu Lys Thr His Gly Val Gly Glu Ser
                245                 250                 255

Gly Val Lys Ser Met Ser Ile Ile Val Trp Val Pro Ile Leu Ile Thr
            260                 265                 270

Ala Ile Ala Leu Ile Glu Gly Arg Lys Arg Ile Ala Asn Asn Met Ala
        275                 280                 285

His Phe Arg Val Gln Ile Ser Lys Asp Leu Pro Gln Phe Ala Thr Val
    290                 295                 300

Gly Ile Ser Leu Phe Ser Ala Leu Ala Ala Ala Asn Ile Met Glu Glu
305                 310                 315                 320

Leu Gly Val Gly Pro Gln Leu Ser Asn Trp Leu Asp Ser Met Asp Leu
                325                 330                 335

Pro Lys Ser Val Met Val Ile Ile Val Cys Ile Met Cys Ile Val Val
            340                 345                 350

Ala Thr Pro Leu Ser Ser Thr Ala Thr Ala Ala Ala Ile Gly Ala Pro
        355                 360                 365

Ala Val Ala Ala Leu Ala Ala Val Gly Ile Asp Pro Thr Val Ala Ile
    370                 375                 380

Val Val Ile Leu Leu Cys Thr Ser Thr Glu Gly Ala Ser Pro Pro Val
385                 390                 395                 400
```

```
Gly Ala Pro Ile Tyr Leu Ser Ala Ala Ile Ala Asp Ala Asn Pro Thr
               405                 410                 415

Lys Met Phe Val Pro Leu Ile Thr Tyr Phe Val Val Pro Met Ile Leu
            420                 425                 430

Leu Ala Trp Leu Val Gly Met Gly Phe Leu Pro Val Ile Val Pro Thr
        435                 440                 445

Gly
```

<210> 209
<211> 983
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(960)
<223> FRXA00362

<400> 209

```
gat gaa aag acg gga tgg act gct gaa agg tcc gca acg tta gtc gcg   48
Asp Glu Lys Thr Gly Trp Thr Ala Glu Arg Ser Ala Thr Leu Val Ala
  1               5                  10                  15

ggc aac tct ggc ctt ggt gtt gcg ttg cct ccc aat tca aca atg ttc   96
Gly Asn Ser Gly Leu Gly Val Ala Leu Pro Pro Asn Ser Thr Met Phe
             20                  25                  30

atc att ttg gca ttg cca gct gca gca gct tct tcg gcc tct cag gtg   144
Ile Ile Leu Ala Leu Pro Ala Ala Ala Ala Ser Ser Ala Ser Gln Val
         35                  40                  45

tac att gct ttg gct tgt ggt ggt gcg tat gca gtg ctc tac cgc tta   192
Tyr Ile Ala Leu Ala Cys Gly Gly Ala Tyr Ala Val Leu Tyr Arg Leu
     50                  55                  60

gcg gtc gtc ttt tac tgg aca cgt aaa gat aaa att cct gcc acc cct   240
Ala Val Val Phe Tyr Trp Thr Arg Lys Asp Lys Ile Pro Ala Thr Pro
 65                  70                  75                  80

gat gat caa cgg gtg tca ttc ggt gag gca atg aag act gga tgg cgt   288
Asp Asp Gln Arg Val Ser Phe Gly Glu Ala Met Lys Thr Gly Trp Arg
                 85                  90                  95

tca ccg ttg atc ttc ctt gga att ttg atc ccc gta atc ctc aca atc   336
Ser Pro Leu Ile Phe Leu Gly Ile Leu Ile Pro Val Ile Leu Thr Ile
            100                 105                 110

ggc cca ttg tct gaa tgg tta aag aca cat gga gtt ggg gag tct ggt   384
Gly Pro Leu Ser Glu Trp Leu Lys Thr His Gly Val Gly Glu Ser Gly
        115                 120                 125

gtt aaa tcg atg tcg atc atc gtg tgg gtg cca att ctg att acg gca   432
Val Lys Ser Met Ser Ile Ile Val Trp Val Pro Ile Leu Ile Thr Ala
    130                 135                 140

att gct ctg att gaa ggg cgt aaa cga att gct aac aac atg gca cac   480
```

```
Ile Ala Leu Ile Glu Gly Arg Lys Arg Ile Ala Asn Asn Met Ala His
145                 150                 155                 160

ttt agg gtt cag atc tcc aag gac ttg cca caa ttt gcc acc gta gga   528
Phe Arg Val Gln Ile Ser Lys Asp Leu Pro Gln Phe Ala Thr Val Gly
                165                 170                 175

att tcg ttg ttt tct gcg ctt gca gca gcg aac atc atg gaa gaa ctg   576
Ile Ser Leu Phe Ser Ala Leu Ala Ala Ala Asn Ile Met Glu Glu Leu
            180                 185                 190

ggt gtt ggc ccg cag ttg tct aac tgg ctt gat tcc atg gac cta cct   624
Gly Val Gly Pro Gln Leu Ser Asn Trp Leu Asp Ser Met Asp Leu Pro
        195                 200                 205

aag tct gtc atg gtg atc att gtc tgc atc atg tgc att gtg gtg gca   672
Lys Ser Val Met Val Ile Ile Val Cys Ile Met Cys Ile Val Val Ala
    210                 215                 220

acg cca ctg tcg tca aca gca acc gcg gct gcg att ggt gct ccc gct   720
Thr Pro Leu Ser Ser Thr Ala Thr Ala Ala Ala Ile Gly Ala Pro Ala
225                 230                 235                 240

gtc gct gcg ttg gct gcg gta ggt att gat cca act gtg gcg atc gta   768
Val Ala Ala Leu Ala Ala Val Gly Ile Asp Pro Thr Val Ala Ile Val
                245                 250                 255

gtg atc ttg ctg tgc act tcc act gaa ggt gca tcc ccg ccg gtg ggc   816
Val Ile Leu Leu Cys Thr Ser Thr Glu Gly Ala Ser Pro Pro Val Gly
            260                 265                 270

gcg ccg att tac ctt tct gct gcg atc gcc gat gca aac cca acg aaa   864
Ala Pro Ile Tyr Leu Ser Ala Ala Ile Ala Asp Ala Asn Pro Thr Lys
        275                 280                 285

atg ttc gta cca ctg att acg tac ttt gtt gtc ccc atg att ctg ctt   912
Met Phe Val Pro Leu Ile Thr Tyr Phe Val Val Pro Met Ile Leu Leu
    290                 295                 300

gct tgg cta gtt gga atg gga ttc tta cca gtg att gtt cct acg ggt   960
Ala Trp Leu Val Gly Met Gly Phe Leu Pro Val Ile Val Pro Thr Gly
305                 310                 315                 320

taaaggggta aaaatgaact caa                                        983
```

<210> 210
<211> 320
<212> PRT
<213> Corynebacterium glutamicum

<400> 210

```
Asp Glu Lys Thr Gly Trp Thr Ala Glu Arg Ser Ala Thr Leu Val Ala
  1               5                  10                  15

Gly Asn Ser Gly Leu Gly Val Ala Leu Pro Pro Asn Ser Thr Met Phe
             20                  25                  30

Ile Ile Leu Ala Leu Pro Ala Ala Ala Ala Ser Ser Ala Ser Gln Val
         35                  40                  45
```

```
Tyr Ile Ala Leu Ala Cys Gly Gly Ala Tyr Ala Val Leu Tyr Arg Leu
     50                  55                  60

Ala Val Val Phe Tyr Trp Thr Arg Lys Asp Lys Ile Pro Ala Thr Pro
 65                  70                  75                  80

Asp Asp Gln Arg Val Ser Phe Gly Glu Ala Met Lys Thr Gly Trp Arg
                 85                  90                  95

Ser Pro Leu Ile Phe Leu Gly Ile Leu Ile Pro Val Ile Leu Thr Ile
            100                 105                 110

Gly Pro Leu Ser Glu Trp Leu Lys Thr His Gly Val Gly Glu Ser Gly
        115                 120                 125

Val Lys Ser Met Ser Ile Ile Val Trp Val Pro Ile Leu Ile Thr Ala
    130                 135                 140

Ile Ala Leu Ile Glu Gly Arg Lys Arg Ile Ala Asn Asn Met Ala His
145                 150                 155                 160

Phe Arg Val Gln Ile Ser Lys Asp Leu Pro Gln Phe Ala Thr Val Gly
                165                 170                 175

Ile Ser Leu Phe Ser Ala Leu Ala Ala Ala Asn Ile Met Glu Glu Leu
            180                 185                 190

Gly Val Gly Pro Gln Leu Ser Asn Trp Leu Asp Ser Met Asp Leu Pro
        195                 200                 205

Lys Ser Val Met Val Ile Ile Val Cys Ile Met Cys Ile Val Val Ala
    210                 215                 220

Thr Pro Leu Ser Ser Thr Ala Thr Ala Ala Ala Ile Gly Ala Pro Ala
225                 230                 235                 240

Val Ala Ala Leu Ala Ala Val Gly Ile Asp Pro Thr Val Ala Ile Val
                245                 250                 255

Val Ile Leu Leu Cys Thr Ser Thr Glu Gly Ala Ser Pro Pro Val Gly
            260                 265                 270

Ala Pro Ile Tyr Leu Ser Ala Ala Ile Ala Asp Ala Asn Pro Thr Lys
        275                 280                 285

Met Phe Val Pro Leu Ile Thr Tyr Phe Val Val Pro Met Ile Leu Leu
    290                 295                 300

Ala Trp Leu Val Gly Met Gly Phe Leu Pro Val Ile Val Pro Thr Gly
305                 310                 315                 320
```

<210> 211
<211> 439
<212> DNA
<213> Corynebacterium glutamicum

<220>

<221> CDS
<222> (101)..(439)
<223> RXN00373

<400> 211
cacgtggcgg atctgcgcgc taagggcgag ctgccgccgc cgaggaagaa acgcaggcgt 60

cgaaaagcgt cttaaaaggt ttttcactag ggtgttgtcc atg gac atc cag cag 115
Met Asp Ile Gln Gln
1 5

cta gac gcc gaa aca aca gca tgg aaa gac agc ctc ctg cgc gcc gca 163
Leu Asp Ala Glu Thr Thr Ala Trp Lys Asp Ser Leu Leu Arg Ala Ala
10 15 20

cag gag gct ggt ttt cat ttt gag cca ccg aaa ctc ttc gag gat ttt 211
Gln Glu Ala Gly Phe His Phe Glu Pro Pro Lys Leu Phe Glu Asp Phe
25 30 35

gag acc atg gtg gag cag tac aag cag gca gct gcg agc gac ccg gac 259
Glu Thr Met Val Glu Gln Tyr Lys Gln Ala Ala Ala Ser Asp Pro Asp
40 45 50

att gat gtc act gat att cag caa atg tgg ggc atc gtg gtg ggg gag 307
Ile Asp Val Thr Asp Ile Gln Gln Met Trp Gly Ile Val Val Gly Glu
55 60 65

tac ctg cgc gaa aaa atg ggc atg gaa tgg gtc gtc atc acc gat gac 355
Tyr Leu Arg Glu Lys Met Gly Met Glu Trp Val Val Ile Thr Asp Asp
70 75 80 85

tac ggc act gac ctc gcg att cta gcc acg gca ccc aac ggg gac cac 403
Tyr Gly Thr Asp Leu Ala Ile Leu Ala Thr Ala Pro Asn Gly Asp His
90 95 100

gta tat tcc tgc ccc atc atc gtg gtg ggc aag cgc 439
Val Tyr Ser Cys Pro Ile Ile Val Val Gly Lys Arg
105 110

<210> 212
<211> 113
<212> PRT
<213> Corynebacterium glutamicum

<400> 212
Met Asp Ile Gln Gln Leu Asp Ala Glu Thr Thr Ala Trp Lys Asp Ser
1 5 10 15

Leu Leu Arg Ala Ala Gln Glu Ala Gly Phe His Phe Glu Pro Pro Lys
20 25 30

Leu Phe Glu Asp Phe Glu Thr Met Val Glu Gln Tyr Lys Gln Ala Ala
35 40 45

Ala Ser Asp Pro Asp Ile Asp Val Thr Asp Ile Gln Gln Met Trp Gly
50 55 60

Ile Val Val Gly Glu Tyr Leu Arg Glu Lys Met Gly Met Glu Trp Val
65 70 75 80

```
Val Ile Thr Asp Asp Tyr Gly Thr Asp Leu Ala Ile Leu Ala Thr Ala
                85                  90                  95

Pro Asn Gly Asp His Val Tyr Ser Cys Pro Ile Ile Val Val Gly Lys
            100                 105                 110

Arg
```

<210> 213
<211> 439
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(439)
<223> FRXA00373

<400> 213

```
cacgtggcgg atctgcgcgc taagggcgag ctgccgccgc cgaggaagaa acgcaggcgt 60

cgaaaagcgt cttaaaaggt ttttcactag ggtgttgtcc atg gac atc cag cag   115
                                            Met Asp Ile Gln Gln
                                              1               5

cta gac gcc gaa aca aca gca tgg aaa gac agc ctc ctg cgc gcc gca   163
Leu Asp Ala Glu Thr Thr Ala Trp Lys Asp Ser Leu Leu Arg Ala Ala
                10                  15                  20

cag gag gct ggt ttt cat ttt gag cca ccg aaa ctc ttc gag gat ttt   211
Gln Glu Ala Gly Phe His Phe Glu Pro Pro Lys Leu Phe Glu Asp Phe
            25                  30                  35

gag acc atg gtg gag cag tac aag cag gca gct gcg agc gac ccg gac   259
Glu Thr Met Val Glu Gln Tyr Lys Gln Ala Ala Ala Ser Asp Pro Asp
        40                  45                  50

att gat gtc act gat att cag caa atg tgg ggc atc gtg gtg ggg gag   307
Ile Asp Val Thr Asp Ile Gln Gln Met Trp Gly Ile Val Val Gly Glu
    55                  60                  65

tac ctg cgc gaa aaa atg ggc atg gaa tgg gtc gtc atc acc gat gac   355
Tyr Leu Arg Glu Lys Met Gly Met Glu Trp Val Val Ile Thr Asp Asp
70                  75                  80                  85

tac ggc act gac ctc gcg att cta gcc acg gca ccc aac ggg gac cac   403
Tyr Gly Thr Asp Leu Ala Ile Leu Ala Thr Ala Pro Asn Gly Asp His
                90                  95                  100

gta tat tcc tgc ccc atc atc gtg gtg ggc aag cgc                   439
Val Tyr Ser Cys Pro Ile Ile Val Val Gly Lys Arg
            105                 110
```

<210> 214
<211> 113
<212> PRT
<213> Corynebacterium glutamicum

<400> 214
Met Asp Ile Gln Gln Leu Asp Ala Glu Thr Thr Ala Trp Lys Asp Ser
1 5 10 15

Leu Leu Arg Ala Ala Gln Glu Ala Gly Phe His Phe Glu Pro Pro Lys
20 25 30

Leu Phe Glu Asp Phe Glu Thr Met Val Glu Gln Tyr Lys Gln Ala Ala
35 40 45

Ala Ser Asp Pro Asp Ile Asp Val Thr Asp Ile Gln Gln Met Trp Gly
50 55 60

Ile Val Val Gly Glu Tyr Leu Arg Glu Lys Met Gly Met Glu Trp Val
65 70 75 80

Val Ile Thr Asp Asp Tyr Gly Thr Asp Leu Ala Ile Leu Ala Thr Ala
85 90 95

Pro Asn Gly Asp His Val Tyr Ser Cys Pro Ile Ile Val Val Gly Lys
100 105 110

Arg

<210> 215
<211> 528
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(505)
<223> RXN00390

<400> 215
ggaaatagac cgttaatagc tggtctttac atttgccaga aagctccgac gaaaccccaa 60

tagttgacac ggaaactaat tcattctagc tttagtgacc atg tca act acc agg 115
Met Ser Thr Thr Arg
1 5

gaa att gca ttc ctc atc gca cgt atc ctc ttg ggc gtc atc ctc atc 163
Glu Ile Ala Phe Leu Ile Ala Arg Ile Leu Leu Gly Val Ile Leu Ile
10 15 20

gcc cac ggc tgg gac aag ttc gcc atc aca gga ctt gaa ggc gtc acc 211
Ala His Gly Trp Asp Lys Phe Ala Ile Thr Gly Leu Glu Gly Val Thr
25 30 35

ggc ttc ttc gat tca ctc ggc atc cca gca gcc ggc atc gcc gca ata 259
Gly Phe Phe Asp Ser Leu Gly Ile Pro Ala Ala Gly Ile Ala Ala Ile
40 45 50

gct gct gca gtc gtc gag ctc cta gga gga atc ctt atc atc cta gga 307
Ala Ala Ala Val Val Glu Leu Leu Gly Gly Ile Leu Ile Ile Leu Gly
55 60 65

gta ttt acc cgc atc gtt gcc gcc ttc gtt gcc ata gac atg ctc ttc 355
Val Phe Thr Arg Ile Val Ala Ala Phe Val Ala Ile Asp Met Leu Phe

```
 70                  75                  80                  85

gca gca ctg ttt gcg cac gtc tcc tcc ggc atc ttt gtc acc aac aat   403
Ala Ala Leu Phe Ala His Val Ser Ser Gly Ile Phe Val Thr Asn Asn
                90                  95                 100

ggt tgg gaa ctc acc ggc gca atc ggc gct ggc gcg ctg ctt ctc atc   451
Gly Trp Glu Leu Thr Gly Ala Ile Gly Ala Gly Ala Leu Leu Leu Ile
            105                 110                 115

gca gtt ggc gca agt gca tgg agc atc gac ggg gtt ctg gca aaa cgc   499
Ala Val Gly Ala Ser Ala Trp Ser Ile Asp Gly Val Leu Ala Lys Arg
        120                 125                 130

aag gcc taaatctagc gccacaactc cga                                 528
Lys Ala
    135


<210> 216
<211> 135
<212> PRT
<213> Corynebacterium glutamicum

<400> 216
Met Ser Thr Thr Arg Glu Ile Ala Phe Leu Ile Ala Arg Ile Leu Leu
  1               5                  10                  15

Gly Val Ile Leu Ile Ala His Gly Trp Asp Lys Phe Ala Ile Thr Gly
             20                  25                  30

Leu Glu Gly Val Thr Gly Phe Phe Asp Ser Leu Gly Ile Pro Ala Ala
         35                  40                  45

Gly Ile Ala Ala Ile Ala Ala Ala Val Val Glu Leu Leu Gly Gly Ile
     50                  55                  60

Leu Ile Ile Leu Gly Val Phe Thr Arg Ile Val Ala Ala Phe Val Ala
 65                  70                  75                  80

Ile Asp Met Leu Phe Ala Ala Leu Phe Ala His Val Ser Ser Gly Ile
                 85                  90                  95

Phe Val Thr Asn Asn Gly Trp Glu Leu Thr Gly Ala Ile Gly Ala Gly
            100                 105                 110

Ala Leu Leu Leu Ile Ala Val Gly Ala Ser Ala Trp Ser Ile Asp Gly
        115                 120                 125

Val Leu Ala Lys Arg Lys Ala
    130                 135


<210> 217
<211> 528
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(505)
```

<223> FRXA00390

<400> 217
ggaaatagac cgttaatagc tggtctttac atttgccaga aagctccgac gaaaccccaa 60

tagttgacac ggaaactaat tcattctagc tttagtgacc atg tca act acc agg 115
Met Ser Thr Thr Arg
1 5

gaa att gca ttc ctc atc gca cgt atc ctc ttg ggc gtc atc ctc atc 163
Glu Ile Ala Phe Leu Ile Ala Arg Ile Leu Leu Gly Val Ile Leu Ile
10 15 20

gcc cac ggc tgg gac aag ttc gcc atc aca gga ctt gaa ggc gtc acc 211
Ala His Gly Trp Asp Lys Phe Ala Ile Thr Gly Leu Glu Gly Val Thr
25 30 35

ggc ttc ttc gat tca ctc ggc atc cca gca gcc ggc atc gcc gca ata 259
Gly Phe Phe Asp Ser Leu Gly Ile Pro Ala Ala Gly Ile Ala Ala Ile
40 45 50

gct gct gca gtc gtc gag ctc cta gga gga atc ctt atc atc cta gga 307
Ala Ala Ala Val Val Glu Leu Leu Gly Gly Ile Leu Ile Ile Leu Gly
55 60 65

gta ttt acc cgc atc gtt gcc gcc ttc gtt gcc ata gac atg ctc ttc 355
Val Phe Thr Arg Ile Val Ala Ala Phe Val Ala Ile Asp Met Leu Phe
70 75 80 85

gca gca ctg ttt gcg cac gtc tcc tcc ggc atc ttt gtc acc aac aat 403
Ala Ala Leu Phe Ala His Val Ser Ser Gly Ile Phe Val Thr Asn Asn
90 95 100

ggt tgg gaa ctc acc ggc gca atc ggc gct ggc gcg ctg ctt ctc atc 451
Gly Trp Glu Leu Thr Gly Ala Ile Gly Ala Gly Ala Leu Leu Leu Ile
105 110 115

gca gtt ggc gca agt gca tgg agc atc gac ggg gtt ctg gca aaa cgc 499
Ala Val Gly Ala Ser Ala Trp Ser Ile Asp Gly Val Leu Ala Lys Arg
120 125 130

aag gcc taaatctagc gccacaactc cga 528
Lys Ala
135

<210> 218
<211> 135
<212> PRT
<213> Corynebacterium glutamicum

<400> 218
Met Ser Thr Thr Arg Glu Ile Ala Phe Leu Ile Ala Arg Ile Leu Leu
1 5 10 15

Gly Val Ile Leu Ile Ala His Gly Trp Asp Lys Phe Ala Ile Thr Gly
20 25 30

Leu Glu Gly Val Thr Gly Phe Phe Asp Ser Leu Gly Ile Pro Ala Ala
35 40 45

```
Gly Ile Ala Ala Ile Ala Ala Ala Val Val Glu Leu Leu Gly Gly Ile
     50                  55                  60

Leu Ile Ile Leu Gly Val Phe Thr Arg Ile Val Ala Ala Phe Val Ala
 65                  70                  75                  80

Ile Asp Met Leu Phe Ala Ala Leu Phe Ala His Val Ser Ser Gly Ile
                 85                  90                  95

Phe Val Thr Asn Asn Gly Trp Glu Leu Thr Gly Ala Ile Gly Ala Gly
            100                 105                 110

Ala Leu Leu Leu Ile Ala Val Gly Ala Ser Ala Trp Ser Ile Asp Gly
        115                 120                 125

Val Leu Ala Lys Arg Lys Ala
    130                 135


<210> 219
<211> 438
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(415)
<223> RXN00399

<400> 219
ggacattgct atgtcgtgag ttgtagtaac cccaaagccc acggattaat caatagtgaa 60

attcaatgat ttttttttcc cacaggccta aacttaaatc atg agc cac aac gac   115
                                            Met Ser His Asn Asp
                                              1               5

agc cca aac ttt gct cgc cga gcg ctc aat tgg ctc cgc caa ggt tat   163
Ser Pro Asn Phe Ala Arg Arg Ala Leu Asn Trp Leu Arg Gln Gly Tyr
                 10                  15                  20

cca acc ggt gtt ccg cgg cac gat act ttc gct ctg ttt tac gtt ttg   211
Pro Thr Gly Val Pro Arg His Asp Thr Phe Ala Leu Phe Tyr Val Leu
             25                  30                  35

gag cgc gaa ctt act gag gaa gat ctc aat gag ctc gca gag ctt ctc   259
Glu Arg Glu Leu Thr Glu Glu Asp Leu Asn Glu Leu Ala Glu Leu Leu
         40                  45                  50

atc gcg gaa ggt gag aac aat ggg ctg cac gat aat ccc att acg cgt   307
Ile Ala Glu Gly Glu Asn Asn Gly Leu His Asp Asn Pro Ile Thr Arg
     55                  60                  65

gaa aaa atc ggc aag ctg atc acg cat gtt cac agt cag cca cct gag   355
Glu Lys Ile Gly Lys Leu Ile Thr His Val His Ser Gln Pro Pro Glu
 70                  75                  80                  85

gat gaa gac atc gat cga att cag aaa aag ctg cag gct gag ggc ttc   403
Asp Glu Asp Ile Asp Arg Ile Gln Lys Lys Leu Gln Ala Glu Gly Phe
                 90                  95                 100

ccc acc cgc aat taattaattg gagttttgtt gtt                        438
```

Pro Thr Arg Asn
105

<210> 220
<211> 105
<212> PRT
<213> Corynebacterium glutamicum

<400> 220
Met Ser His Asn Asp Ser Pro Asn Phe Ala Arg Arg Ala Leu Asn Trp
1 5 10 15

Leu Arg Gln Gly Tyr Pro Thr Gly Val Pro Arg His Asp Thr Phe Ala
20 25 30

Leu Phe Tyr Val Leu Glu Arg Glu Leu Thr Glu Glu Asp Leu Asn Glu
35 40 45

Leu Ala Glu Leu Leu Ile Ala Glu Gly Glu Asn Asn Gly Leu His Asp
50 55 60

Asn Pro Ile Thr Arg Glu Lys Ile Gly Lys Leu Ile Thr His Val His
65 70 75 80

Ser Gln Pro Pro Glu Asp Glu Asp Ile Asp Arg Ile Gln Lys Lys Leu
85 90 95

Gln Ala Glu Gly Phe Pro Thr Arg Asn
100 105

<210> 221
<211> 438
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(415)
<223> FRXA00399

<400> 221
ggacattgct atgtcgtgag ttgtagtaac cccaaagccc acggattaat caatagtgaa 60

attcaatgat tttcttttcc cacaggccta aacttaaatc atg agc cac aac gac 115
Met Ser His Asn Asp
1 5

agc cca aac ttt gct cgc cga gcg ctc aat tgg ctc cgc caa ggt tat 163
Ser Pro Asn Phe Ala Arg Arg Ala Leu Asn Trp Leu Arg Gln Gly Tyr
10 15 20

cca acc ggt gtt ccg cgg cac gat act ttc gct ctg ttt tac gtt ttg 211
Pro Thr Gly Val Pro Arg His Asp Thr Phe Ala Leu Phe Tyr Val Leu
25 30 35

gag cgc gaa ctt act gag gaa gat ctc aat gag ctc gca gag ctt ctc 259
Glu Arg Glu Leu Thr Glu Glu Asp Leu Asn Glu Leu Ala Glu Leu Leu
40 45 50

```
atc gcg gaa ggt gag aac aat ggg ctg cac gat aat ccc att acg cgt   307
Ile Ala Glu Gly Glu Asn Asn Gly Leu His Asp Asn Pro Ile Thr Arg
     55                  60                  65

gaa aaa atc ggc aag ctg atc acg cat gtt cac agt cag cca cct gag   355
Glu Lys Ile Gly Lys Leu Ile Thr His Val His Ser Gln Pro Pro Glu
 70                  75                  80                  85

gat gaa gac atc gat cga att cag aaa aag ctg cag gct gag ggc ttc   403
Asp Glu Asp Ile Asp Arg Ile Gln Lys Lys Leu Gln Ala Glu Gly Phe
                90                  95                 100

ccc acc cgc aat taattaattg gagttttgtt gtt                        438
Pro Thr Arg Asn
            105


<210> 222
<211> 105
<212> PRT
<213> Corynebacterium glutamicum

<400> 222
Met Ser His Asn Asp Ser Pro Asn Phe Ala Arg Arg Ala Leu Asn Trp
  1               5                  10                  15

Leu Arg Gln Gly Tyr Pro Thr Gly Val Pro Arg His Asp Thr Phe Ala
             20                  25                  30

Leu Phe Tyr Val Leu Glu Arg Glu Leu Thr Glu Glu Asp Leu Asn Glu
         35                  40                  45

Leu Ala Glu Leu Leu Ile Ala Glu Gly Glu Asn Asn Gly Leu His Asp
     50                  55                  60

Asn Pro Ile Thr Arg Glu Lys Ile Gly Lys Leu Ile Thr His Val His
 65                  70                  75                  80

Ser Gln Pro Pro Glu Asp Glu Asp Ile Asp Arg Ile Gln Lys Lys Leu
                85                  90                  95

Gln Ala Glu Gly Phe Pro Thr Arg Asn
            100                 105


<210> 223
<211> 1673
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1650)
<223> RXN00416

<400> 223
ctg gcg tct tac tta agc cca act gcg ctg gtg gtt gcg gtg ttg gct   48
Leu Ala Ser Tyr Leu Ser Pro Thr Ala Leu Val Val Ala Val Leu Ala
  1               5                  10                  15

att ccg ctg tct gcg acc cgc ctg tat ttg gac gga atc agc gtt gac   96
```

```
Ile Pro Leu Ser Ala Thr Arg Leu Tyr Leu Asp Gly Ile Ser Val Asp
             20                  25                  30

cag ggc ttt aga act cag ttt tta acc cgc atg gct gac gat atc ggc   144
Gln Gly Phe Arg Thr Gln Phe Leu Thr Arg Met Ala Asp Asp Ile Gly
         35                  40                  45

ttg tcg gac atg aac tac atc gat atg cct acc ttc tac cct gct gga   192
Leu Ser Asp Met Asn Tyr Ile Asp Met Pro Thr Phe Tyr Pro Ala Gly
     50                  55                  60

tgg ttc tgg ctc ggt ggt cgc ttg gcc aat ctt ttg ggg ctg ccc ggt   240
Trp Phe Trp Leu Gly Gly Arg Leu Ala Asn Leu Leu Gly Leu Pro Gly
 65                  70                  75                  80

tgg gaa gct ttc cag cca tgg gca att gtg tcc atg gca gtt gct gct   288
Trp Glu Ala Phe Gln Pro Trp Ala Ile Val Ser Met Ala Val Ala Ala
                 85                  90                  95

tct gtg tta gtt cca gtg tgg cag cgc atc acc ggt tcc ctg ccg gtg   336
Ser Val Leu Val Pro Val Trp Gln Arg Ile Thr Gly Ser Leu Pro Val
            100                 105                 110

gca aca ggc att gcg ttg gtg aca acc tgc att atc ttg gcg atg aat   384
Ala Thr Gly Ile Ala Leu Val Thr Thr Cys Ile Ile Leu Ala Met Asn
        115                 120                 125

tcc gaa gag ccc tac gct gca atc gtt gcg atg ggt att cca gcg atg   432
Ser Glu Glu Pro Tyr Ala Ala Ile Val Ala Met Gly Ile Pro Ala Met
    130                 135                 140

ctc gtg ctg gct tcc cgc att gcc aag ggc gat aag ttt gcg ctt gcc   480
Leu Val Leu Ala Ser Arg Ile Ala Lys Gly Asp Lys Phe Ala Leu Ala
145                 150                 155                 160

ggc ggc att att tac ttg ggt gtt tcg gct act ttc tat act ttg ttc   528
Gly Gly Ile Ile Tyr Leu Gly Val Ser Ala Thr Phe Tyr Thr Leu Phe
                165                 170                 175

acc ggt gct atc gcg ctt tct gcg gtc gcg gtg tgc atc gtg gtg gcg   576
Thr Gly Ala Ile Ala Leu Ser Ala Val Ala Val Cys Ile Val Val Ala
            180                 185                 190

gct att gtg cag cgc tcc atc aaa cca ctg ctg tgg ctt gca gtg ctg   624
Ala Ile Val Gln Arg Ser Ile Lys Pro Leu Leu Trp Leu Ala Val Leu
        195                 200                 205

ggt ggt gga tcc att gtc att gcg ttg att tct tgg ggt cct tac ctt   672
Gly Gly Gly Ser Ile Val Ile Ala Leu Ile Ser Trp Gly Pro Tyr Leu
    210                 215                 220

ctg gcc tcc atc aac gga gcg gag cgc tct ggc gat tcc gca aca cac   720
Leu Ala Ser Ile Asn Gly Ala Glu Arg Ser Gly Asp Ser Ala Thr His
225                 230                 235                 240

tac ctg cct ctt gaa ggc acc caa ttc ccg gtt cct ttc ttg gca tca   768
Tyr Leu Pro Leu Glu Gly Thr Gln Phe Pro Val Pro Phe Leu Ala Ser
                245                 250                 255

agc gtt gtg gga ctg ttg tgt ctt gtt ggc ctg atc tat ttg gtg gtg   816
Ser Val Val Gly Leu Leu Cys Leu Val Gly Leu Ile Tyr Leu Val Val
```

```
            260                 265                 270

cgt ttc cac aac aat gag gtg cgc gcg atg tgg gtc ggc atc gca gtg   864
Arg Phe His Asn Asn Glu Val Arg Ala Met Trp Val Gly Ile Ala Val
        275                 280                 285

ttt tat gcc tgg atg ggc atg tcc atg gcg atc acg ctt ttg ggc aac   912
Phe Tyr Ala Trp Met Gly Met Ser Met Ala Ile Thr Leu Leu Gly Asn
    290                 295                 300

acg ttg ctt gga ttc cgt ctt gat acg gtg ctg gtg ctt att ttt gcc   960
Thr Leu Leu Gly Phe Arg Leu Asp Thr Val Leu Val Leu Ile Phe Ala
305                 310                 315                 320

acg gct gga gtg ttg ggc att gca gat ttc cgc ctt gcc agt gtg tat  1008
Thr Ala Gly Val Leu Gly Ile Ala Asp Phe Arg Leu Ala Ser Val Tyr
                325                 330                 335

cag ctc tac ccc acc caa atc aca gag cgc acg gcc acc cat ctg acc  1056
Gln Leu Tyr Pro Thr Gln Ile Thr Glu Arg Thr Ala Thr His Leu Thr
            340                 345                 350

aat cta att gtg gtc ctc gtg ctg ctt ggc ggc ctc tac tac gcg caa  1104
Asn Leu Ile Val Val Leu Val Leu Leu Gly Gly Leu Tyr Tyr Ala Gln
        355                 360                 365

gat ctg ccg cag aag aac gca cga gct atc gat ctg gcc tat acc gat  1152
Asp Leu Pro Gln Lys Asn Ala Arg Ala Ile Asp Leu Ala Tyr Thr Asp
    370                 375                 380

act gat ggc tac ggc gag cgc gcg gat ctg tat ccg gcc gga gct gca  1200
Thr Asp Gly Tyr Gly Glu Arg Ala Asp Leu Tyr Pro Ala Gly Ala Ala
385                 390                 395                 400

cgt tat tac aag gac atc aac gat cat ctg ctt gat caa gga ttc gag  1248
Arg Tyr Tyr Lys Asp Ile Asn Asp His Leu Leu Asp Gln Gly Phe Glu
                405                 410                 415

cct tcc gaa act gtc gtg ctg aca gac gaa ctc gat ttc atg tcc tac  1296
Pro Ser Glu Thr Val Val Leu Thr Asp Glu Leu Asp Phe Met Ser Tyr
            420                 425                 430

tac cct tat cgc gga tac caa gct ttt act tcc cac tac gcc aac ccg  1344
Tyr Pro Tyr Arg Gly Tyr Gln Ala Phe Thr Ser His Tyr Ala Asn Pro
        435                 440                 445

ctt ggt gag ttc gga aac agg aac gca ttc atc gaa gat ctc gcg atc  1392
Leu Gly Glu Phe Gly Asn Arg Asn Ala Phe Ile Glu Asp Leu Ala Ile
    450                 455                 460

cga agc tgg gat gag ttg gct gat cct caa caa ttc agc gac gcc ttg  1440
Arg Ser Trp Asp Glu Leu Ala Asp Pro Gln Gln Phe Ser Asp Ala Leu
465                 470                 475                 480

aac acc tct cca tgg acg atc cct gag gtg ttc atc ttc cgt ggc tcc  1488
Asn Thr Ser Pro Trp Thr Ile Pro Glu Val Phe Ile Phe Arg Gly Ser
                485                 490                 495

atc gat gat cct gac gcc ggt tgg aaa tac gac gtg gct gaa gat ctg  1536
Ile Asp Asp Pro Asp Ala Gly Trp Lys Tyr Asp Val Ala Glu Asp Leu
            500                 505                 510
```

```
tac ccg aac aat cca aac gtg cgc ttc cgc ggc gtg tac ttt aac ccg   1584
Tyr Pro Asn Asn Pro Asn Val Arg Phe Arg Gly Val Tyr Phe Asn Pro
        515                 520                 525

gag tca ttt gat cag atg tgg cag acc aag caa gtg gga cct ttc gtg   1632
Glu Ser Phe Asp Gln Met Trp Gln Thr Lys Gln Val Gly Pro Phe Val
    530                 535                 540

gtg gta acg cac aat gag taattcctca ccaaacgacc caa                1673
Val Val Thr His Asn Glu
545                 550
```

<210> 224
<211> 550
<212> PRT
<213> Corynebacterium glutamicum

<400> 224

```
Leu Ala Ser Tyr Leu Ser Pro Thr Ala Leu Val Val Ala Val Leu Ala
  1               5                  10                  15

Ile Pro Leu Ser Ala Thr Arg Leu Tyr Leu Asp Gly Ile Ser Val Asp
             20                  25                  30

Gln Gly Phe Arg Thr Gln Phe Leu Thr Arg Met Ala Asp Asp Ile Gly
         35                  40                  45

Leu Ser Asp Met Asn Tyr Ile Asp Met Pro Thr Phe Tyr Pro Ala Gly
     50                  55                  60

Trp Phe Trp Leu Gly Gly Arg Leu Ala Asn Leu Leu Gly Leu Pro Gly
 65                  70                  75                  80

Trp Glu Ala Phe Gln Pro Trp Ala Ile Val Ser Met Ala Val Ala Ala
                 85                  90                  95

Ser Val Leu Val Pro Val Trp Gln Arg Ile Thr Gly Ser Leu Pro Val
            100                 105                 110

Ala Thr Gly Ile Ala Leu Val Thr Thr Cys Ile Ile Leu Ala Met Asn
        115                 120                 125

Ser Glu Glu Pro Tyr Ala Ala Ile Val Ala Met Gly Ile Pro Ala Met
    130                 135                 140

Leu Val Leu Ala Ser Arg Ile Ala Lys Gly Asp Lys Phe Ala Leu Ala
145                 150                 155                 160

Gly Gly Ile Ile Tyr Leu Gly Val Ser Ala Thr Phe Tyr Thr Leu Phe
                165                 170                 175

Thr Gly Ala Ile Ala Leu Ser Ala Val Ala Val Cys Ile Val Val Ala
            180                 185                 190

Ala Ile Val Gln Arg Ser Ile Lys Pro Leu Leu Trp Leu Ala Val Leu
        195                 200                 205

Gly Gly Gly Ser Ile Val Ile Ala Leu Ile Ser Trp Gly Pro Tyr Leu
    210                 215                 220
```

Leu Ala Ser Ile Asn Gly Ala Glu Arg Ser Gly Asp Ser Ala Thr His
225 230 235 240

Tyr Leu Pro Leu Glu Gly Thr Gln Phe Pro Val Pro Phe Leu Ala Ser
245 250 255

Ser Val Val Gly Leu Leu Cys Leu Val Gly Leu Ile Tyr Leu Val Val
260 265 270

Arg Phe His Asn Asn Glu Val Arg Ala Met Trp Val Gly Ile Ala Val
275 280 285

Phe Tyr Ala Trp Met Gly Met Ser Met Ala Ile Thr Leu Leu Gly Asn
290 295 300

Thr Leu Leu Gly Phe Arg Leu Asp Thr Val Leu Val Leu Ile Phe Ala
305 310 315 320

Thr Ala Gly Val Leu Gly Ile Ala Asp Phe Arg Leu Ala Ser Val Tyr
325 330 335

Gln Leu Tyr Pro Thr Gln Ile Thr Glu Arg Thr Ala Thr His Leu Thr
340 345 350

Asn Leu Ile Val Val Leu Val Leu Leu Gly Gly Leu Tyr Tyr Ala Gln
355 360 365

Asp Leu Pro Gln Lys Asn Ala Arg Ala Ile Asp Leu Ala Tyr Thr Asp
370 375 380

Thr Asp Gly Tyr Gly Glu Arg Ala Asp Leu Tyr Pro Ala Gly Ala Ala
385 390 395 400

Arg Tyr Tyr Lys Asp Ile Asn Asp His Leu Leu Asp Gln Gly Phe Glu
405 410 415

Pro Ser Glu Thr Val Val Leu Thr Asp Glu Leu Asp Phe Met Ser Tyr
420 425 430

Tyr Pro Tyr Arg Gly Tyr Gln Ala Phe Thr Ser His Tyr Ala Asn Pro
435 440 445

Leu Gly Glu Phe Gly Asn Arg Asn Ala Phe Ile Glu Asp Leu Ala Ile
450 455 460

Arg Ser Trp Asp Glu Leu Ala Asp Pro Gln Gln Phe Ser Asp Ala Leu
465 470 475 480

Asn Thr Ser Pro Trp Thr Ile Pro Glu Val Phe Ile Phe Arg Gly Ser
485 490 495

Ile Asp Asp Pro Asp Ala Gly Trp Lys Tyr Asp Val Ala Glu Asp Leu
500 505 510

Tyr Pro Asn Asn Pro Asn Val Arg Phe Arg Gly Val Tyr Phe Asn Pro
515 520 525

Glu Ser Phe Asp Gln Met Trp Gln Thr Lys Gln Val Gly Pro Phe Val
530 535 540

Val Val Thr His Asn Glu
545 550

<210> 225
<211> 350
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(327)
<223> FRXA00416

<400> 225
act tcc cac tac gcc aac ccg ctt ggt gag ttc gga aac agg aac gca 48
Thr Ser His Tyr Ala Asn Pro Leu Gly Glu Phe Gly Asn Arg Asn Ala
1 5 10 15

ttc atc gaa gat ctc gcg atc cga agc tgg aat gag ttg gct gat cct 96
Phe Ile Glu Asp Leu Ala Ile Arg Ser Trp Asn Glu Leu Ala Asp Pro
20 25 30

caa caa ttc agc gac gcc ttg aac acc tct cca tgg acg atc cct gag 144
Gln Gln Phe Ser Asp Ala Leu Asn Thr Ser Pro Trp Thr Ile Pro Glu
35 40 45

gtg ttc atc ttc cgt ggc tcc atc gat gat cct gac gcc ggt tgg aaa 192
Val Phe Ile Phe Arg Gly Ser Ile Asp Asp Pro Asp Ala Gly Trp Lys
50 55 60

tac gat gtg gct gaa gat ctg tac ccg aac aat cca aac gtg cgc ttc 240
Tyr Asp Val Ala Glu Asp Leu Tyr Pro Asn Asn Pro Asn Val Arg Phe
65 70 75 80

cgc ggc gtg tac ttt aac ccg gag tca ttt gat cag atg tgg cag acc 288
Arg Gly Val Tyr Phe Asn Pro Glu Ser Phe Asp Gln Met Trp Gln Thr
85 90 95

aag caa gtg gga cct ttc gtg gtg gta acg cac aat gag taattcctca 337
Lys Gln Val Gly Pro Phe Val Val Val Thr His Asn Glu
100 105

ccaaacgacc caa 350

<210> 226
<211> 109
<212> PRT
<213> Corynebacterium glutamicum

<400> 226
Thr Ser His Tyr Ala Asn Pro Leu Gly Glu Phe Gly Asn Arg Asn Ala
1 5 10 15

Phe Ile Glu Asp Leu Ala Ile Arg Ser Trp Asn Glu Leu Ala Asp Pro
20 25 30

Gln Gln Phe Ser Asp Ala Leu Asn Thr Ser Pro Trp Thr Ile Pro Glu
35 40 45

```
Val Phe Ile Phe Arg Gly Ser Ile Asp Asp Pro Asp Ala Gly Trp Lys
     50                  55                  60

Tyr Asp Val Ala Glu Asp Leu Tyr Pro Asn Asn Pro Asn Val Arg Phe
 65                  70                  75                  80

Arg Gly Val Tyr Phe Asn Pro Glu Ser Phe Asp Gln Met Trp Gln Thr
                85                  90                  95

Lys Gln Val Gly Pro Phe Val Val Val Thr His Asn Glu
            100                 105
```

<210> 227
<211> 1065
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1065)
<223> FRXA00418

<400> 227

```
ctg gcg tct tac tta agc cca act gcg ctg gtg gtt gcg gtg ttg gct   48
Leu Ala Ser Tyr Leu Ser Pro Thr Ala Leu Val Val Ala Val Leu Ala
  1               5                  10                  15

att ccg ctg tct gcg acc cgc ctg tat ttg gac gga atc agc gtt gac   96
Ile Pro Leu Ser Ala Thr Arg Leu Tyr Leu Asp Gly Ile Ser Val Asp
             20                  25                  30

cag ggc ttt aga act cag ttt tta acc cgc atg gct gac gat atc ggc   144
Gln Gly Phe Arg Thr Gln Phe Leu Thr Arg Met Ala Asp Asp Ile Gly
         35                  40                  45

ttg tcg gac atg aac tac atc gat atg cct acc ttc tac cct gct gga   192
Leu Ser Asp Met Asn Tyr Ile Asp Met Pro Thr Phe Tyr Pro Ala Gly
     50                  55                  60

tgg ttc tgg ctc ggt ggt cgc ttg gcc aat ctt ttg ggg ctg ccc ggt   240
Trp Phe Trp Leu Gly Gly Arg Leu Ala Asn Leu Leu Gly Leu Pro Gly
 65                  70                  75                  80

tgg gaa gct ttc cag cca tgg gca att gtg tcc atg gca gtt gct gct   288
Trp Glu Ala Phe Gln Pro Trp Ala Ile Val Ser Met Ala Val Ala Ala
                85                  90                  95

tct gtg tta gtt cca gtg tgg cag cgc atc acc ggt tcc ctg ccg gtg   336
Ser Val Leu Val Pro Val Trp Gln Arg Ile Thr Gly Ser Leu Pro Val
            100                 105                 110

gca aca ggc att gcg ttg gtg aca acc tgc att atc ttg gcg atg aat   384
Ala Thr Gly Ile Ala Leu Val Thr Thr Cys Ile Ile Leu Ala Met Asn
        115                 120                 125

tcc gaa gag ccc tac gct gca atc gtt gcg atg ggt att cca gcg atg   432
Ser Glu Glu Pro Tyr Ala Ala Ile Val Ala Met Gly Ile Pro Ala Met
    130                 135                 140

ctc gtg ctg gct tcc cgc att gcc aag ggc gat aag ttt gcg ctt gcc   480
```

```
Leu Val Leu Ala Ser Arg Ile Ala Lys Gly Asp Lys Phe Ala Leu Ala
145                 150                 155                 160

ggc ggc att att tac ttg ggt gtt tcg gct act ttc tat act ttg ttc   528
Gly Gly Ile Ile Tyr Leu Gly Val Ser Ala Thr Phe Tyr Thr Leu Phe
                165                 170                 175

acc ggt gct atc gcg ctt tct gcg gtc gcg gtg tgc atc gtg gtg gcg   576
Thr Gly Ala Ile Ala Leu Ser Ala Val Ala Val Cys Ile Val Val Ala
            180                 185                 190

gct att gtg cag cgc tcc atc aaa cca ctg ctg tgg ctt gca gtg ctg   624
Ala Ile Val Gln Arg Ser Ile Lys Pro Leu Leu Trp Leu Ala Val Leu
        195                 200                 205

ggt ggt gga tcc att gtc att gcg ttg att tct tgg ggt cct tac ctt   672
Gly Gly Gly Ser Ile Val Ile Ala Leu Ile Ser Trp Gly Pro Tyr Leu
    210                 215                 220

ctg gcc tcc atc aac gga gcg gag cgc tct ggc gat tcc gca aca cac   720
Leu Ala Ser Ile Asn Gly Ala Glu Arg Ser Gly Asp Ser Ala Thr His
225                 230                 235                 240

tac ctg cct ctt gaa ggc acc caa ttc ccg gtt cct ttc ttg gca tca   768
Tyr Leu Pro Leu Glu Gly Thr Gln Phe Pro Val Pro Phe Leu Ala Ser
                245                 250                 255

agc gtt gtg gga ctg ttg tgt ctt gtt ggc ctg atc tat ttg gtg gtg   816
Ser Val Val Gly Leu Leu Cys Leu Val Gly Leu Ile Tyr Leu Val Val
            260                 265                 270

cgt ttc cac aac aat gag gtg cgc gcg atg tgg gtc ggc atc gca gtg   864
Arg Phe His Asn Asn Glu Val Arg Ala Met Trp Val Gly Ile Ala Val
        275                 280                 285

ttt tat gcc tgg atg ggc atg tcc atg gcg atc acg ctt ttg ggc aac   912
Phe Tyr Ala Trp Met Gly Met Ser Met Ala Ile Thr Leu Leu Gly Asn
    290                 295                 300

acg ttg ctt gga ttc cgt ctt gat acg gtg ctg gtg ctt att ttt gcc   960
Thr Leu Leu Gly Phe Arg Leu Asp Thr Val Leu Val Leu Ile Phe Ala
305                 310                 315                 320

acg gct gga gtg ttg ggc att gca gat ttc cgc ctt gcc agt gtg tat  1008
Thr Ala Gly Val Leu Gly Ile Ala Asp Phe Arg Leu Ala Ser Val Tyr
                325                 330                 335

cag ctc tac ccc acc caa atc aca gag cgc acg gcc acc cat ctg acc  1056
Gln Leu Tyr Pro Thr Gln Ile Thr Glu Arg Thr Ala Thr His Leu Thr
            340                 345                 350

aat cta att                                                     1065
Asn Leu Ile
        355
```

<210> 228
<211> 355
<212> PRT
<213> Corynebacterium glutamicum

<400> 228

```
Leu Ala Ser Tyr Leu Ser Pro Thr Ala Leu Val Val Ala Val Leu Ala
 1               5                  10                  15

Ile Pro Leu Ser Ala Thr Arg Leu Tyr Leu Asp Gly Ile Ser Val Asp
            20                  25                  30

Gln Gly Phe Arg Thr Gln Phe Leu Thr Arg Met Ala Asp Asp Ile Gly
        35                  40                  45

Leu Ser Asp Met Asn Tyr Ile Asp Met Pro Thr Phe Tyr Pro Ala Gly
    50                  55                  60

Trp Phe Trp Leu Gly Gly Arg Leu Ala Asn Leu Leu Gly Leu Pro Gly
65                  70                  75                  80

Trp Glu Ala Phe Gln Pro Trp Ala Ile Val Ser Met Ala Val Ala Ala
                85                  90                  95

Ser Val Leu Val Pro Val Trp Gln Arg Ile Thr Gly Ser Leu Pro Val
            100                 105                 110

Ala Thr Gly Ile Ala Leu Val Thr Thr Cys Ile Ile Leu Ala Met Asn
        115                 120                 125

Ser Glu Glu Pro Tyr Ala Ala Ile Val Ala Met Gly Ile Pro Ala Met
    130                 135                 140

Leu Val Leu Ala Ser Arg Ile Ala Lys Gly Asp Lys Phe Ala Leu Ala
145                 150                 155                 160

Gly Gly Ile Ile Tyr Leu Gly Val Ser Ala Thr Phe Tyr Thr Leu Phe
                165                 170                 175

Thr Gly Ala Ile Ala Leu Ser Ala Val Ala Val Cys Ile Val Val Ala
            180                 185                 190

Ala Ile Val Gln Arg Ser Ile Lys Pro Leu Leu Trp Leu Ala Val Leu
        195                 200                 205

Gly Gly Gly Ser Ile Val Ile Ala Leu Ile Ser Trp Gly Pro Tyr Leu
    210                 215                 220

Leu Ala Ser Ile Asn Gly Ala Glu Arg Ser Gly Asp Ser Ala Thr His
225                 230                 235                 240

Tyr Leu Pro Leu Glu Gly Thr Gln Phe Pro Val Pro Phe Leu Ala Ser
                245                 250                 255

Ser Val Val Gly Leu Leu Cys Leu Val Gly Leu Ile Tyr Leu Val Val
            260                 265                 270

Arg Phe His Asn Asn Glu Val Arg Ala Met Trp Val Gly Ile Ala Val
        275                 280                 285

Phe Tyr Ala Trp Met Gly Met Ser Met Ala Ile Thr Leu Leu Gly Asn
    290                 295                 300

Thr Leu Leu Gly Phe Arg Leu Asp Thr Val Leu Val Leu Ile Phe Ala
305                 310                 315                 320
```

```
Thr Ala Gly Val Leu Gly Ile Ala Asp Phe Arg Leu Ala Ser Val Tyr
                325                 330                 335

Gln Leu Tyr Pro Thr Gln Ile Thr Glu Arg Thr Ala Thr His Leu Thr
            340                 345                 350

Asn Leu Ile
        355


<210> 229
<211> 1017
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(994)
<223> RXN00422

<400> 229
aagcgccggg cgcggaaggc gctggctgag gccttcggcg cggaggtcca gccactgccg 60

cttgacaccg aataggacaa atgggtctat cctggggcgc atg ccc acg aat tat   115
                                              Met Pro Thr Asn Tyr
                                                1               5

gca cgc gac aac gtc att tcc ttg gcg tct gcc cgc gag cag cgt tcc   163
Ala Arg Asp Asn Val Ile Ser Leu Ala Ser Ala Arg Glu Gln Arg Ser
                10                  15                  20

ggg aaa ccc gag ccc aaa ccc gaa cta aca ctc atc gtc cgc gcc acc   211
Gly Lys Pro Glu Pro Lys Pro Glu Leu Thr Leu Ile Val Arg Ala Thr
            25                  30                  35

aac gtg caa gcg gac ggc gag gtc cac agg caa att ggg ttg aac tcg   259
Asn Val Gln Ala Asp Gly Glu Val His Arg Gln Ile Gly Leu Asn Ser
        40                  45                  50

gcg atg agc ctg gac gag ctg cac aat gta ctc aac atc gtt ttc ggt   307
Ala Met Ser Leu Asp Glu Leu His Asn Val Leu Asn Ile Val Phe Gly
    55                  60                  65

gtt ggc ggc gag cag tca ccc tgg cgt ttc gaa gac caa ttc cac caa   355
Val Gly Gly Glu Gln Ser Pro Trp Arg Phe Glu Asp Gln Phe His Gln
70                  75                  80                  85

ccc agc gcc ccc gac acc aac ctc ggc gaa ctc ctg ccc gaa ccc ggc   403
Pro Ser Ala Pro Asp Thr Asn Leu Gly Glu Leu Leu Pro Glu Pro Gly
                90                  95                 100

gac ttc ctg ttt tac ttc tgg ggc ctg tgg caa ttc aac ctg caa tgc   451
Asp Phe Leu Phe Tyr Phe Trp Gly Leu Trp Gln Phe Asn Leu Gln Cys
            105                 110                 115

gtg gaa atg tac ccg cgc gac aac ggc acc ccg cgc gcg ctg tgc atc   499
Val Glu Met Tyr Pro Arg Asp Asn Gly Thr Pro Arg Ala Leu Cys Ile
        120                 125                 130

ggc ggc tcc ggc ggc ctc ggc gac gac ttc gac caa gcc acc atc aac   547
Gly Gly Ser Gly Gly Leu Gly Asp Asp Phe Asp Gln Ala Thr Ile Asn
```

```
    135                 140                 145

gcc gaa ctc acc ggc acc gac acc atc cgc gac gtc ctc tcc ggc gtg   595
Ala Glu Leu Thr Gly Thr Asp Thr Ile Arg Asp Val Leu Ser Gly Val
150                 155                 160                 165

cgc ccc gaa gtc atc gac ctc gtc gac cgc acc ggc gtc ttc gac ttc   643
Arg Pro Glu Val Ile Asp Leu Val Asp Arg Thr Gly Val Phe Asp Phe
                170                 175                 180

atc cca ctg ctc caa gcg ctc gac ctc aaa aga gaa ccg ctt atc gac   691
Ile Pro Leu Leu Gln Ala Leu Asp Leu Lys Arg Glu Pro Leu Ile Asp
            185                 190                 195

gcc acc cgc tac cac acc tgc cgc acg ctg cca gtg gaa aac agc gcc   739
Ala Thr Arg Tyr His Thr Cys Arg Thr Leu Pro Val Glu Asn Ser Ala
        200                 205                 210

gaa gcc tcc gac gca ttc tgg tcc tgc gta ctc gcc ctg tcc tgc ctc   787
Glu Ala Ser Asp Ala Phe Trp Ser Cys Val Leu Ala Leu Ser Cys Leu
    215                 220                 225

gga aac gac gaa ctt ttc atc gaa gtg atc gaa tcc aca atg agc acc   835
Gly Asn Asp Glu Leu Phe Ile Glu Val Ile Glu Ser Thr Met Ser Thr
230                 235                 240                 245

ctc ggc tgg gtc gcc gac gac ggc tcc cca cta cgt gca cca gag atc   883
Leu Gly Trp Val Ala Asp Asp Gly Ser Pro Leu Arg Ala Pro Glu Ile
                250                 255                 260

acc agc gcc tgc gaa gcc tcc ctg aag ata ctc gcg gaa ctc ggt ggc   931
Thr Ser Ala Cys Glu Ala Ser Leu Lys Ile Leu Ala Glu Leu Gly Gly
            265                 270                 275

tac ggc cca gag cgg ctt gcc ccc gtg gat cgc ctg gac att tat agg   979
Tyr Gly Pro Glu Arg Leu Ala Pro Val Asp Arg Leu Asp Ile Tyr Arg
        280                 285                 290

gag ctg ctg tgt ttc taggtattgt gtaacctcgt gtc                    1017
Glu Leu Leu Cys Phe
    295


<210> 230
<211> 298
<212> PRT
<213> Corynebacterium glutamicum

<400> 230
Met Pro Thr Asn Tyr Ala Arg Asp Asn Val Ile Ser Leu Ala Ser Ala
  1               5                  10                  15

Arg Glu Gln Arg Ser Gly Lys Pro Glu Pro Lys Pro Glu Leu Thr Leu
             20                  25                  30

Ile Val Arg Ala Thr Asn Val Gln Ala Asp Gly Glu Val His Arg Gln
         35                  40                  45

Ile Gly Leu Asn Ser Ala Met Ser Leu Asp Glu Leu His Asn Val Leu
     50                  55                  60
```

```
Asn Ile Val Phe Gly Val Gly Gly Glu Gln Ser Pro Trp Arg Phe Glu
 65                  70                  75                  80

Asp Gln Phe His Gln Pro Ser Ala Pro Asp Thr Asn Leu Gly Glu Leu
                85                  90                  95

Leu Pro Glu Pro Gly Asp Phe Leu Phe Tyr Phe Trp Gly Leu Trp Gln
            100                 105                 110

Phe Asn Leu Gln Cys Val Glu Met Tyr Pro Arg Asp Asn Gly Thr Pro
        115                 120                 125

Arg Ala Leu Cys Ile Gly Gly Ser Gly Gly Leu Gly Asp Asp Phe Asp
    130                 135                 140

Gln Ala Thr Ile Asn Ala Glu Leu Thr Gly Thr Asp Thr Ile Arg Asp
145                 150                 155                 160

Val Leu Ser Gly Val Arg Pro Glu Val Ile Asp Leu Val Asp Arg Thr
                165                 170                 175

Gly Val Phe Asp Phe Ile Pro Leu Leu Gln Ala Leu Asp Leu Lys Arg
            180                 185                 190

Glu Pro Leu Ile Asp Ala Thr Arg Tyr His Thr Cys Arg Thr Leu Pro
        195                 200                 205

Val Glu Asn Ser Ala Glu Ala Ser Asp Ala Phe Trp Ser Cys Val Leu
    210                 215                 220

Ala Leu Ser Cys Leu Gly Asn Asp Glu Leu Phe Ile Glu Val Ile Glu
225                 230                 235                 240

Ser Thr Met Ser Thr Leu Gly Trp Val Ala Asp Asp Gly Ser Pro Leu
                245                 250                 255

Arg Ala Pro Glu Ile Thr Ser Ala Cys Glu Ala Ser Leu Lys Ile Leu
            260                 265                 270

Ala Glu Leu Gly Gly Tyr Gly Pro Glu Arg Leu Ala Pro Val Asp Arg
        275                 280                 285

Leu Asp Ile Tyr Arg Glu Leu Leu Cys Phe
    290                 295


<210> 231
<211> 523
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(523)
<223> FRXA00422

<400> 231
aagcgccggg cgcggaaggc gctggctgag gccttcggcg cggaggtcca gccactgccg 60

cttgacaccg aataggacaa atgggtctat cctggggcgc atg ccc acg aat tat   115
                                              Met Pro Thr Asn Tyr
```

```
                                                    1               5

gca cgc gac aac gtc att tcc ttg gcg tct gcc cgc gag cag cgt tcc   163
Ala Arg Asp Asn Val Ile Ser Leu Ala Ser Ala Arg Glu Gln Arg Ser
                10                  15                  20

ggg aaa ccc gag ccc aaa ccc gaa cta aca ctc atc gtc cgc gcc acc   211
Gly Lys Pro Glu Pro Lys Pro Glu Leu Thr Leu Ile Val Arg Ala Thr
            25                  30                  35

aac gtg caa gcg gac ggc gag gtc cac agg caa att ggg ttg aac tcg   259
Asn Val Gln Ala Asp Gly Glu Val His Arg Gln Ile Gly Leu Asn Ser
        40                  45                  50

gcg atg agc ctg gac gag ctg cac aat gta ctc aac atc gtt ttc ggt   307
Ala Met Ser Leu Asp Glu Leu His Asn Val Leu Asn Ile Val Phe Gly
    55                  60                  65

gtt ggc ggc gag cag tca ccc tgg cgt ttc gaa gac caa ttc cac caa   355
Val Gly Gly Glu Gln Ser Pro Trp Arg Phe Glu Asp Gln Phe His Gln
70                  75                  80                  85

ccc agc gcc ccc gac acc aac ctc ggc gaa ctc ctg ccc gaa ccc ggc   403
Pro Ser Ala Pro Asp Thr Asn Leu Gly Glu Leu Leu Pro Glu Pro Gly
                90                  95                  100

gac ttc ctg ttt tac ttc tgg ggc ctg tgg caa ttc aac ctg caa tgc   451
Asp Phe Leu Phe Tyr Phe Trp Gly Leu Trp Gln Phe Asn Leu Gln Cys
            105                 110                 115

gtg gaa atg tac ccg cgc gac aac ggc acc ccg cgc gcg ctg tgc atc   499
Val Glu Met Tyr Pro Arg Asp Asn Gly Thr Pro Arg Ala Leu Cys Ile
        120                 125                 130

ggc ggc tcc ggc ggc ctc ggc gac                                  523
Gly Gly Ser Gly Gly Leu Gly Asp
    135                 140
```

US 2005-0221449 A1 Oct. 6, 2005

<210> 232
<211> 141
<212> PRT
<213> Corynebacterium glutamicum

<400> 232

```
Met Pro Thr Asn Tyr Ala Arg Asp Asn Val Ile Ser Leu Ala Ser Ala
  1               5                  10                  15

Arg Glu Gln Arg Ser Gly Lys Pro Glu Pro Lys Pro Glu Leu Thr Leu
            20                  25                  30

Ile Val Arg Ala Thr Asn Val Gln Ala Asp Gly Glu Val His Arg Gln
        35                  40                  45

Ile Gly Leu Asn Ser Ala Met Ser Leu Asp Glu Leu His Asn Val Leu
    50                  55                  60

Asn Ile Val Phe Gly Val Gly Gly Glu Gln Ser Pro Trp Arg Phe Glu
65                  70                  75                  80

Asp Gln Phe His Gln Pro Ser Ala Pro Asp Thr Asn Leu Gly Glu Leu
```

```
                85                  90                  95

Leu Pro Glu Pro Gly Asp Phe Leu Phe Tyr Phe Trp Gly Leu Trp Gln
            100                 105                 110

Phe Asn Leu Gln Cys Val Glu Met Tyr Pro Arg Asp Asn Gly Thr Pro
        115                 120                 125

Arg Ala Leu Cys Ile Gly Gly Ser Gly Gly Leu Gly Asp
    130                 135                 140


<210> 233
<211> 543
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(520)
<223> RXN00447

<400> 233
gagcacggca tcgtgattcg cgcgttcccc gagggtgcgc gcatttcggt gaccaacgcc 60

gaggaaactg acaagctgct gcgcgcgtgg gaggccatca atg ctg ggt agt ctt   115
                                              Met Leu Gly Ser Leu
                                                1               5

tgg cgt ttt gcg gtg cgc acc gca gca ggc gcg gtg gcg ttg tgg gtg   163
Trp Arg Phe Ala Val Arg Thr Ala Ala Gly Ala Val Ala Leu Trp Val
                10                  15                  20

gtt att aag ctt atc gac ggc atc tcc ctg agt ttt ccc acc aca cct   211
Val Ile Lys Leu Ile Asp Gly Ile Ser Leu Ser Phe Pro Thr Thr Pro
            25                  30                  35

ctc tat cag gac ggt cag cac gac aat ctg ctg aca ttc ctg gcg gtg   259
Leu Tyr Gln Asp Gly Gln His Asp Asn Leu Leu Thr Phe Leu Ala Val
        40                  45                  50

gca gca atc att gtc gtg ttg aat gcc acg gtg aaa ccc gtc ttg aag   307
Ala Ala Ile Ile Val Val Leu Asn Ala Thr Val Lys Pro Val Leu Lys
    55                  60                  65

ctg ctt ggt ttg ccg ttg aca atc atc acc ttg ggt ctg ttc tcg ctg   355
Leu Leu Gly Leu Pro Leu Thr Ile Ile Thr Leu Gly Leu Phe Ser Leu
70                  75                  80                  85

gtc atc aac gcg gta atc atg ctg ctg gcg gag tat gtg tca gat ttg   403
Val Ile Asn Ala Val Ile Met Leu Leu Ala Glu Tyr Val Ser Asp Leu
                90                  95                  100

atc ggt ttc ggt cta cgc att gaa acc ttc ggt gcg gcc ttc tgg ggt   451
Ile Gly Phe Gly Leu Arg Ile Glu Thr Phe Gly Ala Ala Phe Trp Gly
            105                 110                 115

gcg att gtg ctg gcg tta gtg aac tgg gtt ctt ggc ccc att acc ggc   499
Ala Ile Val Leu Ala Leu Val Asn Trp Val Leu Gly Pro Ile Thr Gly
        120                 125                 130
```

```
ctc ctc ggt gca aaa aag gac taaccatggc ggatctgagc att              543
Leu Leu Gly Ala Lys Lys Asp
    135                 140


<210> 234
<211> 140
<212> PRT
<213> Corynebacterium glutamicum

<400> 234
Met Leu Gly Ser Leu Trp Arg Phe Ala Val Arg Thr Ala Ala Gly Ala
  1               5                  10                  15

Val Ala Leu Trp Val Val Ile Lys Leu Ile Asp Gly Ile Ser Leu Ser
             20                  25                  30

Phe Pro Thr Thr Pro Leu Tyr Gln Asp Gly Gln His Asp Asn Leu Leu
         35                  40                  45

Thr Phe Leu Ala Val Ala Ala Ile Ile Val Val Leu Asn Ala Thr Val
     50                  55                  60

Lys Pro Val Leu Lys Leu Leu Gly Leu Pro Leu Thr Ile Ile Thr Leu
 65                  70                  75                  80

Gly Leu Phe Ser Leu Val Ile Asn Ala Val Ile Met Leu Leu Ala Glu
                 85                  90                  95

Tyr Val Ser Asp Leu Ile Gly Phe Gly Leu Arg Ile Glu Thr Phe Gly
            100                 105                 110

Ala Ala Phe Trp Gly Ala Ile Val Leu Ala Leu Val Asn Trp Val Leu
        115                 120                 125

Gly Pro Ile Thr Gly Leu Leu Gly Ala Lys Lys Asp
    130                 135                 140


<210> 235
<211> 400
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(400)
<223> FRXA00447

<400> 235
gagcacggca tcgtgattcg cgcgttcccc gagggtgcgc gcatttcggt gaccaacgcc 60

gaggaaactg acaagctgct gcgcgcgtgg gaggccatca atg ctg ggt agt ctt   115
                                              Met Leu Gly Ser Leu
                                                1               5

tgg cgt ttt gcg gtg cgc acc gca gca ggc gcg gtg gcg ttg tgg gtg   163
Trp Arg Phe Ala Val Arg Thr Ala Ala Gly Ala Val Ala Leu Trp Val
                10                  15                  20

gtt att aag ctt atc gac ggc atc tcc ctg agt ttt ccc acc aca cct   211
```

```
Val Ile Lys Leu Ile Asp Gly Ile Ser Leu Ser Phe Pro Thr Thr Pro
            25                  30                  35

ctc tat cag gac ggt cag cac gac aat ctg ctg aca ttc ctg gcg gtg   259
Leu Tyr Gln Asp Gly Gln His Asp Asn Leu Leu Thr Phe Leu Ala Val
        40                  45                  50

gca gca atc att gtc gtg ttg aat gcc acg gtg aaa ccc gtc ttg aag   307
Ala Ala Ile Ile Val Val Leu Asn Ala Thr Val Lys Pro Val Leu Lys
    55                  60                  65

ctg ctt ggt ttg ccg ttg aca atc atc acc ttg ggt ctg ttc tcg ctg   355
Leu Leu Gly Leu Pro Leu Thr Ile Ile Thr Leu Gly Leu Phe Ser Leu
70                  75                  80                  85

gtc atc aac gcg gta atc atg ctg ctg gcg gag tat gtg tca gat       400
Val Ile Asn Ala Val Ile Met Leu Leu Ala Glu Tyr Val Ser Asp
                90                  95                  100


<210> 236
<211> 100
<212> PRT
<213> Corynebacterium glutamicum

<400> 236
Met Leu Gly Ser Leu Trp Arg Phe Ala Val Arg Thr Ala Ala Gly Ala
  1               5                  10                  15

Val Ala Leu Trp Val Val Ile Lys Leu Ile Asp Gly Ile Ser Leu Ser
            20                  25                  30

Phe Pro Thr Thr Pro Leu Tyr Gln Asp Gly Gln His Asp Asn Leu Leu
        35                  40                  45

Thr Phe Leu Ala Val Ala Ala Ile Ile Val Val Leu Asn Ala Thr Val
    50                  55                  60

Lys Pro Val Leu Lys Leu Leu Gly Leu Pro Leu Thr Ile Ile Thr Leu
65                  70                  75                  80

Gly Leu Phe Ser Leu Val Ile Asn Ala Val Ile Met Leu Leu Ala Glu
                85                  90                  95

Tyr Val Ser Asp
            100


<210> 237
<211> 873
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(850)
<223> RXN00455

<400> 237
gaagtgtctg gccgattggc taacaatctc tagttaaatc ccgcctcatg aaaccacgat 60
```

```
gaaaccaaca tgagagtttt ttcatccacg ttttctggct atg gtt gtg gac gtg   115
                                              Met Val Val Asp Val
                                                1               5

caa aat caa tca cac acc cca gaa acc cag cct caa cct ggg cag ggc   163
Gln Asn Gln Ser His Thr Pro Glu Thr Gln Pro Gln Pro Gly Gln Gly
                10                  15                  20

gca gcc aag aaa acc ccc gtt gcg tcc gga aac tcc acg ttc att cac   211
Ala Ala Lys Lys Thr Pro Val Ala Ser Gly Asn Ser Thr Phe Ile His
            25                  30                  35

att cag cca agc ttg tac ccc att ttg ctg gcg ctg ttt gtt gca gtc   259
Ile Gln Pro Ser Leu Tyr Pro Ile Leu Leu Ala Leu Phe Val Ala Val
        40                  45                  50

ttt cta att tca aat atc acc gca acc aag ggc gta gaa atc ggc ccg   307
Phe Leu Ile Ser Asn Ile Thr Ala Thr Lys Gly Val Glu Ile Gly Pro
    55                  60                  65

ttg gtg aca gac ggt gcg ttc ttc ctc ttc ccc atc tca tat gtg ttg   355
Leu Val Thr Asp Gly Ala Phe Phe Leu Phe Pro Ile Ser Tyr Val Leu
70                  75                  80                  85

ggc gat gtt cta gcc gaa tgt tac ggc ttc aaa tcc act cgt cgt gcc   403
Gly Asp Val Leu Ala Glu Cys Tyr Gly Phe Lys Ser Thr Arg Arg Ala
                90                  95                  100

att ctt act ggt ttt ggc atc acg atg ctc gcg gcg ctg tct ttc tac   451
Ile Leu Thr Gly Phe Gly Ile Thr Met Leu Ala Ala Leu Ser Phe Tyr
            105                 110                 115

att tcc atc tgg ctg cct ggc gca agt ttc tgg gaa ggc caa gaa gct   499
Ile Ser Ile Trp Leu Pro Gly Ala Ser Phe Trp Glu Gly Gln Glu Ala
        120                 125                 130

ttc gaa gca acg ctc ggc ctt gtt cca cag atc atc gtg gca tca ctg   547
Phe Glu Ala Thr Leu Gly Leu Val Pro Gln Ile Ile Val Ala Ser Leu
    135                 140                 145

gcg ggc tat att gtg ggt cag ctg ctc aac gcc aaa gtt ctg gtg gct   595
Ala Gly Tyr Ile Val Gly Gln Leu Leu Asn Ala Lys Val Leu Val Ala
150                 155                 160                 165

atc aaa aag cgc acg ggt gaa aag tcc ctg tgg gcg cgc ctg att ggt   643
Ile Lys Lys Arg Thr Gly Glu Lys Ser Leu Trp Ala Arg Leu Ile Gly
                170                 175                 180

tcc acc gtt gtc gga gaa ttt gtc gat acc ctg ctg ttt tgc gcc atc   691
Ser Thr Val Val Gly Glu Phe Val Asp Thr Leu Leu Phe Cys Ala Ile
            185                 190                 195

gca gcg cca gtg atc ggt att gcc acc gcc ccg gat ttc atc aac tac   739
Ala Ala Pro Val Ile Gly Ile Ala Thr Ala Pro Asp Phe Ile Asn Tyr
        200                 205                 210

gtt gtg gtg ggc ttc gtg tgg aaa acc ctt cta gag gtc atc ctc atg   787
Val Val Val Gly Phe Val Trp Lys Thr Leu Leu Glu Val Ile Leu Met
    215                 220                 225

ccc atc acc tac gca gtc att agg tgg gtg aaa cgc cgc gaa ggt tat   835
```

```
Pro Ile Thr Tyr Ala Val Ile Arg Trp Val Lys Arg Arg Glu Gly Tyr
230                 235                 240                 245

gaa acc ttc gac gcg tagtaccggc ctaagaattc ttc                    873
Glu Thr Phe Asp Ala
                250


<210> 238
<211> 250
<212> PRT
<213> Corynebacterium glutamicum

<400> 238
Met Val Val Asp Val Gln Asn Gln Ser His Thr Pro Glu Thr Gln Pro
  1               5                  10                  15

Gln Pro Gly Gln Gly Ala Ala Lys Lys Thr Pro Val Ala Ser Gly Asn
             20                  25                  30

Ser Thr Phe Ile His Ile Gln Pro Ser Leu Tyr Pro Ile Leu Leu Ala
         35                  40                  45

Leu Phe Val Ala Val Phe Leu Ile Ser Asn Ile Thr Ala Thr Lys Gly
     50                  55                  60

Val Glu Ile Gly Pro Leu Val Thr Asp Gly Ala Phe Phe Leu Phe Pro
 65                  70                  75                  80

Ile Ser Tyr Val Leu Gly Asp Val Leu Ala Glu Cys Tyr Gly Phe Lys
                 85                  90                  95

Ser Thr Arg Arg Ala Ile Leu Thr Gly Phe Gly Ile Thr Met Leu Ala
            100                 105                 110

Ala Leu Ser Phe Tyr Ile Ser Ile Trp Leu Pro Gly Ala Ser Phe Trp
        115                 120                 125

Glu Gly Gln Glu Ala Phe Glu Ala Thr Leu Gly Leu Val Pro Gln Ile
    130                 135                 140

Ile Val Ala Ser Leu Ala Gly Tyr Ile Val Gly Gln Leu Leu Asn Ala
145                 150                 155                 160

Lys Val Leu Val Ala Ile Lys Lys Arg Thr Gly Glu Lys Ser Leu Trp
                165                 170                 175

Ala Arg Leu Ile Gly Ser Thr Val Val Gly Glu Phe Val Asp Thr Leu
            180                 185                 190

Leu Phe Cys Ala Ile Ala Ala Pro Val Ile Gly Ile Ala Thr Ala Pro
        195                 200                 205

Asp Phe Ile Asn Tyr Val Val Val Gly Phe Val Trp Lys Thr Leu Leu
    210                 215                 220

Glu Val Ile Leu Met Pro Ile Thr Tyr Ala Val Ile Arg Trp Val Lys
225                 230                 235                 240

Arg Arg Glu Gly Tyr Glu Thr Phe Asp Ala
                245                 250
```

<210> 239
<211> 641
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(618)
<223> FRXA00455

<400> 239

```
att ttg ctg gcg ctg ttt gtt gca gtc ttt cta att tca aat atc acc   48
Ile Leu Leu Ala Leu Phe Val Ala Val Phe Leu Ile Ser Asn Ile Thr
  1               5                  10                  15

gca acc aag ggc gta gaa atc ggc ccg ttg gtg aca gac ggt gcg ttc   96
Ala Thr Lys Gly Val Glu Ile Gly Pro Leu Val Thr Asp Gly Ala Phe
            20                  25                  30

ttc ctc ttc ccc atc tca tat gtg ttg ggc gat gtt cta gcc gaa tgt   144
Phe Leu Phe Pro Ile Ser Tyr Val Leu Gly Asp Val Leu Ala Glu Cys
        35                  40                  45

tac ggc ttc aaa tcc act cgt cgt gcc att ctt act ggt ttt ggc atc   192
Tyr Gly Phe Lys Ser Thr Arg Arg Ala Ile Leu Thr Gly Phe Gly Ile
    50                  55                  60

acg atg ctc gcg gcg ctg tct ttc tac att tcc atc tgg ctg cct ggc   240
Thr Met Leu Ala Ala Leu Ser Phe Tyr Ile Ser Ile Trp Leu Pro Gly
65                  70                  75                  80

gca agt ttc tgg gaa ggc caa gaa gct ttc gaa gca acg ctc ggc ctt   288
Ala Ser Phe Trp Glu Gly Gln Glu Ala Phe Glu Ala Thr Leu Gly Leu
                85                  90                  95

gtt cca cag atc atc gtg gca tca ctg gcg ggc tat att gtg ggt cag   336
Val Pro Gln Ile Ile Val Ala Ser Leu Ala Gly Tyr Ile Val Gly Gln
            100                 105                 110

ctg ctc aac gcc aaa gtt ctg gtg gct atc aaa aag cgc acg ggt gaa   384
Leu Leu Asn Ala Lys Val Leu Val Ala Ile Lys Lys Arg Thr Gly Glu
        115                 120                 125

aag tcc ctg tgg gcg cgc ctg att ggt tcc acc gtt gtc gga gaa ttt   432
Lys Ser Leu Trp Ala Arg Leu Ile Gly Ser Thr Val Val Gly Glu Phe
    130                 135                 140

gtc gat acc ctg ctg ttt tgc gcc atc gca gcg cca gtg atc ggt att   480
Val Asp Thr Leu Leu Phe Cys Ala Ile Ala Ala Pro Val Ile Gly Ile
145                 150                 155                 160

gcc acc gcc ccg gat ttc atc aac tac gtt gtg gtg ggc ttc gtg tgg   528
Ala Thr Ala Pro Asp Phe Ile Asn Tyr Val Val Val Gly Phe Val Trp
                165                 170                 175

aaa acc ctt cta gag gtc atc ctc atg ccc atc acc tac gca gtc att   576
Lys Thr Leu Leu Glu Val Ile Leu Met Pro Ile Thr Tyr Ala Val Ile
            180                 185                 190
```

```
agg tgg gtg aaa cgc cgc gaa ggt tat gaa acc ttc gac gcg          618
Arg Trp Val Lys Arg Arg Glu Gly Tyr Glu Thr Phe Asp Ala
        195                 200                 205

tagtaccggc ctaagaattc ttc                                       641


<210> 240
<211> 206
<212> PRT
<213> Corynebacterium glutamicum

<400> 240
Ile Leu Leu Ala Leu Phe Val Ala Val Phe Leu Ile Ser Asn Ile Thr
  1               5                  10                  15

Ala Thr Lys Gly Val Glu Ile Gly Pro Leu Val Thr Asp Gly Ala Phe
             20                  25                  30

Phe Leu Phe Pro Ile Ser Tyr Val Leu Gly Asp Val Leu Ala Glu Cys
         35                  40                  45

Tyr Gly Phe Lys Ser Thr Arg Arg Ala Ile Leu Thr Gly Phe Gly Ile
     50                  55                  60

Thr Met Leu Ala Ala Leu Ser Phe Tyr Ile Ser Ile Trp Leu Pro Gly
 65                  70                  75                  80

Ala Ser Phe Trp Glu Gly Gln Glu Ala Phe Glu Ala Thr Leu Gly Leu
                 85                  90                  95

Val Pro Gln Ile Ile Val Ala Ser Leu Ala Gly Tyr Ile Val Gly Gln
            100                 105                 110

Leu Leu Asn Ala Lys Val Leu Val Ala Ile Lys Lys Arg Thr Gly Glu
        115                 120                 125

Lys Ser Leu Trp Ala Arg Leu Ile Gly Ser Thr Val Val Gly Glu Phe
    130                 135                 140

Val Asp Thr Leu Leu Phe Cys Ala Ile Ala Ala Pro Val Ile Gly Ile
145                 150                 155                 160

Ala Thr Ala Pro Asp Phe Ile Asn Tyr Val Val Val Gly Phe Val Trp
                165                 170                 175

Lys Thr Leu Leu Glu Val Ile Leu Met Pro Ile Thr Tyr Ala Val Ile
            180                 185                 190

Arg Trp Val Lys Arg Arg Glu Gly Tyr Glu Thr Phe Asp Ala
        195                 200                 205


<210> 241
<211> 912
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(889)
```

<223> RXN00473

<400> 241

```
ggggcagctg tggatttttc acaaccaccc cttttctcac accagccccg catgaacagg 60

ctggttgcac accgttgaaa atgagtgttt actggaactc atg agt gga aca ggt   115
                                            Met Ser Gly Thr Gly
                                              1               5

gtt cga aag ttg tgg gga gat ggc act ccg gtg tcg ctc cct gac ctt   163
Val Arg Lys Leu Trp Gly Asp Gly Thr Pro Val Ser Leu Pro Asp Leu
                 10                  15                  20

tca gga tta agt aga gcg gag cgc att gat gcg ttg cgt tca cgc atg   211
Ser Gly Leu Ser Arg Ala Glu Arg Ile Asp Ala Leu Arg Ser Arg Met
             25                  30                  35

tcc acc atg ggt gct gcg gtg cca aag ttt gag ccg tcg gtg gaa gaa   259
Ser Thr Met Gly Ala Ala Val Pro Lys Phe Glu Pro Ser Val Glu Glu
         40                  45                  50

agt gct gaa caa aag cag gat tct ctc gcc gaa aaa cag gac ata gtt   307
Ser Ala Glu Gln Lys Gln Asp Ser Leu Ala Glu Lys Gln Asp Ile Val
     55                  60                  65

gca gtt cct tcc gct ttt tct gat ctt ttc cct ggg gat ggt ttg ccg   355
Ala Val Pro Ser Ala Phe Ser Asp Leu Phe Pro Gly Asp Gly Leu Pro
 70                  75                  80                  85

cgt cgt gcg gtt act caa ttg gtt gaa cag cca ctt gtg gtg gtg gac   403
Arg Arg Ala Val Thr Gln Leu Val Glu Gln Pro Leu Val Val Val Asp
                 90                  95                 100

ttc ctg gct cat att act gcc cag ggt gga cac gct gcg gtg att ggg   451
Phe Leu Ala His Ile Thr Ala Gln Gly Gly His Ala Ala Val Ile Gly
            105                 110                 115

tgg aag gat tta gcc tac gcc ggg gtg att gat tcc gga ggt gtg tgc   499
Trp Lys Asp Leu Ala Tyr Ala Gly Val Ile Asp Ser Gly Gly Val Cys
        120                 125                 130

gag aac atc att gct att cca aat cct ggt acg gag cca ctg aat gtg   547
Glu Asn Ile Ile Ala Ile Pro Asn Pro Gly Thr Glu Pro Leu Asn Val
    135                 140                 145

gca gcg gtg ctg tgt gag ggg ttg gat gtg gtc gtg tac aaa ggc ccg   595
Ala Ala Val Leu Cys Glu Gly Leu Asp Val Val Val Tyr Lys Gly Pro
150                 155                 160                 165

gag att tcc ctg tcg cca acc aga gcg agg ccg ttg ctg gga aag ctg   643
Glu Ile Ser Leu Ser Pro Thr Arg Ala Arg Pro Leu Leu Gly Lys Leu
                170                 175                 180

agg cag ggg act gct gcc ttg gtg atg gtt ggc acg aaa gta agc tca   691
Arg Gln Gly Thr Ala Ala Leu Val Met Val Gly Thr Lys Val Ser Ser
            185                 190                 195

ccg gcg ctg tcg gtg gat gca gag atc act gat tat gtt ggc att ggt   739
Pro Ala Leu Ser Val Asp Ala Glu Ile Thr Asp Tyr Val Gly Ile Gly
        200                 205                 210
```

```
gca ggt agt ggg cgt att cgt ggc gtt gag atg cag gtg cgg gct gtg   787
Ala Gly Ser Gly Arg Ile Arg Gly Val Glu Met Gln Val Arg Ala Val
    215                 220                 225

tcg aaa act cac ggt gtg cgc agc gga aaa gtc ctg atc agt agg cct   835
Ser Lys Thr His Gly Val Arg Ser Gly Lys Val Leu Ile Ser Arg Pro
230                 235                 240                 245

cag gat gca gca ttg ctt gag cct gaa cag cca aca acg ttg cgg gcg   883
Gln Asp Ala Ala Leu Leu Glu Pro Glu Gln Pro Thr Thr Leu Arg Ala
                250                 255                 260

gtc cca tgacgcgggt gatggcattg tgg                                912
Val Pro
```

<210> 242
<211> 263
<212> PRT
<213> Corynebacterium glutamicum

```
<400> 242
Met Ser Gly Thr Gly Val Arg Lys Leu Trp Gly Asp Gly Thr Pro Val
  1               5                  10                  15

Ser Leu Pro Asp Leu Ser Gly Leu Ser Arg Ala Glu Arg Ile Asp Ala
            20                  25                  30

Leu Arg Ser Arg Met Ser Thr Met Gly Ala Ala Val Pro Lys Phe Glu
        35                  40                  45

Pro Ser Val Glu Glu Ser Ala Glu Gln Lys Gln Asp Ser Leu Ala Glu
    50                  55                  60

Lys Gln Asp Ile Val Ala Val Pro Ser Ala Phe Ser Asp Leu Phe Pro
65                  70                  75                  80

Gly Asp Gly Leu Pro Arg Arg Ala Val Thr Gln Leu Val Glu Gln Pro
                85                  90                  95

Leu Val Val Val Asp Phe Leu Ala His Ile Thr Ala Gln Gly Gly His
            100                 105                 110

Ala Ala Val Ile Gly Trp Lys Asp Leu Ala Tyr Ala Gly Val Ile Asp
        115                 120                 125

Ser Gly Gly Val Cys Glu Asn Ile Ile Ala Ile Pro Asn Pro Gly Thr
    130                 135                 140

Glu Pro Leu Asn Val Ala Ala Val Leu Cys Glu Gly Leu Asp Val Val
145                 150                 155                 160

Val Tyr Lys Gly Pro Glu Ile Ser Leu Ser Pro Thr Arg Ala Arg Pro
                165                 170                 175

Leu Leu Gly Lys Leu Arg Gln Gly Thr Ala Ala Leu Val Met Val Gly
            180                 185                 190

Thr Lys Val Ser Ser Pro Ala Leu Ser Val Asp Ala Glu Ile Thr Asp
        195                 200                 205
```

```
Tyr Val Gly Ile Gly Ala Gly Ser Gly Arg Ile Arg Gly Val Glu Met
    210                 215                 220

Gln Val Arg Ala Val Ser Lys Thr His Gly Val Arg Ser Gly Lys Val
225                 230                 235                 240

Leu Ile Ser Arg Pro Gln Asp Ala Ala Leu Leu Glu Pro Glu Gln Pro
                245                 250                 255

Thr Thr Leu Arg Ala Val Pro
            260
```

<210> 243
<211> 888
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(865)
<223> FRXA00473

<400> 243

```
ccaccccttt tctcacacca gccccgcatg aacaggctgg ttgcacaccg ttgaaaatga 60

gtgtttactg gaactcatga gtggaacagg tgttcgaaag ttg tgg gga gat ggc   115
                                              Leu Trp Gly Asp Gly
                                                1               5

act ccg gtg tcg ctc cct gac ctt tca gga tta agt aga gcg gag cgc   163
Thr Pro Val Ser Leu Pro Asp Leu Ser Gly Leu Ser Arg Ala Glu Arg
                10                  15                  20

att gat gcg ttg cgt tca cgc atg tcc acc atg ggt gct gcg gtg cca   211
Ile Asp Ala Leu Arg Ser Arg Met Ser Thr Met Gly Ala Ala Val Pro
            25                  30                  35

aag ttt gag ccg tcg gtg gaa gaa agt gct gaa caa aag cag gat tct   259
Lys Phe Glu Pro Ser Val Glu Glu Ser Ala Glu Gln Lys Gln Asp Ser
        40                  45                  50

ctc gcc gaa aaa cag gac ata gtt gca gtt cct tcc gct ttt tct gat   307
Leu Ala Glu Lys Gln Asp Ile Val Ala Val Pro Ser Ala Phe Ser Asp
    55                  60                  65

ctt ttc cct ggg gat ggt ttg ccg cgt cgt gcg gtt act caa ttg gtt   355
Leu Phe Pro Gly Asp Gly Leu Pro Arg Arg Ala Val Thr Gln Leu Val
70                  75                  80                  85

gaa cag cca ctt gtg gtg gtg gac ttc ctg gct cat att act gcc cag   403
Glu Gln Pro Leu Val Val Val Asp Phe Leu Ala His Ile Thr Ala Gln
                90                  95                  100

ggt gga cac gct gcg gtg att ggg tgg aag gat tta gcc tac gcc ggg   451
Gly Gly His Ala Ala Val Ile Gly Trp Lys Asp Leu Ala Tyr Ala Gly
            105                 110                 115

gtg att gat tcc gga ggt gtg tgc gag aac atc att gct att cca aat   499
Val Ile Asp Ser Gly Gly Val Cys Glu Asn Ile Ile Ala Ile Pro Asn
```

```
        120                 125                 130

cct ggt acg gag cca ctg aat gtg gca gcg gtg ctg tgt gag ggg ttg   547
Pro Gly Thr Glu Pro Leu Asn Val Ala Ala Val Leu Cys Glu Gly Leu
    135                 140                 145

gat gtg gtc gtg tac aaa ggc ccg gag att tcc ctg tcg cca acc aga   595
Asp Val Val Val Tyr Lys Gly Pro Glu Ile Ser Leu Ser Pro Thr Arg
150                 155                 160                 165

gcg agg ccg ttg ctg gga aag ctg agg cag ggg act gct gcc ttg gtg   643
Ala Arg Pro Leu Leu Gly Lys Leu Arg Gln Gly Thr Ala Ala Leu Val
                170                 175                 180

atg gtt ggc acg aaa gta agc tca ccg gcg ctg tcg gtg gat gca gag   691
Met Val Gly Thr Lys Val Ser Ser Pro Ala Leu Ser Val Asp Ala Glu
            185                 190                 195

atc act gat tat gtt ggc att ggt gca ggt agt ggg cgt att cgt ggc   739
Ile Thr Asp Tyr Val Gly Ile Gly Ala Gly Ser Gly Arg Ile Arg Gly
        200                 205                 210

gtt gag atg cag gtg cgg gct gtg tcg aaa act cac ggt gtg cgc agc   787
Val Glu Met Gln Val Arg Ala Val Ser Lys Thr His Gly Val Arg Ser
    215                 220                 225

gga aaa gtc ctg atc agt agg cct cag gat gca gca ttg ctt gag cct   835
Gly Lys Val Leu Ile Ser Arg Pro Gln Asp Ala Ala Leu Leu Glu Pro
230                 235                 240                 245

gaa cag cca aca acg ttg cgg gcg gtc cca tgacgcgggt gatggcattg     885
Glu Gln Pro Thr Thr Leu Arg Ala Val Pro
                250                 255

tgg                                                               888


<210> 244
<211> 255
<212> PRT
<213> Corynebacterium glutamicum

<400> 244
Leu Trp Gly Asp Gly Thr Pro Val Ser Leu Pro Asp Leu Ser Gly Leu
  1               5                  10                  15

Ser Arg Ala Glu Arg Ile Asp Ala Leu Arg Ser Arg Met Ser Thr Met
             20                  25                  30

Gly Ala Ala Val Pro Lys Phe Glu Pro Ser Val Glu Glu Ser Ala Glu
         35                  40                  45

Gln Lys Gln Asp Ser Leu Ala Glu Lys Gln Asp Ile Val Ala Val Pro
     50                  55                  60

Ser Ala Phe Ser Asp Leu Phe Pro Gly Asp Gly Leu Pro Arg Arg Ala
 65                  70                  75                  80

Val Thr Gln Leu Val Glu Gln Pro Leu Val Val Val Asp Phe Leu Ala
                 85                  90                  95
```

```
His Ile Thr Ala Gln Gly Gly His Ala Ala Val Ile Gly Trp Lys Asp
            100                 105                 110

Leu Ala Tyr Ala Gly Val Ile Asp Ser Gly Gly Val Cys Glu Asn Ile
        115                 120                 125

Ile Ala Ile Pro Asn Pro Gly Thr Glu Pro Leu Asn Val Ala Ala Val
    130                 135                 140

Leu Cys Glu Gly Leu Asp Val Val Val Tyr Lys Gly Pro Glu Ile Ser
145                 150                 155                 160

Leu Ser Pro Thr Arg Ala Arg Pro Leu Leu Gly Lys Leu Arg Gln Gly
                165                 170                 175

Thr Ala Ala Leu Val Met Val Gly Thr Lys Val Ser Ser Pro Ala Leu
            180                 185                 190

Ser Val Asp Ala Glu Ile Thr Asp Tyr Val Gly Ile Gly Ala Gly Ser
        195                 200                 205

Gly Arg Ile Arg Gly Val Glu Met Gln Val Arg Ala Val Ser Lys Thr
    210                 215                 220

His Gly Val Arg Ser Gly Lys Val Leu Ile Ser Arg Pro Gln Asp Ala
225                 230                 235                 240

Ala Leu Leu Glu Pro Glu Gln Pro Thr Thr Leu Arg Ala Val Pro
                245                 250                 255
```

<210> 245
<211> 2418
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2395)
<223> RXN00485

<400> 245

```
tcaacttcgg cgacgaggtg ggcgctattt ttcattgttt ttcgcgattt tcgcttcggt 60

tgcattgact gttagcgcca ctgcgttgac aaattctttg gtg tcc agt gtt aat   115
                                            Val Ser Ser Val Asn
                                              1               5

gat ctt ttt gcc aag ccg tat gaa aac gct gat ctt gtg gtc acg gtg   163
Asp Leu Phe Ala Lys Pro Tyr Glu Asn Ala Asp Leu Val Val Thr Val
                 10                  15                  20

tct gcg aaa aac gaa gat tcc ttt gca gct ttt gag caa caa tta gct   211
Ser Ala Lys Asn Glu Asp Ser Phe Ala Ala Phe Glu Gln Gln Leu Ala
             25                  30                  35

acg aca cct ggt gtt gaa gct ctg gct ttt gat caa aat ttt gca gcc   259
Thr Thr Pro Gly Val Glu Ala Leu Ala Phe Asp Gln Asn Phe Ala Ala
         40                  45                  50

tct gta aag caa tca gac ggg att tac gcc agt act tca gtc cag tca   307
```

```
Ser Val Lys Gln Ser Asp Gly Ile Tyr Ala Ser Thr Ser Val Gln Ser
     55                  60                  65

att tcg gaa ggc cca ctg cag tgg cgg cca atc cta gaa ggc cga ttg   355
Ile Ser Glu Gly Pro Leu Gln Trp Arg Pro Ile Leu Glu Gly Arg Leu
 70                  75                  80                  85

ccc caa gga cct ggt gag att gca gta aca acg gcc ccg ggt gcg cct   403
Pro Gln Gly Pro Gly Glu Ile Ala Val Thr Thr Ala Pro Gly Ala Pro
                 90                  95                 100

gaa gtt ggt gag cac gta tcc att cgc ctg tcc caa aac act gag gac   451
Glu Val Gly Glu His Val Ser Ile Arg Leu Ser Gln Asn Thr Glu Asp
            105                 110                 115

act gag gtt ctt gtg gtt ggc gtg gtg gag cca gcg gcg cag gaa act   499
Thr Glu Val Leu Val Val Gly Val Val Glu Pro Ala Ala Gln Glu Thr
        120                 125                 130

tta ggt ggc gca ccg ttc gtt gtg gcg tct cct gat gcg ctg atg gag   547
Leu Gly Gly Ala Pro Phe Val Val Ala Ser Pro Asp Ala Leu Met Glu
    135                 140                 145

tgg aat tct tcc ggt gtg cgg ggt gaa ttc cga gtg gca act tcc gat   595
Trp Asn Ser Ser Gly Val Arg Gly Glu Phe Arg Val Ala Thr Ser Asp
150                 155                 160                 165

cct gcc tcg cta gag gct gca agc ttt agc gac gct acg gtg gtg gtt   643
Pro Ala Ser Leu Glu Ala Ala Ser Phe Ser Asp Ala Thr Val Val Val
                170                 175                 180

gct tcg gcg gag ggg cac gtc gat aag ctt gct gat tct tat ttg ggc   691
Ala Ser Ala Glu Gly His Val Asp Lys Leu Ala Asp Ser Tyr Leu Gly
            185                 190                 195

cag cga gat cgc tat ttc ttg ctg ctc gca gcg ttt gtg gca gtg gct   739
Gln Arg Asp Arg Tyr Phe Leu Leu Leu Ala Ala Phe Val Ala Val Ala
        200                 205                 210

gct gcc gtg gcg ttt ttg gtg gtc ttt tct gca tat tcg gtg ctc act   787
Ala Ala Val Ala Phe Leu Val Val Phe Ser Ala Tyr Ser Val Leu Thr
    215                 220                 225

ggt gag cga gtt cgc gag ttc ggg ctg att cgt tca gtg ggc gca tcg   835
Gly Glu Arg Val Arg Glu Phe Gly Leu Ile Arg Ser Val Gly Ala Ser
230                 235                 240                 245

acg ccg cag att ttg ggg tca gtg att ttt gaa gcc ggc atc ctc ggt   883
Thr Pro Gln Ile Leu Gly Ser Val Ile Phe Glu Ala Gly Ile Leu Gly
                250                 255                 260

gtg gtg gct gct ggt ttt ggt gcg ccc gcc gga ttg atg gcg gcg cgt   931
Val Val Ala Ala Gly Phe Gly Ala Pro Ala Gly Leu Met Ala Ala Arg
            265                 270                 275

ttg ttg gcg gat aat gcc gca cgt ttt ggc att cgt gtg ccc att gat   979
Leu Leu Ala Asp Asn Ala Ala Arg Phe Gly Ile Arg Val Pro Ile Asp
        280                 285                 290

gtg att gat ctg cca agt agc acg atg tgg ctc atc gct ggc gtc ggc   1027
Val Ile Asp Leu Pro Ser Ser Thr Met Trp Leu Ile Ala Gly Val Gly
```

```
    295                 300                 305

gtg gtg atg tcc gtg att gcg gca tta ccg gca gtg ttc agt gtg tgc   1075
Val Val Met Ser Val Ile Ala Ala Leu Pro Ala Val Phe Ser Val Cys
310                 315                 320                 325

aga aaa tcc gca gtg gaa tca ctg agt acg cct gct att tcg agg act   1123
Arg Lys Ser Ala Val Glu Ser Leu Ser Thr Pro Ala Ile Ser Arg Thr
                330                 335                 340

tcc ccc tgg ttc ggt gca tta tgg ttg ctg ctc gcg ggc att gtg ggc   1171
Ser Pro Trp Phe Gly Ala Leu Trp Leu Leu Leu Ala Gly Ile Val Gly
            345                 350                 355

gcc ggc gga atg tgg gcg tat gag gca acc tcg gac tac cgc ggc atg   1219
Ala Gly Gly Met Trp Ala Tyr Glu Ala Thr Ser Asp Tyr Arg Gly Met
        360                 365                 370

cgt tca gtg gct tta tcc atc gcc ggt tca ggc gct ttg gtg tgt gcg   1267
Arg Ser Val Ala Leu Ser Ile Ala Gly Ser Gly Ala Leu Val Cys Ala
    375                 380                 385

ttg ttg att gcc acg gcg gtg ctc gtg ccc tgg tta ttg cac gta ttc   1315
Leu Leu Ile Ala Thr Ala Val Leu Val Pro Trp Leu Leu His Val Phe
390                 395                 400                 405

tcc agg att gtg ggc ggc acc gtc cca aca ctt cag ttg gga ttg gcg   1363
Ser Arg Ile Val Gly Gly Thr Val Pro Thr Leu Gln Leu Gly Leu Ala
                410                 415                 420

ttt gca gca aag cag aaa tct cgt tcg gcg gcg ctg atc gct gtg att   1411
Phe Ala Ala Lys Gln Lys Ser Arg Ser Ala Ala Leu Ile Ala Val Ile
            425                 430                 435

ctt gct ggt tct gca tta agc tcc gct gtt ctg cat ggc cag gca cat   1459
Leu Ala Gly Ser Ala Leu Ser Ser Ala Val Leu His Gly Gln Ala His
        440                 445                 450

atc ggc acg cat ttg gtg gcc gtg gct aaa ggc atg ggc ggc aca gac   1507
Ile Gly Thr His Leu Val Ala Val Ala Lys Gly Met Gly Gly Thr Asp
    455                 460                 465

atg atg gtt aca gcg ctt gat ggg gaa atc ccc gcc gga atg ctg gag   1555
Met Met Val Thr Ala Leu Asp Gly Glu Ile Pro Ala Gly Met Leu Glu
470                 475                 480                 485

gaa atc tct agc atc gac ggc gtg aaa act gcc atc gcg cca gcc acc   1603
Glu Ile Ser Ser Ile Asp Gly Val Lys Thr Ala Ile Ala Pro Ala Thr
                490                 495                 500

acc gct gtg gaa ttg gaa gat tcc ggc aat ttc tct gtg ctc atg ctc   1651
Thr Ala Val Glu Leu Glu Asp Ser Gly Asn Phe Ser Val Leu Met Leu
            505                 510                 515

gct gaa gaa gac gga gcc tcc gtg atg cgc gca ggc gat act ggt gca   1699
Ala Glu Glu Asp Gly Ala Ser Val Met Arg Ala Gly Asp Thr Gly Ala
        520                 525                 530

cca gct ggt ggc ctt gtt ttg ggc aga aac tct cct gac cag gat gct   1747
Pro Ala Gly Gly Leu Val Leu Gly Arg Asn Ser Pro Asp Gln Asp Ala
    535                 540                 545
```

```
tac ccg gcc ggc cag gct gca aac atc att gtc gcg gat acc cca acg   1795
Tyr Pro Ala Gly Gln Ala Ala Asn Ile Ile Val Ala Asp Thr Pro Thr
550                 555                 560                 565

cag gcg gaa atc ttc cac agc gac aac tac ttc tcc atg atc gac cca   1843
Gln Ala Glu Ile Phe His Ser Asp Asn Tyr Phe Ser Met Ile Asp Pro
                570                 575                 580

gca ctc gcc acc ggc ccc agc acc aca cgc aac gta ctg atc ctg ctc   1891
Ala Leu Ala Thr Gly Pro Ser Thr Thr Arg Asn Val Leu Ile Leu Leu
            585                 590                 595

gac ggc gac tcc aac cag gcc ccc gac aac gcc acg gcg cag gcg gta   1939
Asp Gly Asp Ser Asn Gln Ala Pro Asp Asn Ala Thr Ala Gln Ala Val
        600                 605                 610

cgc aag acc att tcg ctt ttc gac gga cga tac tcc atc acc gag ggt   1987
Arg Lys Thr Ile Ser Leu Phe Asp Gly Arg Tyr Ser Ile Thr Glu Gly
    615                 620                 625

ttc tcc gcc cgc caa aac act ttt gaa ctg gtt tcc cgc atc acc acc   2035
Phe Ser Ala Arg Gln Asn Thr Phe Glu Leu Val Ser Arg Ile Thr Thr
630                 635                 640                 645

atg tcc aca ctg ctt gcc atc gtg gcc tta gcg atc gct gcc gtt ggc   2083
Met Ser Thr Leu Leu Ala Ile Val Ala Leu Ala Ile Ala Ala Val Gly
                650                 655                 660

ctg atc aac aca gtg gca ctc acc att tct gag cgt gcc cgc gat cgt   2131
Leu Ile Asn Thr Val Ala Leu Thr Ile Ser Glu Arg Ala Arg Asp Arg
            665                 670                 675

tat ttg ctg cgc acc att gga ctg acc tca act ggt cag att ctg gtg   2179
Tyr Leu Leu Arg Thr Ile Gly Leu Thr Ser Thr Gly Gln Ile Leu Val
        680                 685                 690

atg gct att gaa atg atc gcg ctc tca ttg ccg gct gcc att gtt ggt   2227
Met Ala Ile Glu Met Ile Ala Leu Ser Leu Pro Ala Ala Ile Val Gly
    695                 700                 705

gca gtt tcg gga gga ttc tta ggc aga ttc gtt gcc agt tct gcc acc   2275
Ala Val Ser Gly Gly Phe Leu Gly Arg Phe Val Ala Ser Ser Ala Thr
710                 715                 720                 725

aac acc gct gcg acg gca cca ctt caa gta gac att ctc ggc gga acg   2323
Asn Thr Ala Ala Thr Ala Pro Leu Gln Val Asp Ile Leu Gly Gly Thr
                730                 735                 740

gtt ctc gcg atg gtc gca gga tct gta ctg tgc gcg ctc atc gtg ctg   2371
Val Leu Ala Met Val Ala Gly Ser Val Leu Cys Ala Leu Ile Val Leu
            745                 750                 755

gcg aac aaa cga cgt cgg gtg gtt tgattataaa atccaaaaat cga         2418
Ala Asn Lys Arg Arg Arg Val Val
        760                 765
```

<210> 246
<211> 765
<212> PRT

<213> Corynebacterium glutamicum

<400> 246

```
Val Ser Ser Val Asn Asp Leu Phe Ala Lys Pro Tyr Glu Asn Ala Asp
  1               5                  10                  15

Leu Val Val Thr Val Ser Ala Lys Asn Glu Asp Ser Phe Ala Ala Phe
            20                  25                  30

Glu Gln Gln Leu Ala Thr Thr Pro Gly Val Glu Ala Leu Ala Phe Asp
        35                  40                  45

Gln Asn Phe Ala Ala Ser Val Lys Gln Ser Asp Gly Ile Tyr Ala Ser
    50                  55                  60

Thr Ser Val Gln Ser Ile Ser Glu Gly Pro Leu Gln Trp Arg Pro Ile
65                  70                  75                  80

Leu Glu Gly Arg Leu Pro Gln Gly Pro Gly Glu Ile Ala Val Thr Thr
                85                  90                  95

Ala Pro Gly Ala Pro Glu Val Gly Glu His Val Ser Ile Arg Leu Ser
            100                 105                 110

Gln Asn Thr Glu Asp Thr Glu Val Leu Val Val Gly Val Val Glu Pro
        115                 120                 125

Ala Ala Gln Glu Thr Leu Gly Gly Ala Pro Phe Val Val Ala Ser Pro
    130                 135                 140

Asp Ala Leu Met Glu Trp Asn Ser Ser Gly Val Arg Gly Glu Phe Arg
145                 150                 155                 160

Val Ala Thr Ser Asp Pro Ala Ser Leu Glu Ala Ala Ser Phe Ser Asp
                165                 170                 175

Ala Thr Val Val Val Ala Ser Ala Glu Gly His Val Asp Lys Leu Ala
            180                 185                 190

Asp Ser Tyr Leu Gly Gln Arg Asp Arg Tyr Phe Leu Leu Leu Ala Ala
        195                 200                 205

Phe Val Ala Val Ala Ala Ala Val Ala Phe Leu Val Val Phe Ser Ala
    210                 215                 220

Tyr Ser Val Leu Thr Gly Glu Arg Val Arg Glu Phe Gly Leu Ile Arg
225                 230                 235                 240

Ser Val Gly Ala Ser Thr Pro Gln Ile Leu Gly Ser Val Ile Phe Glu
                245                 250                 255

Ala Gly Ile Leu Gly Val Val Ala Ala Gly Phe Gly Ala Pro Ala Gly
            260                 265                 270

Leu Met Ala Ala Arg Leu Leu Ala Asp Asn Ala Ala Arg Phe Gly Ile
        275                 280                 285

Arg Val Pro Ile Asp Val Ile Asp Leu Pro Ser Ser Thr Met Trp Leu
    290                 295                 300

Ile Ala Gly Val Gly Val Val Met Ser Val Ile Ala Ala Leu Pro Ala
```

```
305                 310                 315                 320

Val Phe Ser Val Cys Arg Lys Ser Ala Val Glu Ser Leu Ser Thr Pro
                325                 330                 335

Ala Ile Ser Arg Thr Ser Pro Trp Phe Gly Ala Leu Trp Leu Leu Leu
            340                 345                 350

Ala Gly Ile Val Gly Ala Gly Gly Met Trp Ala Tyr Glu Ala Thr Ser
        355                 360                 365

Asp Tyr Arg Gly Met Arg Ser Val Ala Leu Ser Ile Ala Gly Ser Gly
    370                 375                 380

Ala Leu Val Cys Ala Leu Leu Ile Ala Thr Ala Val Leu Val Pro Trp
385                 390                 395                 400

Leu Leu His Val Phe Ser Arg Ile Val Gly Gly Thr Val Pro Thr Leu
                405                 410                 415

Gln Leu Gly Leu Ala Phe Ala Ala Lys Gln Lys Ser Arg Ser Ala Ala
            420                 425                 430

Leu Ile Ala Val Ile Leu Ala Gly Ser Ala Leu Ser Ser Ala Val Leu
        435                 440                 445

His Gly Gln Ala His Ile Gly Thr His Leu Val Ala Val Ala Lys Gly
    450                 455                 460

Met Gly Gly Thr Asp Met Met Val Thr Ala Leu Asp Gly Glu Ile Pro
465                 470                 475                 480

Ala Gly Met Leu Glu Glu Ile Ser Ser Ile Asp Gly Val Lys Thr Ala
                485                 490                 495

Ile Ala Pro Ala Thr Thr Ala Val Glu Leu Glu Asp Ser Gly Asn Phe
            500                 505                 510

Ser Val Leu Met Leu Ala Glu Glu Asp Gly Ala Ser Val Met Arg Ala
        515                 520                 525

Gly Asp Thr Gly Ala Pro Ala Gly Gly Leu Val Leu Gly Arg Asn Ser
    530                 535                 540

Pro Asp Gln Asp Ala Tyr Pro Ala Gly Gln Ala Ala Asn Ile Ile Val
545                 550                 555                 560

Ala Asp Thr Pro Thr Gln Ala Glu Ile Phe His Ser Asp Asn Tyr Phe
                565                 570                 575

Ser Met Ile Asp Pro Ala Leu Ala Thr Gly Pro Ser Thr Thr Arg Asn
            580                 585                 590

Val Leu Ile Leu Leu Asp Gly Asp Ser Asn Gln Ala Pro Asp Asn Ala
        595                 600                 605

Thr Ala Gln Ala Val Arg Lys Thr Ile Ser Leu Phe Asp Gly Arg Tyr
    610                 615                 620

Ser Ile Thr Glu Gly Phe Ser Ala Arg Gln Asn Thr Phe Glu Leu Val
625                 630                 635                 640
```

```
Ser Arg Ile Thr Thr Met Ser Thr Leu Leu Ala Ile Val Ala Leu Ala
                645                 650                 655

Ile Ala Ala Val Gly Leu Ile Asn Thr Val Ala Leu Thr Ile Ser Glu
            660                 665                 670

Arg Ala Arg Asp Arg Tyr Leu Leu Arg Thr Ile Gly Leu Thr Ser Thr
        675                 680                 685

Gly Gln Ile Leu Val Met Ala Ile Glu Met Ile Ala Leu Ser Leu Pro
    690                 695                 700

Ala Ala Ile Val Gly Ala Val Ser Gly Gly Phe Leu Gly Arg Phe Val
705                 710                 715                 720

Ala Ser Ser Ala Thr Asn Thr Ala Ala Thr Ala Pro Leu Gln Val Asp
                725                 730                 735

Ile Leu Gly Gly Thr Val Leu Ala Met Val Ala Gly Ser Val Leu Cys
            740                 745                 750

Ala Leu Ile Val Leu Ala Asn Lys Arg Arg Arg Val Val
        755                 760                 765
```

<210> 247
<211> 2166
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2143)
<223> FRXA00485

<400> 247

```
tgcagcctct gtaaagcaat cagacgggat ttacgccagt acttcagtcc agtcaatttc 60

ggaaggccca ctgcagtggc ggccaatcct agaaggccga ttg ccc caa gga cct   115
                                              Leu Pro Gln Gly Pro
                                                1               5

ggt gag att gca gta aca acg gcc ccg ggt gcg cct gaa gtt ggt gag   163
Gly Glu Ile Ala Val Thr Thr Ala Pro Gly Ala Pro Glu Val Gly Glu
               10                  15                  20

cac gta tcc att cgc ctg tcc caa aac act gag gac act gag gtt ctt   211
His Val Ser Ile Arg Leu Ser Gln Asn Thr Glu Asp Thr Glu Val Leu
            25                  30                  35

gtg gtt ggc gtg gtg gag cca gcg gcg cag gaa act tta ggt ggc gca   259
Val Val Gly Val Val Glu Pro Ala Ala Gln Glu Thr Leu Gly Gly Ala
        40                  45                  50

ccg ttc gtt gtg gcg tct cct gat gcg ctg atg gag tgg aat tct tcc   307
Pro Phe Val Val Ala Ser Pro Asp Ala Leu Met Glu Trp Asn Ser Ser
    55                  60                  65

ggt gtg cgg ggt gaa ttc cga gtg gca act tcc gat cct gcc tcg cta   355
Gly Val Arg Gly Glu Phe Arg Val Ala Thr Ser Asp Pro Ala Ser Leu
```

```
 70                  75                  80                  85

gag gct gca agc ttt agc gac gct acg gtg gtg gtt gct tcg gcg gag   403
Glu Ala Ala Ser Phe Ser Asp Ala Thr Val Val Val Ala Ser Ala Glu
                90                  95                 100

ggg cac gtc gat aag ctt gct gat tct tat ttg ggc cag cga gat cgc   451
Gly His Val Asp Lys Leu Ala Asp Ser Tyr Leu Gly Gln Arg Asp Arg
            105                 110                 115

tat ttc ttg ctg ctc gca gcg ttt gtg gca gtg gct gct gcc gtg gcg   499
Tyr Phe Leu Leu Leu Ala Ala Phe Val Ala Val Ala Ala Ala Val Ala
        120                 125                 130

ttt ttg gtg gtc ttt tct gca tat tcg gtg ctc act ggt gag cga gtt   547
Phe Leu Val Val Phe Ser Ala Tyr Ser Val Leu Thr Gly Glu Arg Val
    135                 140                 145

cgc gag ttc ggg ctg att cgt tca gtg ggc gca tcg acg ccg cag att   595
Arg Glu Phe Gly Leu Ile Arg Ser Val Gly Ala Ser Thr Pro Gln Ile
150                 155                 160                 165

ttg ggg tca gtg att ttt gaa gcc ggc atc ctc ggt gtg gtg gct gct   643
Leu Gly Ser Val Ile Phe Glu Ala Gly Ile Leu Gly Val Val Ala Ala
                170                 175                 180

ggt ttt ggt gcg ccc gcc gga ttg atg gcg gcg cgt ttg ttg gcg gat   691
Gly Phe Gly Ala Pro Ala Gly Leu Met Ala Ala Arg Leu Leu Ala Asp
            185                 190                 195

aat gcc gca cgt ttt ggc att cgt gtg ccc att gat gtg att gat ctg   739
Asn Ala Ala Arg Phe Gly Ile Arg Val Pro Ile Asp Val Ile Asp Leu
        200                 205                 210

cca agt agc acg atg tgg ctc atc gct ggc gtc ggc gtg gtg atg tcc   787
Pro Ser Ser Thr Met Trp Leu Ile Ala Gly Val Gly Val Val Met Ser
    215                 220                 225

gtg att gcg gca tta ccg gca gtg ttc agt gtg tgc aga aaa tcc gca   835
Val Ile Ala Ala Leu Pro Ala Val Phe Ser Val Cys Arg Lys Ser Ala
230                 235                 240                 245

gtg gaa tca ctg agt acg cct gct att tcg agg act tcc ccc tgg ttc   883
Val Glu Ser Leu Ser Thr Pro Ala Ile Ser Arg Thr Ser Pro Trp Phe
                250                 255                 260

ggt gca tta tgg ttg ctg ctc gcg ggc att gtg ggc gcc ggc gga atg   931
Gly Ala Leu Trp Leu Leu Leu Ala Gly Ile Val Gly Ala Gly Gly Met
            265                 270                 275

tgg gcg tat gag gca acc tcg gac tac cgc ggc atg cgt tca gtg gct   979
Trp Ala Tyr Glu Ala Thr Ser Asp Tyr Arg Gly Met Arg Ser Val Ala
        280                 285                 290

tta tcc atc gcc ggt tca ggc gct ttg gtg tgt gcg ttg ttg att gcc   1027
Leu Ser Ile Ala Gly Ser Gly Ala Leu Val Cys Ala Leu Leu Ile Ala
    295                 300                 305

acg gcg gtg ctc gtg ccc tgg tta ttg cac gta ttc tcc agg att gtg   1075
Thr Ala Val Leu Val Pro Trp Leu Leu His Val Phe Ser Arg Ile Val
310                 315                 320                 325
```

```
ggc ggc acc gtc cca aca ctt cag ttg gga ttg gcg ttt gca gca aag   1123
Gly Gly Thr Val Pro Thr Leu Gln Leu Gly Leu Ala Phe Ala Ala Lys
                330                 335                 340

cag aaa tct cgt tcg gcg gcg ctg atc gct gtg att ctt gct ggt tct   1171
Gln Lys Ser Arg Ser Ala Ala Leu Ile Ala Val Ile Leu Ala Gly Ser
            345                 350                 355

gca tta agc tcc gct gtt ctg cat ggc cag gca cat atc ggc acg cat   1219
Ala Leu Ser Ser Ala Val Leu His Gly Gln Ala His Ile Gly Thr His
        360                 365                 370

ttg gtg gcc gtg gct aaa ggc atg ggc ggc aca gac atg atg gtt aca   1267
Leu Val Ala Val Ala Lys Gly Met Gly Gly Thr Asp Met Met Val Thr
    375                 380                 385

gcg ctt gat ggg gaa atc ccc gcc gga atg ctg gag gaa atc tct agc   1315
Ala Leu Asp Gly Glu Ile Pro Ala Gly Met Leu Glu Glu Ile Ser Ser
390                 395                 400                 405

atc gac ggc gtg aaa act gcc atc gcg cca gcc acc acc gct gtg gaa   1363
Ile Asp Gly Val Lys Thr Ala Ile Ala Pro Ala Thr Thr Ala Val Glu
                410                 415                 420

ttg gaa gat tcc ggc aat ttc tct gtg ctc atg ctc gct gaa gaa gac   1411
Leu Glu Asp Ser Gly Asn Phe Ser Val Leu Met Leu Ala Glu Glu Asp
            425                 430                 435

gga gcc tcc gtg atg cgc gca ggc gat act ggt gca cca gct ggt ggc   1459
Gly Ala Ser Val Met Arg Ala Gly Asp Thr Gly Ala Pro Ala Gly Gly
        440                 445                 450

ctt gtt ttg ggc aga aac tct cct gac cag gat gct tac ccg gcc ggc   1507
Leu Val Leu Gly Arg Asn Ser Pro Asp Gln Asp Ala Tyr Pro Ala Gly
    455                 460                 465

cag gct gca aac atc att gtc gcg gat acc cca acg cag gcg gaa atc   1555
Gln Ala Ala Asn Ile Ile Val Ala Asp Thr Pro Thr Gln Ala Glu Ile
470                 475                 480                 485

ttc cac agc gac aac tac ttc tcc atg atc gac cca gca ctc gcc acc   1603
Phe His Ser Asp Asn Tyr Phe Ser Met Ile Asp Pro Ala Leu Ala Thr
                490                 495                 500

ggc ccc agc acc aca cgc aac gta ctg atc ctg ctc gac ggc gac tcc   1651
Gly Pro Ser Thr Thr Arg Asn Val Leu Ile Leu Leu Asp Gly Asp Ser
            505                 510                 515

aac cag gcc ccc gac aac gcc acg gcg cag gcg gta cgc aag acc att   1699
Asn Gln Ala Pro Asp Asn Ala Thr Ala Gln Ala Val Arg Lys Thr Ile
        520                 525                 530

tcg ctt ttc gac gga cga tac tcc atc acc gag ggt ttc tcc gcc cgc   1747
Ser Leu Phe Asp Gly Arg Tyr Ser Ile Thr Glu Gly Phe Ser Ala Arg
    535                 540                 545

caa aac act ttt gaa ctg gtt tcc cgc atc acc acc atg tcc aca ctg   1795
Gln Asn Thr Phe Glu Leu Val Ser Arg Ile Thr Thr Met Ser Thr Leu
550                 555                 560                 565
```

```
ctt gcc atc gtg gcc tta gcg atc gct gcc gtt ggc ctg atc aac aca   1843
Leu Ala Ile Val Ala Leu Ala Ile Ala Ala Val Gly Leu Ile Asn Thr
                570                 575                 580

gtg gca ctc acc att tct gag cgt gcc cgc gat cgt tat ttg ctg cgc   1891
Val Ala Leu Thr Ile Ser Glu Arg Ala Arg Asp Arg Tyr Leu Leu Arg
            585                 590                 595

acc att gga ctg acc tca act ggt cag att ctg gtg atg gct att gaa   1939
Thr Ile Gly Leu Thr Ser Thr Gly Gln Ile Leu Val Met Ala Ile Glu
        600                 605                 610

atg atc gcg ctc tca ttg ccg gct gcc att gtt ggt gca gtt tcg gga   1987
Met Ile Ala Leu Ser Leu Pro Ala Ala Ile Val Gly Ala Val Ser Gly
    615                 620                 625

gga ttc tta ggc aga ttc gtt gcc agt tct gcc acc aac acc gct gcg   2035
Gly Phe Leu Gly Arg Phe Val Ala Ser Ser Ala Thr Asn Thr Ala Ala
630                 635                 640                 645

acg gca cca ctt caa gta gac att ctc ggc gga acg gtt ctc gcg atg   2083
Thr Ala Pro Leu Gln Val Asp Ile Leu Gly Gly Thr Val Leu Ala Met
                650                 655                 660

gtc gca gga tct gta ctg tgc gcg ctc atc gtg ctg gcg aac aaa cga   2131
Val Ala Gly Ser Val Leu Cys Ala Leu Ile Val Leu Ala Asn Lys Arg
            665                 670                 675

cgt cgg gtg gtt tgattataaa atccaaaaat cga                        2166
Arg Arg Val Val
        680
```

<210> 248
<211> 681
<212> PRT
<213> Corynebacterium glutamicum

<400> 248

```
Leu Pro Gln Gly Pro Gly Glu Ile Ala Val Thr Thr Ala Pro Gly Ala
  1               5                  10                  15

Pro Glu Val Gly Glu His Val Ser Ile Arg Leu Ser Gln Asn Thr Glu
             20                  25                  30

Asp Thr Glu Val Leu Val Val Gly Val Val Glu Pro Ala Ala Gln Glu
         35                  40                  45

Thr Leu Gly Gly Ala Pro Phe Val Val Ala Ser Pro Asp Ala Leu Met
     50                  55                  60

Glu Trp Asn Ser Ser Gly Val Arg Gly Glu Phe Arg Val Ala Thr Ser
 65                  70                  75                  80

Asp Pro Ala Ser Leu Glu Ala Ala Ser Phe Ser Asp Ala Thr Val Val
                 85                  90                  95

Val Ala Ser Ala Glu Gly His Val Asp Lys Leu Ala Asp Ser Tyr Leu
            100                 105                 110

Gly Gln Arg Asp Arg Tyr Phe Leu Leu Leu Ala Ala Phe Val Ala Val
```

```
        115                 120                 125

Ala Ala Ala Val Ala Phe Leu Val Val Phe Ser Ala Tyr Ser Val Leu
    130                 135                 140

Thr Gly Glu Arg Val Arg Glu Phe Gly Leu Ile Arg Ser Val Gly Ala
145                 150                 155                 160

Ser Thr Pro Gln Ile Leu Gly Ser Val Ile Phe Glu Ala Gly Ile Leu
                165                 170                 175

Gly Val Val Ala Ala Gly Phe Gly Ala Pro Ala Gly Leu Met Ala Ala
            180                 185                 190

Arg Leu Leu Ala Asp Asn Ala Ala Arg Phe Gly Ile Arg Val Pro Ile
        195                 200                 205

Asp Val Ile Asp Leu Pro Ser Ser Thr Met Trp Leu Ile Ala Gly Val
    210                 215                 220

Gly Val Val Met Ser Val Ile Ala Ala Leu Pro Ala Val Phe Ser Val
225                 230                 235                 240

Cys Arg Lys Ser Ala Val Glu Ser Leu Ser Thr Pro Ala Ile Ser Arg
                245                 250                 255

Thr Ser Pro Trp Phe Gly Ala Leu Trp Leu Leu Leu Ala Gly Ile Val
            260                 265                 270

Gly Ala Gly Gly Met Trp Ala Tyr Glu Ala Thr Ser Asp Tyr Arg Gly
        275                 280                 285

Met Arg Ser Val Ala Leu Ser Ile Ala Gly Ser Gly Ala Leu Val Cys
    290                 295                 300

Ala Leu Leu Ile Ala Thr Ala Val Leu Val Pro Trp Leu Leu His Val
305                 310                 315                 320

Phe Ser Arg Ile Val Gly Gly Thr Val Pro Thr Leu Gln Leu Gly Leu
                325                 330                 335

Ala Phe Ala Ala Lys Gln Lys Ser Arg Ser Ala Ala Leu Ile Ala Val
            340                 345                 350

Ile Leu Ala Gly Ser Ala Leu Ser Ser Ala Val Leu His Gly Gln Ala
        355                 360                 365

His Ile Gly Thr His Leu Val Ala Val Ala Lys Gly Met Gly Gly Thr
    370                 375                 380

Asp Met Met Val Thr Ala Leu Asp Gly Glu Ile Pro Ala Gly Met Leu
385                 390                 395                 400

Glu Glu Ile Ser Ser Ile Asp Gly Val Lys Thr Ala Ile Ala Pro Ala
                405                 410                 415

Thr Thr Ala Val Glu Leu Glu Asp Ser Gly Asn Phe Ser Val Leu Met
            420                 425                 430

Leu Ala Glu Glu Asp Gly Ala Ser Val Met Arg Ala Gly Asp Thr Gly
        435                 440                 445
```

```
Ala Pro Ala Gly Gly Leu Val Leu Gly Arg Asn Ser Pro Asp Gln Asp
    450                 455                 460

Ala Tyr Pro Ala Gly Gln Ala Ala Asn Ile Ile Val Ala Asp Thr Pro
465                 470                 475                 480

Thr Gln Ala Glu Ile Phe His Ser Asp Asn Tyr Phe Ser Met Ile Asp
                485                 490                 495

Pro Ala Leu Ala Thr Gly Pro Ser Thr Thr Arg Asn Val Leu Ile Leu
            500                 505                 510

Leu Asp Gly Asp Ser Asn Gln Ala Pro Asp Asn Ala Thr Ala Gln Ala
        515                 520                 525

Val Arg Lys Thr Ile Ser Leu Phe Asp Gly Arg Tyr Ser Ile Thr Glu
    530                 535                 540

Gly Phe Ser Ala Arg Gln Asn Thr Phe Glu Leu Val Ser Arg Ile Thr
545                 550                 555                 560

Thr Met Ser Thr Leu Leu Ala Ile Val Ala Leu Ala Ile Ala Ala Val
                565                 570                 575

Gly Leu Ile Asn Thr Val Ala Leu Thr Ile Ser Glu Arg Ala Arg Asp
            580                 585                 590

Arg Tyr Leu Leu Arg Thr Ile Gly Leu Thr Ser Thr Gly Gln Ile Leu
        595                 600                 605

Val Met Ala Ile Glu Met Ile Ala Leu Ser Leu Pro Ala Ala Ile Val
    610                 615                 620

Gly Ala Val Ser Gly Gly Phe Leu Gly Arg Phe Val Ala Ser Ser Ala
625                 630                 635                 640

Thr Asn Thr Ala Ala Thr Ala Pro Leu Gln Val Asp Ile Leu Gly Gly
                645                 650                 655

Thr Val Leu Ala Met Val Ala Gly Ser Val Leu Cys Ala Leu Ile Val
            660                 665                 670

Leu Ala Asn Lys Arg Arg Arg Val Val
        675                 680
```

<210> 249
<211> 1149
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1126)
<223> RXN00496

<400> 249
ctgcagagat ggtgggcagc accccaggtg ctgtacgagt tgcccaacac agggcactca 60

cgacacttcg aagcacactt gagcagcagg agaacaagta atg act cga cgt cta 115

```
                                                    Met Thr Arg Arg Leu
                                                      1               5

cat ggt ggt gag cag gat ggc cag gaa cac gtt aaa gga cag cta aag   163
His Gly Gly Glu Gln Asp Gly Gln Glu His Val Lys Gly Gln Leu Lys
                  10                  15                  20

cag ctg ttc gac gac gac gcg ttc ttg act gac ctg tcc cgc ggc gtt   211
Gln Leu Phe Asp Asp Asp Ala Phe Leu Thr Asp Leu Ser Arg Gly Val
             25                  30                  35

gat ccc tca gag ggc gat gac gcc ctc gct ggc ctc ctc ctc gat tta   259
Asp Pro Ser Glu Gly Asp Asp Ala Leu Ala Gly Leu Leu Leu Asp Leu
         40                  45                  50

aca aag gaa gct cag gag ccg ccg gca aca atg ccg gat tgg tct act   307
Thr Lys Glu Ala Gln Glu Pro Pro Ala Thr Met Pro Asp Trp Ser Thr
     55                  60                  65

ttg ctc cct gga att ttg gat cag gat cag gat ttg cca gtg gaa tcc   355
Leu Leu Pro Gly Ile Leu Asp Gln Asp Gln Asp Leu Pro Val Glu Ser
 70                  75                  80                  85

act tcg gac acc acg gtt atg cag gca tca aac cct gca acc caa gaa   403
Thr Ser Asp Thr Thr Val Met Gln Ala Ser Asn Pro Ala Thr Gln Glu
                 90                  95                 100

ttc gca cct gtt tct att tct gat acc ccc aac act gca act aat tca   451
Phe Ala Pro Val Ser Ile Ser Asp Thr Pro Asn Thr Ala Thr Asn Ser
            105                 110                 115

gct gat gca gat gag tcc gca act gtt gtt cca ctt gca gca cgc cgt   499
Ala Asp Ala Asp Glu Ser Ala Thr Val Val Pro Leu Ala Ala Arg Arg
        120                 125                 130

gag aag cgt gcc aag agc gga tca agc ggg gtt cat tca ctg gat gct   547
Glu Lys Arg Ala Lys Ser Gly Ser Ser Gly Val His Ser Leu Asp Ala
    135                 140                 145

tcg gca acc cag cgc aaa tct cac cca ttc ctt agc ggt ttg gtg ggt   595
Ser Ala Thr Gln Arg Lys Ser His Pro Phe Leu Ser Gly Leu Val Gly
150                 155                 160                 165

gct gca gct gca act cta gtc atc gca ggc ggt gga gca gca gtg tac   643
Ala Ala Ala Ala Thr Leu Val Ile Ala Gly Gly Gly Ala Ala Val Tyr
                170                 175                 180

aac gct gat gaa aac tcc ccg ttg tat ggc atg aat cag cag ctg ttt   691
Asn Ala Asp Glu Asn Ser Pro Leu Tyr Gly Met Asn Gln Gln Leu Phe
            185                 190                 195

ggc aat caa gat tct cca agc gtg gtg gag ctt gcc tcc acg ctg gaa   739
Gly Asn Gln Asp Ser Pro Ser Val Val Glu Leu Ala Ser Thr Leu Glu
        200                 205                 210

gaa gtt gat agt cgt aca gct agt ggc gat gtg gaa ggg gca cgt gct   787
Glu Val Asp Ser Arg Thr Ala Ser Gly Asp Val Glu Gly Ala Arg Ala
    215                 220                 225

cta ctc gag cag gct cga gca atg ctg gat ggc atg gca cct cct cga   835
Leu Leu Glu Gln Ala Arg Ala Met Leu Asp Gly Met Ala Pro Pro Arg
```

```
230                 235                 240                 245

aag gcg ccg tcg gag gca acc cga acg gtt gaa tct gaa cca ggt act   883
Lys Ala Pro Ser Glu Ala Thr Arg Thr Val Glu Ser Glu Pro Gly Thr
                250                 255                 260

cag acg ttg act gca acg gtt act gaa tcc gca agt ccg gaa cca ccg   931
Gln Thr Leu Thr Ala Thr Val Thr Glu Ser Ala Ser Pro Glu Pro Pro
            265                 270                 275

gtc acg gaa act caa act gtt acc tcc acc gag gta cag aca gtg aca   979
Val Thr Glu Thr Gln Thr Val Thr Ser Thr Glu Val Gln Thr Val Thr
        280                 285                 290

acc act gcg gtt gct cca ccg gtc tgg act cct aat cca gag cca aca   1027
Thr Thr Ala Val Ala Pro Pro Val Trp Thr Pro Asn Pro Glu Pro Thr
    295                 300                 305

acc aca gct gcc ccg act tct acg cct tca act ggt ggc ggt gag gga   1075
Thr Thr Ala Ala Pro Thr Ser Thr Pro Ser Thr Gly Gly Gly Glu Gly
310                 315                 320                 325

acc ggc aat gat ggt gac tct gga ctt gtg cca cct cag act cct gga   1123
Thr Gly Asn Asp Gly Asp Ser Gly Leu Val Pro Pro Gln Thr Pro Gly
                330                 335                 340

aac taggtaaaaa tataaaaact gct                                    1149
Asn
```

<210> 250
<211> 342
<212> PRT
<213> Corynebacterium glutamicum

<400> 250

```
Met Thr Arg Arg Leu His Gly Gly Glu Gln Asp Gly Gln Glu His Val
  1               5                  10                  15

Lys Gly Gln Leu Lys Gln Leu Phe Asp Asp Asp Ala Phe Leu Thr Asp
             20                  25                  30

Leu Ser Arg Gly Val Asp Pro Ser Glu Gly Asp Asp Ala Leu Ala Gly
         35                  40                  45

Leu Leu Leu Asp Leu Thr Lys Glu Ala Gln Glu Pro Pro Ala Thr Met
     50                  55                  60

Pro Asp Trp Ser Thr Leu Leu Pro Gly Ile Leu Asp Gln Asp Gln Asp
 65                  70                  75                  80

Leu Pro Val Glu Ser Thr Ser Asp Thr Thr Val Met Gln Ala Ser Asn
                 85                  90                  95

Pro Ala Thr Gln Glu Phe Ala Pro Val Ser Ile Ser Asp Thr Pro Asn
            100                 105                 110

Thr Ala Thr Asn Ser Ala Asp Ala Asp Glu Ser Ala Thr Val Val Pro
        115                 120                 125
```

```
Leu Ala Ala Arg Arg Glu Lys Arg Ala Lys Ser Gly Ser Ser Gly Val
    130                 135                 140

His Ser Leu Asp Ala Ser Ala Thr Gln Arg Lys Ser His Pro Phe Leu
145                 150                 155                 160

Ser Gly Leu Val Gly Ala Ala Ala Ala Thr Leu Val Ile Ala Gly Gly
                165                 170                 175

Gly Ala Ala Val Tyr Asn Ala Asp Glu Asn Ser Pro Leu Tyr Gly Met
            180                 185                 190

Asn Gln Gln Leu Phe Gly Asn Gln Asp Ser Pro Ser Val Val Glu Leu
        195                 200                 205

Ala Ser Thr Leu Glu Glu Val Asp Ser Arg Thr Ala Ser Gly Asp Val
    210                 215                 220

Glu Gly Ala Arg Ala Leu Leu Glu Gln Ala Arg Ala Met Leu Asp Gly
225                 230                 235                 240

Met Ala Pro Pro Arg Lys Ala Pro Ser Glu Ala Thr Arg Thr Val Glu
                245                 250                 255

Ser Glu Pro Gly Thr Gln Thr Leu Thr Ala Thr Val Thr Glu Ser Ala
            260                 265                 270

Ser Pro Glu Pro Pro Val Thr Glu Thr Gln Thr Val Thr Ser Thr Glu
        275                 280                 285

Val Gln Thr Val Thr Thr Thr Ala Val Ala Pro Pro Val Trp Thr Pro
    290                 295                 300

Asn Pro Glu Pro Thr Thr Thr Ala Ala Pro Thr Ser Thr Pro Ser Thr
305                 310                 315                 320

Gly Gly Gly Glu Gly Thr Gly Asn Asp Gly Asp Ser Gly Leu Val Pro
                325                 330                 335

Pro Gln Thr Pro Gly Asn
            340
```

<210> 251
<211> 502
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(502)
<223> FRXA00496

<400> 251
ctgcagagat ggtgggcagc accccaggtg ctgtacgagt tgcccaacac agggcactca 60

cgacacttcg aagcacactt gagcagcagg agaacaagta atg act cga cgt cta 115
Met Thr Arg Arg Leu
1 5

cat ggt ggt gag cag gat ggc cag gaa cac gtt aaa gga cag cta aag 163

```
His Gly Gly Glu Gln Asp Gly Gln Glu His Val Lys Gly Gln Leu Lys
                10                  15                  20

cag ctg ttc gac gac gac gcg ttc ttg act gac ctg tcc cgc ggc gtt   211
Gln Leu Phe Asp Asp Asp Ala Phe Leu Thr Asp Leu Ser Arg Gly Val
            25                  30                  35

gat ccc tca gag ggc gat gac gcc ctc gct ggc ctc ctc ctc gat tta   259
Asp Pro Ser Glu Gly Asp Asp Ala Leu Ala Gly Leu Leu Leu Asp Leu
        40                  45                  50

aca aag gaa gct cag gag ccg ccg gca aca atg ccg gat tgg tct act   307
Thr Lys Glu Ala Gln Glu Pro Pro Ala Thr Met Pro Asp Trp Ser Thr
    55                  60                  65

ttg ctc cct gga att ttg gat cag gat cag gat ttg cca gtg gaa tcc   355
Leu Leu Pro Gly Ile Leu Asp Gln Asp Gln Asp Leu Pro Val Glu Ser
70                  75                  80                  85

act tcg gac acc acg gtt atg cag gca tca aac cct gca acc caa gaa   403
Thr Ser Asp Thr Thr Val Met Gln Ala Ser Asn Pro Ala Thr Gln Glu
                90                  95                  100

ttc gca cct gtt tct att tct gat acc ccc aac act gca act aat tca   451
Phe Ala Pro Val Ser Ile Ser Asp Thr Pro Asn Thr Ala Thr Asn Ser
            105                 110                 115

gct gat gca gat gag tcc gca act gtt gtt cca ctt gca gca cgc cgt   499
Ala Asp Ala Asp Glu Ser Ala Thr Val Val Pro Leu Ala Ala Arg Arg
        120                 125                 130

gag                                                               502
Glu
```

Replacement Sheet (Rule 26)

<210> 252
<211> 134
<212> PRT
<213> Corynebacterium glutamicum

<400> 252

```
Met Thr Arg Arg Leu His Gly Gly Glu Gln Asp Gly Gln Glu His Val
  1               5                  10                  15

Lys Gly Gln Leu Lys Gln Leu Phe Asp Asp Asp Ala Phe Leu Thr Asp
            20                  25                  30

Leu Ser Arg Gly Val Asp Pro Ser Glu Gly Asp Asp Ala Leu Ala Gly
        35                  40                  45

Leu Leu Leu Asp Leu Thr Lys Glu Ala Gln Glu Pro Pro Ala Thr Met
    50                  55                  60

Pro Asp Trp Ser Thr Leu Leu Pro Gly Ile Leu Asp Gln Asp Gln Asp
65                  70                  75                  80

Leu Pro Val Glu Ser Thr Ser Asp Thr Thr Val Met Gln Ala Ser Asn
                85                  90                  95

Pro Ala Thr Gln Glu Phe Ala Pro Val Ser Ile Ser Asp Thr Pro Asn
```

```
            100                 105                 110

Thr Ala Thr Asn Ser Ala Asp Ala Asp Glu Ser Ala Thr Val Val Pro
        115                 120                 125

Leu Ala Ala Arg Arg Glu
    130


<210> 253
<211> 1845
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1822)
<223> RXN00503

<400> 253
aatccacgaa ggtgcccaag aatcaccaat ttcggtcgga actgatcctt ctttgtccgt 60

tgagacccca caggtgtttt aaacatttag tattagttcc atg aaa cca gtc ttc   115
                                            Met Lys Pro Val Phe
                                              1               5

tcc gtt gac caa atc cga cgc gca gaa aac acc ctt ttt gag ctt cag   163
Ser Val Asp Gln Ile Arg Arg Ala Glu Asn Thr Leu Phe Glu Leu Gln
                10                  15                  20

gca gat ccg gat gag ctg atg atc tcc gcg gca tcg gcg gtg gcc gat   211
Ala Asp Pro Asp Glu Leu Met Ile Ser Ala Ala Ser Ala Val Ala Asp
            25                  30                  35

gtc gcg ttg gca atg gtg gac ggc ccc gct cca gcg gtc tcc agt gag   259
Val Ala Leu Ala Met Val Asp Gly Pro Ala Pro Ala Val Ser Ser Glu
        40                  45                  50

gag tca atc ctg ctg ctg gtc ggc ccc ggt ggc aac ggt ggc gac gcc   307
Glu Ser Ile Leu Leu Leu Val Gly Pro Gly Gly Asn Gly Gly Asp Ala
    55                  60                  65

ttg tat gca ggc gcg ttc ctt gca gaa gaa ggc cac cac gtt gat gct   355
Leu Tyr Ala Gly Ala Phe Leu Ala Glu Glu Gly His His Val Asp Ala
70                  75                  80                  85

ttg ctg ttg gga aac ggc aaa gtc cat caa tca gca ttg gca tat tat   403
Leu Leu Leu Gly Asn Gly Lys Val His Gln Ser Ala Leu Ala Tyr Tyr
                90                  95                  100

gag tct ttg ggc ggg cag atc att tcc gat ttt ccc cct cac tac ctc   451
Glu Ser Leu Gly Gly Gln Ile Ile Ser Asp Phe Pro Pro His Tyr Leu
            105                 110                 115

tac cgc ctg gtg att gat ggt ttg ttt ggc atc ggt ggt cgg gga ggg   499
Tyr Arg Leu Val Ile Asp Gly Leu Phe Gly Ile Gly Gly Arg Gly Gly
        120                 125                 130

ctc acc cca gag ctg gcc agt ttg gtg gag tct ttt tcc gct tca ggt   547
Leu Thr Pro Glu Leu Ala Ser Leu Val Glu Ser Phe Ser Ala Ser Gly
    135                 140                 145
```

```
atc ccc att ttg gcg att gat gtg ccg tct ggc gtg cat gcc gat agt   595
Ile Pro Ile Leu Ala Ile Asp Val Pro Ser Gly Val His Ala Asp Ser
150                 155                 160                 165

ggt gaa ctg ccg ccc ggc gtg atg gtg acg gtg gaa gga ttt gat aat   643
Gly Glu Leu Pro Pro Gly Val Met Val Thr Val Glu Gly Phe Asp Asn
                170                 175                 180

gat gca ccg atg gcg cgt cag aaa att ccg gca cac att gac gct gat   691
Asp Ala Pro Met Ala Arg Gln Lys Ile Pro Ala His Ile Asp Ala Asp
            185                 190                 195

gtc acg atc acg ttt ggc ggt ttg aga cgc gcc cac gcg gtc agt cct   739
Val Thr Ile Thr Phe Gly Gly Leu Arg Arg Ala His Ala Val Ser Pro
        200                 205                 210

gcg tgt ggt gaa gtg ctc tgt gct gat atc aac atc gct ggt ggc ggc   787
Ala Cys Gly Glu Val Leu Cys Ala Asp Ile Asn Ile Ala Gly Gly Gly
    215                 220                 225

gga aaa tcg ctg tcc gct gag ttg agt cag gtg cag gca gaa gac gcg   835
Gly Lys Ser Leu Ser Ala Glu Leu Ser Gln Val Gln Ala Glu Asp Ala
230                 235                 240                 245

acc ccg cag atg ttt gcc tcc aag gcg tat caa cgg aaa gat tcg ctt   883
Thr Pro Gln Met Phe Ala Ser Lys Ala Tyr Gln Arg Lys Asp Ser Leu
                250                 255                 260

ttt gag cgc gcg aat ctc aaa gct acg gcg cca cat atc cat agg atc   931
Phe Glu Arg Ala Asn Leu Lys Ala Thr Ala Pro His Ile His Arg Ile
            265                 270                 275

ggc cag cac ttt acc gtg ttg aac atg gag cct ggc ccg gat cat gat   979
Gly Gln His Phe Thr Val Leu Asn Met Glu Pro Gly Pro Asp His Asp
        280                 285                 290

aaa tac agt ggc gga att gtc ggc att gtt gca ggt agt ggc acc tat  1027
Lys Tyr Ser Gly Gly Ile Val Gly Ile Val Ala Gly Ser Gly Thr Tyr
    295                 300                 305

cca ggt gct gct gtg ctg tcg gtg aag gcg gct gtc agg gcc aca agc  1075
Pro Gly Ala Ala Val Leu Ser Val Lys Ala Ala Val Arg Ala Thr Ser
310                 315                 320                 325

gcc atg gtt cga tac gtt ggc cct gcg tta aat ttt gtc atc cag tcg  1123
Ala Met Val Arg Tyr Val Gly Pro Ala Leu Asn Phe Val Ile Gln Ser
                330                 335                 340

ctg ccg gag gtc gtc gca acg caa tca ctt gcc acc gcc ggc cgc gtg  1171
Leu Pro Glu Val Val Ala Thr Gln Ser Leu Ala Thr Ala Gly Arg Val
            345                 350                 355

caa gcg tgg gtg cac ggc ccc gga cgc ggg ctg gag gct gag caa tca  1219
Gln Ala Trp Val His Gly Pro Gly Arg Gly Leu Glu Ala Glu Gln Ser
        360                 365                 370

gcc gag ctt gcg gag ctt ttg agc cgg cct gag cct gtg ctt atc gac  1267
Ala Glu Leu Ala Glu Leu Leu Ser Arg Pro Glu Pro Val Leu Ile Asp
    375                 380                 385
```

```
gcc gac agc ctc tca tta ctc cag ctc tca gcg gag ctt cgg cag gcg   1315
Ala Asp Ser Leu Ser Leu Leu Gln Leu Ser Ala Glu Leu Arg Gln Ala
390                 395                 400                 405

ttg cgc gag cga aaa gca cca acg gtg ctc act ccg cac aag ggc gaa   1363
Leu Arg Glu Arg Lys Ala Pro Thr Val Leu Thr Pro His Lys Gly Glu
                410                 415                 420

ttt gaa cgc atc gca gca gaa tta cgc tct gaa ggc gtc gag att ccc   1411
Phe Glu Arg Ile Ala Ala Glu Leu Arg Ser Glu Gly Val Glu Ile Pro
            425                 430                 435

caa gcg gac aaa gat ccc att ggt gct gcg caa gcg tta gct aaa gaa   1459
Gln Ala Asp Lys Asp Pro Ile Gly Ala Ala Gln Ala Leu Ala Lys Glu
        440                 445                 450

ttt gat tgt tgc gta ctg ctc aag ggg aaa tac acc gtc att gca gct   1507
Phe Asp Cys Cys Val Leu Leu Lys Gly Lys Tyr Thr Val Ile Ala Ala
    455                 460                 465

cac gac ttt gtg cat gcg atc aac gct ggg cat tcc tgg ttg gct aca   1555
His Asp Phe Val His Ala Ile Asn Ala Gly His Ser Trp Leu Ala Thr
470                 475                 480                 485

cct ggc tct ggc gat gtg ttg tca ggt ctt gtc ggt gca cac ttg gct   1603
Pro Gly Ser Gly Asp Val Leu Ser Gly Leu Val Gly Ala His Leu Ala
                490                 495                 500

caa agc tac gca gaa tta aac cgc ttg ccg gag ttt ttc ccc gat gtg   1651
Gln Ser Tyr Ala Glu Leu Asn Arg Leu Pro Glu Phe Phe Pro Asp Val
            505                 510                 515

acc ttg tct gat tcg gcg att tac acc cag att gca cct gct gcg acc   1699
Thr Leu Ser Asp Ser Ala Ile Tyr Thr Gln Ile Ala Pro Ala Ala Thr
        520                 525                 530

atc cac gcg gtt gct gct ggg ttg gcc gca cga acc gaa ttt ggg ttt   1747
Ile His Ala Val Ala Ala Gly Leu Ala Ala Arg Thr Glu Phe Gly Phe
    535                 540                 545

gcg ccg acc tcc gca agt ttg atc gct gat gcc atc cct gca gcg acc   1795
Ala Pro Thr Ser Ala Ser Leu Ile Ala Asp Ala Ile Pro Ala Ala Thr
550                 555                 560                 565

gcc aag gtg gat ttg aag cga att gtc tagctctgca tgaattccgt         1842
Ala Lys Val Asp Leu Lys Arg Ile Val
                570

atg                                                              1845
```

<210> 254
<211> 574
<212> PRT
<213> Corynebacterium glutamicum

<400> 254

```
Met Lys Pro Val Phe Ser Val Asp Gln Ile Arg Arg Ala Glu Asn Thr
  1               5                  10                  15

Leu Phe Glu Leu Gln Ala Asp Pro Asp Glu Leu Met Ile Ser Ala Ala
```

```
                20                  25                  30

Ser Ala Val Ala Asp Val Ala Leu Ala Met Val Asp Gly Pro Ala Pro
          35                  40                  45

Ala Val Ser Ser Glu Glu Ser Ile Leu Leu Leu Val Gly Pro Gly Gly
      50                  55                  60

Asn Gly Gly Asp Ala Leu Tyr Ala Gly Ala Phe Leu Ala Glu Glu Gly
 65                  70                  75                  80

His His Val Asp Ala Leu Leu Leu Gly Asn Gly Lys Val His Gln Ser
                 85                  90                  95

Ala Leu Ala Tyr Tyr Glu Ser Leu Gly Gly Gln Ile Ile Ser Asp Phe
            100                 105                 110

Pro Pro His Tyr Leu Tyr Arg Leu Val Ile Asp Gly Leu Phe Gly Ile
        115                 120                 125

Gly Gly Arg Gly Gly Leu Thr Pro Glu Leu Ala Ser Leu Val Glu Ser
    130                 135                 140

Phe Ser Ala Ser Gly Ile Pro Ile Leu Ala Ile Asp Val Pro Ser Gly
145                 150                 155                 160

Val His Ala Asp Ser Gly Glu Leu Pro Pro Gly Val Met Val Thr Val
                165                 170                 175

Glu Gly Phe Asp Asn Asp Ala Pro Met Ala Arg Gln Lys Ile Pro Ala
            180                 185                 190

His Ile Asp Ala Asp Val Thr Ile Thr Phe Gly Gly Leu Arg Arg Ala
        195                 200                 205

His Ala Val Ser Pro Ala Cys Gly Glu Val Leu Cys Ala Asp Ile Asn
    210                 215                 220

Ile Ala Gly Gly Gly Gly Lys Ser Leu Ser Ala Glu Leu Ser Gln Val
225                 230                 235                 240

Gln Ala Glu Asp Ala Thr Pro Gln Met Phe Ala Ser Lys Ala Tyr Gln
                245                 250                 255

Arg Lys Asp Ser Leu Phe Glu Arg Ala Asn Leu Lys Ala Thr Ala Pro
            260                 265                 270

His Ile His Arg Ile Gly Gln His Phe Thr Val Leu Asn Met Glu Pro
        275                 280                 285

Gly Pro Asp His Asp Lys Tyr Ser Gly Gly Ile Val Gly Ile Val Ala
    290                 295                 300

Gly Ser Gly Thr Tyr Pro Gly Ala Ala Val Leu Ser Val Lys Ala Ala
305                 310                 315                 320

Val Arg Ala Thr Ser Ala Met Val Arg Tyr Val Gly Pro Ala Leu Asn
                325                 330                 335

Phe Val Ile Gln Ser Leu Pro Glu Val Val Ala Thr Gln Ser Leu Ala
            340                 345                 350
```

```
Thr Ala Gly Arg Val Gln Ala Trp Val His Gly Pro Gly Arg Gly Leu
        355                 360                 365

Glu Ala Glu Gln Ser Ala Glu Leu Ala Glu Leu Leu Ser Arg Pro Glu
    370                 375                 380

Pro Val Leu Ile Asp Ala Asp Ser Leu Ser Leu Leu Gln Leu Ser Ala
385                 390                 395                 400

Glu Leu Arg Gln Ala Leu Arg Glu Arg Lys Ala Pro Thr Val Leu Thr
                405                 410                 415

Pro His Lys Gly Glu Phe Glu Arg Ile Ala Ala Glu Leu Arg Ser Glu
            420                 425                 430

Gly Val Glu Ile Pro Gln Ala Asp Lys Asp Pro Ile Gly Ala Ala Gln
        435                 440                 445

Ala Leu Ala Lys Glu Phe Asp Cys Cys Val Leu Leu Lys Gly Lys Tyr
    450                 455                 460

Thr Val Ile Ala Ala His Asp Phe Val His Ala Ile Asn Ala Gly His
465                 470                 475                 480

Ser Trp Leu Ala Thr Pro Gly Ser Gly Asp Val Leu Ser Gly Leu Val
                485                 490                 495

Gly Ala His Leu Ala Gln Ser Tyr Ala Glu Leu Asn Arg Leu Pro Glu
            500                 505                 510

Phe Phe Pro Asp Val Thr Leu Ser Asp Ser Ala Ile Tyr Thr Gln Ile
        515                 520                 525

Ala Pro Ala Ala Thr Ile His Ala Val Ala Ala Gly Leu Ala Ala Arg
    530                 535                 540

Thr Glu Phe Gly Phe Ala Pro Thr Ser Ala Ser Leu Ile Ala Asp Ala
545                 550                 555                 560

Ile Pro Ala Ala Thr Ala Lys Val Asp Leu Lys Arg Ile Val
                565                 570
```

<210> 255
<211> 543
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(520)
<223> RXN00504

<400> 255
aaggtggatt tgaagcgaat tgtctagctc tgcatgaatt ccgtatgaat tcttttcttt 60

caagtggccg agatgtgaag cgcacggtta attgagaggc atg acc tac gga ttt 115
                                                Met Thr Tyr Gly Phe
                                                  1   5

```
ctt gtc aac aca gat ctc acc cac cgc gcg att gac ttt gat tta gaa   163
Leu Val Asn Thr Asp Leu Thr His Arg Ala Ile Asp Phe Asp Leu Glu
                10                  15                  20

aac gct gcg aag ttc ctc ggc ggt gcc gat gat ggc cgc gtc gct gtc   211
Asn Ala Ala Lys Phe Leu Gly Gly Ala Asp Asp Gly Arg Val Ala Val
            25                  30                  35

gct ttc caa gag gat ggc acc ttg tac gcc gct ctc tac agc gcc agc   259
Ala Phe Gln Glu Asp Gly Thr Leu Tyr Ala Ala Leu Tyr Ser Ala Ser
        40                  45                  50

gca aaa gat gag ggt gcc gca gca aac cca gta gca tcc ctt ggc cgc   307
Ala Lys Asp Glu Gly Ala Ala Ala Asn Pro Val Ala Ser Leu Gly Arg
    55                  60                  65

aac gcc gct gct acc ggt gat ggc tcc ttc ttc tct gat ccg acc act   355
Asn Ala Ala Ala Thr Gly Asp Gly Ser Phe Phe Ser Asp Pro Thr Thr
70                  75                  80                  85

gca atc tgt ggc cct gtg atc ttc gtg ggg gcc gaa ggc gaa gac atc   403
Ala Ile Cys Gly Pro Val Ile Phe Val Gly Ala Glu Gly Glu Asp Ile
                90                  95                  100

acg ttg gat gaa att gag cga att aag gac ggc att cgc gcc gct cgt   451
Thr Leu Asp Glu Ile Glu Arg Ile Lys Asp Gly Ile Arg Ala Ala Arg
            105                 110                 115

aac tac cgc gat gat tat cca gag gaa ttc aac ctg tgg cgc aac gct   499
Asn Tyr Arg Asp Asp Tyr Pro Glu Glu Phe Asn Leu Trp Arg Asn Ala
        120                 125                 130

gta tat aac ctg cgt acg gct taaagtttgg ctgccatgtg aat             543
Val Tyr Asn Leu Arg Thr Ala
    135                 140
```

<210> 256
<211> 140
<212> PRT
<213> Corynebacterium glutamicum

<400> 256

```
Met Thr Tyr Gly Phe Leu Val Asn Thr Asp Leu Thr His Arg Ala Ile
  1               5                  10                  15

Asp Phe Asp Leu Glu Asn Ala Ala Lys Phe Leu Gly Gly Ala Asp Asp
            20                  25                  30

Gly Arg Val Ala Val Ala Phe Gln Glu Asp Gly Thr Leu Tyr Ala Ala
        35                  40                  45

Leu Tyr Ser Ala Ser Ala Lys Asp Glu Gly Ala Ala Ala Asn Pro Val
    50                  55                  60

Ala Ser Leu Gly Arg Asn Ala Ala Ala Thr Gly Asp Gly Ser Phe Phe
65                  70                  75                  80

Ser Asp Pro Thr Thr Ala Ile Cys Gly Pro Val Ile Phe Val Gly Ala
                85                  90                  95
```

```
Glu Gly Glu Asp Ile Thr Leu Asp Glu Ile Glu Arg Ile Lys Asp Gly
            100                 105                 110

Ile Arg Ala Ala Arg Asn Tyr Arg Asp Asp Tyr Pro Glu Glu Phe Asn
        115                 120                 125

Leu Trp Arg Asn Ala Val Tyr Asn Leu Arg Thr Ala
    130                 135                 140


<210> 257
<211> 346
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(346)
<223> FRXA00504

<400> 257
aaggtggatt tgaagcgaat tgtctagctc tgcatgaatt ccgtatgaat tcttttcttt 60

caagtggccg agatgtgaag cgcacggtta attgagaggc atg acc tac gga ttt   115
                                               Met Thr Tyr Gly Phe
                                                 1               5

ctt gtc aac aca gat ctc acc cac cgc gcg att gac ttt gat tta gaa   163
Leu Val Asn Thr Asp Leu Thr His Arg Ala Ile Asp Phe Asp Leu Glu
                10                  15                  20

aac gct gcg aag ttc ctc ggc ggt gcc gat gat ggc cgc gtc gct gtc   211
Asn Ala Ala Lys Phe Leu Gly Gly Ala Asp Asp Gly Arg Val Ala Val
            25                  30                  35

gct ttc caa gag gat ggc acc ttg tac gcc gct ctc tac agc gcc agc   259
Ala Phe Gln Glu Asp Gly Thr Leu Tyr Ala Ala Leu Tyr Ser Ala Ser
        40                  45                  50

gca aaa gat gag ggt gcc gca gca aac cca gta gca tcc ctt ggc cgc   307
Ala Lys Asp Glu Gly Ala Ala Ala Asn Pro Val Ala Ser Leu Gly Arg
    55                  60                  65

aac gcc gct gct acc ggt gat ggc tcc ttc ttc tct gat               346
Asn Ala Ala Ala Thr Gly Asp Gly Ser Phe Phe Ser Asp
70                  75                  80


<210> 258
<211> 82
<212> PRT
<213> Corynebacterium glutamicum

<400> 258
Met Thr Tyr Gly Phe Leu Val Asn Thr Asp Leu Thr His Arg Ala Ile
  1               5                  10                  15

Asp Phe Asp Leu Glu Asn Ala Ala Lys Phe Leu Gly Gly Ala Asp Asp
            20                  25                  30

Gly Arg Val Ala Val Ala Phe Gln Glu Asp Gly Thr Leu Tyr Ala Ala
```

```
         35                  40                  45

Leu Tyr Ser Ala Ser Ala Lys Asp Glu Gly Ala Ala Ala Asn Pro Val
     50                  55                  60

Ala Ser Leu Gly Arg Asn Ala Ala Ala Thr Gly Asp Gly Ser Phe Phe
 65                  70                  75                  80

Ser Asp



<210> 259
<211> 618
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(595)
<223> RXN00505

<400> 259
ttgcggagcg tttagacacc attaactatg aggtagtgtg ccgaccaacc ggccgaactg 60

tccgcgcata tgtttaagtg aatacgttta aggagcagca atg aaa tct gag ttt   115
                                            Met Lys Ser Glu Phe
                                              1               5

ccg gta tcc ggc acg agg cgt ttt gag cat gcc gca gat acc caa aat   163
Pro Val Ser Gly Thr Arg Arg Phe Glu His Ala Ala Asp Thr Gln Asn
                10                  15                  20

ttt ggg gaa gaa tta ggc agg cat cta gaa gct ggc gat gtg gtg att   211
Phe Gly Glu Glu Leu Gly Arg His Leu Glu Ala Gly Asp Val Val Ile
            25                  30                  35

ttg gac ggc ccg ctg ggt gct gga aaa acc aca ttt act caa ggt atc   259
Leu Asp Gly Pro Leu Gly Ala Gly Lys Thr Thr Phe Thr Gln Gly Ile
        40                  45                  50

gct cgt gga ttg cag gtg aag ggg cgg gtg aca tcg ccg acg ttt gtg   307
Ala Arg Gly Leu Gln Val Lys Gly Arg Val Thr Ser Pro Thr Phe Val
    55                  60                  65

atc gcg agg gaa cac cgc tcg gaa atc ggt ggg cca gat ctg atc cac   355
Ile Ala Arg Glu His Arg Ser Glu Ile Gly Gly Pro Asp Leu Ile His
70                  75                  80                  85

atg gat gcc tac cga ttg ctg ggc gaa gac agc gag gat gct gat ccg   403
Met Asp Ala Tyr Arg Leu Leu Gly Glu Asp Ser Glu Asp Ala Asp Pro
                90                  95                 100

atc ggt gcg ctg gac tct ttg gat ttg gat acc gat ttg gac ttg gct   451
Ile Gly Ala Leu Asp Ser Leu Asp Leu Asp Thr Asp Leu Asp Leu Ala
            105                 110                 115

gtg gtt gtt gcg gaa tgg ggc ggt ggc ttg gtg gag cag atc gct gac   499
Val Val Val Ala Glu Trp Gly Gly Gly Leu Val Glu Gln Ile Ala Asp
        120                 125                 130
```

```
tcg tat ctt ttg att acc att gat cga gag acc gct gtg cag gaa gac   547
Ser Tyr Leu Leu Ile Thr Ile Asp Arg Glu Thr Ala Val Gln Glu Asp
    135                 140                 145

ccg gaa tct gag gct cga att ttc cat tgg gaa tgg cgc gaa ggc cgc   595
Pro Glu Ser Glu Ala Arg Ile Phe His Trp Glu Trp Arg Glu Gly Arg
150             155                 160                 165

tgagaaagtt ttccacgcta aaa                                        618
```

<210> 260
<211> 165
<212> PRT
<213> Corynebacterium glutamicum

<400> 260

```
Met Lys Ser Glu Phe Pro Val Ser Gly Thr Arg Arg Phe Glu His Ala
  1               5                  10                  15

Ala Asp Thr Gln Asn Phe Gly Glu Glu Leu Gly Arg His Leu Glu Ala
             20                  25                  30

Gly Asp Val Val Ile Leu Asp Gly Pro Leu Gly Ala Gly Lys Thr Thr
         35                  40                  45

Phe Thr Gln Gly Ile Ala Arg Gly Leu Gln Val Lys Gly Arg Val Thr
     50                  55                  60

Ser Pro Thr Phe Val Ile Ala Arg Glu His Arg Ser Glu Ile Gly Gly
 65                  70                  75                  80

Pro Asp Leu Ile His Met Asp Ala Tyr Arg Leu Leu Gly Glu Asp Ser
                 85                  90                  95

Glu Asp Ala Asp Pro Ile Gly Ala Leu Asp Ser Leu Asp Leu Asp Thr
            100                 105                 110

Asp Leu Asp Leu Ala Val Val Val Ala Glu Trp Gly Gly Gly Leu Val
        115                 120                 125

Glu Gln Ile Ala Asp Ser Tyr Leu Leu Ile Thr Ile Asp Arg Glu Thr
    130                 135                 140

Ala Val Gln Glu Asp Pro Glu Ser Glu Ala Arg Ile Phe His Trp Glu
145                 150                 155                 160

Trp Arg Glu Gly Arg
                165
```

<210> 261
<211> 275
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(252)
<223> FRXA00505

<400> 261
gat ctg atc cac atg gat gcc tac cga ttg ctg ggc gaa gac agc gag 48
Asp Leu Ile His Met Asp Ala Tyr Arg Leu Leu Gly Glu Asp Ser Glu
1 5 10 15

gat gct gat ccg atc ggt gcg ctg gac tct ttg gat ttg gat acc gat 96
Asp Ala Asp Pro Ile Gly Ala Leu Asp Ser Leu Asp Leu Asp Thr Asp
20 25 30

ttg gac ttg gct gtg gtt gtt gcg gaa tgg ggc ggt ggc ttg gtg gag 144
Leu Asp Leu Ala Val Val Val Ala Glu Trp Gly Gly Gly Leu Val Glu
35 40 45

cag atc gct gac tcg tat ctt ttg att acc att gat cga gag acc gct 192
Gln Ile Ala Asp Ser Tyr Leu Leu Ile Thr Ile Asp Arg Glu Thr Ala
50 55 60

gtg cag gaa gac ccg gaa tct gag gct cga att ttc cat tgg gaa tgg 240
Val Gln Glu Asp Pro Glu Ser Glu Ala Arg Ile Phe His Trp Glu Trp
65 70 75 80

cgc gaa ggc cgc tgagaaagtt ttccacgcta aaa 275
Arg Glu Gly Arg

<210> 262
<211> 84
<212> PRT
<213> Corynebacterium glutamicum

<400> 262
Asp Leu Ile His Met Asp Ala Tyr Arg Leu Leu Gly Glu Asp Ser Glu
1 5 10 15

Asp Ala Asp Pro Ile Gly Ala Leu Asp Ser Leu Asp Leu Asp Thr Asp
20 25 30

Leu Asp Leu Ala Val Val Val Ala Glu Trp Gly Gly Gly Leu Val Glu
35 40 45

Gln Ile Ala Asp Ser Tyr Leu Leu Ile Thr Ile Asp Arg Glu Thr Ala
50 55 60

Val Gln Glu Asp Pro Glu Ser Glu Ala Arg Ile Phe His Trp Glu Trp
65 70 75 80

Arg Glu Gly Arg

<210> 263
<211> 978
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(955)
<223> RXN00507

<400> 263
gttcatgttg aactattgtg ccaccaaccg cggacagaaa tacgattggt gccggggtta 60

gtgccagtat tgccccacgc tttcaactat ccttaaacac gtg gct gag aat ctg 115
Val Ala Glu Asn Leu
1 5

aac aaa cac ctg tcc aaa ctg tcc aag cgc gga ccg cac cgc gtg ctg 163
Asn Lys His Leu Ser Lys Leu Ser Lys Arg Gly Pro His Arg Val Leu
10 15 20

gta ggc gat atg aac tac gcc ggc atc ccg ggc aaa atc tac acc cca 211
Val Gly Asp Met Asn Tyr Ala Gly Ile Pro Gly Lys Ile Tyr Thr Pro
25 30 35

gca gaa ggc gac ggc atc cca ggt gta gct ttc ggc cac gac tgg atg 259
Ala Glu Gly Asp Gly Ile Pro Gly Val Ala Phe Gly His Asp Trp Met
40 45 50

aaa tcc atc aag tac tac cac caa act ttg cga cac ctc gcg tcc tgg 307
Lys Ser Ile Lys Tyr Tyr His Gln Thr Leu Arg His Leu Ala Ser Trp
55 60 65

ggc atc gct gtt gcc gcc cca gac acc gaa aat ggc ttc atg cca gac 355
Gly Ile Ala Val Ala Ala Pro Asp Thr Glu Asn Gly Phe Met Pro Asp
70 75 80 85

cac aaa ggt ttc gcc tct gac ctc gaa tcc tcc att cag att ctc ggc 403
His Lys Gly Phe Ala Ser Asp Leu Glu Ser Ser Ile Gln Ile Leu Gly
90 95 100

ggc gta aaa ctc ggc tcc gga aac gtc acc gtc aac cca gcc tgc ctc 451
Gly Val Lys Leu Gly Ser Gly Asn Val Thr Val Asn Pro Ala Cys Leu
105 110 115

ggt gta gta ggc cac ggc atg ggt gct ggg gct gca gta cta tcc gca 499
Gly Val Val Gly His Gly Met Gly Ala Gly Ala Ala Val Leu Ser Ala
120 125 130

gca aac cgc gac ctc gtg cgc gca gtc gga gca atc tac cca gcg aaa 547
Ala Asn Arg Asp Leu Val Arg Ala Val Gly Ala Ile Tyr Pro Ala Lys
135 140 145

acc tcc ccc tca gca atc gac gcc gcc ttc gct gtc aaa gcc cca ggc 595
Thr Ser Pro Ser Ala Ile Asp Ala Ala Phe Ala Val Lys Ala Pro Gly
150 155 160 165

cta gtc atc gga tcc tcc agc ctc ggc ctc ttt gaa tcc ggc gag cca 643
Leu Val Ile Gly Ser Ser Ser Leu Gly Leu Phe Glu Ser Gly Glu Pro
170 175 180

gca aaa ctc gca gcc aac tgg gcc ggc gat gtc tgc tac cgc gaa tca 691
Ala Lys Leu Ala Ala Asn Trp Ala Gly Asp Val Cys Tyr Arg Glu Ser
185 190 195

gaa aaa ggc aac caa cag ggc ttc tct gaa gac acc atg ttc aaa ctt 739
Glu Lys Gly Asn Gln Gln Gly Phe Ser Glu Asp Thr Met Phe Lys Leu
200 205 210

gtc gca gga atc ggc agc cca caa acc gga gct caa gaa acc gtc cgc 787
Val Ala Gly Ile Gly Ser Pro Gln Thr Gly Ala Gln Glu Thr Val Arg

```
    215                 220                 225

ggc ctc ctc acc gga ttc ctt ctc cac caa ctt gcc gga gaa aag aaa   835
Gly Leu Leu Thr Gly Phe Leu Leu His Gln Leu Ala Gly Glu Lys Lys
230                 235                 240                 245

tac aaa gca ttc tcc gaa cca gac gct gaa gct aag aaa gtt gtc tcc   883
Tyr Lys Ala Phe Ser Glu Pro Asp Ala Glu Ala Lys Lys Val Val Ser
                250                 255                 260

tac ttc ggc cag gag ctg cag gaa cat gcc ttc cct aag gac acg tcc   931
Tyr Phe Gly Gln Glu Leu Gln Glu His Ala Phe Pro Lys Asp Thr Ser
            265                 270                 275

cca ttc gcg ttc ctt aac gag aag tagttcgctt ttcttagtgg gtg         978
Pro Phe Ala Phe Leu Asn Glu Lys
        280                 285


<210> 264
<211> 285
<212> PRT
<213> Corynebacterium glutamicum

<400> 264
Val Ala Glu Asn Leu Asn Lys His Leu Ser Lys Leu Ser Lys Arg Gly
  1               5                  10                  15

Pro His Arg Val Leu Val Gly Asp Met Asn Tyr Ala Gly Ile Pro Gly
             20                  25                  30

Lys Ile Tyr Thr Pro Ala Glu Gly Asp Gly Ile Pro Gly Val Ala Phe
         35                  40                  45

Gly His Asp Trp Met Lys Ser Ile Lys Tyr Tyr His Gln Thr Leu Arg
     50                  55                  60

His Leu Ala Ser Trp Gly Ile Ala Val Ala Ala Pro Asp Thr Glu Asn
 65                  70                  75                  80

Gly Phe Met Pro Asp His Lys Gly Phe Ala Ser Asp Leu Glu Ser Ser
                 85                  90                  95

Ile Gln Ile Leu Gly Gly Val Lys Leu Gly Ser Gly Asn Val Thr Val
            100                 105                 110

Asn Pro Ala Cys Leu Gly Val Val Gly His Gly Met Gly Ala Gly Ala
        115                 120                 125

Ala Val Leu Ser Ala Ala Asn Arg Asp Leu Val Arg Ala Val Gly Ala
    130                 135                 140

Ile Tyr Pro Ala Lys Thr Ser Pro Ser Ala Ile Asp Ala Ala Phe Ala
145                 150                 155                 160

Val Lys Ala Pro Gly Leu Val Ile Gly Ser Ser Ser Leu Gly Leu Phe
                165                 170                 175

Glu Ser Gly Glu Pro Ala Lys Leu Ala Ala Asn Trp Ala Gly Asp Val
            180                 185                 190
```

```
Cys Tyr Arg Glu Ser Glu Lys Gly Asn Gln Gln Gly Phe Ser Glu Asp
        195                 200                 205

Thr Met Phe Lys Leu Val Ala Gly Ile Gly Ser Pro Gln Thr Gly Ala
    210                 215                 220

Gln Glu Thr Val Arg Gly Leu Leu Thr Gly Phe Leu Leu His Gln Leu
225                 230                 235                 240

Ala Gly Glu Lys Lys Tyr Lys Ala Phe Ser Glu Pro Asp Ala Glu Ala
                245                 250                 255

Lys Lys Val Val Ser Tyr Phe Gly Gln Glu Leu Gln Glu His Ala Phe
            260                 265                 270

Pro Lys Asp Thr Ser Pro Phe Ala Phe Leu Asn Glu Lys
        275                 280                 285


<210> 265
<211> 978
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(955)
<223> FRXA00507

<400> 265
gttcatgttg aactattgtg ccaccaaccg cggacagaaa tacgattggt gccggggtta 60

gtgccagtat tgccccacgc tttcaactat ccttaaacac gtg gct gag aat ctg   115
                                              Val Ala Glu Asn Leu
                                                1               5

aac aaa cac ctg tcc aaa ctg tcc aag cgc gga ccg cac cgc gtg ctg   163
Asn Lys His Leu Ser Lys Leu Ser Lys Arg Gly Pro His Arg Val Leu
                10                  15                  20

gta ggc gat atg aac tac gcc ggc atc ccg ggc aaa atc tac acc cca   211
Val Gly Asp Met Asn Tyr Ala Gly Ile Pro Gly Lys Ile Tyr Thr Pro
            25                  30                  35

gca gaa ggc gac ggc atc cca ggt gta gct ttc ggc cac gac tgg atg   259
Ala Glu Gly Asp Gly Ile Pro Gly Val Ala Phe Gly His Asp Trp Met
        40                  45                  50

aaa tcc atc aag tac tac cac caa act ttg cga cac ctc gcg tcc tgg   307
Lys Ser Ile Lys Tyr Tyr His Gln Thr Leu Arg His Leu Ala Ser Trp
    55                  60                  65

ggc atc gct gtt gcc gcc cca gac acc gaa aat ggc ttc atg cca gac   355
Gly Ile Ala Val Ala Ala Pro Asp Thr Glu Asn Gly Phe Met Pro Asp
70                  75                  80                  85

cac aaa ggt ttc gcc tct gac ctc gaa tcc tcc att cag att ctc ggc   403
His Lys Gly Phe Ala Ser Asp Leu Glu Ser Ser Ile Gln Ile Leu Gly
                90                  95                  100

ggc gta aaa ctc ggc tcc gga aac gtc acc gtc aac cca gcc tgc ctc   451
```

```
Gly Val Lys Leu Gly Ser Gly Asn Val Thr Val Asn Pro Ala Cys Leu
            105                 110                 115

ggt gta gta ggc cac ggc atg ggt gct ggg gct gca gta cta tcc gca   499
Gly Val Val Gly His Gly Met Gly Ala Gly Ala Ala Val Leu Ser Ala
        120                 125                 130

gca aac cgc gac ctc gtg cgc gca gtc gga gca atc tac cca gcg aaa   547
Ala Asn Arg Asp Leu Val Arg Ala Val Gly Ala Ile Tyr Pro Ala Lys
    135                 140                 145

acc tcc ccc tca gca atc gac gcc gcc ttc gct gtc aaa gcc cca ggc   595
Thr Ser Pro Ser Ala Ile Asp Ala Ala Phe Ala Val Lys Ala Pro Gly
150                 155                 160                 165

cta gtc atc gga tcc tcc agc ctc ggc ctc ttt gaa tcc ggc gag cca   643
Leu Val Ile Gly Ser Ser Ser Leu Gly Leu Phe Glu Ser Gly Glu Pro
                170                 175                 180

gca aaa ctc gca gcc aac tgg gcc ggc gat gtc tgc tac cgc gaa tca   691
Ala Lys Leu Ala Ala Asn Trp Ala Gly Asp Val Cys Tyr Arg Glu Ser
            185                 190                 195

gaa aaa ggc aac caa cag ggc ttc tct gaa gac acc atg ttc aaa ctt   739
Glu Lys Gly Asn Gln Gln Gly Phe Ser Glu Asp Thr Met Phe Lys Leu
        200                 205                 210

gtc gca gga atc ggc agc cca caa acc gga gct caa gaa acc gtc cgc   787
Val Ala Gly Ile Gly Ser Pro Gln Thr Gly Ala Gln Glu Thr Val Arg
    215                 220                 225

ggc ctc ctc acc gga ttc ctt ctc cac caa ctt gcc gga gaa aag aaa   835
Gly Leu Leu Thr Gly Phe Leu Leu His Gln Leu Ala Gly Glu Lys Lys
230                 235                 240                 245

tac aaa gca ttc tcc gaa cca gac gct gaa gct aag aaa gtt gtc tcc   883
Tyr Lys Ala Phe Ser Glu Pro Asp Ala Glu Ala Lys Lys Val Val Ser
                250                 255                 260

tac ttc ggc cag gag ctg cag gaa cat gcc ttc cct aag gac acg tcc   931
Tyr Phe Gly Gln Glu Leu Gln Glu His Ala Phe Pro Lys Asp Thr Ser
            265                 270                 275

cca ttc gcg ttc ctt aac gag aag tagttcgctt ttcttagtgg gtg         978
Pro Phe Ala Phe Leu Asn Glu Lys
        280                 285


<210> 266
<211> 285
<212> PRT
<213> Corynebacterium glutamicum

<400> 266
Val Ala Glu Asn Leu Asn Lys His Leu Ser Lys Leu Ser Lys Arg Gly
  1               5                  10                  15

Pro His Arg Val Leu Val Gly Asp Met Asn Tyr Ala Gly Ile Pro Gly
             20                  25                  30

Lys Ile Tyr Thr Pro Ala Glu Gly Asp Gly Ile Pro Gly Val Ala Phe
```

```
         35                  40                  45

Gly His Asp Trp Met Lys Ser Ile Lys Tyr Tyr His Gln Thr Leu Arg
     50                  55                  60

His Leu Ala Ser Trp Gly Ile Ala Val Ala Ala Pro Asp Thr Glu Asn
 65                  70                  75                  80

Gly Phe Met Pro Asp His Lys Gly Phe Ala Ser Asp Leu Glu Ser Ser
                 85                  90                  95

Ile Gln Ile Leu Gly Gly Val Lys Leu Gly Ser Gly Asn Val Thr Val
            100                 105                 110

Asn Pro Ala Cys Leu Gly Val Val Gly His Gly Met Gly Ala Gly Ala
        115                 120                 125

Ala Val Leu Ser Ala Ala Asn Arg Asp Leu Val Arg Ala Val Gly Ala
    130                 135                 140

Ile Tyr Pro Ala Lys Thr Ser Pro Ser Ala Ile Asp Ala Ala Phe Ala
145                 150                 155                 160

Val Lys Ala Pro Gly Leu Val Ile Gly Ser Ser Ser Leu Gly Leu Phe
                165                 170                 175

Glu Ser Gly Glu Pro Ala Lys Leu Ala Ala Asn Trp Ala Gly Asp Val
            180                 185                 190

Cys Tyr Arg Glu Ser Glu Lys Gly Asn Gln Gln Gly Phe Ser Glu Asp
        195                 200                 205

Thr Met Phe Lys Leu Val Ala Gly Ile Gly Ser Pro Gln Thr Gly Ala
    210                 215                 220

Gln Glu Thr Val Arg Gly Leu Leu Thr Gly Phe Leu Leu His Gln Leu
225                 230                 235                 240

Ala Gly Glu Lys Lys Tyr Lys Ala Phe Ser Glu Pro Asp Ala Glu Ala
                245                 250                 255

Lys Lys Val Val Ser Tyr Phe Gly Gln Glu Leu Gln Glu His Ala Phe
            260                 265                 270

Pro Lys Asp Thr Ser Pro Phe Ala Phe Leu Asn Glu Lys
        275                 280                 285


<210> 267
<211> 1632
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1609)
<223> RXN00510

<400> 267
acgcttttac ccaaacaacc caagccgccg aggaagaagt taaacgattc gacaataccg 60
```

```
acaaagtttt tggtgccgga tttgatggga ttgatccgaa gtg aat gat cct tta   115
                                             Val Asn Asp Pro Leu
                                               1               5

gcc ggc tac gga gca gtg atc tcc gca cta caa ggc gcc agt ggt ggg   163
Ala Gly Tyr Gly Ala Val Ile Ser Ala Leu Gln Gly Ala Ser Gly Gly
                 10                  15                  20

atg tat cgc gga ccg gcg aaa tcc gaa ggc cag ttg cgc gag atg tac   211
Met Tyr Arg Gly Pro Ala Lys Ser Glu Gly Gln Leu Arg Glu Met Tyr
             25                  30                  35

caa acc atc gaa ggg cta gac acc agc tcg ttg cgc gaa gct gcc gaa   259
Gln Thr Ile Glu Gly Leu Asp Thr Ser Ser Leu Arg Glu Ala Ala Glu
         40                  45                  50

gca gca gtg ggc gga acg aac gaa gcc aga ata caa ggg tgg gtc ggc   307
Ala Ala Val Gly Gly Thr Asn Glu Ala Arg Ile Gln Gly Trp Val Gly
     55                  60                  65

ccg ctc ttg aaa ttc ttc ggg acg gtt ggc ggg gga atg atc gcc acg   355
Pro Leu Leu Lys Phe Phe Gly Thr Val Gly Gly Gly Met Ile Ala Thr
 70                  75                  80                  85

gag ata gct gaa cgg gca gtc gat tgg ttc aaa aac cgt aat gat gtg   403
Glu Ile Ala Glu Arg Ala Val Asp Trp Phe Lys Asn Arg Asn Asp Val
                 90                  95                 100

gaa gaa gtc agc gaa gcc gct gat aaa gcc gcc gat gcg atc gac tcc   451
Glu Glu Val Ser Glu Ala Ala Asp Lys Ala Ala Asp Ala Ile Asp Ser
            105                 110                 115

act gtc aca gag tcc gac cag ggc atg atg cac att atc cag cag ctc   499
Thr Val Thr Glu Ser Asp Gln Gly Met Met His Ile Ile Gln Gln Leu
        120                 125                 130

ttg gac att gtg tct acg ttg acg cag att ctt ggc agc atg gat cgg   547
Leu Asp Ile Val Ser Thr Leu Thr Gln Ile Leu Gly Ser Met Asp Arg
    135                 140                 145

ggg aaa ttt cct caa gaa ttc cgg gac tgt gtc caa act gga gct gat   595
Gly Lys Phe Pro Gln Glu Phe Arg Asp Cys Val Gln Thr Gly Ala Asp
150                 155                 160                 165

ctt att gac cag gca ggg gac atg ctt gaa gga ttg tgc gct gat cga   643
Leu Ile Asp Gln Ala Gly Asp Met Leu Glu Gly Leu Cys Ala Asp Arg
                170                 175                 180

gat gat gcg att tca cag tgt ttc tcc gcg ttg acc gat cat gga aaa   691
Asp Asp Ala Ile Ser Gln Cys Phe Ser Ala Leu Thr Asp His Gly Lys
            185                 190                 195

caa gtt tgt gaa act gag cca aag ccg ttg tgt agt gca gct tct ggg   739
Gln Val Cys Glu Thr Glu Pro Lys Pro Leu Cys Ser Ala Ala Ser Gly
        200                 205                 210

ggt tca tct ggt gga gcg act tct tcg gct gcg gcc tct tca ggt ggt   787
Gly Ser Ser Gly Gly Ala Thr Ser Ser Ala Ala Ala Ser Ser Gly Gly
    215                 220                 225

tca agc tcg agc act gct agc tct ggg agt tct ggc gga tcg agc agt   835
```

```
Ser Ser Ser Ser Thr Ala Ser Ser Gly Ser Ser Gly Gly Ser Ser Ser
230                 235                 240                 245

gct gcg gat agt tcg acg tcg acc aat gct gaa tcc agt gtt gaa aag   883
Ala Ala Asp Ser Ser Thr Ser Thr Asn Ala Glu Ser Ser Val Glu Lys
                250                 255                 260

gaa aag acc aca cct gct gcc gtt gag aaa cct gac gag aaa cca gtg   931
Glu Lys Thr Thr Pro Ala Ala Val Glu Lys Pro Asp Glu Lys Pro Val
            265                 270                 275

gag aag ccg gtt gaa aag acg cca gaa aag ccg gta gaa aaa cct gtc   979
Glu Lys Pro Val Glu Lys Thr Pro Glu Lys Pro Val Glu Lys Pro Val
        280                 285                 290

gag aag caa gag tgt gaa gaa aag cct gac cct gac ccg gaa aaa tgc   1027
Glu Lys Gln Glu Cys Glu Glu Lys Pro Asp Pro Asp Pro Glu Lys Cys
    295                 300                 305

aaa aca gag ccg gtc gag tgt gag cca aca ccg aaa cct gaa aca gag   1075
Lys Thr Glu Pro Val Glu Cys Glu Pro Thr Pro Lys Pro Glu Thr Glu
310                 315                 320                 325

cct gaa cca aaa ccg aca ccc acg ccc aca ccc gga aca cca aca cca   1123
Pro Glu Pro Lys Pro Thr Pro Thr Pro Thr Pro Gly Thr Pro Thr Pro
                330                 335                 340

ata cct gag cta gag act gag gat tgt gaa cct ggc aag gag acg ggc   1171
Ile Pro Glu Leu Glu Thr Glu Asp Cys Glu Pro Gly Lys Glu Thr Gly
            345                 350                 355

aca gac tca gaa tct gaa tcg gaa gag tgc gcc ccc gag ctc aat gac   1219
Thr Asp Ser Glu Ser Glu Ser Glu Glu Cys Ala Pro Glu Leu Asn Asp
        360                 365                 370

gtt cca gaa gag tcg gat ctg att ggg caa ctc atc aag gga gca atc   1267
Val Pro Glu Glu Ser Asp Leu Ile Gly Gln Leu Ile Lys Gly Ala Ile
    375                 380                 385

ggt att ggg att gtt gtt gta ggc gtt ggg ctg ttg gtg aat ttc ctg   1315
Gly Ile Gly Ile Val Val Val Gly Val Gly Leu Leu Val Asn Phe Leu
390                 395                 400                 405

gag cag tgc gtc cct gtg att gaa gaa gta cct gtg ccg gag ccc gag   1363
Glu Gln Cys Val Pro Val Ile Glu Glu Val Pro Val Pro Glu Pro Glu
                410                 415                 420

cct ata cct gaa ccc gct ccg cag cct gag cca act tca gtg aaa cca   1411
Pro Ile Pro Glu Pro Ala Pro Gln Pro Glu Pro Thr Ser Val Lys Pro
            425                 430                 435

cca gag tct gaa cta gat aag gtg gct gag cct gcg ccg aag cca att   1459
Pro Glu Ser Glu Leu Asp Lys Val Ala Glu Pro Ala Pro Lys Pro Ile
        440                 445                 450

cca caa gct aat tac act gct gct gca gca act aac tat tcc gct ccc   1507
Pro Gln Ala Asn Tyr Thr Ala Ala Ala Ala Thr Asn Tyr Ser Ala Pro
    455                 460                 465

gcg cac gct ccc gtt gtc cca att acg ccg gca gca cct gaa gtt ccg   1555
Ala His Ala Pro Val Val Pro Ile Thr Pro Ala Ala Pro Glu Val Pro
```

```
470                 475                 480                 485

gca gca cca gaa gtg cct gca ccg gcg gtt aat ctt cac aag gcc ggc   1603
Ala Ala Pro Glu Val Pro Ala Pro Ala Val Asn Leu His Lys Ala Gly
                490                 495                 500

ggg tgg tagcggtgga gtatgcggaa ttt                                 1632
Gly Trp
```

<210> 268
<211> 503
<212> PRT
<213> Corynebacterium glutamicum

<400> 268

```
Val Asn Asp Pro Leu Ala Gly Tyr Gly Ala Val Ile Ser Ala Leu Gln
  1               5                  10                  15

Gly Ala Ser Gly Gly Met Tyr Arg Gly Pro Ala Lys Ser Glu Gly Gln
            20                  25                  30

Leu Arg Glu Met Tyr Gln Thr Ile Glu Gly Leu Asp Thr Ser Ser Leu
         35                  40                  45

Arg Glu Ala Ala Glu Ala Ala Val Gly Gly Thr Asn Glu Ala Arg Ile
     50                  55                  60

Gln Gly Trp Val Gly Pro Leu Leu Lys Phe Phe Gly Thr Val Gly Gly
 65                  70                  75                  80

Gly Met Ile Ala Thr Glu Ile Ala Glu Arg Ala Val Asp Trp Phe Lys
                85                  90                  95

Asn Arg Asn Asp Val Glu Glu Val Ser Glu Ala Ala Asp Lys Ala Ala
            100                 105                 110

Asp Ala Ile Asp Ser Thr Val Thr Glu Ser Asp Gln Gly Met Met His
        115                 120                 125

Ile Ile Gln Gln Leu Leu Asp Ile Val Ser Thr Leu Thr Gln Ile Leu
    130                 135                 140

Gly Ser Met Asp Arg Gly Lys Phe Pro Gln Glu Phe Arg Asp Cys Val
145                 150                 155                 160

Gln Thr Gly Ala Asp Leu Ile Asp Gln Ala Gly Asp Met Leu Glu Gly
                165                 170                 175

Leu Cys Ala Asp Arg Asp Asp Ala Ile Ser Gln Cys Phe Ser Ala Leu
            180                 185                 190

Thr Asp His Gly Lys Gln Val Cys Glu Thr Glu Pro Lys Pro Leu Cys
        195                 200                 205

Ser Ala Ala Ser Gly Gly Ser Ser Gly Gly Ala Thr Ser Ser Ala Ala
    210                 215                 220

Ala Ser Ser Gly Gly Ser Ser Ser Ser Thr Ala Ser Ser Gly Ser Ser
225                 230                 235                 240
```

```
Gly Gly Ser Ser Ser Ala Ala Asp Ser Ser Thr Ser Thr Asn Ala Glu
                245                 250                 255

Ser Ser Val Glu Lys Glu Lys Thr Thr Pro Ala Ala Val Glu Lys Pro
            260                 265                 270

Asp Glu Lys Pro Val Glu Lys Pro Val Glu Lys Thr Pro Glu Lys Pro
        275                 280                 285

Val Glu Lys Pro Val Glu Lys Gln Glu Cys Glu Glu Lys Pro Asp Pro
    290                 295                 300

Asp Pro Glu Lys Cys Lys Thr Glu Pro Val Glu Cys Glu Pro Thr Pro
305                 310                 315                 320

Lys Pro Glu Thr Glu Pro Glu Pro Lys Pro Thr Pro Thr Pro Thr Pro
                325                 330                 335

Gly Thr Pro Thr Pro Ile Pro Glu Leu Glu Thr Glu Asp Cys Glu Pro
            340                 345                 350

Gly Lys Glu Thr Gly Thr Asp Ser Glu Ser Glu Ser Glu Glu Cys Ala
        355                 360                 365

Pro Glu Leu Asn Asp Val Pro Glu Glu Ser Asp Leu Ile Gly Gln Leu
    370                 375                 380

Ile Lys Gly Ala Ile Gly Ile Gly Ile Val Val Val Gly Val Gly Leu
385                 390                 395                 400

Leu Val Asn Phe Leu Glu Gln Cys Val Pro Val Ile Glu Glu Val Pro
                405                 410                 415

Val Pro Glu Pro Glu Pro Ile Pro Glu Pro Ala Pro Gln Pro Glu Pro
            420                 425                 430

Thr Ser Val Lys Pro Pro Glu Ser Glu Leu Asp Lys Val Ala Glu Pro
        435                 440                 445

Ala Pro Lys Pro Ile Pro Gln Ala Asn Tyr Thr Ala Ala Ala Ala Thr
    450                 455                 460

Asn Tyr Ser Ala Pro Ala His Ala Pro Val Val Pro Ile Thr Pro Ala
465                 470                 475                 480

Ala Pro Glu Val Pro Ala Ala Pro Glu Val Pro Ala Pro Ala Val Asn
                485                 490                 495

Leu His Lys Ala Gly Gly Trp
            500
```

<210> 269
<211> 300
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(277)

<223> FRXA00509

<400> 269
cttttctggc gtcttttcaa ccggcttctc cactggtttc tcgtcaggtt tctcaacggc 60

agcaggtgtg gtcttttcct tttcaacact ggattcagca ttg gtc gac gtc gaa 115
Leu Val Asp Val Glu
1 5

cta tcc gca gca ctg ctc gat ccg cca gaa ctc cca gag cta gca gtg 163
Leu Ser Ala Ala Leu Leu Asp Pro Pro Glu Leu Pro Glu Leu Ala Val
10 15 20

ctc gag ctt gaa cca cct gaa gag gcc gca gcc gaa gaa gtc gct cca 211
Leu Glu Leu Glu Pro Pro Glu Glu Ala Ala Ala Glu Glu Val Ala Pro
25 30 35

cca gat gaa ccc cca gaa gct gca cta cac aac ggc ttt ggc tca gtt 259
Pro Asp Glu Pro Pro Glu Ala Ala Leu His Asn Gly Phe Gly Ser Val
40 45 50

tca caa act tgt ttt cca tgatcggtca acgcggagaa aca 300
Ser Gln Thr Cys Phe Pro
55

<210> 270
<211> 59
<212> PRT
<213> Corynebacterium glutamicum

<400> 270
Leu Val Asp Val Glu Leu Ser Ala Ala Leu Leu Asp Pro Pro Glu Leu
1 5 10 15

Pro Glu Leu Ala Val Leu Glu Leu Glu Pro Pro Glu Glu Ala Ala Ala
20 25 30

Glu Glu Val Ala Pro Pro Asp Glu Pro Pro Glu Ala Ala Leu His Asn
35 40 45

Gly Phe Gly Ser Val Ser Gln Thr Cys Phe Pro
50 55

<210> 271
<211> 631
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(631)
<223> FRXA00510

<400> 271
gagcagtgct gcggatagtt cgacgtcgac caatgctgaa tccagtgttg aaaaggaaaa 60

gaccacacct gctgccgttg agaaacctga cgagaaacca gtg gag aag ccg gtt 115
Val Glu Lys Pro Val
1 5

```
gaa aag acg cca gaa aag ccg gta gaa aaa cct gtc gag aag caa gag   163
Glu Lys Thr Pro Glu Lys Pro Val Glu Lys Pro Val Glu Lys Gln Glu
                10                  15                  20

tgt gaa gaa aag cct gac cct gac ccg gaa ana atg caa aan can gag   211
Cys Glu Glu Lys Pro Asp Pro Asp Pro Glu Xaa Met Gln Xaa Xaa Glu
            25                  30                  35

ccg gtc gag tgt gag cca aca ccg aaa cct gaa aca gag cct gaa cca   259
Pro Val Glu Cys Glu Pro Thr Pro Lys Pro Glu Thr Glu Pro Glu Pro
        40                  45                  50

aaa ccn gac acc cac gcc can cna ccc gga aca cca aca cca ata cct   307
Lys Pro Asp Thr His Ala Xaa Xaa Pro Gly Thr Pro Thr Pro Ile Pro
    55                  60                  65

gna gct aga gna ctg agg att gnt gna nac nct gng caa gga gan cgn   355
Xaa Ala Arg Xaa Leu Arg Ile Xaa Xaa Xaa Xaa Xaa Gln Gly Xaa Arg
70                  75                  80                  85

ggc aca gac tca gnn ana tnc tnn nnn nnn gaa tcg gaa gag tgc gcc   403
Gly Thr Asp Ser Xaa Xaa Xaa Xaa Xaa Xaa Glu Ser Glu Glu Cys Ala
                90                  95                  100

ccc gag ctc aat gac gtt cca gaa gag tcg gat ctg att ggg caa ctc   451
Pro Glu Leu Asn Asp Val Pro Glu Glu Ser Asp Leu Ile Gly Gln Leu
            105                 110                 115

atc aag gga gca atc ggt att ggg att gtt gtt gta ggc gtt ggg ctg   499
Ile Lys Gly Ala Ile Gly Ile Gly Ile Val Val Val Gly Val Gly Leu
        120                 125                 130

ttg gtg aat ttc ctg gag cag tgc gtc cct gtg att gaa gaa gta cct   547
Leu Val Asn Phe Leu Glu Gln Cys Val Pro Val Ile Glu Glu Val Pro
    135                 140                 145

gtg ccg gag ccc gag cct ata cct gaa ccc gct ccg cag cct gag cca   595
Val Pro Glu Pro Glu Pro Ile Pro Glu Pro Ala Pro Gln Pro Glu Pro
150                 155                 160                 165

act tca gtg aaa cca cca gag tct gaa cta gat aag                   631
Thr Ser Val Lys Pro Pro Glu Ser Glu Leu Asp Lys
                170                 175
```

<210> 272
<211> 177
<212> PRT
<213> Corynebacterium glutamicum

<400> 272

```
Val Glu Lys Pro Val Glu Lys Thr Pro Glu Lys Pro Val Glu Lys Pro
  1               5                  10                  15

Val Glu Lys Gln Glu Cys Glu Glu Lys Pro Asp Pro Asp Pro Glu Xaa
            20                  25                  30

Met Gln Xaa Xaa Glu Pro Val Glu Cys Glu Pro Thr Pro Lys Pro Glu
        35                  40                  45
```

```
Thr Glu Pro Glu Pro Lys Pro Asp Thr His Ala Xaa Xaa Pro Gly Thr
     50                  55                  60

Pro Thr Pro Ile Pro Xaa Ala Arg Xaa Leu Arg Ile Xaa Xaa Xaa Xaa
 65                  70                  75                  80

Xaa Gln Gly Xaa Arg Gly Thr Asp Ser Xaa Xaa Xaa Xaa Xaa Xaa Glu
                85                  90                  95

Ser Glu Glu Cys Ala Pro Glu Leu Asn Asp Val Pro Glu Glu Ser Asp
            100                 105                 110

Leu Ile Gly Gln Leu Ile Lys Gly Ala Ile Gly Ile Gly Ile Val Val
        115                 120                 125

Val Gly Val Gly Leu Leu Val Asn Phe Leu Glu Gln Cys Val Pro Val
    130                 135                 140

Ile Glu Glu Val Pro Val Pro Glu Pro Glu Pro Ile Pro Glu Pro Ala
145                 150                 155                 160

Pro Gln Pro Glu Pro Thr Ser Val Lys Pro Pro Glu Ser Glu Leu Asp
                165                 170                 175

Lys
```

Sequence Listing Page 334

<210> 273
<211> 825
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(802)
<223> RXN00515

<400> 273

```
gttgacgcac tgaagaagta aagtctcttc acaaaaagcg ctgtgcttcc tcacatggaa 60

gcacagcgct ttttcatatt tttattgcca taatgggcac atg cgt ttt tct cga   115
                                            Met Arg Phe Ser Arg
                                              1               5

gtt ctt ccc gca ctt ctt atc acc acc gcc gtg agc atc cca aca gca   163
Val Leu Pro Ala Leu Leu Ile Thr Thr Ala Val Ser Ile Pro Thr Ala
                10                  15                  20

tct gct gcc aca ctc acc gcc gac acc gac aag gaa ttg tgc atc gcc   211
Ser Ala Ala Thr Leu Thr Ala Asp Thr Asp Lys Glu Leu Cys Ile Ala
            25                  30                  35

agc aac acc gac gat tcc gcg gtg gtt acc ttc tgg aac tcc att gaa   259
Ser Asn Thr Asp Asp Ser Ala Val Val Thr Phe Trp Asn Ser Ile Glu
        40                  45                  50

gac tcc gtg cgc gaa caa cgc ctc gac gaa cta gac gcc caa gat cca   307
Asp Ser Val Arg Glu Gln Arg Leu Asp Glu Leu Asp Ala Gln Asp Pro
    55                  60                  65
```

```
gga atc aaa gcg gcg att gaa agc tac atc gcc caa gat gac aac gcc   355
Gly Ile Lys Ala Ala Ile Glu Ser Tyr Ile Ala Gln Asp Asp Asn Ala
 70                  75                  80                  85

cca act gct gct gaa ctg caa gta cgc ctc gat gcc atc gaa tcc ggc   403
Pro Thr Ala Ala Glu Leu Gln Val Arg Leu Asp Ala Ile Glu Ser Gly
                90                  95                 100

gaa ggc cta gcc atg ctc ctc cca gac gat ccc acg ctg gca gac ccc   451
Glu Gly Leu Ala Met Leu Leu Pro Asp Asp Pro Thr Leu Ala Asp Pro
            105                 110                 115

aac gcc gag gaa agt ttc aaa acg gag tac aca tac gac gaa gcc aaa   499
Asn Ala Glu Glu Ser Phe Lys Thr Glu Tyr Thr Tyr Asp Glu Ala Lys
        120                 125                 130

gac atc atc agc gga ttc tcc agc gat cca gcc agc gat gta ctc agc   547
Asp Ile Ile Ser Gly Phe Ser Ser Asp Pro Ala Ser Asp Val Leu Ser
    135                 140                 145

caa ctt caa caa gcc gcc acc acc ggc acc cgc acc gca gaa atc cgc   595
Gln Leu Gln Gln Ala Ala Thr Thr Gly Thr Arg Thr Ala Glu Ile Arg
150                 155                 160                 165

gcc gaa gta ttc gcc gac cgc acc gat gat tac aac gaa tcc caa acc   643
Ala Glu Val Phe Ala Asp Arg Thr Asp Asp Tyr Asn Glu Ser Gln Thr
                170                 175                 180

gct ctt aaa gag gat ttc caa aac tgc atc gat gcc atc gat gac gcc   691
Ala Leu Lys Glu Asp Phe Gln Asn Cys Ile Asp Ala Ile Asp Asp Ala
            185                 190                 195

cgc cca atc cca ctg cag tac atc ctg att gga ggc gcc atc gct ttg   739
Arg Pro Ile Pro Leu Gln Tyr Ile Leu Ile Gly Gly Ala Ile Ala Leu
        200                 205                 210

gcg gtc atc gtc ctc ggg atc agg gcg tgg act aac tca agg aag cag   787
Ala Val Ile Val Leu Gly Ile Arg Ala Trp Thr Asn Ser Arg Lys Gln
    215                 220                 225

tcc aag cac agc cag taatacgcca agcaaaaaat tgc                    825
Ser Lys His Ser Gln
230
```

<210> 274
<211> 234
<212> PRT
<213> Corynebacterium glutamicum

<400> 274

```
Met Arg Phe Ser Arg Val Leu Pro Ala Leu Leu Ile Thr Thr Ala Val
  1               5                  10                  15

Ser Ile Pro Thr Ala Ser Ala Ala Thr Leu Thr Ala Asp Thr Asp Lys
             20                  25                  30

Glu Leu Cys Ile Ala Ser Asn Thr Asp Asp Ser Ala Val Val Thr Phe
         35                  40                  45

Trp Asn Ser Ile Glu Asp Ser Val Arg Glu Gln Arg Leu Asp Glu Leu
```

```
     50                  55                  60

Asp Ala Gln Asp Pro Gly Ile Lys Ala Ala Ile Glu Ser Tyr Ile Ala
 65                  70                  75                  80

Gln Asp Asp Asn Ala Pro Thr Ala Ala Glu Leu Gln Val Arg Leu Asp
                 85                  90                  95

Ala Ile Glu Ser Gly Glu Gly Leu Ala Met Leu Leu Pro Asp Asp Pro
            100                 105                 110

Thr Leu Ala Asp Pro Asn Ala Glu Glu Ser Phe Lys Thr Glu Tyr Thr
        115                 120                 125

Tyr Asp Glu Ala Lys Asp Ile Ile Ser Gly Phe Ser Ser Asp Pro Ala
    130                 135                 140

Ser Asp Val Leu Ser Gln Leu Gln Gln Ala Ala Thr Thr Gly Thr Arg
145                 150                 155                 160

Thr Ala Glu Ile Arg Ala Glu Val Phe Ala Asp Arg Thr Asp Asp Tyr
                165                 170                 175

Asn Glu Ser Gln Thr Ala Leu Lys Glu Asp Phe Gln Asn Cys Ile Asp
            180                 185                 190

Ala Ile Asp Asp Ala Arg Pro Ile Pro Leu Gln Tyr Ile Leu Ile Gly
        195                 200                 205

Gly Ala Ile Ala Leu Ala Val Ile Val Leu Gly Ile Arg Ala Trp Thr
    210                 215                 220

Asn Ser Arg Lys Gln Ser Lys His Ser Gln
225                 230


<210> 275
<211> 503
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(480)
<223> FRXA00515

<400> 275
att gaa agc tac atc gcc caa gat gac aac gcc cca act gct gct gaa   48
Ile Glu Ser Tyr Ile Ala Gln Asp Asp Asn Ala Pro Thr Ala Ala Glu
  1               5                  10                  15

ctg caa gta cgc ctc gat gcc atc gaa tcc ggc gaa ggc cta gcc atg   96
Leu Gln Val Arg Leu Asp Ala Ile Glu Ser Gly Glu Gly Leu Ala Met
             20                  25                  30

ctc ctc cca gac gat ccc acg ctg gca gac ccc aac gcc gag gaa agt   144
Leu Leu Pro Asp Asp Pro Thr Leu Ala Asp Pro Asn Ala Glu Glu Ser
         35                  40                  45

ttc aaa acg gag tac aca tac gac gaa gcc aaa gac atc atc agc gga   192
Phe Lys Thr Glu Tyr Thr Tyr Asp Glu Ala Lys Asp Ile Ile Ser Gly
```

```
     50                  55                  60

ttc tcc agc gat cca gcc agc gat gta ctc agc caa ctt caa caa gcc   240
Phe Ser Ser Asp Pro Ala Ser Asp Val Leu Ser Gln Leu Gln Gln Ala
 65                  70                  75                  80

gcc acc acc ggc acc cgc acc gca gaa atc cgc gcc gaa gta ttc gcc   288
Ala Thr Thr Gly Thr Arg Thr Ala Glu Ile Arg Ala Glu Val Phe Ala
                85                  90                  95

gac cgc acc gat gat tac aac gaa tcc caa acc gct ctt aaa gag gat   336
Asp Arg Thr Asp Asp Tyr Asn Glu Ser Gln Thr Ala Leu Lys Glu Asp
            100                 105                 110

ttc caa aac tgc atc gat gcc atc gat gac gcc cgc cca atc cca ctg   384
Phe Gln Asn Cys Ile Asp Ala Ile Asp Asp Ala Arg Pro Ile Pro Leu
        115                 120                 125

cag tac atc ctg att gga ggc gcc atc gct ttg gcg gtc atc gtc ctc   432
Gln Tyr Ile Leu Ile Gly Gly Ala Ile Ala Leu Ala Val Ile Val Leu
    130                 135                 140

ggg atc agg gcg tgg act aac tca agg aag cag tcc aag cac agc cag   480
Gly Ile Arg Ala Trp Thr Asn Ser Arg Lys Gln Ser Lys His Ser Gln
145                 150                 155                 160

taatacgcca agcaaaaaat tgc                                        503


<210> 276
<211> 160
<212> PRT
<213> Corynebacterium glutamicum

<400> 276
Ile Glu Ser Tyr Ile Ala Gln Asp Asp Asn Ala Pro Thr Ala Ala Glu
  1               5                  10                  15

Leu Gln Val Arg Leu Asp Ala Ile Glu Ser Gly Glu Gly Leu Ala Met
             20                  25                  30

Leu Leu Pro Asp Asp Pro Thr Leu Ala Asp Pro Asn Ala Glu Glu Ser
         35                  40                  45

Phe Lys Thr Glu Tyr Thr Tyr Asp Glu Ala Lys Asp Ile Ile Ser Gly
     50                  55                  60

Phe Ser Ser Asp Pro Ala Ser Asp Val Leu Ser Gln Leu Gln Gln Ala
 65                  70                  75                  80

Ala Thr Thr Gly Thr Arg Thr Ala Glu Ile Arg Ala Glu Val Phe Ala
                85                  90                  95

Asp Arg Thr Asp Asp Tyr Asn Glu Ser Gln Thr Ala Leu Lys Glu Asp
            100                 105                 110

Phe Gln Asn Cys Ile Asp Ala Ile Asp Asp Ala Arg Pro Ile Pro Leu
        115                 120                 125

Gln Tyr Ile Leu Ile Gly Gly Ala Ile Ala Leu Ala Val Ile Val Leu
    130                 135                 140
```

```
Gly Ile Arg Ala Trp Thr Asn Ser Arg Lys Gln Ser Lys His Ser Gln
145                 150                 155                 160
```

<210> 277
<211> 298
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(298)
<223> FRXA00520

<400> 277
gttgacgcac tgaagaagta aagtctcttc acaaaaagcg ctgtgcttcc tcacatggaa 60

```
gcacagcgct ttttcatatt tttattgcca taatgggcac atg cgt ttt tct cga   115
                                            Met Arg Phe Ser Arg
                                              1               5

gtt ctt ccc gca ctt ctt atc acc acc gcc gtg agc atc cca aca gca   163
Val Leu Pro Ala Leu Leu Ile Thr Thr Ala Val Ser Ile Pro Thr Ala
                10                  15                  20

tct gct gcc aca ctc acc ggc gac acc gac aag gaa ttg tgc atc gcc   211
Ser Ala Ala Thr Leu Thr Gly Asp Thr Asp Lys Glu Leu Cys Ile Ala
            25                  30                  35

agc aac acc gac gat tcc gcg gtg gtt acc ttc tgg aac tcc att gaa   259
Ser Asn Thr Asp Asp Ser Ala Val Val Thr Phe Trp Asn Ser Ile Glu
        40                  45                  50

gac tcc gtg cgc gaa caa cgc ctc gac gaa cta gac gcc               298
Asp Ser Val Arg Glu Gln Arg Leu Asp Glu Leu Asp Ala
    55                  60                  65
```

<210> 278
<211> 66
<212> PRT
<213> Corynebacterium glutamicum

<400> 278

```
Met Arg Phe Ser Arg Val Leu Pro Ala Leu Leu Ile Thr Thr Ala Val
  1               5                  10                  15

Ser Ile Pro Thr Ala Ser Ala Ala Thr Leu Thr Gly Asp Thr Asp Lys
            20                  25                  30

Glu Leu Cys Ile Ala Ser Asn Thr Asp Asp Ser Ala Val Val Thr Phe
        35                  40                  45

Trp Asn Ser Ile Glu Asp Ser Val Arg Glu Gln Arg Leu Asp Glu Leu
    50                  55                  60

Asp Ala
```

65

<210> 279
<211> 1887
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1864)
<223> RXN00527

<400> 279
ttccttggcc ccgaagaaat taatcattgt ggccgtggtc ctgattttga tcattgcggc 60

tgcctcgttt tattttctgc gttcatcatc gaatgaccag gtg att gcc act tct 115
Val Ile Ala Thr Ser
1 5

gat gtt cgg gag att tcc tcc gag gga atc gtg gcg cgt gtg tct gtc 163
Asp Val Arg Glu Ile Ser Ser Glu Gly Ile Val Ala Arg Val Ser Val
10 15 20

aac gga aat att gaa gct gcg cga acc acc acc att tac acc agt ctg 211
Asn Gly Asn Ile Glu Ala Ala Arg Thr Thr Thr Ile Tyr Thr Ser Leu
25 30 35

act gtg ccg gtc gcg aac ttg ccg gtt gcg gtt ggt gac cgt gtg gca 259
Thr Val Pro Val Ala Asn Leu Pro Val Ala Val Gly Asp Arg Val Ala
40 45 50

gct gat cag gtg ttg gct gag ttg gat gcc tct gcc ctg caa cga cag 307
Ala Asp Gln Val Leu Ala Glu Leu Asp Ala Ser Ala Leu Gln Arg Gln
55 60 65

ttg gat gaa act gat gcc aac aat gcg cgt gca gcc atg gcg aac cgc 355
Leu Asp Glu Thr Asp Ala Asn Asn Ala Arg Ala Ala Met Ala Asn Arg
70 75 80 85

aat tcc atc gcg cag tcg cag caa gca tat gag cag tcc agg gaa ctt 403
Asn Ser Ile Ala Gln Ser Gln Gln Ala Tyr Glu Gln Ser Arg Glu Leu
90 95 100

ctt gat agt ggt ttg agc ccg gag atc aac tcg gcg cgg tcc tcg ttg 451
Leu Asp Ser Gly Leu Ser Pro Glu Ile Asn Ser Ala Arg Ser Ser Leu
105 110 115

cgg gcg tcc tca cag gca tat cag gat gcg atc cgc agt ttt gaa gcg 499
Arg Ala Ser Ser Gln Ala Tyr Gln Asp Ala Ile Arg Ser Phe Glu Ala
120 125 130

aag cag cga gat gtg gat ggc gga ttg gat tcc acc atg gtc gct caa 547
Lys Gln Arg Asp Val Asp Gly Gly Leu Asp Ser Thr Met Val Ala Gln
135 140 145

tcg gat gct ctc aag gca gct cgt gag caa gca gat gct gct gaa att 595
Ser Asp Ala Leu Lys Ala Ala Arg Glu Gln Ala Asp Ala Ala Glu Ile
150 155 160 165

gaa cga ctg cgc gcg gac ttc gga ctg ctc aac aac gat cgc agc aac 643

```
Glu Arg Leu Arg Ala Asp Phe Gly Leu Leu Asn Asn Asp Arg Ser Asn
                170                 175                 180

ctc aac gat gtc att ggt ctg ctc gat gag aga gaa tct ttg gct tct   691
Leu Asn Asp Val Ile Gly Leu Leu Asp Glu Arg Glu Ser Leu Ala Ser
            185                 190                 195

gcg gaa tcc gaa cta gct caa gcc cgc gct gca ggt gac cta gag gca   739
Ala Glu Ser Glu Leu Ala Gln Ala Arg Ala Ala Gly Asp Leu Glu Ala
        200                 205                 210

gtc gct gca gct gaa gca aag gtt gca ggc ctg gaa caa tca att gct   787
Val Ala Ala Ala Glu Ala Lys Val Ala Gly Leu Glu Gln Ser Ile Ala
    215                 220                 225

tcc aaa acc tcc acg tgg cct agc caa gat cag act tac ttg cag tcc   835
Ser Lys Thr Ser Thr Trp Pro Ser Gln Asp Gln Thr Tyr Leu Gln Ser
230                 235                 240                 245

tac acc gct ttg gag gaa gct gag cga cgc gtc gca tcc acc act gaa   883
Tyr Thr Ala Leu Glu Glu Ala Glu Arg Arg Val Ala Ser Thr Thr Glu
                250                 255                 260

gct cta gaa ata gcc gag cgg atc tac att gat tca ctc gga aaa gtt   931
Ala Leu Glu Ile Ala Glu Arg Ile Tyr Ile Asp Ser Leu Gly Lys Val
            265                 270                 275

gac tca gaa cta gcc gcc gca cag cgc gcc gtt gcc gaa gcc cac tca   979
Asp Ser Glu Leu Ala Ala Ala Gln Arg Ala Val Ala Glu Ala His Ser
        280                 285                 290

gca caa caa gac gca gca ctt ggc ctc gag acc gcg cag ctt tcc acc   1027
Ala Gln Gln Asp Ala Ala Leu Gly Leu Glu Thr Ala Gln Leu Ser Thr
    295                 300                 305

caa cac caa ttg gaa gcc caa tca agc gcc atc gat gca gct tta ggt   1075
Gln His Gln Leu Glu Ala Gln Ser Ser Ala Ile Asp Ala Ala Leu Gly
310                 315                 320                 325

ttg gca tca gta gat aat gaa gcc gcc acc aga tcc acg tcc cag ctg   1123
Leu Ala Ser Val Asp Asn Glu Ala Ala Thr Arg Ser Thr Ser Gln Leu
                330                 335                 340

cgg atg gat atc aac aac acc acc gtt cgc tcc cca tac tca ggc att   1171
Arg Met Asp Ile Asn Asn Thr Thr Val Arg Ser Pro Tyr Ser Gly Ile
            345                 350                 355

gtt tca tcc gtg cag gca gcc caa ggt caa cca gca gcc ggc gca ctg   1219
Val Ser Ser Val Gln Ala Ala Gln Gly Gln Pro Ala Ala Gly Ala Leu
        360                 365                 370

ttg agt gtt gct gat gat tcc gaa ctg aag atc acc gcg aat gta aaa   1267
Leu Ser Val Ala Asp Asp Ser Glu Leu Lys Ile Thr Ala Asn Val Lys
    375                 380                 385

gaa gcg gag atc agc aac gtc acc atc gga tcc cgc gtc acc ttc act   1315
Glu Ala Glu Ile Ser Asn Val Thr Ile Gly Ser Arg Val Thr Phe Thr
390                 395                 400                 405

acc cca tcg acc gga acc aaa gaa ttc gcc ggc cga gta tcc aaa gtc   1363
Thr Pro Ser Thr Gly Thr Lys Glu Phe Ala Gly Arg Val Ser Lys Val
```

```
                410                 415                 420

tcc ccc att gca gct gcc gcc agt gcc cca gct aca ggt gaa gga gct   1411
Ser Pro Ile Ala Ala Ala Ala Ser Ala Pro Ala Thr Gly Glu Gly Ala
            425                 430                 435

gcc gca ggc gcc aca acc acc aac act gac gtc acc ttc ccc atc gaa   1459
Ala Ala Gly Ala Thr Thr Thr Asn Thr Asp Val Thr Phe Pro Ile Glu
        440                 445                 450

att tcc gtc acc ggc gac cgc gaa ggc ctc aac ctc ggc gga tcc gct   1507
Ile Ser Val Thr Gly Asp Arg Glu Gly Leu Asn Leu Gly Gly Ser Ala
    455                 460                 465

cga gta cgc atc gtc cat gaa atc gca cca cac gta ctg acc gtt cct   1555
Arg Val Arg Ile Val His Glu Ile Ala Pro His Val Leu Thr Val Pro
470                 475                 480                 485

ttg gaa gct gtg tac aaa aat gat gac ggc aaa gac gct gtt ttg atc   1603
Leu Glu Ala Val Tyr Lys Asn Asp Asp Gly Lys Asp Ala Val Leu Ile
                490                 495                 500

atc agc gac gac aac aaa gta gaa gaa gta gaa gta aaa aca gct gaa   1651
Ile Ser Asp Asp Asn Lys Val Glu Glu Val Glu Val Lys Thr Ala Glu
            505                 510                 515

tcc gat gac ttt gat atc gca gtc agc ggt gct gga att tca gaa gac   1699
Ser Asp Asp Phe Asp Ile Ala Val Ser Gly Ala Gly Ile Ser Glu Asp
        520                 525                 530

gct cga gtg ctc acc cag cct gga aac tac cgg ggc ctc atc gga gaa   1747
Ala Arg Val Leu Thr Gln Pro Gly Asn Tyr Arg Gly Leu Ile Gly Glu
    535                 540                 545

act gtg aaa ctt cac gca gat acg gtg gag cag gcg gcg gct cct ttt   1795
Thr Val Lys Leu His Ala Asp Thr Val Glu Gln Ala Ala Ala Pro Phe
550                 555                 560                 565

agt cct gcg gcc cct ttt gac cct gca gcc cct gcc gtt tct gcc aag   1843
Ser Pro Ala Ala Pro Phe Asp Pro Ala Ala Pro Ala Val Ser Ala Lys
                570                 575                 580

caa acc gtg ggc cag gtg att tagcctatga gcctcatcga aat             1887
Gln Thr Val Gly Gln Val Ile
            585
```

<210> 280
<211> 588
<212> PRT
<213> Corynebacterium glutamicum

<400> 280

```
Val Ile Ala Thr Ser Asp Val Arg Glu Ile Ser Ser Glu Gly Ile Val
  1               5                  10                  15

Ala Arg Val Ser Val Asn Gly Asn Ile Glu Ala Ala Arg Thr Thr Thr
             20                  25                  30

Ile Tyr Thr Ser Leu Thr Val Pro Val Ala Asn Leu Pro Val Ala Val
         35                  40                  45
```

```
Gly Asp Arg Val Ala Ala Asp Gln Val Leu Ala Glu Leu Asp Ala Ser
     50                  55                  60

Ala Leu Gln Arg Gln Leu Asp Glu Thr Asp Ala Asn Asn Ala Arg Ala
 65                  70                  75                  80

Ala Met Ala Asn Arg Asn Ser Ile Ala Gln Ser Gln Gln Ala Tyr Glu
                 85                  90                  95

Gln Ser Arg Glu Leu Leu Asp Ser Gly Leu Ser Pro Glu Ile Asn Ser
            100                 105                 110

Ala Arg Ser Ser Leu Arg Ala Ser Ser Gln Ala Tyr Gln Asp Ala Ile
        115                 120                 125

Arg Ser Phe Glu Ala Lys Gln Arg Asp Val Asp Gly Gly Leu Asp Ser
    130                 135                 140

Thr Met Val Ala Gln Ser Asp Ala Leu Lys Ala Ala Arg Glu Gln Ala
145                 150                 155                 160

Asp Ala Ala Glu Ile Glu Arg Leu Arg Ala Asp Phe Gly Leu Leu Asn
                165                 170                 175

Asn Asp Arg Ser Asn Leu Asn Asp Val Ile Gly Leu Leu Asp Glu Arg
            180                 185                 190

Glu Ser Leu Ala Ser Ala Glu Ser Glu Leu Ala Gln Ala Arg Ala Ala
        195                 200                 205

Gly Asp Leu Glu Ala Val Ala Ala Ala Glu Ala Lys Val Ala Gly Leu
    210                 215                 220

Glu Gln Ser Ile Ala Ser Lys Thr Ser Thr Trp Pro Ser Gln Asp Gln
225                 230                 235                 240

Thr Tyr Leu Gln Ser Tyr Thr Ala Leu Glu Glu Ala Glu Arg Arg Val
                245                 250                 255

Ala Ser Thr Thr Glu Ala Leu Glu Ile Ala Glu Arg Ile Tyr Ile Asp
            260                 265                 270

Ser Leu Gly Lys Val Asp Ser Glu Leu Ala Ala Ala Gln Arg Ala Val
        275                 280                 285

Ala Glu Ala His Ser Ala Gln Gln Asp Ala Ala Leu Gly Leu Glu Thr
    290                 295                 300

Ala Gln Leu Ser Thr Gln His Gln Leu Glu Ala Gln Ser Ser Ala Ile
305                 310                 315                 320

Asp Ala Ala Leu Gly Leu Ala Ser Val Asp Asn Glu Ala Ala Thr Arg
                325                 330                 335

Ser Thr Ser Gln Leu Arg Met Asp Ile Asn Asn Thr Thr Val Arg Ser
            340                 345                 350

Pro Tyr Ser Gly Ile Val Ser Ser Val Gln Ala Ala Gln Gly Gln Pro
        355                 360                 365
```

```
Ala Ala Gly Ala Leu Leu Ser Val Ala Asp Asp Ser Glu Leu Lys Ile
    370                 375                 380

Thr Ala Asn Val Lys Glu Ala Glu Ile Ser Asn Val Thr Ile Gly Ser
385                 390                 395                 400

Arg Val Thr Phe Thr Thr Pro Ser Thr Gly Thr Lys Glu Phe Ala Gly
                405                 410                 415

Arg Val Ser Lys Val Ser Pro Ile Ala Ala Ala Ala Ser Ala Pro Ala
            420                 425                 430

Thr Gly Glu Gly Ala Ala Ala Gly Ala Thr Thr Thr Asn Thr Asp Val
        435                 440                 445

Thr Phe Pro Ile Glu Ile Ser Val Thr Gly Asp Arg Glu Gly Leu Asn
    450                 455                 460

Leu Gly Gly Ser Ala Arg Val Arg Ile Val His Glu Ile Ala Pro His
465                 470                 475                 480

Val Leu Thr Val Pro Leu Glu Ala Val Tyr Lys Asn Asp Asp Gly Lys
                485                 490                 495

Asp Ala Val Leu Ile Ile Ser Asp Asp Asn Lys Val Glu Glu Val Glu
            500                 505                 510

Val Lys Thr Ala Glu Ser Asp Asp Phe Asp Ile Ala Val Ser Gly Ala
        515                 520                 525

Gly Ile Ser Glu Asp Ala Arg Val Leu Thr Gln Pro Gly Asn Tyr Arg
    530                 535                 540

Gly Leu Ile Gly Glu Thr Val Lys Leu His Ala Asp Thr Val Glu Gln
545                 550                 555                 560

Ala Ala Ala Pro Phe Ser Pro Ala Ala Pro Phe Asp Pro Ala Ala Pro
                565                 570                 575

Ala Val Ser Ala Lys Gln Thr Val Gly Gln Val Ile
            580                 585
```

<210> 281
<211> 1887
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1864)
<223> FRXA00527

<400> 281
ttccttggcc ccgaagaaat taatcattgt ggccgtggtc ctgattttga tcattgcggc 60

tgcctcgttt tattttctgc gttcatcatc gaatgaccag gtg att gcc act tct 115
                                                Val Ile Ala Thr Ser
                                                  1   5

gat gtt cgg gag att tcc tcc gag gga atc gtg gcg cgt gtg tct gtc 163

```
Asp Val Arg Glu Ile Ser Ser Glu Gly Ile Val Ala Arg Val Ser Val
                10                  15                  20

aac gga aat att gaa gct gcg cga acc acc acc att tac acc agt ctg   211
Asn Gly Asn Ile Glu Ala Ala Arg Thr Thr Thr Ile Tyr Thr Ser Leu
            25                  30                  35

act gtg ccg gtc gcg aac ttg ccg gtt gcg gtt ggt gac cgt gtg gca   259
Thr Val Pro Val Ala Asn Leu Pro Val Ala Val Gly Asp Arg Val Ala
        40                  45                  50

gct gat cag gtg ttg gct gag ttg gat gcc tct gcc ctg caa cga cag   307
Ala Asp Gln Val Leu Ala Glu Leu Asp Ala Ser Ala Leu Gln Arg Gln
    55                  60                  65

ttg gat gaa act gat gcc aac aat gcg cgt gca gcc atg gcg aac cgc   355
Leu Asp Glu Thr Asp Ala Asn Asn Ala Arg Ala Ala Met Ala Asn Arg
70                  75                  80                  85

aat tcc atc gcg cag tcg cag caa gca tat gag cag tcc agg gaa ctt   403
Asn Ser Ile Ala Gln Ser Gln Gln Ala Tyr Glu Gln Ser Arg Glu Leu
                90                  95                  100

ctt gat agt ggt ttg agc ccg gag atc aac tcg gcg cgg tcc tcg ttg   451
Leu Asp Ser Gly Leu Ser Pro Glu Ile Asn Ser Ala Arg Ser Ser Leu
            105                 110                 115

cgg gcg tcc tca cag gca tat cag gat gcg atc cgc agt ttt gaa gcg   499
Arg Ala Ser Ser Gln Ala Tyr Gln Asp Ala Ile Arg Ser Phe Glu Ala
        120                 125                 130

aag cag cga gat gtg gat ggc gga ttg gat tcc acc atg gtc gct caa   547
Lys Gln Arg Asp Val Asp Gly Gly Leu Asp Ser Thr Met Val Ala Gln
    135                 140                 145

tcg gat gct ctc aag gca gct cgt gag caa gca gat gct gct gaa att   595
Ser Asp Ala Leu Lys Ala Ala Arg Glu Gln Ala Asp Ala Ala Glu Ile
150                 155                 160                 165

gaa cga ctg cgc gcg gac ttc gga ctg ctc aac aac gat cgc agc aac   643
Glu Arg Leu Arg Ala Asp Phe Gly Leu Leu Asn Asn Asp Arg Ser Asn
                170                 175                 180

ctc aac gat gtc att ggt ctg ctc gat gag aga gaa tct ttg gct tct   691
Leu Asn Asp Val Ile Gly Leu Leu Asp Glu Arg Glu Ser Leu Ala Ser
            185                 190                 195

gcg gaa tcc gaa cta gct caa gcc cgc gct gca ggt gac cta gag gca   739
Ala Glu Ser Glu Leu Ala Gln Ala Arg Ala Ala Gly Asp Leu Glu Ala
        200                 205                 210

gtc gct gca gct gaa gca aag gtt gca ggc ctg gaa caa tca att gct   787
Val Ala Ala Ala Glu Ala Lys Val Ala Gly Leu Glu Gln Ser Ile Ala
    215                 220                 225

tcc aaa acc tcc acg tgg cct agc caa gat cag act tac ttg cag tcc   835
Ser Lys Thr Ser Thr Trp Pro Ser Gln Asp Gln Thr Tyr Leu Gln Ser
230                 235                 240                 245

tac acc gct ttg gag gaa gct gag cga cgc gtc gca tcc acc act gaa   883
Tyr Thr Ala Leu Glu Glu Ala Glu Arg Arg Val Ala Ser Thr Thr Glu
```

```
                250                 255                 260

gct cta gaa ata gcc gag cgg atc tac att gat tca ctc gga aaa gtt   931
Ala Leu Glu Ile Ala Glu Arg Ile Tyr Ile Asp Ser Leu Gly Lys Val
            265                 270                 275

gac tca gaa cta gcc gcc gca cag cgc gcc gtt gcc gaa gcc cac tca   979
Asp Ser Glu Leu Ala Ala Ala Gln Arg Ala Val Ala Glu Ala His Ser
        280                 285                 290

gca caa caa gac gca gca ctt ggc ctc gag acc gcg cag ctt tcc acc   1027
Ala Gln Gln Asp Ala Ala Leu Gly Leu Glu Thr Ala Gln Leu Ser Thr
    295                 300                 305

caa cac caa ttg gaa gcc caa tca agc gcc atc gat gca gct tta ggt   1075
Gln His Gln Leu Glu Ala Gln Ser Ser Ala Ile Asp Ala Ala Leu Gly
310                 315                 320                 325

ttg gca tca gta gat aat gaa gcc gcc acc aga tcc acg tcc cag ctg   1123
Leu Ala Ser Val Asp Asn Glu Ala Ala Thr Arg Ser Thr Ser Gln Leu
                330                 335                 340

cgg atg gat atc aac aac acc acc gtt cgc tcc cca tac tca ggc att   1171
Arg Met Asp Ile Asn Asn Thr Thr Val Arg Ser Pro Tyr Ser Gly Ile
            345                 350                 355

gtt tca tcc gtg cag gca gcc caa ggt caa cca gca gcc ggc gca ctg   1219
Val Ser Ser Val Gln Ala Ala Gln Gly Gln Pro Ala Ala Gly Ala Leu
        360                 365                 370

ttg agt gtt gct gat gat tcc gaa ctg aag atc acc gcg aat gta aaa   1267
Leu Ser Val Ala Asp Asp Ser Glu Leu Lys Ile Thr Ala Asn Val Lys
    375                 380                 385

gaa gcg gag atc agc aac gtc acc atc gga tcc cgc gtc acc ttc act   1315
Glu Ala Glu Ile Ser Asn Val Thr Ile Gly Ser Arg Val Thr Phe Thr
390                 395                 400                 405

acc cca tcg acc gga acc aaa gaa ttc gcc ggc cga gta tcc aaa gtc   1363
Thr Pro Ser Thr Gly Thr Lys Glu Phe Ala Gly Arg Val Ser Lys Val
                410                 415                 420

tcc ccc att gca gct gcc gcc agt gcc cca gct aca ggt gaa gga gct   1411
Ser Pro Ile Ala Ala Ala Ala Ser Ala Pro Ala Thr Gly Glu Gly Ala
            425                 430                 435

gcc gca ggc gcc aca acc acc aac act gac gtc acc ttc ccc atc gaa   1459
Ala Ala Gly Ala Thr Thr Thr Asn Thr Asp Val Thr Phe Pro Ile Glu
        440                 445                 450

att tcc gtc acc ggc gac cgc gaa ggc ctc aac ctc ggc gga tcc gct   1507
Ile Ser Val Thr Gly Asp Arg Glu Gly Leu Asn Leu Gly Gly Ser Ala
    455                 460                 465

cga gta cgc atc gtc cat gaa atc gca cca cac gta ctg acc gtt cct   1555
Arg Val Arg Ile Val His Glu Ile Ala Pro His Val Leu Thr Val Pro
470                 475                 480                 485

ttg gaa gct gtg tac aaa aat gat gac ggc aaa gac gct gtt ttg atc   1603
Leu Glu Ala Val Tyr Lys Asn Asp Asp Gly Lys Asp Ala Val Leu Ile
                490                 495                 500
```

```
atc agc gac gac aac aaa gta gaa gaa gta gaa gta aaa aca gct gaa   1651
Ile Ser Asp Asp Asn Lys Val Glu Glu Val Glu Val Lys Thr Ala Glu
            505                 510                 515

tcc gat gac ttt gat atc gca gtc agc ggt gct gga att tca gaa gac   1699
Ser Asp Asp Phe Asp Ile Ala Val Ser Gly Ala Gly Ile Ser Glu Asp
        520                 525                 530

gct cga gtg ctc acc cag cct gga aac tac cgg ggc ctc atc gga gaa   1747
Ala Arg Val Leu Thr Gln Pro Gly Asn Tyr Arg Gly Leu Ile Gly Glu
    535                 540                 545

act gtg aaa ctt cac gca gat acg gtg gag cag gcg gcg gct cct ttt   1795
Thr Val Lys Leu His Ala Asp Thr Val Glu Gln Ala Ala Ala Pro Phe
550                 555                 560                 565

agt cct gcg gcc cct ttt gac cct gca gcc cct gcc gtt tct gcc aag   1843
Ser Pro Ala Ala Pro Phe Asp Pro Ala Ala Pro Ala Val Ser Ala Lys
                570                 575                 580

caa acc gtg ggc cag gtg att tagcctatga gcctcatcga aat             1887
Gln Thr Val Gly Gln Val Ile
            585
```

<210> 282
<211> 588
<212> PRT
<213> Corynebacterium glutamicum

<400> 282

```
Val Ile Ala Thr Ser Asp Val Arg Glu Ile Ser Ser Glu Gly Ile Val
  1               5                  10                  15

Ala Arg Val Ser Val Asn Gly Asn Ile Glu Ala Ala Arg Thr Thr Thr
             20                  25                  30

Ile Tyr Thr Ser Leu Thr Val Pro Val Ala Asn Leu Pro Val Ala Val
         35                  40                  45

Gly Asp Arg Val Ala Ala Asp Gln Val Leu Ala Glu Leu Asp Ala Ser
     50                  55                  60

Ala Leu Gln Arg Gln Leu Asp Glu Thr Asp Ala Asn Asn Ala Arg Ala
 65                  70                  75                  80

Ala Met Ala Asn Arg Asn Ser Ile Ala Gln Ser Gln Gln Ala Tyr Glu
                 85                  90                  95

Gln Ser Arg Glu Leu Leu Asp Ser Gly Leu Ser Pro Glu Ile Asn Ser
            100                 105                 110

Ala Arg Ser Ser Leu Arg Ala Ser Ser Gln Ala Tyr Gln Asp Ala Ile
        115                 120                 125

Arg Ser Phe Glu Ala Lys Gln Arg Asp Val Asp Gly Gly Leu Asp Ser
    130                 135                 140

Thr Met Val Ala Gln Ser Asp Ala Leu Lys Ala Ala Arg Glu Gln Ala
145                 150                 155                 160
```

```
Asp Ala Ala Glu Ile Glu Arg Leu Arg Ala Asp Phe Gly Leu Leu Asn
                165                 170                 175

Asn Asp Arg Ser Asn Leu Asn Asp Val Ile Gly Leu Leu Asp Glu Arg
            180                 185                 190

Glu Ser Leu Ala Ser Ala Glu Ser Glu Leu Ala Gln Ala Arg Ala Ala
        195                 200                 205

Gly Asp Leu Glu Ala Val Ala Ala Ala Glu Ala Lys Val Ala Gly Leu
    210                 215                 220

Glu Gln Ser Ile Ala Ser Lys Thr Ser Thr Trp Pro Ser Gln Asp Gln
225                 230                 235                 240

Thr Tyr Leu Gln Ser Tyr Thr Ala Leu Glu Glu Ala Glu Arg Arg Val
                245                 250                 255

Ala Ser Thr Thr Glu Ala Leu Glu Ile Ala Glu Arg Ile Tyr Ile Asp
            260                 265                 270

Ser Leu Gly Lys Val Asp Ser Glu Leu Ala Ala Ala Gln Arg Ala Val
        275                 280                 285

Ala Glu Ala His Ser Ala Gln Gln Asp Ala Ala Leu Gly Leu Glu Thr
    290                 295                 300

Ala Gln Leu Ser Thr Gln His Gln Leu Glu Ala Gln Ser Ser Ala Ile
305                 310                 315                 320

Asp Ala Ala Leu Gly Leu Ala Ser Val Asp Asn Glu Ala Ala Thr Arg
                325                 330                 335

Ser Thr Ser Gln Leu Arg Met Asp Ile Asn Asn Thr Thr Val Arg Ser
            340                 345                 350

Pro Tyr Ser Gly Ile Val Ser Ser Val Gln Ala Ala Gln Gly Gln Pro
        355                 360                 365

Ala Ala Gly Ala Leu Leu Ser Val Ala Asp Asp Ser Glu Leu Lys Ile
    370                 375                 380

Thr Ala Asn Val Lys Glu Ala Glu Ile Ser Asn Val Thr Ile Gly Ser
385                 390                 395                 400

Arg Val Thr Phe Thr Thr Pro Ser Thr Gly Thr Lys Glu Phe Ala Gly
                405                 410                 415

Arg Val Ser Lys Val Ser Pro Ile Ala Ala Ala Ala Ser Ala Pro Ala
            420                 425                 430

Thr Gly Glu Gly Ala Ala Ala Gly Ala Thr Thr Thr Asn Thr Asp Val
        435                 440                 445

Thr Phe Pro Ile Glu Ile Ser Val Thr Gly Asp Arg Glu Gly Leu Asn
    450                 455                 460

Leu Gly Gly Ser Ala Arg Val Arg Ile Val His Glu Ile Ala Pro His
465                 470                 475                 480
```

```
Val Leu Thr Val Pro Leu Glu Ala Val Tyr Lys Asn Asp Asp Gly Lys
                485                 490                 495

Asp Ala Val Leu Ile Ile Ser Asp Asp Asn Lys Val Glu Glu Val Glu
            500                 505                 510

Val Lys Thr Ala Glu Ser Asp Asp Phe Asp Ile Ala Val Ser Gly Ala
        515                 520                 525

Gly Ile Ser Glu Asp Ala Arg Val Leu Thr Gln Pro Gly Asn Tyr Arg
    530                 535                 540

Gly Leu Ile Gly Glu Thr Val Lys Leu His Ala Asp Thr Val Glu Gln
545                 550                 555                 560

Ala Ala Ala Pro Phe Ser Pro Ala Ala Pro Phe Asp Pro Ala Ala Pro
                565                 570                 575

Ala Val Ser Ala Lys Gln Thr Val Gly Gln Val Ile
            580                 585
```

<210> 283
<211> 1521
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1498)
<223> RXN00547

<400> 283

```
ggtcgtagcc taaacgacct taaaaaggag ccgaccgccg atggaccaga aattggacca 60

gcagaaggta gaccgcgtat cgcccggtga tagtgaaccg gtg gca cgg gat ttt   115
                                          Val Ala Arg Asp Phe
                                            1               5

atc aat gca atc ggc ggt cgg ttt ggt cgt ttt gcg cag gtg ggc act   163
Ile Asn Ala Ile Gly Gly Arg Phe Gly Arg Phe Ala Gln Val Gly Thr
                10                  15                  20

cag cgg ttc tgg act ccc ctg cgt gtt ttg atc acc act tcc ctg gtg   211
Gln Arg Phe Trp Thr Pro Leu Arg Val Leu Ile Thr Thr Ser Leu Val
            25                  30                  35

ttt ttg gcc atg ggg ttt tta aca aaa gcc aat tgc atc cag ggt tct   259
Phe Leu Ala Met Gly Phe Leu Thr Lys Ala Asn Cys Ile Gln Gly Ser
        40                  45                  50

aga ggt act gat ggt gtg gtt tct ttg aac tgg tcg gga agt cgc cag   307
Arg Gly Thr Asp Gly Val Val Ser Leu Asn Trp Ser Gly Ser Arg Gln
    55                  60                  65

tac acc tca gcc tgt tac aac gac atc gtt ccg ctc tat ggg ggg cgc   355
Tyr Thr Ser Ala Cys Tyr Asn Asp Ile Val Pro Leu Tyr Gly Gly Arg
70                  75                  80                  85

gga att gat gcg cca ggt ttc cct tat gcc ttt tcg tgg cag gaa ggt   403
Gly Ile Asp Ala Pro Gly Phe Pro Tyr Ala Phe Ser Trp Gln Glu Gly
```

```
                90                  95                 100

gat ctc acc agg tac atg gag tac ccg gtg ttg ggc gga att ttc cag   451
Asp Leu Thr Arg Tyr Met Glu Tyr Pro Val Leu Gly Gly Ile Phe Gln
            105                 110                 115

tgg att tgt ggc att atc acg cgg ttt ttg tac ccg gtt gtt gat gtc   499
Trp Ile Cys Gly Ile Ile Thr Arg Phe Leu Tyr Pro Val Val Asp Val
        120                 125                 130

att ccg ttt cat acg ctg cct gaa tct ggt ctt tat ttc atc gtc acc   547
Ile Pro Phe His Thr Leu Pro Glu Ser Gly Leu Tyr Phe Ile Val Thr
    135                 140                 145

gcg ctt gcg ttg gcg ttc ttt tgg gtg ttg gtc atc cgc atg atg gtg   595
Ala Leu Ala Leu Ala Phe Phe Trp Val Leu Val Ile Arg Met Met Val
150                 155                 160                 165

gag ctc act ggc aat cga gtg tgg gat acc gtc ctt gtt gcg gcg tct   643
Glu Leu Thr Gly Asn Arg Val Trp Asp Thr Val Leu Val Ala Ala Ser
                170                 175                 180

ccc ctg gtt gct gtg cat gcg ttt acc aac tgg gat act cca gcc att   691
Pro Leu Val Ala Val His Ala Phe Thr Asn Trp Asp Thr Pro Ala Ile
            185                 190                 195

gcg gcg gtg att ggt gcg atg ctt gcg gtg aaa cgc gga aac ccc ttg   739
Ala Ala Val Ile Gly Ala Met Leu Ala Val Lys Arg Gly Asn Pro Leu
        200                 205                 210

gtt gcg ggt gtg ctg atc ggc gcg ggt acg gcg ttc aaa ttg tgg ccg   787
Val Ala Gly Val Leu Ile Gly Ala Gly Thr Ala Phe Lys Leu Trp Pro
    215                 220                 225

ctt tat ctt ctt ggt gcg tat ttg gtg ctg gcg gtc aag aat aag aat   835
Leu Tyr Leu Leu Gly Ala Tyr Leu Val Leu Ala Val Lys Asn Lys Asn
230                 235                 240                 245

ctc aag ccg ttt atc acc atg gct gca gcg gct gcg gtg aca tgg ctc   883
Leu Lys Pro Phe Ile Thr Met Ala Ala Ala Ala Ala Val Thr Trp Leu
                250                 255                 260

gtg gtg aat gtg cca gtg atg atc gcg tac ccc aag gcg tgg aat gaa   931
Val Val Asn Val Pro Val Met Ile Ala Tyr Pro Lys Ala Trp Asn Glu
            265                 270                 275

ttc ttg cgc ctg aac cgg gag cgt ggt gcg gag tgg acc acg att tac   979
Phe Leu Arg Leu Asn Arg Glu Arg Gly Ala Glu Trp Thr Thr Ile Tyr
        280                 285                 290

cag gtc atc gac cgt aat ttg ccg atc aat ttg aat gat cca gtg ctg   1027
Gln Val Ile Asp Arg Asn Leu Pro Ile Asn Leu Asn Asp Pro Val Leu
    295                 300                 305

ctt aat gtg ctg agc ttc ggc ttg ttt ggt gca tcg tgt gtg gcc att   1075
Leu Asn Val Leu Ser Phe Gly Leu Phe Gly Ala Ser Cys Val Ala Ile
310                 315                 320                 325

ttg atc ctt ggg ctc aag gtg cag cgc act ccc cga gtc gct gag ctg   1123
Leu Ile Leu Gly Leu Lys Val Gln Arg Thr Pro Arg Val Ala Glu Leu
                330                 335                 340
```

```
gcc ttt ttg att gtc gcg gcg ttt ttg ctg ttt aac aag gtg tgg agt   1171
Ala Phe Leu Ile Val Ala Ala Phe Leu Leu Phe Asn Lys Val Trp Ser
            345                 350                 355

cct cag tat tca ctg tgg ctg gtc ccg ttg gct gtt ctg gca ttt cct   1219
Pro Gln Tyr Ser Leu Trp Leu Val Pro Leu Ala Val Leu Ala Phe Pro
        360                 365                 370

cag tgg aaa gtg ctg ttc ccg tgg atg gtt aca gac gcc atg gtg tgg   1267
Gln Trp Lys Val Leu Phe Pro Trp Met Val Thr Asp Ala Met Val Trp
    375                 380                 385

cca att ttg atg tgg cac atg ctc ggc acg gac aac aag gga ctc ccc   1315
Pro Ile Leu Met Trp His Met Leu Gly Thr Asp Asn Lys Gly Leu Pro
390                 395                 400                 405

cat gaa atg ttg gat ctc atc gtg att tcc cga gat gcc ttc att gtg   1363
His Glu Met Leu Asp Leu Ile Val Ile Ser Arg Asp Ala Phe Ile Val
                410                 415                 420

gtc atg ata gta ggt gta atc cgg cag atg ctc gga cga cgt gca gat   1411
Val Met Ile Val Gly Val Ile Arg Gln Met Leu Gly Arg Arg Ala Asp
            425                 430                 435

ccg gtg atg gat gcg cac gcc ggg cgc gat ttg ttg gcc ggg ccc ttc   1459
Pro Val Met Asp Ala His Ala Gly Arg Asp Leu Leu Ala Gly Pro Phe
        440                 445                 450

ggc gca ggc gag cgt cga aaa gca ttg aag gaa gta agt tgagcacaac    1508
Gly Ala Gly Glu Arg Arg Lys Ala Leu Lys Glu Val Ser
    455                 460                 465

agttttgctg gtc                                                   1521


<210> 284
<211> 466
<212> PRT
<213> Corynebacterium glutamicum

<400> 284
Val Ala Arg Asp Phe Ile Asn Ala Ile Gly Gly Arg Phe Gly Arg Phe
  1               5                  10                  15

Ala Gln Val Gly Thr Gln Arg Phe Trp Thr Pro Leu Arg Val Leu Ile
             20                  25                  30

Thr Thr Ser Leu Val Phe Leu Ala Met Gly Phe Leu Thr Lys Ala Asn
         35                  40                  45

Cys Ile Gln Gly Ser Arg Gly Thr Asp Gly Val Val Ser Leu Asn Trp
     50                  55                  60

Ser Gly Ser Arg Gln Tyr Thr Ser Ala Cys Tyr Asn Asp Ile Val Pro
 65                  70                  75                  80

Leu Tyr Gly Gly Arg Gly Ile Asp Ala Pro Gly Phe Pro Tyr Ala Phe
                 85                  90                  95

Ser Trp Gln Glu Gly Asp Leu Thr Arg Tyr Met Glu Tyr Pro Val Leu
```

```
            100                 105                 110

Gly Gly Ile Phe Gln Trp Ile Cys Gly Ile Ile Thr Arg Phe Leu Tyr
        115                 120                 125

Pro Val Val Asp Val Ile Pro Phe His Thr Leu Pro Glu Ser Gly Leu
    130                 135                 140

Tyr Phe Ile Val Thr Ala Leu Ala Leu Ala Phe Phe Trp Val Leu Val
145                 150                 155                 160

Ile Arg Met Met Val Glu Leu Thr Gly Asn Arg Val Trp Asp Thr Val
                165                 170                 175

Leu Val Ala Ala Ser Pro Leu Val Ala Val His Ala Phe Thr Asn Trp
            180                 185                 190

Asp Thr Pro Ala Ile Ala Ala Val Ile Gly Ala Met Leu Ala Val Lys
        195                 200                 205

Arg Gly Asn Pro Leu Val Ala Gly Val Leu Ile Gly Ala Gly Thr Ala
    210                 215                 220

Phe Lys Leu Trp Pro Leu Tyr Leu Leu Gly Ala Tyr Leu Val Leu Ala
225                 230                 235                 240

Val Lys Asn Lys Asn Leu Lys Pro Phe Ile Thr Met Ala Ala Ala Ala
                245                 250                 255

Ala Val Thr Trp Leu Val Val Asn Val Pro Val Met Ile Ala Tyr Pro
            260                 265                 270

Lys Ala Trp Asn Glu Phe Leu Arg Leu Asn Arg Glu Arg Gly Ala Glu
        275                 280                 285

Trp Thr Thr Ile Tyr Gln Val Ile Asp Arg Asn Leu Pro Ile Asn Leu
    290                 295                 300

Asn Asp Pro Val Leu Leu Asn Val Leu Ser Phe Gly Leu Phe Gly Ala
305                 310                 315                 320

Ser Cys Val Ala Ile Leu Ile Leu Gly Leu Lys Val Gln Arg Thr Pro
                325                 330                 335

Arg Val Ala Glu Leu Ala Phe Leu Ile Val Ala Ala Phe Leu Leu Phe
            340                 345                 350

Asn Lys Val Trp Ser Pro Gln Tyr Ser Leu Trp Leu Val Pro Leu Ala
        355                 360                 365

Val Leu Ala Phe Pro Gln Trp Lys Val Leu Phe Pro Trp Met Val Thr
    370                 375                 380

Asp Ala Met Val Trp Pro Ile Leu Met Trp His Met Leu Gly Thr Asp
385                 390                 395                 400

Asn Lys Gly Leu Pro His Glu Met Leu Asp Leu Ile Val Ile Ser Arg
                405                 410                 415

Asp Ala Phe Ile Val Val Met Ile Val Gly Val Ile Arg Gln Met Leu
            420                 425                 430
```

```
Gly Arg Arg Ala Asp Pro Val Met Asp Ala His Ala Gly Arg Asp Leu
        435                 440                 445

Leu Ala Gly Pro Phe Gly Ala Gly Glu Arg Arg Lys Ala Leu Lys Glu
    450                 455                 460

Val Ser
465


<210> 285
<211> 514
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(514)
<223> FRXA00547

<400> 285
accacgattt accaggtcat cgaccgtaat ttgccgatca atttgaatga tccagtgctg 60

cttaatgtgc tgagcttcgg cttgtttggt gcatcagtgt gtg gcc att ttg atc   115
                                    Val Ala Ile Leu Ile
                                      1               5

ctt ggg ctc aag gtg cag cgc act ccc cga gtc gct gag ctg gcc ttt   163
Leu Gly Leu Lys Val Gln Arg Thr Pro Arg Val Ala Glu Leu Ala Phe
                10                  15                  20

ttg att gtc gcg gcg ttt ttg ctg ttt aac aag gtg tgg agt cct cag   211
Leu Ile Val Ala Ala Phe Leu Leu Phe Asn Lys Val Trp Ser Pro Gln
            25                  30                  35

tat tca ctg tgg ctg gtc ccg ttg gct gtt ctg gca ttt cct cag tgg   259
Tyr Ser Leu Trp Leu Val Pro Leu Ala Val Leu Ala Phe Pro Gln Trp
        40                  45                  50

aaa gtg ctg ttc ccg tgg atg gtt aca gac gcc atg gtg tgg cca att   307
Lys Val Leu Phe Pro Trp Met Val Thr Asp Ala Met Val Trp Pro Ile
    55                  60                  65

ttg atg tgg cac atg ctc ggc acg gac aac aag gga ctc ccc cat gaa   355
Leu Met Trp His Met Leu Gly Thr Asp Asn Lys Gly Leu Pro His Glu
70                  75                  80                  85

atg ttg gat ctc atc gtg att tcc cga gat gcc ttc att gtg gtc atg   403
Met Leu Asp Leu Ile Val Ile Ser Arg Asp Ala Phe Ile Val Val Met
                90                  95                  100

ata agt agg tgt aat ccg gca gat gct cgg acg acg tgc aaa tcc ggt   451
Ile Ser Arg Cys Asn Pro Ala Asp Ala Arg Thr Thr Cys Lys Ser Gly
            105                 110                 115

gat gga tgc gca cgc cgg gcg cga att gtt ggc cgg gcc ctt cgg cgc   499
Asp Gly Cys Ala Arg Arg Ala Arg Ile Val Gly Arg Ala Leu Arg Arg
        120                 125                 130

aag cga agc gtc gaa                                             514
```

Lys Arg Ser Val Glu
135

<210> 286
<211> 138
<212> PRT
<213> Corynebacterium glutamicum

<400> 286
Val Ala Ile Leu Ile Leu Gly Leu Lys Val Gln Arg Thr Pro Arg Val
1 5 10 15

Ala Glu Leu Ala Phe Leu Ile Val Ala Ala Phe Leu Leu Phe Asn Lys
20 25 30

Val Trp Ser Pro Gln Tyr Ser Leu Trp Leu Val Pro Leu Ala Val Leu
35 40 45

Ala Phe Pro Gln Trp Lys Val Leu Phe Pro Trp Met Val Thr Asp Ala
50 55 60

Met Val Trp Pro Ile Leu Met Trp His Met Leu Gly Thr Asp Asn Lys
65 70 75 80

Gly Leu Pro His Glu Met Leu Asp Leu Ile Val Ile Ser Arg Asp Ala
85 90 95

Phe Ile Val Val Met Ile Ser Arg Cys Asn Pro Ala Asp Ala Arg Thr
100 105 110

Thr Cys Lys Ser Gly Asp Gly Cys Ala Arg Arg Ala Arg Ile Val Gly
115 120 125

Arg Ala Leu Arg Arg Lys Arg Ser Val Glu
130 135

<210> 287
<211> 713
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(690)
<223> FRXA00546

<400> 287
ccg gtg ttg ggc gga att ttc cag tgg att tgt ggc att atc acg cgg 48
Pro Val Leu Gly Gly Ile Phe Gln Trp Ile Cys Gly Ile Ile Thr Arg
1 5 10 15

ttt ttg tac ccg gtt gtt gat gtc att ccg ttt cat acg ctg cct gaa 96
Phe Leu Tyr Pro Val Val Asp Val Ile Pro Phe His Thr Leu Pro Glu
20 25 30

tct ggt ctt tat ttc atc gtc acc gcg ctt gcg ttg gcg ttc ttt tgg 144
Ser Gly Leu Tyr Phe Ile Val Thr Ala Leu Ala Leu Ala Phe Phe Trp
35 40 45

```
gtg ttg gtc atc cgc atg atg gtg gag ctc act ggc aat cga gtg tgg   192
Val Leu Val Ile Arg Met Met Val Glu Leu Thr Gly Asn Arg Val Trp
     50                  55                  60

gat acc gtc ctt gtt gcg gcg tct ccc ctg gtt gct gtg cat gcg ttt   240
Asp Thr Val Leu Val Ala Ala Ser Pro Leu Val Ala Val His Ala Phe
 65                  70                  75                  80

acc aac tgg gat act cca gcc att gcg gcg gtg att ggt gcg atg ctt   288
Thr Asn Trp Asp Thr Pro Ala Ile Ala Ala Val Ile Gly Ala Met Leu
                 85                  90                  95

gcg gtg aaa cgc gga aac ccc ttg gtt gcg ggt gtg ctg atc ggc gcg   336
Ala Val Lys Arg Gly Asn Pro Leu Val Ala Gly Val Leu Ile Gly Ala
            100                 105                 110

ggt acg gcg ttc aaa ttg tgg ccg ctt tat ctt ctt ggt gcg tat ttg   384
Gly Thr Ala Phe Lys Leu Trp Pro Leu Tyr Leu Leu Gly Ala Tyr Leu
        115                 120                 125

gtg ctg gcg gtc aag aat aag aat ctc aag ccg ttt atc acc atg gct   432
Val Leu Ala Val Lys Asn Lys Asn Leu Lys Pro Phe Ile Thr Met Ala
    130                 135                 140

gca gcg gct gcg gtg aca tgg ctc gtg gtg aat gtg cca gtg atg atc   480
Ala Ala Ala Ala Val Thr Trp Leu Val Val Asn Val Pro Val Met Ile
145                 150                 155                 160

gcg tac ccc aag gcg tgg aat gaa ttc ttg cgc ctg aac cgg gag cgt   528
Ala Tyr Pro Lys Ala Trp Asn Glu Phe Leu Arg Leu Asn Arg Glu Arg
                165                 170                 175

ggt gcg gag tgg acc acg att tac cag gtc atc gac cgt aat ttg ccg   576
Gly Ala Glu Trp Thr Thr Ile Tyr Gln Val Ile Asp Arg Asn Leu Pro
            180                 185                 190

atc aat ttg aat gat cca gtg ctg ctt aat gtg ctg agc ttc ggc ttg   624
Ile Asn Leu Asn Asp Pro Val Leu Leu Asn Val Leu Ser Phe Gly Leu
        195                 200                 205

ttt ggt gca tca gtg tgt ggc cat ttt gat cct tgg gct caa ggt gca   672
Phe Gly Ala Ser Val Cys Gly His Phe Asp Pro Trp Ala Gln Gly Ala
    210                 215                 220

gcg cac tcc ccg agt cgc tgagctggcc tttttgattg tcg                713
Ala His Ser Pro Ser Arg
225                 230
```

<210> 288
<211> 230
<212> PRT
<213> Corynebacterium glutamicum

<400> 288

```
Pro Val Leu Gly Gly Ile Phe Gln Trp Ile Cys Gly Ile Ile Thr Arg
  1               5                  10                  15

Phe Leu Tyr Pro Val Val Asp Val Ile Pro Phe His Thr Leu Pro Glu
             20                  25                  30
```

```
Ser Gly Leu Tyr Phe Ile Val Thr Ala Leu Ala Leu Ala Phe Phe Trp
         35                  40                  45

Val Leu Val Ile Arg Met Met Val Glu Leu Thr Gly Asn Arg Val Trp
     50                  55                  60

Asp Thr Val Leu Val Ala Ala Ser Pro Leu Val Ala Val His Ala Phe
 65                  70                  75                  80

Thr Asn Trp Asp Thr Pro Ala Ile Ala Ala Val Ile Gly Ala Met Leu
                 85                  90                  95

Ala Val Lys Arg Gly Asn Pro Leu Val Ala Gly Val Leu Ile Gly Ala
            100                 105                 110

Gly Thr Ala Phe Lys Leu Trp Pro Leu Tyr Leu Leu Gly Ala Tyr Leu
        115                 120                 125

Val Leu Ala Val Lys Asn Lys Asn Leu Lys Pro Phe Ile Thr Met Ala
    130                 135                 140

Ala Ala Ala Ala Val Thr Trp Leu Val Val Asn Val Pro Val Met Ile
145                 150                 155                 160

Ala Tyr Pro Lys Ala Trp Asn Glu Phe Leu Arg Leu Asn Arg Glu Arg
                165                 170                 175

Gly Ala Glu Trp Thr Thr Ile Tyr Gln Val Ile Asp Arg Asn Leu Pro
            180                 185                 190

Ile Asn Leu Asn Asp Pro Val Leu Leu Asn Val Leu Ser Phe Gly Leu
        195                 200                 205

Phe Gly Ala Ser Val Cys Gly His Phe Asp Pro Trp Ala Gln Gly Ala
    210                 215                 220

Ala His Ser Pro Ser Arg
225                 230
```

<210> 289
<211> 1059
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1036)
<223> RXN00552

<400> 289
ccgccaacaa ggcagcaaag ctcgatccaa ttgacgcctt gcgttatgag taaaagcctc 60

gtttttaagg tagccacaca tcgcactaga ctgaagaact gtg gct acc tca aaa 115
                                                Val Ala Thr Ser Lys
                                                  1   5

att ctt ctt tat tac gca ttc acc ccg ctc tct gac cct aaa gcg gtt 163
Ile Leu Leu Tyr Tyr Ala Phe Thr Pro Leu Ser Asp Pro Lys Ala Val
                 10   15   20

```
cag ctg tgg cag cgt gag ctc tgc gag tca ctg aat ctt cgt ggc cgc   211
Gln Leu Trp Gln Arg Glu Leu Cys Glu Ser Leu Asn Leu Arg Gly Arg
            25                  30                  35

atc ctg atc tcc act cac ggc atc aat gga acc gtg ggc gga gat att   259
Ile Leu Ile Ser Thr His Gly Ile Asn Gly Thr Val Gly Gly Asp Ile
        40                  45                  50

gat gat tgc aag gcg tac att aaa aag acc cgc gag tac cca ggt ttc   307
Asp Asp Cys Lys Ala Tyr Ile Lys Lys Thr Arg Glu Tyr Pro Gly Phe
    55                  60                  65

aac cgc atg cag ttt aag tgg tcc gag ggt ggc gct gag gat ttc cca   355
Asn Arg Met Gln Phe Lys Trp Ser Glu Gly Gly Ala Glu Asp Phe Pro
70                  75                  80                  85

aag ctc agt gtc aaa gtc cgc gat gag atc gtt gcc ttc ggc gct cca   403
Lys Leu Ser Val Lys Val Arg Asp Glu Ile Val Ala Phe Gly Ala Pro
                90                  95                  100

gat gag ctc aaa gtg gat gaa aac ggc gtc gtc ggt ggc ggc gtt cac   451
Asp Glu Leu Lys Val Asp Glu Asn Gly Val Val Gly Gly Gly Val His
            105                 110                 115

ctg aaa cca cag cag gtc aat gag ctt gtg gaa gcc cgt ggc gat gaa   499
Leu Lys Pro Gln Gln Val Asn Glu Leu Val Glu Ala Arg Gly Asp Glu
        120                 125                 130

gtt gtg ttc ttt gac ggc cgc aac gca atg gaa gcc cag atc ggc aag   547
Val Val Phe Phe Asp Gly Arg Asn Ala Met Glu Ala Gln Ile Gly Lys
    135                 140                 145

ttc aag gac gct gtt gtc cct gac gta gaa acc act cat gat ttc atc   595
Phe Lys Asp Ala Val Val Pro Asp Val Glu Thr Thr His Asp Phe Ile
150                 155                 160                 165

gca gaa att gag tct gga aaa tac gac gat ctc aaa gac aag cct gtg   643
Ala Glu Ile Glu Ser Gly Lys Tyr Asp Asp Leu Lys Asp Lys Pro Val
                170                 175                 180

gtc acc tac tgc acc ggc gga att cgt tgt gag atc ctg agt tca ctc   691
Val Thr Tyr Cys Thr Gly Gly Ile Arg Cys Glu Ile Leu Ser Ser Leu
            185                 190                 195

atg atc aac cgt ggt ttc aaa gag gtc tac caa atc gat ggc ggc atc   739
Met Ile Asn Arg Gly Phe Lys Glu Val Tyr Gln Ile Asp Gly Gly Ile
        200                 205                 210

gtt cgc tac ggc gag cag ttt ggc aac aag ggc ctg tgg gaa ggc tcc   787
Val Arg Tyr Gly Glu Gln Phe Gly Asn Lys Gly Leu Trp Glu Gly Ser
    215                 220                 225

ctc tac gtt ttc gat aag cgc atg cat atg gaa ttc ggc gag gat tac   835
Leu Tyr Val Phe Asp Lys Arg Met His Met Glu Phe Gly Glu Asp Tyr
230                 235                 240                 245

aaa gag gtc gga cac tgc atc cat tgc gat act ccc acc aac aaa ttt   883
Lys Glu Val Gly His Cys Ile His Cys Asp Thr Pro Thr Asn Lys Phe
                250                 255                 260

gag cac tgc ctc aac gaa gat gat tgc cgc gag ctc gtg ttg atg tgc   931
```

```
Glu His Cys Leu Asn Glu Asp Asp Cys Arg Glu Leu Val Leu Met Cys
            265                 270                 275

cct gat tgc ttc gcc aat gtt gag acc cgt cat tgc aag cgc gaa cgc   979
Pro Asp Cys Phe Ala Asn Val Glu Thr Arg His Cys Lys Arg Glu Arg
        280                 285                 290

tgt gca gca att gct gcg gat ttc gct gag caa gga att gat ccg ctc   1027
Cys Ala Ala Ile Ala Ala Asp Phe Ala Glu Gln Gly Ile Asp Pro Leu
    295                 300                 305

gtt act tct taaaaagggt atggtggctg ggt                            1059
Val Thr Ser
310
```

<210> 290
<211> 312
<212> PRT
<213> Corynebacterium glutamicum

<400> 290

```
Val Ala Thr Ser Lys Ile Leu Leu Tyr Tyr Ala Phe Thr Pro Leu Ser
  1               5                  10                  15

Asp Pro Lys Ala Val Gln Leu Trp Gln Arg Glu Leu Cys Glu Ser Leu
             20                  25                  30

Asn Leu Arg Gly Arg Ile Leu Ile Ser Thr His Gly Ile Asn Gly Thr
         35                  40                  45

Val Gly Gly Asp Ile Asp Asp Cys Lys Ala Tyr Ile Lys Lys Thr Arg
     50                  55                  60

Glu Tyr Pro Gly Phe Asn Arg Met Gln Phe Lys Trp Ser Glu Gly Gly
 65                  70                  75                  80

Ala Glu Asp Phe Pro Lys Leu Ser Val Lys Val Arg Asp Glu Ile Val
                 85                  90                  95

Ala Phe Gly Ala Pro Asp Glu Leu Lys Val Asp Glu Asn Gly Val Val
            100                 105                 110

Gly Gly Gly Val His Leu Lys Pro Gln Gln Val Asn Glu Leu Val Glu
        115                 120                 125

Ala Arg Gly Asp Glu Val Val Phe Phe Asp Gly Arg Asn Ala Met Glu
    130                 135                 140

Ala Gln Ile Gly Lys Phe Lys Asp Ala Val Val Pro Asp Val Glu Thr
145                 150                 155                 160

Thr His Asp Phe Ile Ala Glu Ile Glu Ser Gly Lys Tyr Asp Asp Leu
                165                 170                 175

Lys Asp Lys Pro Val Val Thr Tyr Cys Thr Gly Gly Ile Arg Cys Glu
            180                 185                 190

Ile Leu Ser Ser Leu Met Ile Asn Arg Gly Phe Lys Glu Val Tyr Gln
        195                 200                 205
```

```
Ile Asp Gly Gly Ile Val Arg Tyr Gly Glu Gln Phe Gly Asn Lys Gly
    210                 215                 220

Leu Trp Glu Gly Ser Leu Tyr Val Phe Asp Lys Arg Met His Met Glu
225                 230                 235                 240

Phe Gly Glu Asp Tyr Lys Glu Val Gly His Cys Ile His Cys Asp Thr
                245                 250                 255

Pro Thr Asn Lys Phe Glu His Cys Leu Asn Glu Asp Asp Cys Arg Glu
            260                 265                 270

Leu Val Leu Met Cys Pro Asp Cys Phe Ala Asn Val Glu Thr Arg His
        275                 280                 285

Cys Lys Arg Glu Arg Cys Ala Ala Ile Ala Ala Asp Phe Ala Glu Gln
    290                 295                 300

Gly Ile Asp Pro Leu Val Thr Ser
305                 310
```

Sequence Listing

<210> 291
<211> 740
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(717)
<223> FRXA00552

<400> 291

```
ttt aag tgg tcc gag ggt ggc gct gag gat ttc cca aag ctc agt gtc   48
Phe Lys Trp Ser Glu Gly Gly Ala Glu Asp Phe Pro Lys Leu Ser Val
  1               5                  10                  15

aaa gtc cgc gat gag atc gtt gcc ttc ggc gct cca gat gag ctc aaa   96
Lys Val Arg Asp Glu Ile Val Ala Phe Gly Ala Pro Asp Glu Leu Lys
            20                  25                  30

gtg gat gaa aac ggc gtc gtc ggt ggc ggc gtt cac ctg aaa cca cag   144
Val Asp Glu Asn Gly Val Val Gly Gly Gly Val His Leu Lys Pro Gln
        35                  40                  45

cag gtc aat gag ctt gtg gaa gcc cgt ggc gat gaa gtt gtg ttc ttt   192
Gln Val Asn Glu Leu Val Glu Ala Arg Gly Asp Glu Val Val Phe Phe
    50                  55                  60

gac ggc cgc aac gca atg gaa gcc cag atc ggc aag ttc aag gac gct   240
Asp Gly Arg Asn Ala Met Glu Ala Gln Ile Gly Lys Phe Lys Asp Ala
65                  70                  75                  80

gtt gtc cct gac gta gaa acc act cat gat ttc atc gca gaa att gag   288
Val Val Pro Asp Val Glu Thr Thr His Asp Phe Ile Ala Glu Ile Glu
                85                  90                  95

tct gga aaa tac gac gat ctc aaa gac aag cct gtg gtc acc tac tgc   336
Ser Gly Lys Tyr Asp Asp Leu Lys Asp Lys Pro Val Val Thr Tyr Cys
            100                 105                 110
```

```
acc ggc gga att cgt tgt gag atc ctg agt tca ctc atg atc aac cgt   384
Thr Gly Gly Ile Arg Cys Glu Ile Leu Ser Ser Leu Met Ile Asn Arg
        115                 120                 125

ggt ttc aaa gag gtc tac caa atc gat ggc ggc atc gtt cgc tac ggc   432
Gly Phe Lys Glu Val Tyr Gln Ile Asp Gly Gly Ile Val Arg Tyr Gly
    130                 135                 140

gag cag ttt ggc aac aag ggc ctg tgg gaa ggc tcc ctc tac gtt ttc   480
Glu Gln Phe Gly Asn Lys Gly Leu Trp Glu Gly Ser Leu Tyr Val Phe
145                 150                 155                 160

gat aag cgc atg cat atg gaa ttc ggc gag gat tac aaa gag gtc gga   528
Asp Lys Arg Met His Met Glu Phe Gly Glu Asp Tyr Lys Glu Val Gly
                165                 170                 175

cac tgc atc cat tgc gat act ccc acc aac aaa ttt gag cac tgc ctc   576
His Cys Ile His Cys Asp Thr Pro Thr Asn Lys Phe Glu His Cys Leu
            180                 185                 190

aac gaa gat gat tgc cgc gag ctc gtg ttg atg tgc cct gat tgc ttc   624
Asn Glu Asp Asp Cys Arg Glu Leu Val Leu Met Cys Pro Asp Cys Phe
        195                 200                 205

gcc aat gtt gag acc cgt cat tgc aag cgc gaa cgc tgt gca gca att   672
Ala Asn Val Glu Thr Arg His Cys Lys Arg Glu Arg Cys Ala Ala Ile
    210                 215                 220

gct gcg gat ttc gct gag caa gga att gat ccg ctc gtt act tct       717
Ala Ala Asp Phe Ala Glu Gln Gly Ile Asp Pro Leu Val Thr Ser
225                 230                 235

taaaaagggt atggtggctg ggt                                        740


<210> 292
<211> 239
<212> PRT
<213> Corynebacterium glutamicum

<400> 292
Phe Lys Trp Ser Glu Gly Gly Ala Glu Asp Phe Pro Lys Leu Ser Val
  1               5                  10                  15

Lys Val Arg Asp Glu Ile Val Ala Phe Gly Ala Pro Asp Glu Leu Lys
            20                  25                  30

Val Asp Glu Asn Gly Val Val Gly Gly Gly Val His Leu Lys Pro Gln
        35                  40                  45

Gln Val Asn Glu Leu Val Glu Ala Arg Gly Asp Glu Val Val Phe Phe
    50                  55                  60

Asp Gly Arg Asn Ala Met Glu Ala Gln Ile Gly Lys Phe Lys Asp Ala
65                  70                  75                  80

Val Val Pro Asp Val Glu Thr Thr His Asp Phe Ile Ala Glu Ile Glu
                85                  90                  95

Ser Gly Lys Tyr Asp Asp Leu Lys Asp Lys Pro Val Val Thr Tyr Cys
            100                 105                 110
```

```
Thr Gly Gly Ile Arg Cys Glu Ile Leu Ser Ser Leu Met Ile Asn Arg
        115                 120                 125

Gly Phe Lys Glu Val Tyr Gln Ile Asp Gly Gly Ile Val Arg Tyr Gly
    130                 135                 140

Glu Gln Phe Gly Asn Lys Gly Leu Trp Glu Gly Ser Leu Tyr Val Phe
145                 150                 155                 160

Asp Lys Arg Met His Met Glu Phe Gly Glu Asp Tyr Lys Glu Val Gly
                165                 170                 175

His Cys Ile His Cys Asp Thr Pro Thr Asn Lys Phe Glu His Cys Leu
            180                 185                 190

Asn Glu Asp Asp Cys Arg Glu Leu Val Leu Met Cys Pro Asp Cys Phe
        195                 200                 205

Ala Asn Val Glu Thr Arg His Cys Lys Arg Glu Arg Cys Ala Ala Ile
    210                 215                 220

Ala Ala Asp Phe Ala Glu Gln Gly Ile Asp Pro Leu Val Thr Ser
225                 230                 235


<210> 293
<211> 1062
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1039)
<223> RXN00555

<400> 293
cctggtggat atcattactg agcttgcaga ggtgtacggt agctggaaag agaccgacag 60

cggttcttaa cagttttctc catctcaact ccggaatttg atg aaa caa ccc ctt   115
                                              Met Lys Gln Pro Leu
                                                1               5

cgc gta ctt att tct tgt cga ccc gaa gaa aat tcg ggt ggc aaa cgt   163
Arg Val Leu Ile Ser Cys Arg Pro Glu Glu Asn Ser Gly Gly Lys Arg
                  10                  15                  20

agt gaa caa aat gat gct gtt ttt gag ttc gcc gca tgg cta gct cgt   211
Ser Glu Gln Asn Asp Ala Val Phe Glu Phe Ala Ala Trp Leu Ala Arg
              25                  30                  35

act tca gac atc aat gtt cgt gga atc aca act ttc ata cgc cct tgg   259
Thr Ser Asp Ile Asn Val Arg Gly Ile Thr Thr Phe Ile Arg Pro Trp
          40                  45                  50

ccg tct tcc tcc atc agt aag ctc gga gga aaa tat cat aag tgg tat   307
Pro Ser Ser Ser Ile Ser Lys Leu Gly Gly Lys Tyr His Lys Trp Tyr
      55                  60                  65

aag aat tta gat tct tac tac cgc agt cgc acg atc aag gga ctc aaa   355
Lys Asn Leu Asp Ser Tyr Tyr Arg Ser Arg Thr Ile Lys Gly Leu Lys
```

```
 70                  75                  80                  85

gag gcc gga gtt gag aag tcc caa tgg gac gat gat gtt tca gtt ttt   403
Glu Ala Gly Val Glu Lys Ser Gln Trp Asp Asp Asp Val Ser Val Phe
                90                  95                 100

gta gat ggt cct tct gaa tcc acg ctg ctc acc cat gct gct gaa gaa   451
Val Asp Gly Pro Ser Glu Ser Thr Leu Leu Thr His Ala Ala Glu Glu
            105                 110                 115

ttc gaa gcg gac ctc att ctg ctt ggc tct gat gcg acc gca cca aaa   499
Phe Glu Ala Asp Leu Ile Leu Leu Gly Ser Asp Ala Thr Ala Pro Lys
        120                 125                 130

ggc cgc ttt ctg gcc agc tcc acc gca gat gcc ctc ctt cac tcc tcg   547
Gly Arg Phe Leu Ala Ser Ser Thr Ala Asp Ala Leu Leu His Ser Ser
    135                 140                 145

ccc gtc cca cta gga ctt gtg ccg cga ggg gtg aag ctt tcc aaa aag   595
Pro Val Pro Leu Gly Leu Val Pro Arg Gly Val Lys Leu Ser Lys Lys
150                 155                 160                 165

ggt gtc acc cgc gtc aac tac gct ttc acc aat gaa agc gat gac ttt   643
Gly Val Thr Arg Val Asn Tyr Ala Phe Thr Asn Glu Ser Asp Asp Phe
                170                 175                 180

gag caa ggt tta cgc tct tcc gcg gag ctc gcc acc aat tgg aac gtt   691
Glu Gln Gly Leu Arg Ser Ser Ala Glu Leu Ala Thr Asn Trp Asn Val
            185                 190                 195

cct ctt cgg atc ctt gct ttt tca ccc aca ggc att act tcc gca cca   739
Pro Leu Arg Ile Leu Ala Phe Ser Pro Thr Gly Ile Thr Ser Ala Pro
        200                 205                 210

acg tcg cgg agc ttg gat att tcc act gag ctt tcc tcc gag tgg cgt   787
Thr Ser Arg Ser Leu Asp Ile Ser Thr Glu Leu Ser Ser Glu Trp Arg
    215                 220                 225

gaa cta acg ctc gcc atg ctt gat cga gcc cgt gat ggc gtc ctc aca   835
Glu Leu Thr Leu Ala Met Leu Asp Arg Ala Arg Asp Gly Val Leu Thr
230                 235                 240                 245

gac cac cca aac ttg agc gtg agc agt gaa acc ggt tct ggc tgg ggt   883
Asp His Pro Asn Leu Ser Val Ser Ser Glu Thr Gly Ser Gly Trp Gly
                250                 255                 260

tgg agc ggt gca att gat gct ttg cga tgg aag aaa ggt gac ctg ctg   931
Trp Ser Gly Ala Ile Asp Ala Leu Arg Trp Lys Lys Gly Asp Leu Leu
            265                 270                 275

tgc atg gga agc cat cgc aca gac acc ctt tca cgt gtc ttt gtc ggt   979
Cys Met Gly Ser His Arg Thr Asp Thr Leu Ser Arg Val Phe Val Gly
        280                 285                 290

tcg gaa aca atg gaa att atc cga aac tct cct gta ccg acc atc att   1027
Ser Glu Thr Met Glu Ile Ile Arg Asn Ser Pro Val Pro Thr Ile Ile
    295                 300                 305

tat ccc ggt ctt taggctctcc aacagcagag gac                        1062
Tyr Pro Gly Leu
310
```

<210> 294
<211> 313
<212> PRT
<213> Corynebacterium glutamicum

<400> 294

```
Met Lys Gln Pro Leu Arg Val Leu Ile Ser Cys Arg Pro Glu Glu Asn
  1               5                  10                  15

Ser Gly Gly Lys Arg Ser Glu Gln Asn Asp Ala Val Phe Glu Phe Ala
             20                  25                  30

Ala Trp Leu Ala Arg Thr Ser Asp Ile Asn Val Arg Gly Ile Thr Thr
         35                  40                  45

Phe Ile Arg Pro Trp Pro Ser Ser Ser Ile Ser Lys Leu Gly Gly Lys
     50                  55                  60

Tyr His Lys Trp Tyr Lys Asn Leu Asp Ser Tyr Tyr Arg Ser Arg Thr
 65                  70                  75                  80

Ile Lys Gly Leu Lys Glu Ala Gly Val Glu Lys Ser Gln Trp Asp Asp
                 85                  90                  95

Asp Val Ser Val Phe Val Asp Gly Pro Ser Glu Ser Thr Leu Leu Thr
            100                 105                 110

His Ala Ala Glu Glu Phe Glu Ala Asp Leu Ile Leu Leu Gly Ser Asp
        115                 120                 125

Ala Thr Ala Pro Lys Gly Arg Phe Leu Ala Ser Ser Thr Ala Asp Ala
    130                 135                 140

Leu Leu His Ser Ser Pro Val Pro Leu Gly Leu Val Pro Arg Gly Val
145                 150                 155                 160

Lys Leu Ser Lys Lys Gly Val Thr Arg Val Asn Tyr Ala Phe Thr Asn
                165                 170                 175

Glu Ser Asp Asp Phe Glu Gln Gly Leu Arg Ser Ser Ala Glu Leu Ala
            180                 185                 190

Thr Asn Trp Asn Val Pro Leu Arg Ile Leu Ala Phe Ser Pro Thr Gly
        195                 200                 205

Ile Thr Ser Ala Pro Thr Ser Arg Ser Leu Asp Ile Ser Thr Glu Leu
    210                 215                 220

Ser Ser Glu Trp Arg Glu Leu Thr Leu Ala Met Leu Asp Arg Ala Arg
225                 230                 235                 240

Asp Gly Val Leu Thr Asp His Pro Asn Leu Ser Val Ser Ser Glu Thr
                245                 250                 255

Gly Ser Gly Trp Gly Trp Ser Gly Ala Ile Asp Ala Leu Arg Trp Lys
            260                 265                 270

Lys Gly Asp Leu Leu Cys Met Gly Ser His Arg Thr Asp Thr Leu Ser
        275                 280                 285
```

```
Arg Val Phe Val Gly Ser Glu Thr Met Glu Ile Ile Arg Asn Ser Pro
    290                 295                 300

Val Pro Thr Ile Ile Tyr Pro Gly Leu
305                 310


<210> 295
<211> 914
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(891)
<223> FRXA00555

<400> 295
tcg ggt ggc aaa cgt agt gaa caa aat gat gct gtt ttt gag ttc gcc   48
Ser Gly Gly Lys Arg Ser Glu Gln Asn Asp Ala Val Phe Glu Phe Ala
  1               5                  10                  15

gca tgg cta gct cgt act tca gac atc aat gtt cgt gga atc aca act   96
Ala Trp Leu Ala Arg Thr Ser Asp Ile Asn Val Arg Gly Ile Thr Thr
             20                  25                  30

ttc ata cgc cct tgg ccg tct tcc tcc atc agt aag ctc gga gga aaa   144
Phe Ile Arg Pro Trp Pro Ser Ser Ser Ile Ser Lys Leu Gly Gly Lys
         35                  40                  45

tat cat aag tgg tat aag aat tta gat tct tac tac cgc agt cgc acg   192
Tyr His Lys Trp Tyr Lys Asn Leu Asp Ser Tyr Tyr Arg Ser Arg Thr
     50                  55                  60

atc aag gga ctc aaa gag gcc gga gtt gag aag tcc caa tgg gac gat   240
Ile Lys Gly Leu Lys Glu Ala Gly Val Glu Lys Ser Gln Trp Asp Asp
 65                  70                  75                  80

gat gtt tca gtt ttt gta gat ggt cct tct gaa tcc acg ctg ctc acc   288
Asp Val Ser Val Phe Val Asp Gly Pro Ser Glu Ser Thr Leu Leu Thr
                 85                  90                  95

cat gct gct gaa gaa ttc gaa gcg gac ctc att ctg ctt ggc tct gat   336
His Ala Ala Glu Glu Phe Glu Ala Asp Leu Ile Leu Leu Gly Ser Asp
            100                 105                 110

gcg acc gca cca aaa ggc cgc ttt ctg gcc agc tcc acc gca gat gcc   384
Ala Thr Ala Pro Lys Gly Arg Phe Leu Ala Ser Ser Thr Ala Asp Ala
        115                 120                 125

ctc ctt cac tcc tcg ccc gtc cca cta gga ctt gtg ccg cga ggg gtg   432
Leu Leu His Ser Ser Pro Val Pro Leu Gly Leu Val Pro Arg Gly Val
    130                 135                 140

aag ctt tcc aaa aag ggt gtc acc cgc gtc aac tac gct ttc acc aat   480
Lys Leu Ser Lys Lys Gly Val Thr Arg Val Asn Tyr Ala Phe Thr Asn
145                 150                 155                 160

gaa agc gat gac ttt gag caa ggt tta cgc tct tcc gcg gag ctc gcc   528
Glu Ser Asp Asp Phe Glu Gln Gly Leu Arg Ser Ser Ala Glu Leu Ala
```

```
                165                 170                 175

acc aat tgg aac gtt cct ctt cgg atc ctt gct ttt tca ccc aca ggc   576
Thr Asn Trp Asn Val Pro Leu Arg Ile Leu Ala Phe Ser Pro Thr Gly
            180                 185                 190

att act tcc gca cca acg tcg cgg agc ttg gat att tcc act gag ctt   624
Ile Thr Ser Ala Pro Thr Ser Arg Ser Leu Asp Ile Ser Thr Glu Leu
        195                 200                 205

tcc tcc gag tgg cgt gaa cta acg ctc gcc atg ctt gat cga gcc cgt   672
Ser Ser Glu Trp Arg Glu Leu Thr Leu Ala Met Leu Asp Arg Ala Arg
    210                 215                 220

gat ggc gtc ctc aca gac cac cca aac ttg agc gtg agc agt gaa acc   720
Asp Gly Val Leu Thr Asp His Pro Asn Leu Ser Val Ser Ser Glu Thr
225                 230                 235                 240

ggt tct ggc tgg ggt tgg agc ggt gca att gat gct ttg cga tgg aag   768
Gly Ser Gly Trp Gly Trp Ser Gly Ala Ile Asp Ala Leu Arg Trp Lys
                245                 250                 255

aaa ggt gac ctg ctg tgc atg gga agc cat cgc aca gac acc ctt tca   816
Lys Gly Asp Leu Leu Cys Met Gly Ser His Arg Thr Asp Thr Leu Ser
            260                 265                 270

cgt gtc ttt gtc ggt tcg gaa aca atg gaa att atc cga aac tct cct   864
Arg Val Phe Val Gly Ser Glu Thr Met Glu Ile Ile Arg Asn Ser Pro
        275                 280                 285

gta ccg acc atc att tat ccc ggt ctt taggctctcc aacagcagag         911
Val Pro Thr Ile Ile Tyr Pro Gly Leu
    290                 295

gac                                                               914


<210> 296
<211> 297
<212> PRT
<213> Corynebacterium glutamicum

<400> 296
Ser Gly Gly Lys Arg Ser Glu Gln Asn Asp Ala Val Phe Glu Phe Ala
  1               5                  10                  15

Ala Trp Leu Ala Arg Thr Ser Asp Ile Asn Val Arg Gly Ile Thr Thr
             20                  25                  30

Phe Ile Arg Pro Trp Pro Ser Ser Ser Ile Ser Lys Leu Gly Gly Lys
         35                  40                  45

Tyr His Lys Trp Tyr Lys Asn Leu Asp Ser Tyr Tyr Arg Ser Arg Thr
     50                  55                  60

Ile Lys Gly Leu Lys Glu Ala Gly Val Glu Lys Ser Gln Trp Asp Asp
 65                  70                  75                  80

Asp Val Ser Val Phe Val Asp Gly Pro Ser Glu Ser Thr Leu Leu Thr
                 85                  90                  95
```

```
His Ala Ala Glu Glu Phe Glu Ala Asp Leu Ile Leu Leu Gly Ser Asp
            100                 105                 110

Ala Thr Ala Pro Lys Gly Arg Phe Leu Ala Ser Ser Thr Ala Asp Ala
        115                 120                 125

Leu Leu His Ser Ser Pro Val Pro Leu Gly Leu Val Pro Arg Gly Val
    130                 135                 140

Lys Leu Ser Lys Lys Gly Val Thr Arg Val Asn Tyr Ala Phe Thr Asn
145                 150                 155                 160

Glu Ser Asp Asp Phe Glu Gln Gly Leu Arg Ser Ser Ala Glu Leu Ala
                165                 170                 175

Thr Asn Trp Asn Val Pro Leu Arg Ile Leu Ala Phe Ser Pro Thr Gly
            180                 185                 190

Ile Thr Ser Ala Pro Thr Ser Arg Ser Leu Asp Ile Ser Thr Glu Leu
        195                 200                 205

Ser Ser Glu Trp Arg Glu Leu Thr Leu Ala Met Leu Asp Arg Ala Arg
    210                 215                 220

Asp Gly Val Leu Thr Asp His Pro Asn Leu Ser Val Ser Ser Glu Thr
225                 230                 235                 240

Gly Ser Gly Trp Gly Trp Ser Gly Ala Ile Asp Ala Leu Arg Trp Lys
                245                 250                 255

Lys Gly Asp Leu Leu Cys Met Gly Ser His Arg Thr Asp Thr Leu Ser
            260                 265                 270

Arg Val Phe Val Gly Ser Glu Thr Met Glu Ile Ile Arg Asn Ser Pro
        275                 280                 285

Val Pro Thr Ile Ile Tyr Pro Gly Leu
    290                 295


<210> 297
<211> 498
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(475)
<223> RXN00560

<400> 297
aaggacgact tctggggagc ggtgtggatt ctcacgggga ttctcatgcg gattatcaga 60

catatggaca ctttaacggt tcgtactagg ctgatgcttc atg agg att gat ccg   115
                                          Met Arg Ile Asp Pro
                                            1               5

ctg gaa acc cgg caa gcc gta ttg gcc gtc aaa gac tgg att gaa ggg   163
Leu Glu Thr Arg Gln Ala Val Leu Ala Val Lys Asp Trp Ile Glu Gly
                10                  15                  20
```

```
gag gga gac gtc aaa aag cct ggt cgt gcg gca ctt gcc gcc gca act   211
Glu Gly Asp Val Lys Lys Pro Gly Arg Ala Ala Leu Ala Ala Ala Thr
            25                  30                  35

cgc ctg agc gtc cga ctg ctc gcg caa cac gcg ccg gga aac agc gtg   259
Arg Leu Ser Val Arg Leu Leu Ala Gln His Ala Pro Gly Asn Ser Val
        40                  45                  50

gag gtg cgg gta ccc cca ttt gtt gcg gtg caa tgc ata gag ggg cca   307
Glu Val Arg Val Pro Pro Phe Val Ala Val Gln Cys Ile Glu Gly Pro
    55                  60                  65

aaa cat aca cgc ggc aca cca ccc aac gtg gtg gag acc gac gcc aag   355
Lys His Thr Arg Gly Thr Pro Pro Asn Val Val Glu Thr Asp Ala Lys
70                  75                  80                  85

acc tgg tta cgc tta gca cct ggg caa acc aca ttt gat gca gaa ttt   403
Thr Trp Leu Arg Leu Ala Pro Gly Gln Thr Thr Phe Asp Ala Glu Phe
                90                  95                  100

gaa agc gga aaa att agc gca tca ggt acc cga gcc aaa gag att gcg   451
Glu Ser Gly Lys Ile Ser Ala Ser Gly Thr Arg Ala Lys Glu Ile Ala
            105                 110                 115

gac tgg tta cca gtg gtc aaa ctt tagatttcct aatgctcatt agt         498
Asp Trp Leu Pro Val Val Lys Leu
        120                 125
```

<210> 298
<211> 125
<212> PRT
<213> Corynebacterium glutamicum

<400> 298

```
Met Arg Ile Asp Pro Leu Glu Thr Arg Gln Ala Val Leu Ala Val Lys
  1               5                  10                  15

Asp Trp Ile Glu Gly Glu Gly Asp Val Lys Lys Pro Gly Arg Ala Ala
            20                  25                  30

Leu Ala Ala Ala Thr Arg Leu Ser Val Arg Leu Leu Ala Gln His Ala
        35                  40                  45

Pro Gly Asn Ser Val Glu Val Arg Val Pro Pro Phe Val Ala Val Gln
    50                  55                  60

Cys Ile Glu Gly Pro Lys His Thr Arg Gly Thr Pro Pro Asn Val Val
65                  70                  75                  80

Glu Thr Asp Ala Lys Thr Trp Leu Arg Leu Ala Pro Gly Gln Thr Thr
                85                  90                  95

Phe Asp Ala Glu Phe Glu Ser Gly Lys Ile Ser Ala Ser Gly Thr Arg
            100                 105                 110

Ala Lys Glu Ile Ala Asp Trp Leu Pro Val Val Lys Leu
        115                 120                 125
```

<210> 299

<211> 337
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(337)
<223> FRXA00560

<400> 299
aaggacgact tctggggagc ggtgtggatt ctcacgggga ttctcatgcg gattatcaga 60

catatggaca ctttaacggt tcgtactagg ctgatgcttc atg agg att gat ccg 115
Met Arg Ile Asp Pro
1 5

ctg gaa acc cgg caa gcc gta ttg gcc gtc aaa gac tgg att gaa ggg 163
Leu Glu Thr Arg Gln Ala Val Leu Ala Val Lys Asp Trp Ile Glu Gly
10 15 20

gag gga gac gtc aaa aag cct ggt cgt gcg gca ctt gcc gcc gca act 211
Glu Gly Asp Val Lys Lys Pro Gly Arg Ala Ala Leu Ala Ala Ala Thr
25 30 35

cgc ctg agc gtc cga ctg ctc gcg caa cac gcg ccg gga aac agc gtg 259
Arg Leu Ser Val Arg Leu Leu Ala Gln His Ala Pro Gly Asn Ser Val
40 45 50

gag gtg cgg gta ccc cca ttt gtt gcg gtg caa tgc ata gag ggg cca 307
Glu Val Arg Val Pro Pro Phe Val Ala Val Gln Cys Ile Glu Gly Pro
55 60 65

aaa cat aca cgc ggc aca cca ccc aac gtg 337
Lys His Thr Arg Gly Thr Pro Pro Asn Val
70 75

<210> 300
<211> 79
<212> PRT
<213> Corynebacterium glutamicum

<400> 300
Met Arg Ile Asp Pro Leu Glu Thr Arg Gln Ala Val Leu Ala Val Lys
1 5 10 15

Asp Trp Ile Glu Gly Glu Gly Asp Val Lys Lys Pro Gly Arg Ala Ala
20 25 30

Leu Ala Ala Ala Thr Arg Leu Ser Val Arg Leu Leu Ala Gln His Ala
35 40 45

Pro Gly Asn Ser Val Glu Val Arg Val Pro Pro Phe Val Ala Val Gln
50 55 60

Cys Ile Glu Gly Pro Lys His Thr Arg Gly Thr Pro Pro Asn Val
65 70 75

<210> 301
<211> 1002

<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(979)
<223> RXN00574

<400> 301
aactgctggg cactactgag attcccatgt gggatgtgga ccggtggcaa ccatcgcttc 60

tcaagcccgg tgattcagtt cgatttgtgc aggtgaagaa atg agc ttc aaa gta 115
Met Ser Phe Lys Val
1 5

att tcc act ggc ccc caa gcc atc ttc caa gac cga ggt cgc ttc ggt 163
Ile Ser Thr Gly Pro Gln Ala Ile Phe Gln Asp Arg Gly Arg Phe Gly
10 15 20

ttt gcc agc gct ggt gtt gga acc tca gga tcc ttt gat cgt tta tcc 211
Phe Ala Ser Ala Gly Val Gly Thr Ser Gly Ser Phe Asp Arg Leu Ser
25 30 35

gct gct cgc gcg aat cac gct tta ggt aat gat ccc aat gca acc gtg 259
Ala Ala Arg Ala Asn His Ala Leu Gly Asn Asp Pro Asn Ala Thr Val
40 45 50

gta gag att ctg ctc ggt ggc ttt gag gtg gag gcg ttg cac acc acc 307
Val Glu Ile Leu Leu Gly Gly Phe Glu Val Glu Ala Leu His Thr Thr
55 60 65

tcg atc gtg ttc acg gga act gaa gct gaa gtg atg gtt cga acg gct 355
Ser Ile Val Phe Thr Gly Thr Glu Ala Glu Val Met Val Arg Thr Ala
70 75 80 85

ggt gga caa tcc aaa aat gcc acc acc aac acc atc atc gat gtt gca 403
Gly Gly Gln Ser Lys Asn Ala Thr Thr Asn Thr Ile Ile Asp Val Ala
90 95 100

gct ggt gaa cgt atc cgc gtc gag ccc gca acc tat ggc atg cgt gcc 451
Ala Gly Glu Arg Ile Arg Val Glu Pro Ala Thr Tyr Gly Met Arg Ala
105 110 115

tac ttt gct gct cgc ggt gga ttt gca gta aaa aaa act ttg gga tct 499
Tyr Phe Ala Ala Arg Gly Gly Phe Ala Val Lys Lys Thr Leu Gly Ser
120 125 130

gct tca acc gat ctg atc tcc cac atg ggc cct tgc ccg atc gag ccc 547
Ala Ser Thr Asp Leu Ile Ser His Met Gly Pro Cys Pro Ile Glu Pro
135 140 145

ggg gat gtc att gac gta gca aca gac att gca gat tct cag tgg tgg 595
Gly Asp Val Ile Asp Val Ala Thr Asp Ile Ala Asp Ser Gln Trp Trp
150 155 160 165

cca aaa ctt cgg caa ctg ccc acc tta tgg aaa cgc atg cca aca gaa 643
Pro Lys Leu Arg Gln Leu Pro Thr Leu Trp Lys Arg Met Pro Thr Glu
170 175 180

acg ctt acc gtc atc cga ggt cca cgt gac aaa tgg ttc acg caa gaa 691
Thr Leu Thr Val Ile Arg Gly Pro Arg Asp Lys Trp Phe Thr Gln Glu

```
            185                 190                 195

tcc ctc aac aac ttt ttt act cag gtg ttt acg gtg agc aat gac tcc   739
Ser Leu Asn Asn Phe Phe Thr Gln Val Phe Thr Val Ser Asn Asp Ser
        200                 205                 210

aac cgg att ggt ttg cgc atg cac tca agc gag ccg atc caa cat cgt   787
Asn Arg Ile Gly Leu Arg Met His Ser Ser Glu Pro Ile Gln His Arg
    215                 220                 225

gtg gaa ggc gag ctg aaa agt gaa gga atg gtc cgg ggg tcc atc cag   835
Val Glu Gly Glu Leu Lys Ser Glu Gly Met Val Arg Gly Ser Ile Gln
230                 235                 240                 245

att ccg cct ggt gga aac ccc gtg gtg ttt ggt ccc gat cat cct gtg   883
Ile Pro Pro Gly Gly Asn Pro Val Val Phe Gly Pro Asp His Pro Val
                250                 255                 260

acc ggt ggc tat cca gta ata gca gta ctt aca tca agg tcg tgt gat   931
Thr Gly Gly Tyr Pro Val Ile Ala Val Leu Thr Ser Arg Ser Cys Asp
            265                 270                 275

cgt tcg gcc cag ctg ttg ccg ggc gat aaa gtc aga ttt aaa ttg ctt   979
Arg Ser Ala Gln Leu Leu Pro Gly Asp Lys Val Arg Phe Lys Leu Leu
        280                 285                 290

taggaacttt gagcttgctc tgg                                        1002


<210> 302
<211> 293
<212> PRT
<213> Corynebacterium glutamicum

<400> 302
Met Ser Phe Lys Val Ile Ser Thr Gly Pro Gln Ala Ile Phe Gln Asp
  1               5                  10                  15

Arg Gly Arg Phe Gly Phe Ala Ser Ala Gly Val Gly Thr Ser Gly Ser
             20                  25                  30

Phe Asp Arg Leu Ser Ala Ala Arg Ala Asn His Ala Leu Gly Asn Asp
         35                  40                  45

Pro Asn Ala Thr Val Val Glu Ile Leu Leu Gly Gly Phe Glu Val Glu
     50                  55                  60

Ala Leu His Thr Thr Ser Ile Val Phe Thr Gly Thr Glu Ala Glu Val
 65                  70                  75                  80

Met Val Arg Thr Ala Gly Gly Gln Ser Lys Asn Ala Thr Thr Asn Thr
                 85                  90                  95

Ile Ile Asp Val Ala Ala Gly Glu Arg Ile Arg Val Glu Pro Ala Thr
            100                 105                 110

Tyr Gly Met Arg Ala Tyr Phe Ala Ala Arg Gly Gly Phe Ala Val Lys
        115                 120                 125

Lys Thr Leu Gly Ser Ala Ser Thr Asp Leu Ile Ser His Met Gly Pro
    130                 135                 140
```

```
Cys Pro Ile Glu Pro Gly Asp Val Ile Asp Val Ala Thr Asp Ile Ala
145                 150                 155                 160

Asp Ser Gln Trp Trp Pro Lys Leu Arg Gln Leu Pro Thr Leu Trp Lys
                165                 170                 175

Arg Met Pro Thr Glu Thr Leu Thr Val Ile Arg Gly Pro Arg Asp Lys
            180                 185                 190

Trp Phe Thr Gln Glu Ser Leu Asn Asn Phe Phe Thr Gln Val Phe Thr
        195                 200                 205

Val Ser Asn Asp Ser Asn Arg Ile Gly Leu Arg Met His Ser Ser Glu
    210                 215                 220

Pro Ile Gln His Arg Val Glu Gly Glu Leu Lys Ser Glu Gly Met Val
225                 230                 235                 240

Arg Gly Ser Ile Gln Ile Pro Pro Gly Gly Asn Pro Val Val Phe Gly
                245                 250                 255

Pro Asp His Pro Val Thr Gly Gly Tyr Pro Val Ile Ala Val Leu Thr
            260                 265                 270

Ser Arg Ser Cys Asp Arg Ser Ala Gln Leu Leu Pro Gly Asp Lys Val
        275                 280                 285

Arg Phe Lys Leu Leu
    290


<210> 303
<211> 1002
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(979)
<223> FRXA00574

<400> 303
aactgctggg cactactgag attcccatgt gggatgtgga ccggtggcaa ccatcgcttc 60

tcaagcccgg tgattcagtt cgatttgtgc aggtgaagaa atg agc ttc aaa gta   115
                                            Met Ser Phe Lys Val
                                              1               5

att tcc act ggc ccc caa gcc atc ttc caa gac cga ggt cgc ttc ggt   163
Ile Ser Thr Gly Pro Gln Ala Ile Phe Gln Asp Arg Gly Arg Phe Gly
                 10                  15                  20

ttt gcc agc gct ggt gtt gga acc tca gga tcc ttt gat cgt tta tcc   211
Phe Ala Ser Ala Gly Val Gly Thr Ser Gly Ser Phe Asp Arg Leu Ser
             25                  30                  35

gct gct cgc gcg aat cac gct tta ggt aat gat ccc aat gca acc gtg   259
Ala Ala Arg Ala Asn His Ala Leu Gly Asn Asp Pro Asn Ala Thr Val
         40                  45                  50
```

```
gta gag att ctg ctc ggt ggc ttt gag gtg gag gcg ttg cac acc acc   307
Val Glu Ile Leu Leu Gly Gly Phe Glu Val Glu Ala Leu His Thr Thr
     55                  60                  65

tcg atc gtg ttc acg gga act gaa gct gaa gtg atg gtt cga acg gct   355
Ser Ile Val Phe Thr Gly Thr Glu Ala Glu Val Met Val Arg Thr Ala
 70                  75                  80                  85

ggt gga caa tcc aaa aat gcc acc acc aac acc atc atc gat gtt gca   403
Gly Gly Gln Ser Lys Asn Ala Thr Thr Asn Thr Ile Ile Asp Val Ala
                90                  95                 100

gct ggt gaa cgt atc cgc gtc gag ccc gca acc tat ggc atg cgt gcc   451
Ala Gly Glu Arg Ile Arg Val Glu Pro Ala Thr Tyr Gly Met Arg Ala
            105                 110                 115

tac ttt gct gct cgc ggt gga ttt gca gta aaa aaa act ttg gga tct   499
Tyr Phe Ala Ala Arg Gly Gly Phe Ala Val Lys Lys Thr Leu Gly Ser
        120                 125                 130

gct tca acc gat ctg atc tcc cac atg ggc cct tgc ccg atc gag ccc   547
Ala Ser Thr Asp Leu Ile Ser His Met Gly Pro Cys Pro Ile Glu Pro
    135                 140                 145

ggg gat gtc att gac gta gca aca gac att gca gat tct cag tgg tgg   595
Gly Asp Val Ile Asp Val Ala Thr Asp Ile Ala Asp Ser Gln Trp Trp
150                 155                 160                 165

cca aaa ctt cgg caa ctg ccc acc tta tgg aaa cgc atg cca aca gaa   643
Pro Lys Leu Arg Gln Leu Pro Thr Leu Trp Lys Arg Met Pro Thr Glu
                170                 175                 180

acg ctt acc gtc atc cga ggt cca cgt gac aaa tgg ttc acg caa gaa   691
Thr Leu Thr Val Ile Arg Gly Pro Arg Asp Lys Trp Phe Thr Gln Glu
            185                 190                 195

tcc ctc aac aac ttt ttt act cag gtg ttt acg gtg agc aat gac tcc   739
Ser Leu Asn Asn Phe Phe Thr Gln Val Phe Thr Val Ser Asn Asp Ser
        200                 205                 210

aac cgg att ggt ttg cgc atg cac tca agc gag ccg atc caa cat cgt   787
Asn Arg Ile Gly Leu Arg Met His Ser Ser Glu Pro Ile Gln His Arg
    215                 220                 225

gtg gaa ggc gag ctg aaa agt gaa gga atg gtc cgg ggg tcc atc cag   835
Val Glu Gly Glu Leu Lys Ser Glu Gly Met Val Arg Gly Ser Ile Gln
230                 235                 240                 245

att ccg cct ggt gga aac ccc gtg gtg ttt ggt ccc gat cat cct gtg   883
Ile Pro Pro Gly Gly Asn Pro Val Val Phe Gly Pro Asp His Pro Val
                250                 255                 260

acc ggt ggc tat cca gta ata gca gta ctt aca tca agg tcg tgt gat   931
Thr Gly Gly Tyr Pro Val Ile Ala Val Leu Thr Ser Arg Ser Cys Asp
            265                 270                 275

cgt tcg gcc cag ctg ttg ccg ggc gat aaa gtc aga ttt aaa ttg ctt   979
Arg Ser Ala Gln Leu Leu Pro Gly Asp Lys Val Arg Phe Lys Leu Leu
        280                 285                 290

taggaacttt gagcttgctc tgg                                        1002
```

<210> 304
<211> 293
<212> PRT
<213> Corynebacterium glutamicum

<400> 304
Met Ser Phe Lys Val Ile Ser Thr Gly Pro Gln Ala Ile Phe Gln Asp
1 5 10 15

Arg Gly Arg Phe Gly Phe Ala Ser Ala Gly Val Gly Thr Ser Gly Ser
20 25 30

Phe Asp Arg Leu Ser Ala Ala Arg Ala Asn His Ala Leu Gly Asn Asp
35 40 45

Pro Asn Ala Thr Val Val Glu Ile Leu Leu Gly Gly Phe Glu Val Glu
50 55 60

Ala Leu His Thr Thr Ser Ile Val Phe Thr Gly Thr Glu Ala Glu Val
65 70 75 80

Met Val Arg Thr Ala Gly Gly Gln Ser Lys Asn Ala Thr Thr Asn Thr
85 90 95

Ile Ile Asp Val Ala Ala Gly Glu Arg Ile Arg Val Glu Pro Ala Thr
100 105 110

Tyr Gly Met Arg Ala Tyr Phe Ala Ala Arg Gly Gly Phe Ala Val Lys
115 120 125

Lys Thr Leu Gly Ser Ala Ser Thr Asp Leu Ile Ser His Met Gly Pro
130 135 140

Cys Pro Ile Glu Pro Gly Asp Val Ile Asp Val Ala Thr Asp Ile Ala
145 150 155 160

Asp Ser Gln Trp Trp Pro Lys Leu Arg Gln Leu Pro Thr Leu Trp Lys
165 170 175

Arg Met Pro Thr Glu Thr Leu Thr Val Ile Arg Gly Pro Arg Asp Lys
180 185 190

Trp Phe Thr Gln Glu Ser Leu Asn Asn Phe Phe Thr Gln Val Phe Thr
195 200 205

Val Ser Asn Asp Ser Asn Arg Ile Gly Leu Arg Met His Ser Ser Glu
210 215 220

Pro Ile Gln His Arg Val Glu Gly Glu Leu Lys Ser Glu Gly Met Val
225 230 235 240

Arg Gly Ser Ile Gln Ile Pro Pro Gly Gly Asn Pro Val Val Phe Gly
245 250 255

Pro Asp His Pro Val Thr Gly Gly Tyr Pro Val Ile Ala Val Leu Thr
260 265 270

Ser Arg Ser Cys Asp Arg Ser Ala Gln Leu Leu Pro Gly Asp Lys Val
275 280 285

Arg Phe Lys Leu Leu
290

<210> 305
<211> 573
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(550)
<223> RXN00589

<400> 305
ccgttatctc cgtaactgtt gtttctgcag aaccatacaa ctcagcaaaa gccgcgacac 60

tccgcggcaa aaactaacca aggatttaaa agtcttcaaa atg aca act ctt tca 115
Met Thr Thr Leu Ser
1 5

cgt aag ttc ttc gtt tct gct acc aca gcc ctg gcg gca gtc gca ctg 163
Arg Lys Phe Phe Val Ser Ala Thr Thr Ala Leu Ala Ala Val Ala Leu
10 15 20

gtt gcg tgt tcc cct aat gag att gat tct gaa ctg aag gtg cca acg 211
Val Ala Cys Ser Pro Asn Glu Ile Asp Ser Glu Leu Lys Val Pro Thr
25 30 35

gca act ggc gtt tct tta cct tcg aag aac gtt tcc gcg acc tca act 259
Ala Thr Gly Val Ser Leu Pro Ser Lys Asn Val Ser Ala Thr Ser Thr
40 45 50

gct act aca gat gag gat gcg cct ggc tac att gat tgc gta gcc gca 307
Ala Thr Thr Asp Glu Asp Ala Pro Gly Tyr Ile Asp Cys Val Ala Ala
55 60 65

cca act cag caa cct gct gaa atc tca cta aac tgt gca atg gat att 355
Pro Thr Gln Gln Pro Ala Glu Ile Ser Leu Asn Cys Ala Met Asp Ile
70 75 80 85

gat cgg ctc acg gat att tct tgg agc gaa tgg gat act gat tcc gca 403
Asp Arg Leu Thr Asp Ile Ser Trp Ser Glu Trp Asp Thr Asp Ser Ala
90 95 100

act gga acc ggt acc cgc atc gta acc gct gca aat ggt caa gag acc 451
Thr Gly Thr Gly Thr Arg Ile Val Thr Ala Ala Asn Gly Gln Glu Thr
105 110 115

gaa acc gaa gat att gag gtg aag ctt tcc ttc ccc acc gag tct tcc 499
Glu Thr Glu Asp Ile Glu Val Lys Leu Ser Phe Pro Thr Glu Ser Ser
120 125 130

caa ggc cta gtg ttc act cag gtc acc gtc gat gga cag gtt ctc ttc 547
Gln Gly Leu Val Phe Thr Gln Val Thr Val Asp Gly Gln Val Leu Phe
135 140 145

ctc taatcctcca taattagaga gcg 573
Leu
150

<210> 306
<211> 150
<212> PRT
<213> Corynebacterium glutamicum

<400> 306
Met Thr Thr Leu Ser Arg Lys Phe Phe Val Ser Ala Thr Thr Ala Leu
1 5 10 15

Ala Ala Val Ala Leu Val Ala Cys Ser Pro Asn Glu Ile Asp Ser Glu
20 25 30

Leu Lys Val Pro Thr Ala Thr Gly Val Ser Leu Pro Ser Lys Asn Val
35 40 45

Ser Ala Thr Ser Thr Ala Thr Thr Asp Glu Asp Ala Pro Gly Tyr Ile
50 55 60

Asp Cys Val Ala Ala Pro Thr Gln Gln Pro Ala Glu Ile Ser Leu Asn
65 70 75 80

Cys Ala Met Asp Ile Asp Arg Leu Thr Asp Ile Ser Trp Ser Glu Trp
85 90 95

Asp Thr Asp Ser Ala Thr Gly Thr Gly Thr Arg Ile Val Thr Ala Ala
100 105 110

Asn Gly Gln Glu Thr Glu Thr Glu Asp Ile Glu Val Lys Leu Ser Phe
115 120 125

Pro Thr Glu Ser Ser Gln Gly Leu Val Phe Thr Gln Val Thr Val Asp
130 135 140

Gly Gln Val Leu Phe Leu
145 150

<210> 307
<211> 463
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(463)
<223> FRXA00589

<400> 307
ccgttatctc cgtaactgtt gtttctgcag aaccatacaa ctcagcaaaa gccgcgacac 60

tccgcggcaa aaactaacca aggatttaaa agtcttcaaa atg aca act ctt tca 115
Met Thr Thr Leu Ser
1 5

cgt aag ttc ttc gtt tct gct acc aca gcc ctg gcg gca gtc gca ctg 163
Arg Lys Phe Phe Val Ser Ala Thr Thr Ala Leu Ala Ala Val Ala Leu
10 15 20

gtt gcg tgt tcc cct aat gag att gat tct gaa ctg aag gtg cca acg 211

```
Val Ala Cys Ser Pro Asn Glu Ile Asp Ser Glu Leu Lys Val Pro Thr
            25                  30                  35

gca act ggc gtt tct tta cct tcg aag aac gtt tcc gcg acc tca act   259
Ala Thr Gly Val Ser Leu Pro Ser Lys Asn Val Ser Ala Thr Ser Thr
        40                  45                  50

gct act aca gat gag gat gcg cct ggc tac att gat tgc gta gcc gca   307
Ala Thr Thr Asp Glu Asp Ala Pro Gly Tyr Ile Asp Cys Val Ala Ala
    55                  60                  65

cca act cag caa cct gct gaa atc tca cta aac tgt gca atg gat att   355
Pro Thr Gln Gln Pro Ala Glu Ile Ser Leu Asn Cys Ala Met Asp Ile
70                  75                  80                  85

gat cgg ctc acg gat att tct tgg agc gaa tgg gat act gat tcc gca   403
Asp Arg Leu Thr Asp Ile Ser Trp Ser Glu Trp Asp Thr Asp Ser Ala
                90                  95                  100

act gga acc ggt acc cgc atc gta acc gct gca aat ggt caa gag acc   451
Thr Gly Thr Gly Thr Arg Ile Val Thr Ala Ala Asn Gly Gln Glu Thr
            105                 110                 115

gaa acc gaa gat                                                  463
Glu Thr Glu Asp
        120


<210> 308
<211> 121
<212> PRT
<213> Corynebacterium glutamicum

<400> 308
Met Thr Thr Leu Ser Arg Lys Phe Phe Val Ser Ala Thr Thr Ala Leu
  1               5                  10                  15

Ala Ala Val Ala Leu Val Ala Cys Ser Pro Asn Glu Ile Asp Ser Glu
            20                  25                  30

Leu Lys Val Pro Thr Ala Thr Gly Val Ser Leu Pro Ser Lys Asn Val
        35                  40                  45

Ser Ala Thr Ser Thr Ala Thr Thr Asp Glu Asp Ala Pro Gly Tyr Ile
    50                  55                  60

Asp Cys Val Ala Ala Pro Thr Gln Gln Pro Ala Glu Ile Ser Leu Asn
65                  70                  75                  80

Cys Ala Met Asp Ile Asp Arg Leu Thr Asp Ile Ser Trp Ser Glu Trp
                85                  90                  95

Asp Thr Asp Ser Ala Thr Gly Thr Gly Thr Arg Ile Val Thr Ala Ala
            100                 105                 110

Asn Gly Gln Glu Thr Glu Thr Glu Asp
        115                 120


<210> 309
<211> 468
```

<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(445)
<223> RXN00616

<400> 309
aaccgcaacc tcgcgcactt ggagtgaaaa ttctcatctt catttcatct tggtgcctaa 60

caatggaata cagattgagt tgatcaaagg agaaccccca atg aaa tca ctc ccc 115
Met Lys Ser Leu Pro
1 5

cgt ttc gcc cca ctg att acg att ctg gct ctg ctc gta ctc gtt gcc 163
Arg Phe Ala Pro Leu Ile Thr Ile Leu Ala Leu Leu Val Leu Val Ala
10 15 20

atc gga gga tct gca ctg gca aat aat cgt gct acc cct aat gtg gaa 211
Ile Gly Gly Ser Ala Leu Ala Asn Asn Arg Ala Thr Pro Asn Val Glu
25 30 35

agt gaa ccc gcc acg gtc aac cag cgt tcc act ccc aca act tcc gcg 259
Ser Glu Pro Ala Thr Val Asn Gln Arg Ser Thr Pro Thr Thr Ser Ala
40 45 50

tat gag ccc cct gct aca gaa tct ccg gaa gaa cca acc aca caa att 307
Tyr Glu Pro Pro Ala Thr Glu Ser Pro Glu Glu Pro Thr Thr Gln Ile
55 60 65

caa gaa tcc cca gta caa ccc cca gtt cct gcc ccc gct caa att cct 355
Gln Glu Ser Pro Val Gln Pro Pro Val Pro Ala Pro Ala Gln Ile Pro
70 75 80 85

caa gcc cca caa gtt cca ctc aat tat cag tac tat gac gat gac tgg 403
Gln Ala Pro Gln Val Pro Leu Asn Tyr Gln Tyr Tyr Asp Asp Asp Trp
90 95 100

gac gac gac gat gat gac ttc gac gac gac tgg gac gac gac 445
Asp Asp Asp Asp Asp Asp Phe Asp Asp Asp Trp Asp Asp Asp
105 110 115

taactaaccc ctgaggcact ttc 468

<210> 310
<211> 115
<212> PRT
<213> Corynebacterium glutamicum

<400> 310
Met Lys Ser Leu Pro Arg Phe Ala Pro Leu Ile Thr Ile Leu Ala Leu
1 5 10 15

Leu Val Leu Val Ala Ile Gly Gly Ser Ala Leu Ala Asn Asn Arg Ala
20 25 30

Thr Pro Asn Val Glu Ser Glu Pro Ala Thr Val Asn Gln Arg Ser Thr
35 40 45

```
Pro Thr Thr Ser Ala Tyr Glu Pro Pro Ala Thr Glu Ser Pro Glu Glu
     50                  55                  60

Pro Thr Thr Gln Ile Gln Glu Ser Pro Val Gln Pro Pro Val Pro Ala
 65                  70                  75                  80

Pro Ala Gln Ile Pro Gln Ala Pro Gln Val Pro Leu Asn Tyr Gln Tyr
                 85                  90                  95

Tyr Asp Asp Asp Trp Asp Asp Asp Asp Asp Asp Phe Asp Asp Asp Trp
            100                 105                 110

Asp Asp Asp
        115
```

<210> 311
<211> 468
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(445)
<223> FRXA00616

<400> 311

```
aaccgcaacc tcgcgcactt ggagtgaaaa ttctcatctt catttcatct tggtgcctaa 60

caatggaata cagattgagt tgatcaaagg agaaccccca atg aaa tca ctc ccc   115
                                              Met Lys Ser Leu Pro
                                                1               5

cgt ttc gcc cca ctg att acg att ctg gct ctg ctc gta ctc gtt gcc   163
Arg Phe Ala Pro Leu Ile Thr Ile Leu Ala Leu Leu Val Leu Val Ala
                10                  15                  20

atc gga gga tct gca ctg gca aat aat cgt gct acc cct aat gtg gaa   211
Ile Gly Gly Ser Ala Leu Ala Asn Asn Arg Ala Thr Pro Asn Val Glu
            25                  30                  35

agt gaa ccc gcc acg gtc aac cag cgt tcc act ccc aca act tcc gcg   259
Ser Glu Pro Ala Thr Val Asn Gln Arg Ser Thr Pro Thr Thr Ser Ala
        40                  45                  50

tat gag ccc cct gct aca gaa tct ccg gaa gaa cca acc aca caa att   307
Tyr Glu Pro Pro Ala Thr Glu Ser Pro Glu Glu Pro Thr Thr Gln Ile
    55                  60                  65

caa gaa tcc cca gta caa ccc cca gtt cct gcc ccc gct caa att cct   355
Gln Glu Ser Pro Val Gln Pro Pro Val Pro Ala Pro Ala Gln Ile Pro
70                  75                  80                  85

caa gcc cca caa gtt cca ctc aat tat cag tac tat gac gat gac tgg   403
Gln Ala Pro Gln Val Pro Leu Asn Tyr Gln Tyr Tyr Asp Asp Asp Trp
                90                  95                 100

gac gac gac gat gat gac ttc gac gac gac tgg gac gac gac           445
Asp Asp Asp Asp Asp Asp Phe Asp Asp Asp Trp Asp Asp Asp
            105                 110                 115
```

taactaaccc ctgaggcact ttc 468

<210> 312
<211> 115
<212> PRT
<213> Corynebacterium glutamicum

<400> 312
Met Lys Ser Leu Pro Arg Phe Ala Pro Leu Ile Thr Ile Leu Ala Leu
1 5 10 15

Leu Val Leu Val Ala Ile Gly Gly Ser Ala Leu Ala Asn Asn Arg Ala
20 25 30

Thr Pro Asn Val Glu Ser Glu Pro Ala Thr Val Asn Gln Arg Ser Thr
35 40 45

Pro Thr Thr Ser Ala Tyr Glu Pro Pro Ala Thr Glu Ser Pro Glu Glu
50 55 60

Pro Thr Thr Gln Ile Gln Glu Ser Pro Val Gln Pro Pro Val Pro Ala
65 70 75 80

Pro Ala Gln Ile Pro Gln Ala Pro Gln Val Pro Leu Asn Tyr Gln Tyr
85 90 95

Tyr Asp Asp Asp Trp Asp Asp Asp Asp Asp Asp Phe Asp Asp Asp Trp
100 105 110

Asp Asp Asp
115

<210> 313
<211> 756
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(733)
<223> RXN00647

<400> 313
tgcattcttc ccacaatgac atgagcttat tgcaacatcg tgggtaaagt tgaatcgaga 60

agtcgagaaa taaccgaccg atgaaagagt tgagacgata atg ggc atc ttc gaa 115
Met Gly Ile Phe Glu
1 5

gcc atc cga gcc gca cgc gcg aag acc aaa gct gag atc aaa gca gcc 163
Ala Ile Arg Ala Ala Arg Ala Lys Thr Lys Ala Glu Ile Lys Ala Ala
10 15 20

gag gca aaa gta aaa act gag gcg aaa aac aaa gca aag cta gat ctc 211
Glu Ala Lys Val Lys Thr Glu Ala Lys Asn Lys Ala Lys Leu Asp Leu
25 30 35

aag cgc gag aag ctt ctt gtc cag cag gaa aag aat ctg ctc aag gtt 259
Lys Arg Glu Lys Leu Leu Val Gln Gln Glu Lys Asn Leu Leu Lys Val

```
         40                  45                  50

gaa gaa aag ggc ctg aag aag cgc aac aag cat gag ctg aag atg gcc   307
Glu Glu Lys Gly Leu Lys Lys Arg Asn Lys His Glu Leu Lys Met Ala
     55                  60                  65

aaa aat atc ctt gag caa aag cgc caa gga cgc cta aac aaa gac aag   355
Lys Asn Ile Leu Glu Gln Lys Arg Gln Gly Arg Leu Asn Lys Asp Lys
 70                  75                  80                  85

gtg aag cgc tgg gct ggc acc gca cgt gtg ctc act cca cta ctg ctg   403
Val Lys Arg Trp Ala Gly Thr Ala Arg Val Leu Thr Pro Leu Leu Leu
                 90                  95                 100

cct att att tat cga ctc tcc acc gaa gca cgc gat cag gtt gtt aag   451
Pro Ile Ile Tyr Arg Leu Ser Thr Glu Ala Arg Asp Gln Val Val Lys
            105                 110                 115

gga cgt gcc cgt cgt gca ggt gtc acc gcg gag cag ctt agc caa ttc   499
Gly Arg Ala Arg Arg Ala Gly Val Thr Ala Glu Gln Leu Ser Gln Phe
        120                 125                 130

gca ggt cac gca gca gcg ctg aag gct cgt att caa ggt gtt cgc gaa   547
Ala Gly His Ala Ala Ala Leu Lys Ala Arg Ile Gln Gly Val Arg Glu
    135                 140                 145

acc gca aag aac tcc agc ctc cct gct ggc ttt gta cgc gat gtt gaa   595
Thr Ala Lys Asn Ser Ser Leu Pro Ala Gly Phe Val Arg Asp Val Glu
150                 155                 160                 165

gag cgt ctc aat gag ctc gag gct gct gcg aat aac tct gag ttc atg   643
Glu Arg Leu Asn Glu Leu Glu Ala Ala Ala Asn Asn Ser Glu Phe Met
                170                 175                 180

tct cca cag cag agg aac cgt gcg cac cag tcg atc agt cgt gat ctg   691
Ser Pro Gln Gln Arg Asn Arg Ala His Gln Ser Ile Ser Arg Asp Leu
            185                 190                 195

aac cag gtg tca gat cag att cag gat cga cta ctg gac aag           733
Asn Gln Val Ser Asp Gln Ile Gln Asp Arg Leu Leu Asp Lys
        200                 205                 210

tagctgctgg tcgagtcgct gcc                                        756


<210> 314
<211> 211
<212> PRT
<213> Corynebacterium glutamicum

<400> 314
Met Gly Ile Phe Glu Ala Ile Arg Ala Ala Arg Ala Lys Thr Lys Ala
  1               5                  10                  15

Glu Ile Lys Ala Ala Glu Ala Lys Val Lys Thr Glu Ala Lys Asn Lys
             20                  25                  30

Ala Lys Leu Asp Leu Lys Arg Glu Lys Leu Leu Val Gln Gln Glu Lys
         35                  40                  45

Asn Leu Leu Lys Val Glu Glu Lys Gly Leu Lys Lys Arg Asn Lys His
```

```
     50                  55                  60

Glu Leu Lys Met Ala Lys Asn Ile Leu Glu Gln Lys Arg Gln Gly Arg
 65                  70                  75                  80

Leu Asn Lys Asp Lys Val Lys Arg Trp Ala Gly Thr Ala Arg Val Leu
                85                  90                  95

Thr Pro Leu Leu Leu Pro Ile Ile Tyr Arg Leu Ser Thr Glu Ala Arg
            100                 105                 110

Asp Gln Val Val Lys Gly Arg Ala Arg Arg Ala Gly Val Thr Ala Glu
        115                 120                 125

Gln Leu Ser Gln Phe Ala Gly His Ala Ala Ala Leu Lys Ala Arg Ile
    130                 135                 140

Gln Gly Val Arg Glu Thr Ala Lys Asn Ser Ser Leu Pro Ala Gly Phe
145                 150                 155                 160

Val Arg Asp Val Glu Glu Arg Leu Asn Glu Leu Glu Ala Ala Ala Asn
                165                 170                 175

Asn Ser Glu Phe Met Ser Pro Gln Gln Arg Asn Arg Ala His Gln Ser
            180                 185                 190

Ile Ser Arg Asp Leu Asn Gln Val Ser Asp Gln Ile Gln Asp Arg Leu
        195                 200                 205

Leu Asp Lys
    210


<210> 315
<211> 756
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(733)
<223> FRXA00647

<400> 315
tgcattcttc ccacaatgac atgagcttat tgcaacatcg tgggtaaagt tgaatcgaga 60

agtcgagaaa taaccgaccg atgaaagagt tgagacgata atg ggc atc ttc gaa   115
                                              Met Gly Ile Phe Glu
                                                1               5

gcc atc cga gcc gca cgc gcg aag acc aaa gct gag atc aaa gca gcc   163
Ala Ile Arg Ala Ala Arg Ala Lys Thr Lys Ala Glu Ile Lys Ala Ala
                10                  15                  20

gag gca aaa gta aaa act gag gcg aaa aac aaa gca aag cta gat ctc   211
Glu Ala Lys Val Lys Thr Glu Ala Lys Asn Lys Ala Lys Leu Asp Leu
            25                  30                  35

aag cgc gag aag ctt ctt gtc cag cag gaa aag aat ctg ctc aag gtt   259
Lys Arg Glu Lys Leu Leu Val Gln Gln Glu Lys Asn Leu Leu Lys Val
        40                  45                  50
```

```
gaa gaa aag ggc ctg aag aag cgc aac aag cat gag ctg aag atg gcc   307
Glu Glu Lys Gly Leu Lys Lys Arg Asn Lys His Glu Leu Lys Met Ala
     55                  60                  65

aaa aat atc ctt gag caa aag cgc caa gga cgc cta aac aaa gac aag   355
Lys Asn Ile Leu Glu Gln Lys Arg Gln Gly Arg Leu Asn Lys Asp Lys
 70                  75                  80                  85

gtg aag cgc tgg gct ggc acc gca cgt gtg ctc act cca cta ctg ctg   403
Val Lys Arg Trp Ala Gly Thr Ala Arg Val Leu Thr Pro Leu Leu Leu
                 90                  95                 100

cct att att tat cga ctc tcc acc gaa gca cgc gat cag gtt gtt aag   451
Pro Ile Ile Tyr Arg Leu Ser Thr Glu Ala Arg Asp Gln Val Val Lys
            105                 110                 115

gga cgt gcc cgt cgt gca ggt gtc acc gcg gag cag ctt agc caa ttc   499
Gly Arg Ala Arg Arg Ala Gly Val Thr Ala Glu Gln Leu Ser Gln Phe
        120                 125                 130

gca ggt cac gca gca gcg ctg aag gct cgt att caa ggt gtt cgc gaa   547
Ala Gly His Ala Ala Ala Leu Lys Ala Arg Ile Gln Gly Val Arg Glu
    135                 140                 145

acc gca aag aac tcc agc ctc cct gct ggc ttt gta cgc gat gtt gaa   595
Thr Ala Lys Asn Ser Ser Leu Pro Ala Gly Phe Val Arg Asp Val Glu
150                 155                 160                 165

gag cgt ctc aat gag ctc gag gct gct gcg aat aac tct gag ttc atg   643
Glu Arg Leu Asn Glu Leu Glu Ala Ala Ala Asn Asn Ser Glu Phe Met
                170                 175                 180

tct cca cag cag agg aac cgt gcg cac cag tcg atc agt cgt gat ctg   691
Ser Pro Gln Gln Arg Asn Arg Ala His Gln Ser Ile Ser Arg Asp Leu
            185                 190                 195

aac cag gtg tca gat cag att cag gat cga cta ctg gac aag           733
Asn Gln Val Ser Asp Gln Ile Gln Asp Arg Leu Leu Asp Lys
        200                 205                 210

tagctgctgg tcgagtcgct gcc                                        756
```

<210> 316
<211> 211
<212> PRT
<213> Corynebacterium glutamicum

<400> 316

```
Met Gly Ile Phe Glu Ala Ile Arg Ala Ala Arg Ala Lys Thr Lys Ala
  1               5                  10                  15

Glu Ile Lys Ala Ala Glu Ala Lys Val Lys Thr Glu Ala Lys Asn Lys
             20                  25                  30

Ala Lys Leu Asp Leu Lys Arg Glu Lys Leu Leu Val Gln Gln Glu Lys
         35                  40                  45

Asn Leu Leu Lys Val Glu Glu Lys Gly Leu Lys Lys Arg Asn Lys His
     50                  55                  60
```

```
Glu Leu Lys Met Ala Lys Asn Ile Leu Glu Gln Lys Arg Gln Gly Arg
 65                  70                  75                  80

Leu Asn Lys Asp Lys Val Lys Arg Trp Ala Gly Thr Ala Arg Val Leu
                85                  90                  95

Thr Pro Leu Leu Leu Pro Ile Ile Tyr Arg Leu Ser Thr Glu Ala Arg
            100                 105                 110

Asp Gln Val Val Lys Gly Arg Ala Arg Arg Ala Gly Val Thr Ala Glu
        115                 120                 125

Gln Leu Ser Gln Phe Ala Gly His Ala Ala Ala Leu Lys Ala Arg Ile
    130                 135                 140

Gln Gly Val Arg Glu Thr Ala Lys Asn Ser Ser Leu Pro Ala Gly Phe
145                 150                 155                 160

Val Arg Asp Val Glu Glu Arg Leu Asn Glu Leu Glu Ala Ala Ala Asn
                165                 170                 175

Asn Ser Glu Phe Met Ser Pro Gln Gln Arg Asn Arg Ala His Gln Ser
            180                 185                 190

Ile Ser Arg Asp Leu Asn Gln Val Ser Asp Gln Ile Gln Asp Arg Leu
        195                 200                 205

Leu Asp Lys
    210


<210> 317
<211> 888
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(865)
<223> RXN00653

<400> 317
gttgagattc gcctaacaaa gattttggac gaaaacagta acgatgacag ccacgttaag 60

cgcggaatct tctcgcaatg gtaaaaagcc gcggcctcga gtg agt gtt tcc cag   115
                                            Val Ser Val Ser Gln
                                              1               5

gtt gtt ggt gaa atc ttg ctc acc gta ggc att ttg gcc ttg tta ttc   163
Val Val Gly Glu Ile Leu Leu Thr Val Gly Ile Leu Ala Leu Leu Phe
                10                  15                  20

gca tac tat gag gcc tat tgg acc aac gtg gaa tct ggg aaa tta caa   211
Ala Tyr Tyr Glu Ala Tyr Trp Thr Asn Val Glu Ser Gly Lys Leu Gln
            25                  30                  35

gaa tcg gct ggt caa aag ctt gat gaa gac tgg aat gaa gct cgg gtg   259
Glu Ser Ala Gly Gln Lys Leu Asp Glu Asp Trp Asn Glu Ala Arg Val
        40                  45                  50
```

```
aat cct cga caa aag ctc acc ccg gaa ctt ggt gag gca ttt gcc cgg   307
Asn Pro Arg Gln Lys Leu Thr Pro Glu Leu Gly Glu Ala Phe Ala Arg
     55                  60                  65

atg tat gtt cca gct ttc ggc tct gac ttc aac ttc gca gtg att gaa   355
Met Tyr Val Pro Ala Phe Gly Ser Asp Phe Asn Phe Ala Val Ile Glu
 70                  75                  80                  85

gga acc gat gag gaa gac ctt ctt gcc ggt cct ggc cgt tat gtg gat   403
Gly Thr Asp Glu Glu Asp Leu Leu Ala Gly Pro Gly Arg Tyr Val Asp
                90                  95                 100

tcc caa atg cct ggt gaa gcc gga aac ttt gca gtg gca ggc cac cga   451
Ser Gln Met Pro Gly Glu Ala Gly Asn Phe Ala Val Ala Gly His Arg
            105                 110                 115

gtg ggc aag ggt gcg cca ttc aat gat cta gga aac ctg gaa gtc tgc   499
Val Gly Lys Gly Ala Pro Phe Asn Asp Leu Gly Asn Leu Glu Val Cys
        120                 125                 130

gat gcg atc gtg gtg gag act tac aat tcc tgg gat gtg tac cgc gtg   547
Asp Ala Ile Val Val Glu Thr Tyr Asn Ser Trp Asp Val Tyr Arg Val
    135                 140                 145

atg ccg atg tcc acc aac ggt gca gat cgt gca gca gaa gct gcg gat   595
Met Pro Met Ser Thr Asn Gly Ala Asp Arg Ala Ala Glu Ala Ala Asp
150                 155                 160                 165

tgc ttc aac gaa aac cag gtc agc cgc atg gct gaa ggt gac tat gtg   643
Cys Phe Asn Glu Asn Gln Val Ser Arg Met Ala Glu Gly Asp Tyr Val
                170                 175                 180

aat gtg tcc gga cga agc atc acc act ccg gat cgc atc gat gcc acc   691
Asn Val Ser Gly Arg Ser Ile Thr Thr Pro Asp Arg Ile Asp Ala Thr
            185                 190                 195

tac ccc aca ccg ggc gtc ttc gac act gca gtg cgt gaa gga tca gaa   739
Tyr Pro Thr Pro Gly Val Phe Asp Thr Ala Val Arg Glu Gly Ser Glu
        200                 205                 210

gct ctg ctt acc ttg acc acg tgt cac ccg cag ttc tcc aac gct gag   787
Ala Leu Leu Thr Leu Thr Thr Cys His Pro Gln Phe Ser Asn Ala Glu
    215                 220                 225

cgc atg att gtg cac gca atg ttg gtg gaa gaa atc gat aaa tca agt   835
Arg Met Ile Val His Ala Met Leu Val Glu Glu Ile Asp Lys Ser Ser
230                 235                 240                 245

ggc gaa cgc cct gca gct ttg gag gaa aac taaatgtatt cacttctgtg     885
Gly Glu Arg Pro Ala Ala Leu Glu Glu Asn
                250                 255

gca                                                               888
```

<210> 318
<211> 255
<212> PRT
<213> Corynebacterium glutamicum

<400> 318

```
Val Ser Val Ser Gln Val Val Gly Glu Ile Leu Leu Thr Val Gly Ile
  1               5                  10                  15

Leu Ala Leu Leu Phe Ala Tyr Tyr Glu Ala Tyr Trp Thr Asn Val Glu
             20                  25                  30

Ser Gly Lys Leu Gln Glu Ser Ala Gly Gln Lys Leu Asp Glu Asp Trp
         35                  40                  45

Asn Glu Ala Arg Val Asn Pro Arg Gln Lys Leu Thr Pro Glu Leu Gly
     50                  55                  60

Glu Ala Phe Ala Arg Met Tyr Val Pro Ala Phe Gly Ser Asp Phe Asn
 65                  70                  75                  80

Phe Ala Val Ile Glu Gly Thr Asp Glu Glu Asp Leu Leu Ala Gly Pro
                 85                  90                  95

Gly Arg Tyr Val Asp Ser Gln Met Pro Gly Glu Ala Gly Asn Phe Ala
            100                 105                 110

Val Ala Gly His Arg Val Gly Lys Gly Ala Pro Phe Asn Asp Leu Gly
        115                 120                 125

Asn Leu Glu Val Cys Asp Ala Ile Val Val Glu Thr Tyr Asn Ser Trp
    130                 135                 140

Asp Val Tyr Arg Val Met Pro Met Ser Thr Asn Gly Ala Asp Arg Ala
145                 150                 155                 160

Ala Glu Ala Ala Asp Cys Phe Asn Glu Asn Gln Val Ser Arg Met Ala
                165                 170                 175

Glu Gly Asp Tyr Val Asn Val Ser Gly Arg Ser Ile Thr Thr Pro Asp
            180                 185                 190

Arg Ile Asp Ala Thr Tyr Pro Thr Pro Gly Val Phe Asp Thr Ala Val
        195                 200                 205

Arg Glu Gly Ser Glu Ala Leu Leu Thr Leu Thr Thr Cys His Pro Gln
    210                 215                 220

Phe Ser Asn Ala Glu Arg Met Ile Val His Ala Met Leu Val Glu Glu
225                 230                 235                 240

Ile Asp Lys Ser Ser Gly Glu Arg Pro Ala Ala Leu Glu Glu Asn
                245                 250                 255
```

<210> 319
<211> 888
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(865)
<223> FRXA00653

<400> 319
gttgagattc gcctaacaaa gattttggac gaaaacagta acgatgacag ccacgttaag 60

```
cgcggaatct tctcgcaatg gtaaaaagcc gcggcctcga gtg agt gtt tcc cag   115
                                            Val Ser Val Ser Gln
                                              1               5

gtt gtt ggt gaa atc ttg ctc acc gta ggc att ttg gcc ttg tta ttc   163
Val Val Gly Glu Ile Leu Leu Thr Val Gly Ile Leu Ala Leu Leu Phe
                10                  15                  20

gca tac tat gag gcc tat tgg acc aac gtg gaa tct ggg aaa tta caa   211
Ala Tyr Tyr Glu Ala Tyr Trp Thr Asn Val Glu Ser Gly Lys Leu Gln
            25                  30                  35

gaa tcg gct ggt caa aag ctt gat gaa gac tgg aat gaa gct cgg gtg   259
Glu Ser Ala Gly Gln Lys Leu Asp Glu Asp Trp Asn Glu Ala Arg Val
        40                  45                  50

aat cct cga caa aag ctc acc ccg gaa ctt ggt gag gca ttt gcc cgg   307
Asn Pro Arg Gln Lys Leu Thr Pro Glu Leu Gly Glu Ala Phe Ala Arg
    55                  60                  65

atg tat gtt cca gct ttc ggc tct gac ttc aac ttc gca gtg att gaa   355
Met Tyr Val Pro Ala Phe Gly Ser Asp Phe Asn Phe Ala Val Ile Glu
70                  75                  80                  85

gga acc gat gag gaa gac ctt ctt gcc ggt cct ggc cgt tat gtg gat   403
Gly Thr Asp Glu Glu Asp Leu Leu Ala Gly Pro Gly Arg Tyr Val Asp
                90                  95                  100

tcc caa atg cct ggt gaa gcc gga aac ttt gca gtg gca ggc cac cga   451
Ser Gln Met Pro Gly Glu Ala Gly Asn Phe Ala Val Ala Gly His Arg
            105                 110                 115

gtg ggc aag ggt gcg cca ttc aat gat cta gga aac ctg gaa gtc tgc   499
Val Gly Lys Gly Ala Pro Phe Asn Asp Leu Gly Asn Leu Glu Val Cys
        120                 125                 130

gat gcg atc gtg gtg gag act tac aat tcc tgg gat gtg tac cgc gtg   547
Asp Ala Ile Val Val Glu Thr Tyr Asn Ser Trp Asp Val Tyr Arg Val
    135                 140                 145

atg ccg atg tcc acc aac ggt gca gat cgt gca gca gaa gct gcg gat   595
Met Pro Met Ser Thr Asn Gly Ala Asp Arg Ala Ala Glu Ala Ala Asp
150                 155                 160                 165

tgc ttc aac gaa aac cag gtc agc cgc atg gct gaa ggt gac tat gtg   643
Cys Phe Asn Glu Asn Gln Val Ser Arg Met Ala Glu Gly Asp Tyr Val
                170                 175                 180

aat gtg tcc gga cga agc atc acc act ccg gat cgc atc gat gcc acc   691
Asn Val Ser Gly Arg Ser Ile Thr Thr Pro Asp Arg Ile Asp Ala Thr
            185                 190                 195

tac ccc aca ccg ggc gtc ttc gac act gca gtg cgt gaa gga tca gaa   739
Tyr Pro Thr Pro Gly Val Phe Asp Thr Ala Val Arg Glu Gly Ser Glu
        200                 205                 210

gct ctg ctt acc ttg acc acg tgt cac ccg cag ttc tcc aac gct gag   787
Ala Leu Leu Thr Leu Thr Thr Cys His Pro Gln Phe Ser Asn Ala Glu
    215                 220                 225
```

```
cgc atg att gtg cac gca atg ttg gtg gaa gaa atc gat aaa tca agt   835
Arg Met Ile Val His Ala Met Leu Val Glu Glu Ile Asp Lys Ser Ser
230                 235                 240                 245

ggc gaa cgc cct gca gct ttg gag gaa aac taaatgtatt cacttctgtg     885
Gly Glu Arg Pro Ala Ala Leu Glu Glu Asn
                250                 255

gca                                                               888
```

<210> 320
<211> 255
<212> PRT
<213> Corynebacterium glutamicum

<400> 320

```
Val Ser Val Ser Gln Val Val Gly Glu Ile Leu Leu Thr Val Gly Ile
  1               5                  10                  15

Leu Ala Leu Leu Phe Ala Tyr Tyr Glu Ala Tyr Trp Thr Asn Val Glu
             20                  25                  30

Ser Gly Lys Leu Gln Glu Ser Ala Gly Gln Lys Leu Asp Glu Asp Trp
         35                  40                  45

Asn Glu Ala Arg Val Asn Pro Arg Gln Lys Leu Thr Pro Glu Leu Gly
     50                  55                  60

Glu Ala Phe Ala Arg Met Tyr Val Pro Ala Phe Gly Ser Asp Phe Asn
 65                  70                  75                  80

Phe Ala Val Ile Glu Gly Thr Asp Glu Glu Asp Leu Leu Ala Gly Pro
                 85                  90                  95

Gly Arg Tyr Val Asp Ser Gln Met Pro Gly Glu Ala Gly Asn Phe Ala
            100                 105                 110

Val Ala Gly His Arg Val Gly Lys Gly Ala Pro Phe Asn Asp Leu Gly
        115                 120                 125

Asn Leu Glu Val Cys Asp Ala Ile Val Val Glu Thr Tyr Asn Ser Trp
    130                 135                 140

Asp Val Tyr Arg Val Met Pro Met Ser Thr Asn Gly Ala Asp Arg Ala
145                 150                 155                 160

Ala Glu Ala Ala Asp Cys Phe Asn Glu Asn Gln Val Ser Arg Met Ala
                165                 170                 175

Glu Gly Asp Tyr Val Asn Val Ser Gly Arg Ser Ile Thr Thr Pro Asp
            180                 185                 190

Arg Ile Asp Ala Thr Tyr Pro Thr Pro Gly Val Phe Asp Thr Ala Val
        195                 200                 205

Arg Glu Gly Ser Glu Ala Leu Leu Thr Leu Thr Thr Cys His Pro Gln
    210                 215                 220

Phe Ser Asn Ala Glu Arg Met Ile Val His Ala Met Leu Val Glu Glu
225                 230                 235                 240
```

```
Ile Asp Lys Ser Ser Gly Glu Arg Pro Ala Ala Leu Glu Glu Asn
                245                 250                 255


<210> 321
<211> 1392
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1369)
<223> RXN00662

<400> 321
ccctcatcat agttttaaat ctggggcaga ggcgggaatt taaacacctc tgatacagcg 60

tttactggct atagtgttgc gcgtgccaaa tcgagttcct gtg tca acc att ccg   115
                                        Val Ser Thr Ile Pro
                                          1               5

ctg aat cgt cta gcc gtt atc gct gcc atc att ggt gtc ggt acc ggg   163
Leu Asn Arg Leu Ala Val Ile Ala Ala Ile Ile Gly Val Gly Thr Gly
               10                  15                  20

ctg ttt gtt gct gca ctg aac tgg tct gcc att ggc gtg gag cgt tta   211
Leu Phe Val Ala Ala Leu Asn Trp Ser Ala Ile Gly Val Glu Arg Leu
            25                  30                  35

gtt tat ggc gct gac cat ttg cat aat tac aat ccg gtg gcc aat gtg   259
Val Tyr Gly Ala Asp His Leu His Asn Tyr Asn Pro Val Ala Asn Val
         40                  45                  50

tcg cca ctt cgc ctg tcc atc acg gtg att gtg ctt agc gtg gtg gcc   307
Ser Pro Leu Arg Leu Ser Ile Thr Val Ile Val Leu Ser Val Val Ala
     55                  60                  65

tcc tgg gcg tgg ttt ttt gtg cac cgc acg ggg ccg aaa gag gtt tcg   355
Ser Trp Ala Trp Phe Phe Val His Arg Thr Gly Pro Lys Glu Val Ser
 70                  75                  80                  85

att gtg ggt gcg atc cgg ggc gag aag atg ccg att ttg gag acc ata   403
Ile Val Gly Ala Ile Arg Gly Glu Lys Met Pro Ile Leu Glu Thr Ile
               90                  95                 100

gcg tcc gca ttt ttg cag gtc acc acg gtt gct gcg ggt gcg ccg gtg   451
Ala Ser Ala Phe Leu Gln Val Thr Thr Val Ala Ala Gly Ala Pro Val
            105                 110                 115

ggt gca gag aac gct cca cgt att gct gga gcc ttg gtg gga gag cgg   499
Gly Ala Glu Asn Ala Pro Arg Ile Ala Gly Ala Leu Val Gly Glu Arg
        120                 125                 130

ttt agt cgg tgg ttg cag ctc gat att gat gca aag cgc atc ttg gtg   547
Phe Ser Arg Trp Leu Gln Leu Asp Ile Asp Ala Lys Arg Ile Leu Val
    135                 140                 145

gcc tct gcc gcg gga gct ggt ttg gga gca agc ttc cac ctt ccc cta   595
Ala Ser Ala Ala Gly Ala Gly Leu Gly Ala Ser Phe His Leu Pro Leu
150                 155                 160                 165
```

```
gca ggc gtg ctg ttt gcc ctt gag gtc cta ctg gtt gag gcc tcc act   643
Ala Gly Val Leu Phe Ala Leu Glu Val Leu Leu Val Glu Ala Ser Thr
                170                 175                 180

cgg acc gtg gtt atc gca att atc acc acg acc gcc gcc gtt gcc acc   691
Arg Thr Val Val Ile Ala Ile Ile Thr Thr Thr Ala Ala Val Ala Thr
            185                 190                 195

act gga ttt ttc gtg caa acc cca gat gtg ttc agc act gtc ccg ctg   739
Thr Gly Phe Phe Val Gln Thr Pro Asp Val Phe Ser Thr Val Pro Leu
        200                 205                 210

acg gaa agc cca tgg atg ctg ctt gcc gcg atg gtc acc gga gta gtc   787
Thr Glu Ser Pro Trp Met Leu Leu Ala Ala Met Val Thr Gly Val Val
    215                 220                 225

gcc ggc atg tgc ggg cac tgg ttt tca gcg gcg gcg cac aaa atg gcg   835
Ala Gly Met Cys Gly His Trp Phe Ser Ala Ala Ala His Lys Met Ala
230                 235                 240                 245

cag gcc tcg ccc aag ggt gtg aag att ttg tgg cag atg ccg ttg ggt   883
Gln Ala Ser Pro Lys Gly Val Lys Ile Leu Trp Gln Met Pro Leu Gly
                250                 255                 260

ttc gtg gtg atc gct gcg gtg att tat ttc ttc ccc gaa acc ctg gcg   931
Phe Val Val Ile Ala Ala Val Ile Tyr Phe Phe Pro Glu Thr Leu Ala
            265                 270                 275

aat ccc cgt tgg ctt gcc gat tcc atg ctc ggc gat ggc ctg atc ctc   979
Asn Pro Arg Trp Leu Ala Asp Ser Met Leu Gly Asp Gly Leu Ile Leu
        280                 285                 290

agc acc att tta ttg gta ctt gtt ctg cgc acc gcc atg ttt ttg ctc   1027
Ser Thr Ile Leu Leu Val Leu Val Leu Arg Thr Ala Met Phe Leu Leu
    295                 300                 305

gcc ttc cgc gtg ggc atg gtc ggc ggt aac ctg atc ccc gca ttc gca   1075
Ala Phe Arg Val Gly Met Val Gly Gly Asn Leu Ile Pro Ala Phe Ala
310                 315                 320                 325

ctc gga tcc atg gtc ggt ggg gta gtg ggt gct gta ttg gaa ccc atc   1123
Leu Gly Ser Met Val Gly Gly Val Val Gly Ala Val Leu Glu Pro Ile
                330                 335                 340

act aac gtc ccg atc gcc gct ttt gcg ctg ctt ggc gcc gcc gca ttt   1171
Thr Asn Val Pro Ile Ala Ala Phe Ala Leu Leu Gly Ala Ala Ala Phe
            345                 350                 355

ttg tcc acc acc atg gca gcg cca ctg ttc ggg ctc atc gcc gca gtg   1219
Leu Ser Thr Thr Met Ala Ala Pro Leu Phe Gly Leu Ile Ala Ala Val
        360                 365                 370

gaa ttc acc gac atg gaa gcc caa ggc tac ctt ccg att ttc ctc gca   1267
Glu Phe Thr Asp Met Glu Ala Gln Gly Tyr Leu Pro Ile Phe Leu Ala
    375                 380                 385

gta gcc tcc gcg gtc ctc gcc gtg cgc gtg tgg tct gtc atc gcc aag   1315
Val Ala Ser Ala Val Leu Ala Val Arg Val Trp Ser Val Ile Ala Lys
390                 395                 400                 405
```

```
cac gag ctc cgc gcc atc ccg atc acg tac gcg agc tgg acg ggc gag   1363
His Glu Leu Arg Ala Ile Pro Ile Thr Tyr Ala Ser Trp Thr Gly Glu
                410                 415                 420

ctt aaa taagcttgtc gacgcctccc tcc                                 1392
Leu Lys
```

<210> 322
<211> 423
<212> PRT
<213> Corynebacterium glutamicum

<400> 322

```
Val Ser Thr Ile Pro Leu Asn Arg Leu Ala Val Ile Ala Ala Ile Ile
  1               5                  10                  15

Gly Val Gly Thr Gly Leu Phe Val Ala Ala Leu Asn Trp Ser Ala Ile
             20                  25                  30

Gly Val Glu Arg Leu Val Tyr Gly Ala Asp His Leu His Asn Tyr Asn
         35                  40                  45

Pro Val Ala Asn Val Ser Pro Leu Arg Leu Ser Ile Thr Val Ile Val
     50                  55                  60

Leu Ser Val Val Ala Ser Trp Ala Trp Phe Phe Val His Arg Thr Gly
 65                  70                  75                  80

Pro Lys Glu Val Ser Ile Val Gly Ala Ile Arg Gly Glu Lys Met Pro
                 85                  90                  95

Ile Leu Glu Thr Ile Ala Ser Ala Phe Leu Gln Val Thr Thr Val Ala
            100                 105                 110

Ala Gly Ala Pro Val Gly Ala Glu Asn Ala Pro Arg Ile Ala Gly Ala
        115                 120                 125

Leu Val Gly Glu Arg Phe Ser Arg Trp Leu Gln Leu Asp Ile Asp Ala
    130                 135                 140

Lys Arg Ile Leu Val Ala Ser Ala Ala Gly Ala Gly Leu Gly Ala Ser
145                 150                 155                 160

Phe His Leu Pro Leu Ala Gly Val Leu Phe Ala Leu Glu Val Leu Leu
                165                 170                 175

Val Glu Ala Ser Thr Arg Thr Val Val Ile Ala Ile Ile Thr Thr Thr
            180                 185                 190

Ala Ala Val Ala Thr Thr Gly Phe Phe Val Gln Thr Pro Asp Val Phe
        195                 200                 205

Ser Thr Val Pro Leu Thr Glu Ser Pro Trp Met Leu Leu Ala Ala Met
    210                 215                 220

Val Thr Gly Val Val Ala Gly Met Cys Gly His Trp Phe Ser Ala Ala
225                 230                 235                 240

Ala His Lys Met Ala Gln Ala Ser Pro Lys Gly Val Lys Ile Leu Trp
```

```
                245                 250                 255

Gln Met Pro Leu Gly Phe Val Val Ile Ala Ala Val Ile Tyr Phe Phe
            260                 265                 270

Pro Glu Thr Leu Ala Asn Pro Arg Trp Leu Ala Asp Ser Met Leu Gly
        275                 280                 285

Asp Gly Leu Ile Leu Ser Thr Ile Leu Leu Val Leu Val Leu Arg Thr
    290                 295                 300

Ala Met Phe Leu Leu Ala Phe Arg Val Gly Met Val Gly Gly Asn Leu
305                 310                 315                 320

Ile Pro Ala Phe Ala Leu Gly Ser Met Val Gly Gly Val Val Gly Ala
                325                 330                 335

Val Leu Glu Pro Ile Thr Asn Val Pro Ile Ala Ala Phe Ala Leu Leu
            340                 345                 350

Gly Ala Ala Ala Phe Leu Ser Thr Thr Met Ala Ala Pro Leu Phe Gly
        355                 360                 365

Leu Ile Ala Ala Val Glu Phe Thr Asp Met Glu Ala Gln Gly Tyr Leu
    370                 375                 380

Pro Ile Phe Leu Ala Val Ala Ser Ala Val Leu Ala Val Arg Val Trp
385                 390                 395                 400

Ser Val Ile Ala Lys His Glu Leu Arg Ala Ile Pro Ile Thr Tyr Ala
                405                 410                 415

Ser Trp Thr Gly Glu Leu Lys
            420


<210> 323
<211> 1392
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1369)
<223> FRXA00662

<400> 323
ccctcatcat agttttaaat ctggggcaga ggcgggaatt taaacacctc tgatacagcg 60

tttactggct atagtgttgc gcgtgccaaa tcgagttcct gtg tca acc att ccg  115
                                        Val Ser Thr Ile Pro
                                          1               5

ctg aat cgt cta gcc gtt atc gct gcc atc att ggt gtc ggt acc ggg  163
Leu Asn Arg Leu Ala Val Ile Ala Ala Ile Ile Gly Val Gly Thr Gly
                  10                  15                  20

ctg ttt gtt gct gca ctg aac tgg tct gcc att ggc gtg gag cgt tta  211
Leu Phe Val Ala Ala Leu Asn Trp Ser Ala Ile Gly Val Glu Arg Leu
              25                  30                  35
```

```
gtt tat ggc gct gac cat ttg cat aat tac aat ccg gtg gcc aat gtg   259
Val Tyr Gly Ala Asp His Leu His Asn Tyr Asn Pro Val Ala Asn Val
         40                  45                  50

tcg cca ctt cgc ctg tcc atc acg gtg att gtg ctt agc gtg gtg gcc   307
Ser Pro Leu Arg Leu Ser Ile Thr Val Ile Val Leu Ser Val Val Ala
     55                  60                  65

tcc tgg gcg tgg ttt ttt gtg cac cgc acg ggg ccg aaa gag gtt tcg   355
Ser Trp Ala Trp Phe Phe Val His Arg Thr Gly Pro Lys Glu Val Ser
 70                  75                  80                  85

att gtg ggt gcg atc cgg ggc gag aag atg ccg att ttg gag acc ata   403
Ile Val Gly Ala Ile Arg Gly Glu Lys Met Pro Ile Leu Glu Thr Ile
                 90                  95                 100

gcg tcc gca ttt ttg cag gtc acc acg gtt gct gcg ggt gcg ccg gtg   451
Ala Ser Ala Phe Leu Gln Val Thr Thr Val Ala Ala Gly Ala Pro Val
            105                 110                 115

ggt gca gag aac gct cca cgt att gct gga gcc ttg gtg gga gag cgg   499
Gly Ala Glu Asn Ala Pro Arg Ile Ala Gly Ala Leu Val Gly Glu Arg
        120                 125                 130

ttt agt cgg tgg ttg cag ctc gat att gat gca aag cgc atc ttg gtg   547
Phe Ser Arg Trp Leu Gln Leu Asp Ile Asp Ala Lys Arg Ile Leu Val
    135                 140                 145

gcc tct gcc gcg gga gct ggt ttg gga gca agc ttc cac ctt ccc cta   595
Ala Ser Ala Ala Gly Ala Gly Leu Gly Ala Ser Phe His Leu Pro Leu
150                 155                 160                 165

gca ggc gtg ctg ttt gcc ctt gag gtc cta ctg gtt gag gcc tcc act   643
Ala Gly Val Leu Phe Ala Leu Glu Val Leu Leu Val Glu Ala Ser Thr
                170                 175                 180

cgg acc gtg gtt atc gca att atc acc acg acc gcc gcc gtt gcc acc   691
Arg Thr Val Val Ile Ala Ile Ile Thr Thr Thr Ala Ala Val Ala Thr
            185                 190                 195

act gga ttt ttc gtg caa acc cca gat gtg ttc agc act gtc ccg ctg   739
Thr Gly Phe Phe Val Gln Thr Pro Asp Val Phe Ser Thr Val Pro Leu
        200                 205                 210

acg gaa agc cca tgg atg ctg ctt gcc gcg atg gtc acc gga gta gtc   787
Thr Glu Ser Pro Trp Met Leu Leu Ala Ala Met Val Thr Gly Val Val
    215                 220                 225

gcc ggc atg tgc ggg cac tgg ttt tca gcg gcg gcg cac aaa atg gcg   835
Ala Gly Met Cys Gly His Trp Phe Ser Ala Ala Ala His Lys Met Ala
230                 235                 240                 245

cag gcc tcg ccc aag ggt gtg aag att ttg tgg cag atg ccg ttg ggt   883
Gln Ala Ser Pro Lys Gly Val Lys Ile Leu Trp Gln Met Pro Leu Gly
                250                 255                 260

ttc gtg gtg atc gct gcg gtg att tat ttc ttc ccc gaa acc ctg gcg   931
Phe Val Val Ile Ala Ala Val Ile Tyr Phe Phe Pro Glu Thr Leu Ala
            265                 270                 275

aat ccc cgt tgg ctt gcc gat tcc atg ctc ggc gat ggc ctg atc ctc   979
```

```
Asn Pro Arg Trp Leu Ala Asp Ser Met Leu Gly Asp Gly Leu Ile Leu
        280                 285                 290

agc acc att tta ttg gta ctt gtt ctg cgc acc gcc atg ttt ttg ctc   1027
Ser Thr Ile Leu Leu Val Leu Val Leu Arg Thr Ala Met Phe Leu Leu
    295                 300                 305

gcc ttc cgc gtg ggc atg gtc ggc ggt aac ctg atc ccc gca ttc gca   1075
Ala Phe Arg Val Gly Met Val Gly Gly Asn Leu Ile Pro Ala Phe Ala
310                 315                 320                 325

ctc gga tcc atg gtc ggt ggg gta gtg ggt gct gta ttg gaa ccc atc   1123
Leu Gly Ser Met Val Gly Gly Val Val Gly Ala Val Leu Glu Pro Ile
                330                 335                 340

act aac gtc ccg atc gcc gct ttt gcg ctg ctt ggc gcc gcc gca ttt   1171
Thr Asn Val Pro Ile Ala Ala Phe Ala Leu Leu Gly Ala Ala Ala Phe
            345                 350                 355

ttg tcc acc acc atg gca gcg cca ctg ttc ggg ctc atc gcc gca gtg   1219
Leu Ser Thr Thr Met Ala Ala Pro Leu Phe Gly Leu Ile Ala Ala Val
        360                 365                 370

gaa ttc acc gac atg gaa gcc caa ggc tac ctt ccg att ttc ctc gca   1267
Glu Phe Thr Asp Met Glu Ala Gln Gly Tyr Leu Pro Ile Phe Leu Ala
    375                 380                 385

gta gcc tcc gcg gtc ctc gcc gtg cgc gtg tgg tct gtc atc gcc aag   1315
Val Ala Ser Ala Val Leu Ala Val Arg Val Trp Ser Val Ile Ala Lys
390                 395                 400                 405

cac gag ctc cgc gcc atc ccg atc acg tac gcg agc tgg acg ggc gag   1363
His Glu Leu Arg Ala Ile Pro Ile Thr Tyr Ala Ser Trp Thr Gly Glu
                410                 415                 420

ctt aaa taagcttgtc gacgcctccc tcc                                 1392
Leu Lys
```

Substitute Sheet (Rule 26)

<210> 324
<211> 423
<212> PRT
<213> Corynebacterium glutamicum

<400> 324

```
Val Ser Thr Ile Pro Leu Asn Arg Leu Ala Val Ile Ala Ala Ile Ile
  1               5                  10                  15

Gly Val Gly Thr Gly Leu Phe Val Ala Ala Leu Asn Trp Ser Ala Ile
             20                  25                  30

Gly Val Glu Arg Leu Val Tyr Gly Ala Asp His Leu His Asn Tyr Asn
         35                  40                  45

Pro Val Ala Asn Val Ser Pro Leu Arg Leu Ser Ile Thr Val Ile Val
     50                  55                  60

Leu Ser Val Val Ala Ser Trp Ala Trp Phe Phe Val His Arg Thr Gly
 65                  70                  75                  80
```

```
Pro Lys Glu Val Ser Ile Val Gly Ala Ile Arg Gly Glu Lys Met Pro
                 85                  90                  95

Ile Leu Glu Thr Ile Ala Ser Ala Phe Leu Gln Val Thr Thr Val Ala
            100                 105                 110

Ala Gly Ala Pro Val Gly Ala Glu Asn Ala Pro Arg Ile Ala Gly Ala
        115                 120                 125

Leu Val Gly Glu Arg Phe Ser Arg Trp Leu Gln Leu Asp Ile Asp Ala
    130                 135                 140

Lys Arg Ile Leu Val Ala Ser Ala Ala Gly Ala Gly Leu Gly Ala Ser
145                 150                 155                 160

Phe His Leu Pro Leu Ala Gly Val Leu Phe Ala Leu Glu Val Leu Leu
                165                 170                 175

Val Glu Ala Ser Thr Arg Thr Val Val Ile Ala Ile Ile Thr Thr Thr
            180                 185                 190

Ala Ala Val Ala Thr Thr Gly Phe Phe Val Gln Thr Pro Asp Val Phe
        195                 200                 205

Ser Thr Val Pro Leu Thr Glu Ser Pro Trp Met Leu Leu Ala Ala Met
    210                 215                 220

Val Thr Gly Val Val Ala Gly Met Cys Gly His Trp Phe Ser Ala Ala
225                 230                 235                 240

Ala His Lys Met Ala Gln Ala Ser Pro Lys Gly Val Lys Ile Leu Trp
                245                 250                 255

Gln Met Pro Leu Gly Phe Val Val Ile Ala Ala Val Ile Tyr Phe Phe
            260                 265                 270

Pro Glu Thr Leu Ala Asn Pro Arg Trp Leu Ala Asp Ser Met Leu Gly
        275                 280                 285

Asp Gly Leu Ile Leu Ser Thr Ile Leu Leu Val Leu Val Leu Arg Thr
    290                 295                 300

Ala Met Phe Leu Leu Ala Phe Arg Val Gly Met Val Gly Gly Asn Leu
305                 310                 315                 320

Ile Pro Ala Phe Ala Leu Gly Ser Met Val Gly Gly Val Val Gly Ala
                325                 330                 335

Val Leu Glu Pro Ile Thr Asn Val Pro Ile Ala Ala Phe Ala Leu Leu
            340                 345                 350

Gly Ala Ala Ala Phe Leu Ser Thr Thr Met Ala Ala Pro Leu Phe Gly
        355                 360                 365

Leu Ile Ala Ala Val Glu Phe Thr Asp Met Glu Ala Gln Gly Tyr Leu
    370                 375                 380

Pro Ile Phe Leu Ala Val Ala Ser Ala Val Leu Ala Val Arg Val Trp
385                 390                 395                 400

Ser Val Ile Ala Lys His Glu Leu Arg Ala Ile Pro Ile Thr Tyr Ala
```

```
                405                 410                 415

Ser Trp Thr Gly Glu Leu Lys
            420


<210> 325
<211> 1038
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1015)
<223> RXN00666

<400> 325
agtggtgaat gctggataag tttttaacat gtctagtgta gtcggggaag gcccaaaacc 60

acgattgagc gtgcttgatc tcgtcgcgct gagtgaaggg atg acg gcc ggc gag   115
                                            Met Thr Ala Gly Glu
                                              1               5

gcc att gca cac agt gtt cgc gct gcg cag atc gcc gaa gag cac aat   163
Ala Ile Ala His Ser Val Arg Ala Ala Gln Ile Ala Glu Glu His Asn
                 10                  15                  20

tat gcg cgt ttc tgg gtg gcg gag cac cac aac tcg gaa ggc ttg gca   211
Tyr Ala Arg Phe Trp Val Ala Glu His His Asn Ser Glu Gly Leu Ala
             25                  30                  35

tct tcc gcg acg acg ctg ctc atg ggt cat att gca ggc cac act tca   259
Ser Ser Ala Thr Thr Leu Leu Met Gly His Ile Ala Gly His Thr Ser
         40                  45                  50

cgc att cgc gtt ggc tcc ggt ggc atc atg atg ccc aac cac tcc gcg   307
Arg Ile Arg Val Gly Ser Gly Gly Ile Met Met Pro Asn His Ser Ala
     55                  60                  65

ctg cac gtc gcc gaa gaa ctc ggc acc ctt gag gcc att tac ccc ggc   355
Leu His Val Ala Glu Glu Leu Gly Thr Leu Glu Ala Ile Tyr Pro Gly
 70                  75                  80                  85

cgc atc gag gcc ggc cta ggg cgc gca cca gga acc gac ccc atg acg   403
Arg Ile Glu Ala Gly Leu Gly Arg Ala Pro Gly Thr Asp Pro Met Thr
                 90                  95                 100

gcg cgg gaa ttg ggt cgg gca agt tcg ctt gtc gac gac gtc ctc tcc   451
Ala Arg Glu Leu Gly Arg Ala Ser Ser Leu Val Asp Asp Val Leu Ser
            105                 110                 115

aca atc gtc tcc ctc cag aat tat ttg gac acc ccc gaa gaa cgc ccg   499
Thr Ile Val Ser Leu Gln Asn Tyr Leu Asp Thr Pro Glu Glu Arg Pro
        120                 125                 130

aac atc atc gcg cat cca gga ata aat tcc cgt gtg ccg cta ttc atg   547
Asn Ile Ile Ala His Pro Gly Ile Asn Ser Arg Val Pro Leu Phe Met
    135                 140                 145

ctg gga tct tcc ctc aac ggc gct gcg atg gcc gct aaa tta gac ctt   595
Leu Gly Ser Ser Leu Asn Gly Ala Ala Met Ala Ala Lys Leu Asp Leu
```

```
150                 155                 160                 165

cca ttc gcc ttc gcc agc cac ttc gca ccc ttc caa atg ggg ccc gcc   643
Pro Phe Ala Phe Ala Ser His Phe Ala Pro Phe Gln Met Gly Pro Ala
                170                 175                 180

atc gcc tcc tat cgc gaa cta gca gcc aat cct tat gtc atg gcc gca   691
Ile Ala Ser Tyr Arg Glu Leu Ala Ala Asn Pro Tyr Val Met Ala Ala
            185                 190                 195

gcg aat gtc ctg gtg tgc gac acc gag gaa gaa gcc gaa ttc cag atc   739
Ala Asn Val Leu Val Cys Asp Thr Glu Glu Glu Ala Glu Phe Gln Ile
        200                 205                 210

tcc aca ctg cac caa atg ttc gcc gga atc gtg acg aac tcc cgc ggc   787
Ser Thr Leu His Gln Met Phe Ala Gly Ile Val Thr Asn Ser Arg Gly
    215                 220                 225

aaa ctt gcc cca cca gtg cgg aat ctg aaa gac aaa ctc gac ccg atg   835
Lys Leu Ala Pro Pro Val Arg Asn Leu Lys Asp Lys Leu Asp Pro Met
230                 235                 240                 245

atc tgg aaa cac atc gaa gat tca ttg gaa atg act ttc atc gga aca   883
Ile Trp Lys His Ile Glu Asp Ser Leu Glu Met Thr Phe Ile Gly Thr
                250                 255                 260

gcc gaa tca gtg gta tta caa ctg cag gaa ttc gct gat cgc tac aag   931
Ala Glu Ser Val Val Leu Gln Leu Gln Glu Phe Ala Asp Arg Tyr Lys
            265                 270                 275

tta gat gag atc att aca gtc acc tac tcc tac gac ccc gaa gtc agg   979
Leu Asp Glu Ile Ile Thr Val Thr Tyr Ser Tyr Asp Pro Glu Val Arg
        280                 285                 290

ttc cgc tcc ata gct gca ctt ggc acg gca tgg aat tagtgtcaaa        1025
Phe Arg Ser Ile Ala Ala Leu Gly Thr Ala Trp Asn
    295                 300                 305

agcctcaaaa ata                                                   1038
```

Sequence Listing Page 395 of 2048

<210> 326
<211> 305
<212> PRT
<213> Corynebacterium glutamicum

<400> 326

```
Met Thr Ala Gly Glu Ala Ile Ala His Ser Val Arg Ala Ala Gln Ile
  1               5                  10                  15

Ala Glu Glu His Asn Tyr Ala Arg Phe Trp Val Ala Glu His His Asn
             20                  25                  30

Ser Glu Gly Leu Ala Ser Ser Ala Thr Thr Leu Leu Met Gly His Ile
         35                  40                  45

Ala Gly His Thr Ser Arg Ile Arg Val Gly Ser Gly Gly Ile Met Met
     50                  55                  60

Pro Asn His Ser Ala Leu His Val Ala Glu Glu Leu Gly Thr Leu Glu
 65                  70                  75                  80
```

```
Ala Ile Tyr Pro Gly Arg Ile Glu Ala Gly Leu Gly Arg Ala Pro Gly
                85                  90                  95

Thr Asp Pro Met Thr Ala Arg Glu Leu Gly Arg Ala Ser Ser Leu Val
            100                 105                 110

Asp Asp Val Leu Ser Thr Ile Val Ser Leu Gln Asn Tyr Leu Asp Thr
        115                 120                 125

Pro Glu Glu Arg Pro Asn Ile Ile Ala His Pro Gly Ile Asn Ser Arg
    130                 135                 140

Val Pro Leu Phe Met Leu Gly Ser Ser Leu Asn Gly Ala Ala Met Ala
145                 150                 155                 160

Ala Lys Leu Asp Leu Pro Phe Ala Phe Ala Ser His Phe Ala Pro Phe
                165                 170                 175

Gln Met Gly Pro Ala Ile Ala Ser Tyr Arg Glu Leu Ala Ala Asn Pro
            180                 185                 190

Tyr Val Met Ala Ala Ala Asn Val Leu Val Cys Asp Thr Glu Glu Glu
        195                 200                 205

Ala Glu Phe Gln Ile Ser Thr Leu His Gln Met Phe Ala Gly Ile Val
    210                 215                 220

Thr Asn Ser Arg Gly Lys Leu Ala Pro Pro Val Arg Asn Leu Lys Asp
225                 230                 235                 240

Lys Leu Asp Pro Met Ile Trp Lys His Ile Glu Asp Ser Leu Glu Met
                245                 250                 255

Thr Phe Ile Gly Thr Ala Glu Ser Val Val Leu Gln Leu Gln Glu Phe
            260                 265                 270

Ala Asp Arg Tyr Lys Leu Asp Glu Ile Ile Thr Val Thr Tyr Ser Tyr
        275                 280                 285

Asp Pro Glu Val Arg Phe Arg Ser Ile Ala Ala Leu Gly Thr Ala Trp
    290                 295                 300

Asn
305
```

<210> 327
<211> 487
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(487)
<223> FRXA00666

<400> 327
agtggtgaat gctggataag tttttaacat gtctagtgta gtcggggaag gcccaaaacc 60

acgattgagc gtgcttgatc tcgtcgcgct gagtgaaggg atg acg gcc ggc gag 115

```
                                                    Met Thr Ala Gly Glu
                                                      1               5

gcc att gca cac agt gtt cgc gct gcg cag atc gcc gaa gag cac aat   163
Ala Ile Ala His Ser Val Arg Ala Ala Gln Ile Ala Glu Glu His Asn
                 10                  15                  20

tat gcg cgt ttc tgg gtg gcg gag cac cac aac tcg gaa ggc ttg gca   211
Tyr Ala Arg Phe Trp Val Ala Glu His His Asn Ser Glu Gly Leu Ala
             25                  30                  35

tct tcc gcg acg acg ctg ctc atg ggt cat att gca ggc cac act tca   259
Ser Ser Ala Thr Thr Leu Leu Met Gly His Ile Ala Gly His Thr Ser
         40                  45                  50

cgc att cgc gtt ggc tcc ggt ggc atc atg atg ccc aac cac tcc gcg   307
Arg Ile Arg Val Gly Ser Gly Gly Ile Met Met Pro Asn His Ser Ala
     55                  60                  65

ctg cac gtc gcc gaa gaa ctc ggc acc ctt gag gcc att tac ccc ggc   355
Leu His Val Ala Glu Glu Leu Gly Thr Leu Glu Ala Ile Tyr Pro Gly
 70                  75                  80                  85

cgc atc gag gcc ggc cta ggg cgc gca cca gga acc gac ccc atg acg   403
Arg Ile Glu Ala Gly Leu Gly Arg Ala Pro Gly Thr Asp Pro Met Thr
                 90                  95                 100

gcg cgg gaa ttg ggt cgg gca agt tcg ctt gtc gac gac gtc ctc tcc   451
Ala Arg Glu Leu Gly Arg Ala Ser Ser Leu Val Asp Asp Val Leu Ser
            105                 110                 115

aca atc gtc tcc ctc cag aat tat ttg gac acc ccc                   487
Thr Ile Val Ser Leu Gln Asn Tyr Leu Asp Thr Pro
        120                 125
```

<210> 328
<211> 129
<212> PRT
<213> Corynebacterium glutamicum

<400> 328

```
Met Thr Ala Gly Glu Ala Ile Ala His Ser Val Arg Ala Ala Gln Ile
 1               5                  10                  15

Ala Glu Glu His Asn Tyr Ala Arg Phe Trp Val Ala Glu His His Asn
            20                  25                  30

Ser Glu Gly Leu Ala Ser Ser Ala Thr Thr Leu Leu Met Gly His Ile
        35                  40                  45

Ala Gly His Thr Ser Arg Ile Arg Val Gly Ser Gly Gly Ile Met Met
    50                  55                  60

Pro Asn His Ser Ala Leu His Val Ala Glu Glu Leu Gly Thr Leu Glu
65                  70                  75                  80

Ala Ile Tyr Pro Gly Arg Ile Glu Ala Gly Leu Gly Arg Ala Pro Gly
                85                  90                  95

Thr Asp Pro Met Thr Ala Arg Glu Leu Gly Arg Ala Ser Ser Leu Val
```

```
           100                 105                 110

Asp Asp Val Leu Ser Thr Ile Val Ser Leu Gln Asn Tyr Leu Asp Thr
        115                 120                 125

Pro



<210> 329
<211> 750
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(727)
<223> RXN00704

<400> 329
tcaaattctg cgcacaaagt gttctaagac gacgtctgcc catcggcgct ctaatgcaca 60

ttacagcgtt tacagaattg aaaatgaaag gttcaaagcc ttg acc att act ttt   115
                                          Leu Thr Ile Thr Phe
                                            1               5

agc cgc gtt gct ctg acc acc ctg gca gtc acc gca acc act ttg tcc   163
Ser Arg Val Ala Leu Thr Thr Leu Ala Val Thr Ala Thr Thr Leu Ser
                10                  15                  20

ctg agc act gct gcg aat gca cag tct tcc ttg ttg gat aag act ctt   211
Leu Ser Thr Ala Ala Asn Ala Gln Ser Ser Leu Leu Asp Lys Thr Leu
            25                  30                  35

gat gcc cgt cag tgc atc gat gca gac aac gtc tgg gtc tca gtt gac   259
Asp Ala Arg Gln Cys Ile Asp Ala Asp Asn Val Trp Val Ser Val Asp
        40                  45                  50

tat ggt gca gat tcc gaa aaa gaa cca gag ggc gca tgt gcc acc gag   307
Tyr Gly Ala Asp Ser Glu Lys Glu Pro Glu Gly Ala Cys Ala Thr Glu
    55                  60                  65

ttc act gat ggt gtt gta gct ctt gaa tct gct ggg ttc aaa ctg acc   355
Phe Thr Asp Gly Val Val Ala Leu Glu Ser Ala Gly Phe Lys Leu Thr
70                  75                  80                  85

ttt gac gaa tct gaa atg ggc aaa tac atg acc ggt atc aac gga gtt   403
Phe Asp Glu Ser Glu Met Gly Lys Tyr Met Thr Gly Ile Asn Gly Val
                90                  95                  100

gtt cct gat tgg gtt gaa act gga act tac tgg agt tac tac tct ggt   451
Val Pro Asp Trp Val Glu Thr Gly Thr Tyr Trp Ser Tyr Tyr Ser Gly
            105                 110                 115

gaa gtc gca gat gat tac agc gtg gac tac acc tac tac gag gtt ggt   499
Glu Val Ala Asp Asp Tyr Ser Val Asp Tyr Thr Tyr Tyr Glu Val Gly
        120                 125                 130

gca tct aat tct gaa cct gaa ggt gga act gtt gag gct tgg gtt gtt   547
Ala Ser Asn Ser Glu Pro Glu Gly Gly Thr Val Glu Ala Trp Val Val
    135                 140                 145
```

```
ggc acc ggc gag gaa aca cca gca ctc gag act ctt cct gaa act cca   595
Gly Thr Gly Glu Glu Thr Pro Ala Leu Glu Thr Leu Pro Glu Thr Pro
150                 155                 160                 165

gca gca acc gga tct tct gaa gac ggc ggc tgg att gca gtc atc gca   643
Ala Ala Thr Gly Ser Ser Glu Asp Gly Gly Trp Ile Ala Val Ile Ala
                170                 175                 180

ggt ctt ctc gca ctg atc ggt ggt gga gtt gca gct ttg tac cag ggc   691
Gly Leu Leu Ala Leu Ile Gly Gly Gly Val Ala Ala Leu Tyr Gln Gly
            185                 190                 195

ttg atc act atc cca ggt ctg gtt ctg cct aag ttt taagcaacct       737
Leu Ile Thr Ile Pro Gly Leu Val Leu Pro Lys Phe
        200                 205

aacctaaagc ttc                                                   750
```

<210> 330
<211> 209
<212> PRT
<213> Corynebacterium glutamicum

<400> 330

```
Leu Thr Ile Thr Phe Ser Arg Val Ala Leu Thr Thr Leu Ala Val Thr
  1               5                  10                  15

Ala Thr Thr Leu Ser Leu Ser Thr Ala Ala Asn Ala Gln Ser Ser Leu
             20                  25                  30

Leu Asp Lys Thr Leu Asp Ala Arg Gln Cys Ile Asp Ala Asp Asn Val
         35                  40                  45

Trp Val Ser Val Asp Tyr Gly Ala Asp Ser Glu Lys Glu Pro Glu Gly
     50                  55                  60

Ala Cys Ala Thr Glu Phe Thr Asp Gly Val Val Ala Leu Glu Ser Ala
 65                  70                  75                  80

Gly Phe Lys Leu Thr Phe Asp Glu Ser Glu Met Gly Lys Tyr Met Thr
                 85                  90                  95

Gly Ile Asn Gly Val Val Pro Asp Trp Val Glu Thr Gly Thr Tyr Trp
            100                 105                 110

Ser Tyr Tyr Ser Gly Glu Val Ala Asp Asp Tyr Ser Val Asp Tyr Thr
        115                 120                 125

Tyr Tyr Glu Val Gly Ala Ser Asn Ser Glu Pro Glu Gly Gly Thr Val
    130                 135                 140

Glu Ala Trp Val Val Gly Thr Gly Glu Glu Thr Pro Ala Leu Glu Thr
145                 150                 155                 160

Leu Pro Glu Thr Pro Ala Ala Thr Gly Ser Ser Glu Asp Gly Gly Trp
                165                 170                 175

Ile Ala Val Ile Ala Gly Leu Leu Ala Leu Ile Gly Gly Gly Val Ala
            180                 185                 190
```

```
Ala Leu Tyr Gln Gly Leu Ile Thr Ile Pro Gly Leu Val Leu Pro Lys
        195                 200                 205

Phe
```

<210> 331
<211> 636
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(613)
<223> FRXA00704

<400> 331

```
tcaaattctg cgcacaaagt gttctaagac gacgtctgcc catcggcgct ctaatgcaca 60

ttacagcgtt tacagaattg aaaatgaaag gttcaaagcc ttg acc att act ttt   115
                                          Leu Thr Ile Thr Phe
                                            1               5

agc cgc gtt gct ctg acc acc ctg gca gtc acc gca acc act ttg tcc   163
Ser Arg Val Ala Leu Thr Thr Leu Ala Val Thr Ala Thr Thr Leu Ser
                10                  15                  20

ctg agc act gct gcg aat gca cag tct tcc ttg ttg gat aag act ctt   211
Leu Ser Thr Ala Ala Asn Ala Gln Ser Ser Leu Leu Asp Lys Thr Leu
            25                  30                  35

gat gcc cgt cag tgc atc gat gca gac aac gtc tgg gtc tca gtt gac   259
Asp Ala Arg Gln Cys Ile Asp Ala Asp Asn Val Trp Val Ser Val Asp
        40                  45                  50

tat ggt gca gat tcc gaa aaa gaa cca gag ggc gca tgt gcc acc gag   307
Tyr Gly Ala Asp Ser Glu Lys Glu Pro Glu Gly Ala Cys Ala Thr Glu
    55                  60                  65

ttc act gat ggt gtt gta gct ctt gaa tct gct ggg ttc aaa ctg acc   355
Phe Thr Asp Gly Val Val Ala Leu Glu Ser Ala Gly Phe Lys Leu Thr
70                  75                  80                  85

ttt gac gaa tct gaa atg ggc aaa tac atg acc ggt atc aac gga gtt   403
Phe Asp Glu Ser Glu Met Gly Lys Tyr Met Thr Gly Ile Asn Gly Val
                90                  95                  100

gtt cct gat tgg gtt gaa act gga act tac tgg agt tac tac tct ggt   451
Val Pro Asp Trp Val Glu Thr Gly Thr Tyr Trp Ser Tyr Tyr Ser Gly
            105                 110                 115

gaa gtc gca gat gat tac agc gtg gac tac acc tac tac gag gtt ggt   499
Glu Val Ala Asp Asp Tyr Ser Val Asp Tyr Thr Tyr Tyr Glu Val Gly
        120                 125                 130

gca tct aat tct gaa cct gaa ggt gga act gtt gag gct tgg gtt gtt   547
Ala Ser Asn Ser Glu Pro Glu Gly Gly Thr Val Glu Ala Trp Val Val
    135                 140                 145
```

```
ggc acc ggc gag gaa aca cca gca ctc gag act ctt tct gaa act tca   595
Gly Thr Gly Glu Glu Thr Pro Ala Leu Glu Thr Leu Ser Glu Thr Ser
150                 155                 160                 165

gca gca acc gga tct tct taagacggcg gctggattgc agt                636
Ala Ala Thr Gly Ser Ser
               170
```

<210> 332
<211> 171
<212> PRT
<213> Corynebacterium glutamicum

<400> 332

```
Leu Thr Ile Thr Phe Ser Arg Val Ala Leu Thr Thr Leu Ala Val Thr
  1               5                  10                  15

Ala Thr Thr Leu Ser Leu Ser Thr Ala Ala Asn Ala Gln Ser Ser Leu
             20                  25                  30

Leu Asp Lys Thr Leu Asp Ala Arg Gln Cys Ile Asp Ala Asp Asn Val
         35                  40                  45

Trp Val Ser Val Asp Tyr Gly Ala Asp Ser Glu Lys Glu Pro Glu Gly
     50                  55                  60

Ala Cys Ala Thr Glu Phe Thr Asp Gly Val Val Ala Leu Glu Ser Ala
 65                  70                  75                  80

Gly Phe Lys Leu Thr Phe Asp Glu Ser Glu Met Gly Lys Tyr Met Thr
                 85                  90                  95

Gly Ile Asn Gly Val Val Pro Asp Trp Val Glu Thr Gly Thr Tyr Trp
            100                 105                 110

Ser Tyr Tyr Ser Gly Glu Val Ala Asp Asp Tyr Ser Val Asp Tyr Thr
        115                 120                 125

Tyr Tyr Glu Val Gly Ala Ser Asn Ser Glu Pro Glu Gly Gly Thr Val
    130                 135                 140

Glu Ala Trp Val Val Gly Thr Gly Glu Glu Thr Pro Ala Leu Glu Thr
145                 150                 155                 160

Leu Ser Glu Thr Ser Ala Ala Thr Gly Ser Ser
                165                 170
```

<210> 333
<211> 819
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(796)
<223> RXN00712

<400> 333

```
tgttgcgcgt taataaggaa caatatcggt gtgattcgcg atatattaat cagcttgttt 60
```

```
tcccagcata agtagtcgcc tagtttagga ggtacatggc atg tcc cta cgc aag   115
                                            Met Ser Leu Arg Lys
                                              1               5

aat ctc gcc ctc gga agc agc aca gta cta ctc aca gcc gtg cta agc   163
Asn Leu Ala Leu Gly Ser Ser Thr Val Leu Leu Thr Ala Val Leu Ser
                  10                  15                  20

ggg tgt gtt tcc ctt gat gag cgc tcc act gat aca tcc acg gag aat   211
Gly Cys Val Ser Leu Asp Glu Arg Ser Thr Asp Thr Ser Thr Glu Asn
             25                  30                  35

gtc acc acg gta act gcc aca ctc act tcc acc gcc gca gca gaa ccc   259
Val Thr Thr Val Thr Ala Thr Leu Thr Ser Thr Ala Ala Ala Glu Pro
         40                  45                  50

acc act aga acg act gtg caa agt gct aca gaa gcc tcc act act gca   307
Thr Thr Arg Thr Thr Val Gln Ser Ala Thr Glu Ala Ser Thr Thr Ala
     55                  60                  65

cca gtg caa tgc aat ttg gat ccc cgt acc tcg gat ttt ggg cca tat   355
Pro Val Gln Cys Asn Leu Asp Pro Arg Thr Ser Asp Phe Gly Pro Tyr
 70                  75                  80                  85

ctt gca caa tct cgc acc ccg gtt ggt gag cta gct gga tct gca gat   403
Leu Ala Gln Ser Arg Thr Pro Val Gly Glu Leu Ala Gly Ser Ala Asp
                 90                  95                 100

tcc gtc gtg cag gtt cct gac tgg ttc tat cac ttc caa atg ggc gac   451
Ser Val Val Gln Val Pro Asp Trp Phe Tyr His Phe Gln Met Gly Asp
            105                 110                 115

aac ggc tac gat tcc tgt tcc aag ctc agc tat gtg gtt ctc aac ggt   499
Asn Gly Tyr Asp Ser Cys Ser Lys Leu Ser Tyr Val Val Leu Asn Gly
        120                 125                 130

tcc aat gga gac gcc gaa cgt tct act gga acg ggt gct gcg atc gcc   547
Ser Asn Gly Asp Ala Glu Arg Ser Thr Gly Thr Gly Ala Ala Ile Ala
    135                 140                 145

gac gtg gtg gtg ctg ttt atc gac ggc cat atg gtt gct cgt cct gct   595
Asp Val Val Val Leu Phe Ile Asp Gly His Met Val Ala Arg Pro Ala
150                 155                 160                 165

cct ttt gaa atg aag acc gtg gaa tcc gtc acc aga gtg tca gat tca   643
Pro Phe Glu Met Lys Thr Val Glu Ser Val Thr Arg Val Ser Asp Ser
                170                 175                 180

gaa atc caa gtt gtt tac gga cat gcc ggc cga tct act gcc gaa ggt   691
Glu Ile Gln Val Val Tyr Gly His Ala Gly Arg Ser Thr Ala Glu Gly
            185                 190                 195

gtt acg gac tat ttc acc ttt aac ttc ttc gtt gac aac ggc gtt ctt   739
Val Thr Asp Tyr Phe Thr Phe Asn Phe Phe Val Asp Asn Gly Val Leu
        200                 205                 210

tca gga cgc ggc gat ctc cca gaa cac atc gat act cac atg cgt cta   787
Ser Gly Arg Gly Asp Leu Pro Glu His Ile Asp Thr His Met Arg Leu
    215                 220                 225
```

tat ctg ctg tagccccatc taaaaactct tga 819
Tyr Leu Leu
230

<210> 334
<211> 232
<212> PRT
<213> Corynebacterium glutamicum

<400> 334
Met Ser Leu Arg Lys Asn Leu Ala Leu Gly Ser Ser Thr Val Leu Leu
1 5 10 15

Thr Ala Val Leu Ser Gly Cys Val Ser Leu Asp Glu Arg Ser Thr Asp
20 25 30

Thr Ser Thr Glu Asn Val Thr Thr Val Thr Ala Thr Leu Thr Ser Thr
35 40 45

Ala Ala Ala Glu Pro Thr Thr Arg Thr Thr Val Gln Ser Ala Thr Glu
50 55 60

Ala Ser Thr Thr Ala Pro Val Gln Cys Asn Leu Asp Pro Arg Thr Ser
65 70 75 80

Asp Phe Gly Pro Tyr Leu Ala Gln Ser Arg Thr Pro Val Gly Glu Leu
85 90 95

Ala Gly Ser Ala Asp Ser Val Val Gln Val Pro Asp Trp Phe Tyr His
100 105 110

Phe Gln Met Gly Asp Asn Gly Tyr Asp Ser Cys Ser Lys Leu Ser Tyr
115 120 125

Val Val Leu Asn Gly Ser Asn Gly Asp Ala Glu Arg Ser Thr Gly Thr
130 135 140

Gly Ala Ala Ile Ala Asp Val Val Val Leu Phe Ile Asp Gly His Met
145 150 155 160

Val Ala Arg Pro Ala Pro Phe Glu Met Lys Thr Val Glu Ser Val Thr
165 170 175

Arg Val Ser Asp Ser Glu Ile Gln Val Val Tyr Gly His Ala Gly Arg
180 185 190

Ser Thr Ala Glu Gly Val Thr Asp Tyr Phe Thr Phe Asn Phe Phe Val
195 200 205

Asp Asn Gly Val Leu Ser Gly Arg Gly Asp Leu Pro Glu His Ile Asp
210 215 220

Thr His Met Arg Leu Tyr Leu Leu
225 230

<210> 335
<211> 572
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(549)
<223> FRXA00712

<400> 335

```
gca gca gaa ccc acc act aga acg act gtg caa agt gct aca gaa gcc   48
Ala Ala Glu Pro Thr Thr Arg Thr Thr Val Gln Ser Ala Thr Glu Ala
  1               5                  10                  15

tcc act act gca cca gtg caa tgc aat ttg gat ccc cgt acc tcg gat   96
Ser Thr Thr Ala Pro Val Gln Cys Asn Leu Asp Pro Arg Thr Ser Asp
             20                  25                  30

ttt ggg cca tat ctt gca caa tct cgc acc ccg gtt ggt gag cta gct  144
Phe Gly Pro Tyr Leu Ala Gln Ser Arg Thr Pro Val Gly Glu Leu Ala
         35                  40                  45

gga tct gca gat tcc gtc gtg cag gtt cct gac tgg ttc tat cac ttc  192
Gly Ser Ala Asp Ser Val Val Gln Val Pro Asp Trp Phe Tyr His Phe
     50                  55                  60

caa atg ggc gac aac ggc tac gat tcc tgt tcc aag ctc agc tat gtg  240
Gln Met Gly Asp Asn Gly Tyr Asp Ser Cys Ser Lys Leu Ser Tyr Val
 65                  70                  75                  80

gtt ctc aac ggt tcc aat gga gac gcc gaa cgt tct act gga acg ggt  288
Val Leu Asn Gly Ser Asn Gly Asp Ala Glu Arg Ser Thr Gly Thr Gly
                 85                  90                  95

gct gcg atc gcc gac gtg gtg gtg ctg ttt atc gac ggc cat atg gtt  336
Ala Ala Ile Ala Asp Val Val Val Leu Phe Ile Asp Gly His Met Val
            100                 105                 110

gct cgt cct gct cct ttt gaa atg aag acc gtg gaa tcc gtc acc aga  384
Ala Arg Pro Ala Pro Phe Glu Met Lys Thr Val Glu Ser Val Thr Arg
        115                 120                 125

gtg tca gat tca gaa atc caa gtt gtt tac gga cat gcc ggc cga tct  432
Val Ser Asp Ser Glu Ile Gln Val Val Tyr Gly His Ala Gly Arg Ser
    130                 135                 140

act gcc gaa ggt gtt acg gac tat ttc acc ttt aac ttc ttc gtt gac  480
Thr Ala Glu Gly Val Thr Asp Tyr Phe Thr Phe Asn Phe Phe Val Asp
145                 150                 155                 160

aac ggc gtt ctt tca gga cgc ggc gat ctc cca gaa cac atc gat act  528
Asn Gly Val Leu Ser Gly Arg Gly Asp Leu Pro Glu His Ile Asp Thr
                165                 170                 175

cac atg cgt cta tat ctg ctg tagccccatc taaaaactct tga            572
His Met Arg Leu Tyr Leu Leu
            180
```

<210> 336
<211> 183
<212> PRT
<213> Corynebacterium glutamicum

<400> 336
Ala Ala Glu Pro Thr Thr Arg Thr Thr Val Gln Ser Ala Thr Glu Ala
1 5 10 15

Ser Thr Thr Ala Pro Val Gln Cys Asn Leu Asp Pro Arg Thr Ser Asp
20 25 30

Phe Gly Pro Tyr Leu Ala Gln Ser Arg Thr Pro Val Gly Glu Leu Ala
35 40 45

Gly Ser Ala Asp Ser Val Val Gln Val Pro Asp Trp Phe Tyr His Phe
50 55 60

Gln Met Gly Asp Asn Gly Tyr Asp Ser Cys Ser Lys Leu Ser Tyr Val
65 70 75 80

Val Leu Asn Gly Ser Asn Gly Asp Ala Glu Arg Ser Thr Gly Thr Gly
85 90 95

Ala Ala Ile Ala Asp Val Val Val Leu Phe Ile Asp Gly His Met Val
100 105 110

Ala Arg Pro Ala Pro Phe Glu Met Lys Thr Val Glu Ser Val Thr Arg
115 120 125

Val Ser Asp Ser Glu Ile Gln Val Val Tyr Gly His Ala Gly Arg Ser
130 135 140

Thr Ala Glu Gly Val Thr Asp Tyr Phe Thr Phe Asn Phe Phe Val Asp
145 150 155 160

Asn Gly Val Leu Ser Gly Arg Gly Asp Leu Pro Glu His Ile Asp Thr
165 170 175

His Met Arg Leu Tyr Leu Leu
180

<210> 337
<211> 789
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(766)
<223> RXN00720

<400> 337
ctgatctata cgtcctgttg aagtagagaa gctttctggt caagttcctt gagtatggtg 60

gtcgaagacc agcactccag attcaaggaa cttataaaac atg gca tca ccg cgc 115
Met Ala Ser Pro Arg
1 5

cgc cca cag gtt gca gca cca cgc atc aaa gaa ctt cgc cta aca ggc 163
Arg Pro Gln Val Ala Ala Pro Arg Ile Lys Glu Leu Arg Leu Thr Gly
10 15 20

ctt gac aac gct gac cct caa gac atc gaa tcg aat gag cag ata gag 211
Leu Asp Asn Ala Asp Pro Gln Asp Ile Glu Ser Asn Glu Gln Ile Glu

```
            25                  30                  35

tca tgc cgt ttt aac gag gcc gag ctt tcc gaa cgc gat ctt tct ggt   259
Ser Cys Arg Phe Asn Glu Ala Glu Leu Ser Glu Arg Asp Leu Ser Gly
         40                  45                  50

gct ggt ttc att gaa tgt gaa ttc ctt ggg ctg gaa gca cac gaa acc   307
Ala Gly Phe Ile Glu Cys Glu Phe Leu Gly Leu Glu Ala His Glu Thr
     55                  60                  65

gag cta cgc cgg gct caa ttc gtg gaa aca cgc atc gaa aga gcc aat   355
Glu Leu Arg Arg Ala Gln Phe Val Glu Thr Arg Ile Glu Arg Ala Asn
 70                  75                  80                  85

gct cca tct ttt aag gca gcc cgc tcc atc tgg cgc aac gca acg att   403
Ala Pro Ser Phe Lys Ala Ala Arg Ser Ile Trp Arg Asn Ala Thr Ile
                 90                  95                 100

tcc gac tcc cgc ttt ggt gcc gtc gaa atg tat gaa gca acc gtc caa   451
Ser Asp Ser Arg Phe Gly Ala Val Glu Met Tyr Glu Ala Thr Val Gln
            105                 110                 115

gct ttg aaa atc tct gat tct aag ctg tcg ttt gtc aat ctg cgg ggt   499
Ala Leu Lys Ile Ser Asp Ser Lys Leu Ser Phe Val Asn Leu Arg Gly
        120                 125                 130

gca tcg tta cgg gat gtg ctc ttt gag aac tgt gtc atc gac gag ctt   547
Ala Ser Leu Arg Asp Val Leu Phe Glu Asn Cys Val Ile Asp Glu Leu
    135                 140                 145

gat ctt ggc caa gcc aga gca gaa cgc atc gct ttt aaa gac tgc acg   595
Asp Leu Gly Gln Ala Arg Ala Glu Arg Ile Ala Phe Lys Asp Cys Thr
150                 155                 160                 165

gtg cat tcg ctc acc ttt gat cat gcc gtg ctc agc aat gtg gat ctt   643
Val His Ser Leu Thr Phe Asp His Ala Val Leu Ser Asn Val Asp Leu
                170                 175                 180

cgc ggt tta gat atc gag cgc atc agt ggc gtg gag tcc atg tcc gga   691
Arg Gly Leu Asp Ile Glu Arg Ile Ser Gly Val Glu Ser Met Ser Gly
            185                 190                 195

acc gtg atc tca tcc ctg cag gct gct gac ctg tcg gga gca ttt gca   739
Thr Val Ile Ser Ser Leu Gln Ala Ala Asp Leu Ser Gly Ala Phe Ala
        200                 205                 210

cgg cat tta gga att act gta aac gat tagaaatccg ctcttttgaa         786
Arg His Leu Gly Ile Thr Val Asn Asp
    215                 220

caa                                                               789


<210> 338
<211> 222
<212> PRT
<213> Corynebacterium glutamicum

<400> 338
Met Ala Ser Pro Arg Arg Pro Gln Val Ala Ala Pro Arg Ile Lys Glu
  1               5                  10                  15
```

```
Leu Arg Leu Thr Gly Leu Asp Asn Ala Asp Pro Gln Asp Ile Glu Ser
            20                  25                  30

Asn Glu Gln Ile Glu Ser Cys Arg Phe Asn Glu Ala Glu Leu Ser Glu
        35                  40                  45

Arg Asp Leu Ser Gly Ala Gly Phe Ile Glu Cys Glu Phe Leu Gly Leu
    50                  55                  60

Glu Ala His Glu Thr Glu Leu Arg Arg Ala Gln Phe Val Glu Thr Arg
65                  70                  75                  80

Ile Glu Arg Ala Asn Ala Pro Ser Phe Lys Ala Ala Arg Ser Ile Trp
                85                  90                  95

Arg Asn Ala Thr Ile Ser Asp Ser Arg Phe Gly Ala Val Glu Met Tyr
            100                 105                 110

Glu Ala Thr Val Gln Ala Leu Lys Ile Ser Asp Ser Lys Leu Ser Phe
        115                 120                 125

Val Asn Leu Arg Gly Ala Ser Leu Arg Asp Val Leu Phe Glu Asn Cys
    130                 135                 140

Val Ile Asp Glu Leu Asp Leu Gly Gln Ala Arg Ala Glu Arg Ile Ala
145                 150                 155                 160

Phe Lys Asp Cys Thr Val His Ser Leu Thr Phe Asp His Ala Val Leu
                165                 170                 175

Ser Asn Val Asp Leu Arg Gly Leu Asp Ile Glu Arg Ile Ser Gly Val
            180                 185                 190

Glu Ser Met Ser Gly Thr Val Ile Ser Ser Leu Gln Ala Ala Asp Leu
        195                 200                 205

Ser Gly Ala Phe Ala Arg His Leu Gly Ile Thr Val Asn Asp
    210                 215                 220
```

<210> 339
<211> 789
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(766)
<223> FRXA00720

<400> 339

```
ctgatctata cgtcctgttg aagtagagaa gctttctggt caagttcctt gagtatggtg 60

gtcgaagacc agcactccag attcaaggaa cttataaaac atg gca tca ccg cgc   115
                                            Met Ala Ser Pro Arg
                                              1               5

cgc cca cag gtt gca gca cca cgc atc aaa gaa ctt cgc cta aca ggc   163
Arg Pro Gln Val Ala Ala Pro Arg Ile Lys Glu Leu Arg Leu Thr Gly
                10                  15                  20
```

```
ctt gac aac gct gac cct caa gac atc gaa tcg aat gag cag ata gag   211
Leu Asp Asn Ala Asp Pro Gln Asp Ile Glu Ser Asn Glu Gln Ile Glu
             25                  30                  35

tca tgc cgt ttt aac gag gcc gag ctt tcc gaa cgc gat ctt tct ggt   259
Ser Cys Arg Phe Asn Glu Ala Glu Leu Ser Glu Arg Asp Leu Ser Gly
         40                  45                  50

gct ggt ttc att gaa tgt gaa ttc ctt ggg ctg gaa gca cac gaa acc   307
Ala Gly Phe Ile Glu Cys Glu Phe Leu Gly Leu Glu Ala His Glu Thr
     55                  60                  65

gag cta cgc cgg gct caa ttc gtg gaa aca cgc atc gaa aga gcc aat   355
Glu Leu Arg Arg Ala Gln Phe Val Glu Thr Arg Ile Glu Arg Ala Asn
 70                  75                  80                  85

gct cca tct ttt aag gca gcc cgc tcc atc tgg cgc aac gca acg att   403
Ala Pro Ser Phe Lys Ala Ala Arg Ser Ile Trp Arg Asn Ala Thr Ile
                 90                  95                 100

tcc gac tcc cgc ttt ggt gcc gtc gaa atg tat gaa gca acc gtc caa   451
Ser Asp Ser Arg Phe Gly Ala Val Glu Met Tyr Glu Ala Thr Val Gln
            105                 110                 115

gct ttg aaa atc tct gat tct aag ctg tcg ttt gtc aat ctg cgg ggt   499
Ala Leu Lys Ile Ser Asp Ser Lys Leu Ser Phe Val Asn Leu Arg Gly
        120                 125                 130

gca tcg tta cgg gat gtg ctc ttt gag aac tgt gtc atc gac gag ctt   547
Ala Ser Leu Arg Asp Val Leu Phe Glu Asn Cys Val Ile Asp Glu Leu
    135                 140                 145

gat ctt ggc caa gcc aga gca gaa cgc atc gct ttt aaa gac tgc acg   595
Asp Leu Gly Gln Ala Arg Ala Glu Arg Ile Ala Phe Lys Asp Cys Thr
150                 155                 160                 165

gtg cat tcg ctc acc ttt gat cat gcc gtg ctc agc aat gtg gat ctt   643
Val His Ser Leu Thr Phe Asp His Ala Val Leu Ser Asn Val Asp Leu
                170                 175                 180

cgc ggt tta gat atc gag cgc atc agt ggc gtg gag tcc atg tcc gga   691
Arg Gly Leu Asp Ile Glu Arg Ile Ser Gly Val Glu Ser Met Ser Gly
            185                 190                 195

acc gtg atc tca tcc ctg cag gct gct gac ctg tcg gga gca ttt gca   739
Thr Val Ile Ser Ser Leu Gln Ala Ala Asp Leu Ser Gly Ala Phe Ala
        200                 205                 210

cgg cat tta gga att act gta aac gat tagaaatccg ctcttttgaa         786
Arg His Leu Gly Ile Thr Val Asn Asp
    215                 220

caa                                                              789
```

<210> 340
<211> 222
<212> PRT
<213> Corynebacterium glutamicum

<400> 340
Met Ala Ser Pro Arg Arg Pro Gln Val Ala Ala Pro Arg Ile Lys Glu
1 5 10 15

Leu Arg Leu Thr Gly Leu Asp Asn Ala Asp Pro Gln Asp Ile Glu Ser
20 25 30

Asn Glu Gln Ile Glu Ser Cys Arg Phe Asn Glu Ala Glu Leu Ser Glu
35 40 45

Arg Asp Leu Ser Gly Ala Gly Phe Ile Glu Cys Glu Phe Leu Gly Leu
50 55 60

Glu Ala His Glu Thr Glu Leu Arg Arg Ala Gln Phe Val Glu Thr Arg
65 70 75 80

Ile Glu Arg Ala Asn Ala Pro Ser Phe Lys Ala Ala Arg Ser Ile Trp
85 90 95

Arg Asn Ala Thr Ile Ser Asp Ser Arg Phe Gly Ala Val Glu Met Tyr
100 105 110

Glu Ala Thr Val Gln Ala Leu Lys Ile Ser Asp Ser Lys Leu Ser Phe
115 120 125

Val Asn Leu Arg Gly Ala Ser Leu Arg Asp Val Leu Phe Glu Asn Cys
130 135 140

Val Ile Asp Glu Leu Asp Leu Gly Gln Ala Arg Ala Glu Arg Ile Ala
145 150 155 160

Phe Lys Asp Cys Thr Val His Ser Leu Thr Phe Asp His Ala Val Leu
165 170 175

Ser Asn Val Asp Leu Arg Gly Leu Asp Ile Glu Arg Ile Ser Gly Val
180 185 190

Glu Ser Met Ser Gly Thr Val Ile Ser Ser Leu Gln Ala Ala Asp Leu
195 200 205

Ser Gly Ala Phe Ala Arg His Leu Gly Ile Thr Val Asn Asp
210 215 220

<210> 341
<211> 1088
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1065)
<223> RXN00722

<400> 341
gct gtt ctc cga gaa gcc gga gtt gtt gat gcc ggg gga cag ggc cta 48
Ala Val Leu Arg Glu Ala Gly Val Val Asp Ala Gly Gly Gln Gly Leu
1 5 10 15

gtt att ctc ctg gag tcc ctg gcc gaa caa atc aac gga aac cca cct 96
Val Ile Leu Leu Glu Ser Leu Ala Glu Gln Ile Asn Gly Asn Pro Pro

```
                20                  25                  30

cac cat cca tcg cac cac agt gaa cca gcc gaa gaa ccc tcc ttc cac   144
His His Pro Ser His His Ser Glu Pro Ala Glu Glu Pro Ser Phe His
         35                  40                  45

ggc aaa acc ggc gac cta gaa gtg atg ttt tac att gca tgc gac tcc   192
Gly Lys Thr Gly Asp Leu Glu Val Met Phe Tyr Ile Ala Cys Asp Ser
     50                  55                  60

gcg caa aca ctc gat gct ctc cac aac gaa ctt gaa aca cta ggc gac   240
Ala Gln Thr Leu Asp Ala Leu His Asn Glu Leu Glu Thr Leu Gly Asp
 65                  70                  75                  80

agc ctg ctc atc gcc cga gaa acc aat acc cgc ggc acc gtt cac atc   288
Ser Leu Leu Ile Ala Arg Glu Thr Asn Thr Arg Gly Thr Val His Ile
                85                  90                  95

cat tcg cgc cgg gca ggc gag gtc atc caa aaa gca ttt gcc gca gga   336
His Ser Arg Arg Ala Gly Glu Val Ile Gln Lys Ala Phe Ala Ala Gly
            100                 105                 110

gac gtc agc gaa ctc cgc ctt gaa atc ctc ccc gat act tcc ggc agc   384
Asp Val Ser Glu Leu Arg Leu Glu Ile Leu Pro Asp Thr Ser Gly Ser
        115                 120                 125

ttc acg gaa gaa cca cgc cgg gtc ctc atg gct gtc gca cct gac ggc   432
Phe Thr Glu Glu Pro Arg Arg Val Leu Met Ala Val Ala Pro Asp Gly
    130                 135                 140

ctg gtg gcg gag ctg tac cgc agc gct gga gtg aag gtg gtg gcc cgc   480
Leu Val Ala Glu Leu Tyr Arg Ser Ala Gly Val Lys Val Val Ala Arg
145                 150                 155                 160

aac atc gcg caa tcc aag tct gat gat gtg gtg gca aag atc gtt tcc   528
Asn Ile Ala Gln Ser Lys Ser Asp Asp Val Val Ala Lys Ile Val Ser
                165                 170                 175

atc gcg cgc aag tct ggt gcc gat gag gtg atc ttg ctg ccc aac ggt   576
Ile Ala Arg Lys Ser Gly Ala Asp Glu Val Ile Leu Leu Pro Asn Gly
            180                 185                 190

ctt ttg acc aag cgt gag ctg gtt tcc att gag cgt tcc agc cat gct   624
Leu Leu Thr Lys Arg Glu Leu Val Ser Ile Glu Arg Ser Ser His Ala
        195                 200                 205

ttt gag caa agt gtg gtt att ttg cct act gcc acg ttg gtt gca ggt   672
Phe Glu Gln Ser Val Val Ile Leu Pro Thr Ala Thr Leu Val Ala Gly
    210                 215                 220

ctt gca gcg gtg tcc gtt cat gag cca gcg caa ccc ctg gcg gtg gat   720
Leu Ala Ala Val Ser Val His Glu Pro Ala Gln Pro Leu Ala Val Asp
225                 230                 235                 240

tcc tat gcc atg gca gag gcc gcc ggt tcc atg cgc acg gcc acg atc   768
Ser Tyr Ala Met Ala Glu Ala Ala Gly Ser Met Arg Thr Ala Thr Ile
                245                 250                 255

cgc gcc gcc acc agc gcc gcg ctc acc cag gcc ggc gca tgc tcc aag   816
Arg Ala Ala Thr Ser Ala Ala Leu Thr Gln Ala Gly Ala Cys Ser Lys
            260                 265                 270
```

```
ggt gat cta tta agc ttc atc ggc ccg gag ata gct ctg gtc tcc gag   864
Gly Asp Leu Leu Ser Phe Ile Gly Pro Glu Ile Ala Leu Val Ser Glu
        275                 280                 285

gag ctc aac gac gcg cta tcg cgc acc gct tta agg ctt ctc gac ggc   912
Glu Leu Asn Asp Ala Leu Ser Arg Thr Ala Leu Arg Leu Leu Asp Gly
    290                 295                 300

tcc agc gag caa att acc ctt ctc ata gcg caa gac cgt cag tcc gcc   960
Ser Ser Glu Gln Ile Thr Leu Leu Ile Ala Gln Asp Arg Gln Ser Ala
305                 310                 315                 320

ttc gac gaa gat gtt ttc cgc cgt ggc ctg gga act cac acg gat gtg   1008
Phe Asp Glu Asp Val Phe Arg Arg Gly Leu Gly Thr His Thr Asp Val
                325                 330                 335

gag atc acg gtc tat cct gct act gga atg gag aat ctg gta gag atc   1056
Glu Ile Thr Val Tyr Pro Ala Thr Gly Met Glu Asn Leu Val Glu Ile
            340                 345                 350

gga gtg gag tagccacatg ttgggttggc atg                            1088
Gly Val Glu
        355
```

<210> 342
<211> 355
<212> PRT
<213> Corynebacterium glutamicum

<400> 342

```
Ala Val Leu Arg Glu Ala Gly Val Val Asp Ala Gly Gly Gln Gly Leu
  1               5                  10                  15

Val Ile Leu Leu Glu Ser Leu Ala Glu Gln Ile Asn Gly Asn Pro Pro
             20                  25                  30

His His Pro Ser His His Ser Glu Pro Ala Glu Glu Pro Ser Phe His
         35                  40                  45

Gly Lys Thr Gly Asp Leu Glu Val Met Phe Tyr Ile Ala Cys Asp Ser
     50                  55                  60

Ala Gln Thr Leu Asp Ala Leu His Asn Glu Leu Glu Thr Leu Gly Asp
 65                  70                  75                  80

Ser Leu Leu Ile Ala Arg Glu Thr Asn Thr Arg Gly Thr Val His Ile
                 85                  90                  95

His Ser Arg Arg Ala Gly Glu Val Ile Gln Lys Ala Phe Ala Ala Gly
            100                 105                 110

Asp Val Ser Glu Leu Arg Leu Glu Ile Leu Pro Asp Thr Ser Gly Ser
        115                 120                 125

Phe Thr Glu Glu Pro Arg Arg Val Leu Met Ala Val Ala Pro Asp Gly
    130                 135                 140

Leu Val Ala Glu Leu Tyr Arg Ser Ala Gly Val Lys Val Val Ala Arg
145                 150                 155                 160
```

```
Asn Ile Ala Gln Ser Lys Ser Asp Asp Val Val Ala Lys Ile Val Ser
                165                 170                 175

Ile Ala Arg Lys Ser Gly Ala Asp Glu Val Ile Leu Leu Pro Asn Gly
            180                 185                 190

Leu Leu Thr Lys Arg Glu Leu Val Ser Ile Glu Arg Ser Ser His Ala
        195                 200                 205

Phe Glu Gln Ser Val Val Ile Leu Pro Thr Ala Thr Leu Val Ala Gly
    210                 215                 220

Leu Ala Ala Val Ser Val His Glu Pro Ala Gln Pro Leu Ala Val Asp
225                 230                 235                 240

Ser Tyr Ala Met Ala Glu Ala Ala Gly Ser Met Arg Thr Ala Thr Ile
                245                 250                 255

Arg Ala Ala Thr Ser Ala Ala Leu Thr Gln Ala Gly Ala Cys Ser Lys
            260                 265                 270

Gly Asp Leu Leu Ser Phe Ile Gly Pro Glu Ile Ala Leu Val Ser Glu
        275                 280                 285

Glu Leu Asn Asp Ala Leu Ser Arg Thr Ala Leu Arg Leu Leu Asp Gly
    290                 295                 300

Ser Ser Glu Gln Ile Thr Leu Leu Ile Ala Gln Asp Arg Gln Ser Ala
305                 310                 315                 320

Phe Asp Glu Asp Val Phe Arg Arg Gly Leu Gly Thr His Thr Asp Val
                325                 330                 335

Glu Ile Thr Val Tyr Pro Ala Thr Gly Met Glu Asn Leu Val Glu Ile
            340                 345                 350

Gly Val Glu
        355
```

<210> 343
<211> 542
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (16)..(519)
<223> FRXA00722

<400> 343

```
ccccccccgg tgatcttg ctg ccc aac ggt ctt ttg acc aag cgt gag ctg   51
                Leu Leu Pro Asn Gly Leu Leu Thr Lys Arg Glu Leu
                  1               5                  10

gtt tcc att gag cgt tcc agc cat gct ttt gag caa agt gtg gtt att   99
Val Ser Ile Glu Arg Ser Ser His Ala Phe Glu Gln Ser Val Val Ile
         15                  20                  25

ttg cct act gcc acg ttg gtt gca ggt ctt gca gcg gtg tcc gtt cat   147
```

```
Leu Pro Thr Ala Thr Leu Val Ala Gly Leu Ala Ala Val Ser Val His
     30                  35                  40

gag cca gcg caa ccc ctg gcg gtg gat tcc tat gcc atg gca gag gcc   195
Glu Pro Ala Gln Pro Leu Ala Val Asp Ser Tyr Ala Met Ala Glu Ala
 45                  50                  55                  60

gcc ggt tcc atg cgc acg gcc acg atc cgc gcc gcc acc agc gcc gcg   243
Ala Gly Ser Met Arg Thr Ala Thr Ile Arg Ala Ala Thr Ser Ala Ala
                 65                  70                  75

ctc acc cag gcc ggc gca tgc tcc aag ggt gat cta tta agc ttc atc   291
Leu Thr Gln Ala Gly Ala Cys Ser Lys Gly Asp Leu Leu Ser Phe Ile
             80                  85                  90

ggc ccg gag ata gct ctg gtc tcc gag gag ctc aac gac gcg cta tcg   339
Gly Pro Glu Ile Ala Leu Val Ser Glu Glu Leu Asn Asp Ala Leu Ser
         95                 100                 105

cgc acc gct tta agg ctt ctc gac ggc tcc agc gag caa att acc ctt   387
Arg Thr Ala Leu Arg Leu Leu Asp Gly Ser Ser Glu Gln Ile Thr Leu
    110                 115                 120

ctc ata gcg caa gac cgt cag tcc gcc ttc gac gaa gat gtt ttc cgc   435
Leu Ile Ala Gln Asp Arg Gln Ser Ala Phe Asp Glu Asp Val Phe Arg
125                 130                 135                 140

cgt ggc ctg gga act cac acg gat gtg gag atc acg gtc tat cct gct   483
Arg Gly Leu Gly Thr His Thr Asp Val Glu Ile Thr Val Tyr Pro Ala
                145                 150                 155

act gga atg gag aat ctg gta gag atc gga gtg gag tagccacatg        529
Thr Gly Met Glu Asn Leu Val Glu Ile Gly Val Glu
            160                 165

ttgggttggc atg                                                   542


<210> 344
<211> 168
<212> PRT
<213> Corynebacterium glutamicum

<400> 344
Leu Leu Pro Asn Gly Leu Leu Thr Lys Arg Glu Leu Val Ser Ile Glu
  1               5                  10                  15

Arg Ser Ser His Ala Phe Glu Gln Ser Val Val Ile Leu Pro Thr Ala
             20                  25                  30

Thr Leu Val Ala Gly Leu Ala Ala Val Ser Val His Glu Pro Ala Gln
         35                  40                  45

Pro Leu Ala Val Asp Ser Tyr Ala Met Ala Glu Ala Ala Gly Ser Met
     50                  55                  60

Arg Thr Ala Thr Ile Arg Ala Ala Thr Ser Ala Ala Leu Thr Gln Ala
 65                  70                  75                  80

Gly Ala Cys Ser Lys Gly Asp Leu Leu Ser Phe Ile Gly Pro Glu Ile
                 85                  90                  95
```

```
Ala Leu Val Ser Glu Glu Leu Asn Asp Ala Leu Ser Arg Thr Ala Leu
            100                 105                 110

Arg Leu Leu Asp Gly Ser Ser Glu Gln Ile Thr Leu Leu Ile Ala Gln
        115                 120                 125

Asp Arg Gln Ser Ala Phe Asp Glu Asp Val Phe Arg Arg Gly Leu Gly
    130                 135                 140

Thr His Thr Asp Val Glu Ile Thr Val Tyr Pro Ala Thr Gly Met Glu
145                 150                 155                 160

Asn Leu Val Glu Ile Gly Val Glu
                165
```

<210> 345
<211> 1101
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1078)
<223> RXN00729

<400> 345

```
ttcagcacag atcacccttt gccagctacc gacttagttt cgtaacacgt atagtgggag 60

gcgttttgcc agacgccaaa gaaagataat tggattacct atg agc gcc acc aac   115
                                              Met Ser Ala Thr Asn
                                                1               5

cct gat gcc cta gac gtg cag cac gtc tat ccc atc aag acg aaa aag   163
Pro Asp Ala Leu Asp Val Gln His Val Tyr Pro Ile Lys Thr Lys Lys
                10                  15                  20

act cca ctt gcg gtg att ttc aac atc att agc ggt ggt ttg att gga   211
Thr Pro Leu Ala Val Ile Phe Asn Ile Ile Ser Gly Gly Leu Ile Gly
            25                  30                  35

atg gcg gag ttg gtg cca gga att tcc ggc gga act gtc gct ttg gtt   259
Met Ala Glu Leu Val Pro Gly Ile Ser Gly Gly Thr Val Ala Leu Val
        40                  45                  50

ctt gga att tat gag cgc gca ctg cac aac ggt gat ctc ctc att gat   307
Leu Gly Ile Tyr Glu Arg Ala Leu His Asn Gly Asp Leu Leu Ile Asp
    55                  60                  65

ctg atc aag gtg ttg atc aag gac cgc tcg aag gtt aag gaa gct gcg   355
Leu Ile Lys Val Leu Ile Lys Asp Arg Ser Lys Val Lys Glu Ala Ala
70                  75                  80                  85

gcg aaa atc gac tgg tgg ttc ctc ggc gct atc ggc gtt ggc atg gtc   403
Ala Lys Ile Asp Trp Trp Phe Leu Gly Ala Ile Gly Val Gly Met Val
                90                  95                 100

gtg atg gtc ttc tcg atg tca tcg att ttg cat aca gtt gtt gag gac   451
Val Met Val Phe Ser Met Ser Ser Ile Leu His Thr Val Val Glu Asp
            105                 110                 115
```

```
tac cca gag atc act cgc ggt ctg ttc ctt gga atg gtt gcc gtg tct   499
Tyr Pro Glu Ile Thr Arg Gly Leu Phe Leu Gly Met Val Ala Val Ser
        120                 125                 130

atc ctt gtt ccg ttg gga atg atg gat atg cgg gat gcc aag aag cgc   547
Ile Leu Val Pro Leu Gly Met Met Asp Met Arg Asp Ala Lys Lys Arg
    135                 140                 145

ctc gca atc gtc atc ccg cta ttt ata atc tgc gcc atg ctg gga ttc   595
Leu Ala Ile Val Ile Pro Leu Phe Ile Ile Cys Ala Met Leu Gly Phe
150                 155                 160                 165

ttt gga aca tcc ttc act agt gcg cct cgc acc gat cct tca ctg atc   643
Phe Gly Thr Ser Phe Thr Ser Ala Pro Arg Thr Asp Pro Ser Leu Ile
                170                 175                 180

ttt gtc ttc atc tgt gct gcg atc gct gtg tgt gct ctt gtt ctt cct   691
Phe Val Phe Ile Cys Ala Ala Ile Ala Val Cys Ala Leu Val Leu Pro
            185                 190                 195

ggt gtt tca gga tca ttc ttc ttg ctg gcg gtc ggt atg tac gcg cca   739
Gly Val Ser Gly Ser Phe Phe Leu Leu Ala Val Gly Met Tyr Ala Pro
        200                 205                 210

atc atg gaa tct ctg tcc aac cgt gac ttg tcg gtc atc ggc gtg ttc   787
Ile Met Glu Ser Leu Ser Asn Arg Asp Leu Ser Val Ile Gly Val Phe
    215                 220                 225

ttg ctt ggc gcg ctc acc ggt gtg atc ttg ttt gtg aag gtt ttg tct   835
Leu Leu Gly Ala Leu Thr Gly Val Ile Leu Phe Val Lys Val Leu Ser
230                 235                 240                 245

tat gtt ctc gag cac cac cgc acc atc acg ctg acc atc atg gct ggt   883
Tyr Val Leu Glu His His Arg Thr Ile Thr Leu Thr Ile Met Ala Gly
                250                 255                 260

ctc atg ctg ggt tca ctt cgt gcg ctg tgg cct tgg cag gac ggt gac   931
Leu Met Leu Gly Ser Leu Arg Ala Leu Trp Pro Trp Gln Asp Gly Asp
            265                 270                 275

gct aat cta ctt gct cct ggc gat aac gcc gtg atg att ttc agc atc   979
Ala Asn Leu Leu Ala Pro Gly Asp Asn Ala Val Met Ile Phe Ser Ile
        280                 285                 290

atc att ctt ggt ggc gcg att gtc gct gct ttg atg ttt gct gag cgt   1027
Ile Ile Leu Gly Gly Ala Ile Val Ala Ala Leu Met Phe Ala Glu Arg
    295                 300                 305

gtg tct tcc aag aac att gat tct gag acc gtg gca gaa gag cac ccg   1075
Val Ser Ser Lys Asn Ile Asp Ser Glu Thr Val Ala Glu Glu His Pro
310                 315                 320                 325

cgc taaataagaa ctccacaaag aaa                                    1101
Arg
```

<210> 346
<211> 326
<212> PRT

<213> Corynebacterium glutamicum

<400> 346

```
Met Ser Ala Thr Asn Pro Asp Ala Leu Asp Val Gln His Val Tyr Pro
  1               5                  10                  15

Ile Lys Thr Lys Lys Thr Pro Leu Ala Val Ile Phe Asn Ile Ile Ser
             20                  25                  30

Gly Gly Leu Ile Gly Met Ala Glu Leu Val Pro Gly Ile Ser Gly Gly
          35                  40                  45

Thr Val Ala Leu Val Leu Gly Ile Tyr Glu Arg Ala Leu His Asn Gly
      50                  55                  60

Asp Leu Leu Ile Asp Leu Ile Lys Val Leu Ile Lys Asp Arg Ser Lys
 65                  70                  75                  80

Val Lys Glu Ala Ala Ala Lys Ile Asp Trp Trp Phe Leu Gly Ala Ile
                 85                  90                  95

Gly Val Gly Met Val Val Met Val Phe Ser Met Ser Ser Ile Leu His
            100                 105                 110

Thr Val Val Glu Asp Tyr Pro Glu Ile Thr Arg Gly Leu Phe Leu Gly
        115                 120                 125

Met Val Ala Val Ser Ile Leu Val Pro Leu Gly Met Met Asp Met Arg
    130                 135                 140

Asp Ala Lys Lys Arg Leu Ala Ile Val Ile Pro Leu Phe Ile Ile Cys
145                 150                 155                 160

Ala Met Leu Gly Phe Phe Gly Thr Ser Phe Thr Ser Ala Pro Arg Thr
                165                 170                 175

Asp Pro Ser Leu Ile Phe Val Phe Ile Cys Ala Ala Ile Ala Val Cys
            180                 185                 190

Ala Leu Val Leu Pro Gly Val Ser Gly Ser Phe Phe Leu Leu Ala Val
        195                 200                 205

Gly Met Tyr Ala Pro Ile Met Glu Ser Leu Ser Asn Arg Asp Leu Ser
    210                 215                 220

Val Ile Gly Val Phe Leu Leu Gly Ala Leu Thr Gly Val Ile Leu Phe
225                 230                 235                 240

Val Lys Val Leu Ser Tyr Val Leu Glu His His Arg Thr Ile Thr Leu
                245                 250                 255

Thr Ile Met Ala Gly Leu Met Leu Gly Ser Leu Arg Ala Leu Trp Pro
            260                 265                 270

Trp Gln Asp Gly Asp Ala Asn Leu Leu Ala Pro Gly Asp Asn Ala Val
        275                 280                 285

Met Ile Phe Ser Ile Ile Ile Leu Gly Gly Ala Ile Val Ala Ala Leu
    290                 295                 300

Met Phe Ala Glu Arg Val Ser Ser Lys Asn Ile Asp Ser Glu Thr Val
```

```
305                 310                 315                 320

Ala Glu Glu His Pro Arg
                325
```

<210> 347
<211> 665
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(642)
<223> FRXA00729

<400> 347

```
aca gtt gtt gag gac tac caa gag ttc act cgc ggt ctg ttc ctt gga   48
Thr Val Val Glu Asp Tyr Gln Glu Phe Thr Arg Gly Leu Phe Leu Gly
  1               5                  10                  15

atg gtt gcc gtg tct atc ctt gtt ccg ttg gga atg atg gat atg cgg   96
Met Val Ala Val Ser Ile Leu Val Pro Leu Gly Met Met Asp Met Arg
             20                  25                  30

gat gcc aag aag cgc ctc gca atc gtc atc ccg cta ttt ata atc tgc   144
Asp Ala Lys Lys Arg Leu Ala Ile Val Ile Pro Leu Phe Ile Ile Cys
         35                  40                  45

gcc atg ctg gga ttc ttt gga aca tcc ttc act agt gcg cct cgc acc   192
Ala Met Leu Gly Phe Phe Gly Thr Ser Phe Thr Ser Ala Pro Arg Thr
     50                  55                  60

gat cct tca ctg atc ttt gtc ttc atc tgt gct gcg atc gct gtg tgt   240
Asp Pro Ser Leu Ile Phe Val Phe Ile Cys Ala Ala Ile Ala Val Cys
 65                  70                  75                  80

gct ctt gtt ctt cct ggt gtt tca gga tca ttc ttc ttg ctg gcg gtc   288
Ala Leu Val Leu Pro Gly Val Ser Gly Ser Phe Phe Leu Leu Ala Val
                 85                  90                  95

ggt atg tac gcg cca atc atg gaa tct ctg tcc aac cgt gac ttg tcg   336
Gly Met Tyr Ala Pro Ile Met Glu Ser Leu Ser Asn Arg Asp Leu Ser
            100                 105                 110

gtc atc ggc gtg ttc ttg ctt ggc gcg ctc acc ggt gtg atc ttg ttt   384
Val Ile Gly Val Phe Leu Leu Gly Ala Leu Thr Gly Val Ile Leu Phe
        115                 120                 125

gtg aag gtt ttg tct tat gtt ctc gag cac cac cgc acc atc acg ctg   432
Val Lys Val Leu Ser Tyr Val Leu Glu His His Arg Thr Ile Thr Leu
    130                 135                 140

acc atc atg gct ggt ctc atg ctg ggt tca ctt cgt gcg ctg tgg cct   480
Thr Ile Met Ala Gly Leu Met Leu Gly Ser Leu Arg Ala Leu Trp Pro
145                 150                 155                 160

tgg cag gac ggt gac gct aat cta ctt gct cct ggc gat aac gcc gtg   528
Trp Gln Asp Gly Asp Ala Asn Leu Leu Ala Pro Gly Asp Asn Ala Val
                165                 170                 175
```

```
atg att ttc agc atc atc att ctt ggt ggc gcg att gtc gct gct ttg   576
Met Ile Phe Ser Ile Ile Ile Leu Gly Gly Ala Ile Val Ala Ala Leu
            180                 185                 190

atg ttt gct gag cgt gtg tct tcc aag aac att gat tct gag acc gtg   624
Met Phe Ala Glu Arg Val Ser Ser Lys Asn Ile Asp Ser Glu Thr Val
        195                 200                 205

gca gaa gag cac ccg cgc taaataagaa ctccacaaag aaa                 665
Ala Glu Glu His Pro Arg
    210
```

<210> 348
<211> 214
<212> PRT
<213> Corynebacterium glutamicum

<400> 348

```
Thr Val Val Glu Asp Tyr Gln Glu Phe Thr Arg Gly Leu Phe Leu Gly
  1               5                  10                  15

Met Val Ala Val Ser Ile Leu Val Pro Leu Gly Met Met Asp Met Arg
             20                  25                  30

Asp Ala Lys Lys Arg Leu Ala Ile Val Ile Pro Leu Phe Ile Ile Cys
         35                  40                  45

Ala Met Leu Gly Phe Phe Gly Thr Ser Phe Thr Ser Ala Pro Arg Thr
     50                  55                  60

Asp Pro Ser Leu Ile Phe Val Phe Ile Cys Ala Ala Ile Ala Val Cys
 65                  70                  75                  80

Ala Leu Val Leu Pro Gly Val Ser Gly Ser Phe Phe Leu Leu Ala Val
                 85                  90                  95

Gly Met Tyr Ala Pro Ile Met Glu Ser Leu Ser Asn Arg Asp Leu Ser
            100                 105                 110

Val Ile Gly Val Phe Leu Leu Gly Ala Leu Thr Gly Val Ile Leu Phe
        115                 120                 125

Val Lys Val Leu Ser Tyr Val Leu Glu His His Arg Thr Ile Thr Leu
    130                 135                 140

Thr Ile Met Ala Gly Leu Met Leu Gly Ser Leu Arg Ala Leu Trp Pro
145                 150                 155                 160

Trp Gln Asp Gly Asp Ala Asn Leu Leu Ala Pro Gly Asp Asn Ala Val
                165                 170                 175

Met Ile Phe Ser Ile Ile Ile Leu Gly Gly Ala Ile Val Ala Ala Leu
            180                 185                 190

Met Phe Ala Glu Arg Val Ser Ser Lys Asn Ile Asp Ser Glu Thr Val
        195                 200                 205

Ala Glu Glu His Pro Arg
    210
```

<210> 349
<211> 706
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(706)
<223> FRXA02867

<400> 349
ttcagcacag atcacccttt gccagctacc gacttagttt cgtaacacgt atagtgggag 60

gcgttttgcc agacgccaaa gaaagataat tggattacct atg agc gcc acc aac 115
Met Ser Ala Thr Asn
1 5

cct gat gcc cta gac gtg cag cac gtc tat ccc atc aag acg aaa aag 163
Pro Asp Ala Leu Asp Val Gln His Val Tyr Pro Ile Lys Thr Lys Lys
10 15 20

act cca ctt gcg gtg att ttc aac atc att agc ggt ggt ttg att gga 211
Thr Pro Leu Ala Val Ile Phe Asn Ile Ile Ser Gly Gly Leu Ile Gly
25 30 35

atg gcg gag ttg gtg cca gga att tcc ggc gga act gtc gct ttg gtt 259
Met Ala Glu Leu Val Pro Gly Ile Ser Gly Gly Thr Val Ala Leu Val
40 45 50

ctt gga att tat gag cgc gca ctg cac aac ggt gat ctc ctc att gat 307
Leu Gly Ile Tyr Glu Arg Ala Leu His Asn Gly Asp Leu Leu Ile Asp
55 60 65

ctg atc aag gtg ttg atc aag gac cgc tcg aag gtt aag gaa gct gcg 355
Leu Ile Lys Val Leu Ile Lys Asp Arg Ser Lys Val Lys Glu Ala Ala
70 75 80 85

gcg aaa atc gac tgg tgg ttc ctc ggc gct atc ggc gtt ggc atg gtc 403
Ala Lys Ile Asp Trp Trp Phe Leu Gly Ala Ile Gly Val Gly Met Val
90 95 100

gtg atg gtc ttc tcg atg tca tcg att ttg cat aca gtt gtt gag gac 451
Val Met Val Phe Ser Met Ser Ser Ile Leu His Thr Val Val Glu Asp
105 110 115

tac cca gag atc act cgc ggt ctg ttc ctt gga atg gtt gcc gtg tct 499
Tyr Pro Glu Ile Thr Arg Gly Leu Phe Leu Gly Met Val Ala Val Ser
120 125 130

atc ctt gtt ccg ttg gga atg atg gat atg cgg gat gcc aag aag cgc 547
Ile Leu Val Pro Leu Gly Met Met Asp Met Arg Asp Ala Lys Lys Arg
135 140 145

ctc gca atc gtc atc ccg cta ttt ata atc tgc gcc atg ctg gga ttc 595
Leu Ala Ile Val Ile Pro Leu Phe Ile Ile Cys Ala Met Leu Gly Phe
150 155 160 165

ttt gga aca tcc ttc act agt gcg cct cgc acc gat cct tca ctg atc 643
Phe Gly Thr Ser Phe Thr Ser Ala Pro Arg Thr Asp Pro Ser Leu Ile
170 175 180

```
ttt gtc ttc atc tgt gct gcg atc gct gtg tgt gct ctt gtt ctt cct   691
Phe Val Phe Ile Cys Ala Ala Ile Ala Val Cys Ala Leu Val Leu Pro
            185                 190                 195

ggt gtt cag gat cac                                               706
Gly Val Gln Asp His
        200
```

<210> 350
<211> 202
<212> PRT
<213> Corynebacterium glutamicum

<400> 350

```
Met Ser Ala Thr Asn Pro Asp Ala Leu Asp Val Gln His Val Tyr Pro
  1               5                  10                  15

Ile Lys Thr Lys Lys Thr Pro Leu Ala Val Ile Phe Asn Ile Ile Ser
             20                  25                  30

Gly Gly Leu Ile Gly Met Ala Glu Leu Val Pro Gly Ile Ser Gly Gly
         35                  40                  45

Thr Val Ala Leu Val Leu Gly Ile Tyr Glu Arg Ala Leu His Asn Gly
     50                  55                  60

Asp Leu Leu Ile Asp Leu Ile Lys Val Leu Ile Lys Asp Arg Ser Lys
 65                  70                  75                  80

Val Lys Glu Ala Ala Ala Lys Ile Asp Trp Trp Phe Leu Gly Ala Ile
                 85                  90                  95

Gly Val Gly Met Val Val Met Val Phe Ser Met Ser Ser Ile Leu His
            100                 105                 110

Thr Val Val Glu Asp Tyr Pro Glu Ile Thr Arg Gly Leu Phe Leu Gly
        115                 120                 125

Met Val Ala Val Ser Ile Leu Val Pro Leu Gly Met Met Asp Met Arg
    130                 135                 140

Asp Ala Lys Lys Arg Leu Ala Ile Val Ile Pro Leu Phe Ile Ile Cys
145                 150                 155                 160

Ala Met Leu Gly Phe Phe Gly Thr Ser Phe Thr Ser Ala Pro Arg Thr
                165                 170                 175

Asp Pro Ser Leu Ile Phe Val Phe Ile Cys Ala Ala Ile Ala Val Cys
            180                 185                 190

Ala Leu Val Leu Pro Gly Val Gln Asp His
        195                 200
```

<210> 351
<211> 930
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(907)
<223> RXN00730

<400> 351
tggtgcaata accttaagtg aggctggatt ttgcgttggc aggcgctcgg gttttgtttt 60

atccggcatg ggctcgggag ggactttaaa ataaacagct atg tcg agc caa caa 115
Met Ser Ser Gln Gln
1 5

acg atc ttc atc att ttg ctc ttt gcc gca gtg att ctc att tcc ata 163
Thr Ile Phe Ile Ile Leu Leu Phe Ala Ala Val Ile Leu Ile Ser Ile
10 15 20

gta atg att aca gct gcc ttc aaa acc cgg aaa aag cgc ttt gcc gcg 211
Val Met Ile Thr Ala Ala Phe Lys Thr Arg Lys Lys Arg Phe Ala Ala
25 30 35

cgg gct gaa gga atg gcc aac cct aca att cct gcg cca act gtg ccg 259
Arg Ala Glu Gly Met Ala Asn Pro Thr Ile Pro Ala Pro Thr Val Pro
40 45 50

tgg cag cgc ttc gcc gga gca ctt gca gcc ttg tac gct agg cct gaa 307
Trp Gln Arg Phe Ala Gly Ala Leu Ala Ala Leu Tyr Ala Arg Pro Glu
55 60 65

tgg cac aag acc cgc gga gcg aaa cga gtg tac tca gct gaa cag act 355
Trp His Lys Thr Arg Gly Ala Lys Arg Val Tyr Ser Ala Glu Gln Thr
70 75 80 85

tat ttt ggg ttt gtc tca gca atg cca ctg ggg atg gtg caa aac atg 403
Tyr Phe Gly Phe Val Ser Ala Met Pro Leu Gly Met Val Gln Asn Met
90 95 100

ctg caa aca gac tgg ggt gtg aaa aag tct gag cat gca gtt gat cag 451
Leu Gln Thr Asp Trp Gly Val Lys Lys Ser Glu His Ala Val Asp Gln
105 110 115

ctt tct aaa gga gtg gaa gtg atc gtt ggg gta gcc gca ggc aac tgg 499
Leu Ser Lys Gly Val Glu Val Ile Val Gly Val Ala Ala Gly Asn Trp
120 125 130

cgt aaa aac gga gta tca ccc gca caa gtg gaa gag gca ggc cag cgg 547
Arg Lys Asn Gly Val Ser Pro Ala Gln Val Glu Glu Ala Gly Gln Arg
135 140 145

tta gca gct gaa gga ttg gct cat cca cac ttt gtt gta ttc caa aag 595
Leu Ala Ala Glu Gly Leu Ala His Pro His Phe Val Val Phe Gln Lys
150 155 160 165

cag ctt caa cag gca gat cca aat gca gaa tat gat ctc gat gtg ctc 643
Gln Leu Gln Gln Ala Asp Pro Asn Ala Glu Tyr Asp Leu Asp Val Leu
170 175 180

gca ttt gat atc gca cgc gta gcc aac ctc ctt cgc tgg gct gct tat 691
Ala Phe Asp Ile Ala Arg Val Ala Asn Leu Leu Arg Trp Ala Ala Tyr
185 190 195

aca gat ctg ttg ctc cct gca gaa gcc cgt tgg ttc caa gac cag ctg 739

```
Thr Asp Leu Leu Leu Pro Ala Glu Ala Arg Trp Phe Gln Asp Gln Leu
        200                 205                 210

gga att gcg gct gct gtg tcc ttt ggg agc tgg gaa gaa tac gga gag   787
Gly Ile Ala Ala Ala Val Ser Phe Gly Ser Trp Glu Glu Tyr Gly Glu
    215                 220                 225

cga tac gtc cgt gga cta cag aag aac ttc aag ggc gga aac aag cca   835
Arg Tyr Val Arg Gly Leu Gln Lys Asn Phe Lys Gly Gly Asn Lys Pro
230                 235                 240                 245

tat atc gaa gga gaa cgc tgg ctc aac act gag gct gaa agt cca tgg   883
Tyr Ile Glu Gly Glu Arg Trp Leu Asn Thr Glu Ala Glu Ser Pro Trp
                250                 255                 260

aag acc caa aag tgg att agc gcc taactgctca tgagctaagc ggc         930
Lys Thr Gln Lys Trp Ile Ser Ala
            265
```

<210> 352
<211> 269
<212> PRT
<213> Corynebacterium glutamicum

<400> 352

```
Met Ser Ser Gln Gln Thr Ile Phe Ile Ile Leu Leu Phe Ala Ala Val
  1               5                  10                  15

Ile Leu Ile Ser Ile Val Met Ile Thr Ala Ala Phe Lys Thr Arg Lys
             20                  25                  30

Lys Arg Phe Ala Ala Arg Ala Glu Gly Met Ala Asn Pro Thr Ile Pro
         35                  40                  45

Ala Pro Thr Val Pro Trp Gln Arg Phe Ala Gly Ala Leu Ala Ala Leu
     50                  55                  60

Tyr Ala Arg Pro Glu Trp His Lys Thr Arg Gly Ala Lys Arg Val Tyr
 65                  70                  75                  80

Ser Ala Glu Gln Thr Tyr Phe Gly Phe Val Ser Ala Met Pro Leu Gly
                 85                  90                  95

Met Val Gln Asn Met Leu Gln Thr Asp Trp Gly Val Lys Lys Ser Glu
            100                 105                 110

His Ala Val Asp Gln Leu Ser Lys Gly Val Glu Val Ile Val Gly Val
        115                 120                 125

Ala Ala Gly Asn Trp Arg Lys Asn Gly Val Ser Pro Ala Gln Val Glu
    130                 135                 140

Glu Ala Gly Gln Arg Leu Ala Ala Glu Gly Leu Ala His Pro His Phe
145                 150                 155                 160

Val Val Phe Gln Lys Gln Leu Gln Gln Ala Asp Pro Asn Ala Glu Tyr
                165                 170                 175

Asp Leu Asp Val Leu Ala Phe Asp Ile Ala Arg Val Ala Asn Leu Leu
            180                 185                 190
```

```
Arg Trp Ala Ala Tyr Thr Asp Leu Leu Leu Pro Ala Glu Ala Arg Trp
        195                 200                 205

Phe Gln Asp Gln Leu Gly Ile Ala Ala Ala Val Ser Phe Gly Ser Trp
    210                 215                 220

Glu Glu Tyr Gly Glu Arg Tyr Val Arg Gly Leu Gln Lys Asn Phe Lys
225                 230                 235                 240

Gly Gly Asn Lys Pro Tyr Ile Glu Gly Glu Arg Trp Leu Asn Thr Glu
                245                 250                 255

Ala Glu Ser Pro Trp Lys Thr Gln Lys Trp Ile Ser Ala
            260                 265


<210> 353
<211> 356
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(333)
<223> FRXA00730

<400> 353
cac ttt gtt gta ttc caa aag cag ctt caa cag gca gat cca aat gca   48
His Phe Val Val Phe Gln Lys Gln Leu Gln Gln Ala Asp Pro Asn Ala
  1               5                  10                  15

gaa tat gat ctc gat gtg ctc gca ttt gat atc gca cgc gta gcc aac   96
Glu Tyr Asp Leu Asp Val Leu Ala Phe Asp Ile Ala Arg Val Ala Asn
             20                  25                  30

ctc ctt cgc tgg gct gct tat aca gat ctg ttg ctc cct gca gaa gcc   144
Leu Leu Arg Trp Ala Ala Tyr Thr Asp Leu Leu Leu Pro Ala Glu Ala
         35                  40                  45

cgt tgg ttc caa gac cag ctg gga att gcg gct gct gtg tcc ttt ggg   192
Arg Trp Phe Gln Asp Gln Leu Gly Ile Ala Ala Ala Val Ser Phe Gly
     50                  55                  60

agc tgg gaa gaa tac gga gag cga tac gtc cgt gga cta cag aag aac   240
Ser Trp Glu Glu Tyr Gly Glu Arg Tyr Val Arg Gly Leu Gln Lys Asn
 65                  70                  75                  80

ttc aag ggc gga aac aag cca tat atc gaa gga gaa cgc tgg ctc aac   288
Phe Lys Gly Gly Asn Lys Pro Tyr Ile Glu Gly Glu Arg Trp Leu Asn
                 85                  90                  95

act gag gct gaa agt cca tgg aag acc caa aag tgg att agc gcc       333
Thr Glu Ala Glu Ser Pro Trp Lys Thr Gln Lys Trp Ile Ser Ala
            100                 105                 110

taactgctca tgagctaagc ggc                                        356


<210> 354
<211> 111
```

<212> PRT
<213> Corynebacterium glutamicum

<400> 354
His Phe Val Val Phe Gln Lys Gln Leu Gln Gln Ala Asp Pro Asn Ala
1 5 10 15

Glu Tyr Asp Leu Asp Val Leu Ala Phe Asp Ile Ala Arg Val Ala Asn
20 25 30

Leu Leu Arg Trp Ala Ala Tyr Thr Asp Leu Leu Leu Pro Ala Glu Ala
35 40 45

Arg Trp Phe Gln Asp Gln Leu Gly Ile Ala Ala Ala Val Ser Phe Gly
50 55 60

Ser Trp Glu Glu Tyr Gly Glu Arg Tyr Val Arg Gly Leu Gln Lys Asn
65 70 75 80

Phe Lys Gly Gly Asn Lys Pro Tyr Ile Glu Gly Glu Arg Trp Leu Asn
85 90 95

Thr Glu Ala Glu Ser Pro Trp Lys Thr Gln Lys Trp Ile Ser Ala
100 105 110

<210> 355
<211> 2619
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2596)
<223> RXN00731

<400> 355
ttgataccgt ggccggtgga cattccttcc aggtgtggcg cgtggcttta gcgaatactt 60

ttgattgggt tgccaagcgc ggcggattgc aggtttaaca atg aaa gac gct tca 115
Met Lys Asp Ala Ser
1 5

cag tcc tac tta tta ttc ggt ctg aga tgg ctg ggc agg tcc ctg cgt 163
Gln Ser Tyr Leu Leu Phe Gly Leu Arg Trp Leu Gly Arg Ser Leu Arg
10 15 20

ttc gca ccg tta agc ctg ctc atg atc gtt gtc atg cgg ggt ttg agg 211
Phe Ala Pro Leu Ser Leu Leu Met Ile Val Val Met Arg Gly Leu Arg
25 30 35

gaa gtg ttt ggc gcc gaa gat ccc gca aat agc tct ttg gta gac aac 259
Glu Val Phe Gly Ala Glu Asp Pro Ala Asn Ser Ser Leu Val Asp Asn
40 45 50

ctt ggg ctc acc ctg ccg tgg tct ctt aat gat ccg cat ttt ctc acc 307
Leu Gly Leu Thr Leu Pro Trp Ser Leu Asn Asp Pro His Phe Leu Thr
55 60 65

gca ggg ttt agc gct tcc acc acc aca gca gcg ctc atg tcc acg ttg 355
Ala Gly Phe Ser Ala Ser Thr Thr Thr Ala Ala Leu Met Ser Thr Leu

```
 70                  75                  80                  85

tgg atc atc gtg ttt gcg gtg ccc tct gaa cgg att ctg ggc agc ctc   403
Trp Ile Ile Val Phe Ala Val Pro Ser Glu Arg Ile Leu Gly Ser Leu
                90                  95                 100

aaa ttc gcg atc aca gca gcg ctt atc cac atc act tcc att ccg ctg   451
Lys Phe Ala Ile Thr Ala Ala Leu Ile His Ile Thr Ser Ile Pro Leu
            105                 110                 115

ggc atc ggc atc gcc cac ctc atc gaa gaa gcc gat ctc aac cgc tgg   499
Gly Ile Gly Ile Ala His Leu Ile Glu Glu Ala Asp Leu Asn Arg Trp
        120                 125                 130

ggc aac aac atg ttg gcc gat gtg ctg ctc acc cca gat ttc tgg gtc   547
Gly Asn Asn Met Leu Ala Asp Val Leu Leu Thr Pro Asp Phe Trp Val
    135                 140                 145

ttc ggc gtc gcc gct ttc gca tcc gcc tcc atg cca ctg ctc tgg cga   595
Phe Gly Val Ala Ala Phe Ala Ser Ala Ser Met Pro Leu Leu Trp Arg
150                 155                 160                 165

cgg cgc acc cga ttg ttc ctc ttt act atc acc ttg acg ctg ctg ctt   643
Arg Arg Thr Arg Leu Phe Leu Phe Thr Ile Thr Leu Thr Leu Leu Leu
                170                 175                 180

tat acg ggc acg ctt gcc gac gtc acc atg ctc acc gcg acc atc atc   691
Tyr Thr Gly Thr Leu Ala Asp Val Thr Met Leu Thr Ala Thr Ile Ile
            185                 190                 195

ggc acc gtt gcc ggc gag ttg aac agg cat cgg aaa acc cca ggt ggc   739
Gly Thr Val Ala Gly Glu Leu Asn Arg His Arg Lys Thr Pro Gly Gly
        200                 205                 210

cgc tgg ctt ccc ggt tcc ctc acc gtg cgt gaa gcg cgc att atg acg   787
Arg Trp Leu Pro Gly Ser Leu Thr Val Arg Glu Ala Arg Ile Met Thr
    215                 220                 225

gcc att ttg gtc act gcc gta gca gca ggt cca gtg ctt gct gcg ctt   835
Ala Ile Leu Val Thr Ala Val Ala Ala Gly Pro Val Leu Ala Ala Leu
230                 235                 240                 245

aat cca ctc acc cac ggc cct ttt tcc agt gca acg aaa ttg atc tgg   883
Asn Pro Leu Thr His Gly Pro Phe Ser Ser Ala Thr Lys Leu Ile Trp
                250                 255                 260

cag ccc ctt gtc act gaa gaa cac atg cat cac ctc tgc cac aca gac   931
Gln Pro Leu Val Thr Glu Glu His Met His His Leu Cys His Thr Asp
            265                 270                 275

agc acc tct gat gca tgc caa ggt gcg ctt gat cag ctc caa cag cac   979
Ser Thr Ser Asp Ala Cys Gln Gly Ala Leu Asp Gln Leu Gln Gln His
        280                 285                 290

ggt gtt ggc cct tcc gtt gcc aac ctg att cca ctg atc ctc acc gtg   1027
Gly Val Gly Pro Ser Val Ala Asn Leu Ile Pro Leu Ile Leu Thr Val
    295                 300                 305

gtc ctt gcg atg ggg ctt agc cgc gga cgt cga ctt gca tgg att ttg   1075
Val Leu Ala Met Gly Leu Ser Arg Gly Arg Arg Leu Ala Trp Ile Leu
310                 315                 320                 325
```

```
gcg gtt ttg gcc cag ctc att tcc atc gca gtg ttg atg ttc cag ctg   1123
Ala Val Leu Ala Gln Leu Ile Ser Ile Ala Val Leu Met Phe Gln Leu
                330                 335                 340

acc aaa cta tcg gct gat tcc acc gat ctt cta tgg tca gtc aat gcc   1171
Thr Lys Leu Ser Ala Asp Ser Thr Asp Leu Leu Trp Ser Val Asn Ala
            345                 350                 355

ttt agc gtg atc gtt cct tgg ctg gtg gcg ctc gcc gtc ttg gtg ttt   1219
Phe Ser Val Ile Val Pro Trp Leu Val Ala Leu Ala Val Leu Val Phe
        360                 365                 370

tcc cgc cgt gca ttc cag gtg aag att gat acc acc cgg att tct aaa   1267
Ser Arg Arg Ala Phe Gln Val Lys Ile Asp Thr Thr Arg Ile Ser Lys
    375                 380                 385

tcc tta ggc gct ctc atg gtt aca tgg ttg gca acg gca gca ttg tgg   1315
Ser Leu Gly Ala Leu Met Val Thr Trp Leu Ala Thr Ala Ala Leu Trp
390                 395                 400                 405

atc ctt gcc aca ttg ttc ctg cca cac gca ttc cac cca cat cca aca   1363
Ile Leu Ala Thr Leu Phe Leu Pro His Ala Phe His Pro His Pro Thr
                410                 415                 420

ttg ggg ctg gct ttc aaa gaa ctc ccc ttc cgc tat ctc cca cca act   1411
Leu Gly Leu Ala Phe Lys Glu Leu Pro Phe Arg Tyr Leu Pro Pro Thr
            425                 430                 435

atc gaa acg gtg tta agc cat caa ctc ttc ccc aga agc cct gct ggg   1459
Ile Glu Thr Val Leu Ser His Gln Leu Phe Pro Arg Ser Pro Ala Gly
        440                 445                 450

tgg gca gtg ttt gaa tgg act gga acg cta ttc tgg ctg gtc gta gca   1507
Trp Ala Val Phe Glu Trp Thr Gly Thr Leu Phe Trp Leu Val Val Ala
    455                 460                 465

gca act ctt tat cat ctg ctc atg ggt gtg ccc agc aac aaa gcg cac   1555
Ala Thr Leu Tyr His Leu Leu Met Gly Val Pro Ser Asn Lys Ala His
470                 475                 480                 485

gag gac caa gaa aac gca gcg act ctc ctg cgc tct ggc agc ggc gat   1603
Glu Asp Gln Glu Asn Ala Ala Thr Leu Leu Arg Ser Gly Ser Gly Asp
                490                 495                 500

cac ttg tcc tgg atg acc att tgg ggt ggc aat acg tat tgg tgg gca   1651
His Leu Ser Trp Met Thr Ile Trp Gly Gly Asn Thr Tyr Trp Trp Ala
            505                 510                 515

cca gaa aat gca gga tat gtg gcc tac cgc gtg aaa agg ggc atc gca   1699
Pro Glu Asn Ala Gly Tyr Val Ala Tyr Arg Val Lys Arg Gly Ile Ala
        520                 525                 530

att aca ttg ggt gag cct att ctg ggt ccg gat tca tcc gtc tct aaa   1747
Ile Thr Leu Gly Glu Pro Ile Leu Gly Pro Asp Ser Ser Val Ser Lys
    535                 540                 545

gca gag ctg gcc gca cag ttt gaa gaa ttt gcc agc aac caa ggc tgg   1795
Ala Glu Leu Ala Ala Gln Phe Glu Glu Phe Ala Ser Asn Gln Gly Trp
550                 555                 560                 565
```

```
att gtt gcg tgg tat tcc gtt tgt gaa gaa ttc tca aag gaa cgc atc   1843
Ile Val Ala Trp Tyr Ser Val Cys Glu Glu Phe Ser Lys Glu Arg Ile
                570                 575                 580

aac gct ggc cac cac aca ctt cgt gtg gct gag gaa gca gtc tta agc   1891
Asn Ala Gly His His Thr Leu Arg Val Ala Glu Glu Ala Val Leu Ser
            585                 590                 595

tca gct aat gcg gat ttc aaa ggt aag cac ttc caa aat gtc cgc acc   1939
Ser Ala Asn Ala Asp Phe Lys Gly Lys His Phe Gln Asn Val Arg Thr
        600                 605                 610

gcc cga aac cgc gcg gcc aaa gag ggc gta agt tcc atc tgg aca acc   1987
Ala Arg Asn Arg Ala Ala Lys Glu Gly Val Ser Ser Ile Trp Thr Thr
    615                 620                 625

tgg gct gat ttg agt gcc gaa atg cag cac aag atc atc acg ctg tcg   2035
Trp Ala Asp Leu Ser Ala Glu Met Gln His Lys Ile Ile Thr Leu Ser
630                 635                 640                 645

gaa gaa tgg gtc tct gat aaa gct ctg ccg gag atg ggc ttc acg ctt   2083
Glu Glu Trp Val Ser Asp Lys Ala Leu Pro Glu Met Gly Phe Thr Leu
                650                 655                 660

ggc act gtc aac gag ctc tca gat cca gat acc tat ctt ctt ctc gcg   2131
Gly Thr Val Asn Glu Leu Ser Asp Pro Asp Thr Tyr Leu Leu Leu Ala
            665                 670                 675

att gat gag gaa gag cat ctg cac ggt gtg acc agt tgg ttg ccg gtc   2179
Ile Asp Glu Glu Glu His Leu His Gly Val Thr Ser Trp Leu Pro Val
        680                 685                 690

tat gaa aaa gga cgc atc gtc ggc tac aca ctt gat gtg atg cgc cgt   2227
Tyr Glu Lys Gly Arg Ile Val Gly Tyr Thr Leu Asp Val Met Arg Arg
    695                 700                 705

gat ccg caa ggc ttt aaa tct gtc atc gag ttt ctc att tcc gag gcc   2275
Asp Pro Gln Gly Phe Lys Ser Val Ile Glu Phe Leu Ile Ser Glu Ala
710                 715                 720                 725

gtc gtt atc gca agg gat cac gat ctg gaa tgg atg tcg atg tcc ggc   2323
Val Val Ile Ala Arg Asp His Asp Leu Glu Trp Met Ser Met Ser Gly
                730                 735                 740

gct cct ttg agt acg ccc cca ggt gtg gcc gac gac ggc acc atc gga   2371
Ala Pro Leu Ser Thr Pro Pro Gly Val Ala Asp Asp Gly Thr Ile Gly
            745                 750                 755

caa att ttg gag ctt ttg ggc cga gca atg gag ccg ttc tac ggt ttc   2419
Gln Ile Leu Glu Leu Leu Gly Arg Ala Met Glu Pro Phe Tyr Gly Phe
        760                 765                 770

cgt tcc ctc gct gcg tcc aag aac aaa ttc cac cca gaa cac cac ggt   2467
Arg Ser Leu Ala Ala Ser Lys Asn Lys Phe His Pro Glu His His Gly
    775                 780                 785

tgg tac ttg tgt tac cgc gat gaa tta tcg tta cca agc att ggc ctt   2515
Trp Tyr Leu Cys Tyr Arg Asp Glu Leu Ser Leu Pro Ser Ile Gly Leu
790                 795                 800                 805

gcc gtt gct gcc tgc tac ctc aac gag ttt ccg ctg ccg aat tgg ctg   2563
```

```
Ala Val Ala Ala Cys Tyr Leu Asn Glu Phe Pro Leu Pro Asn Trp Leu
                810                 815                 820

aaa aag acc gcc act tcc gcc cca agc cac agc tagaaaaacg cgtaaccttg 2616
Lys Lys Thr Ala Thr Ser Ala Pro Ser His Ser
            825                 830

gtg                                                               2619


<210> 356
<211> 832
<212> PRT
<213> Corynebacterium glutamicum

<400> 356
Met Lys Asp Ala Ser Gln Ser Tyr Leu Leu Phe Gly Leu Arg Trp Leu
  1               5                  10                  15

Gly Arg Ser Leu Arg Phe Ala Pro Leu Ser Leu Leu Met Ile Val Val
             20                  25                  30

Met Arg Gly Leu Arg Glu Val Phe Gly Ala Glu Asp Pro Ala Asn Ser
         35                  40                  45

Ser Leu Val Asp Asn Leu Gly Leu Thr Leu Pro Trp Ser Leu Asn Asp
     50                  55                  60

Pro His Phe Leu Thr Ala Gly Phe Ser Ala Ser Thr Thr Thr Ala Ala
 65                  70                  75                  80

Leu Met Ser Thr Leu Trp Ile Ile Val Phe Ala Val Pro Ser Glu Arg
                 85                  90                  95

Ile Leu Gly Ser Leu Lys Phe Ala Ile Thr Ala Ala Leu Ile His Ile
            100                 105                 110

Thr Ser Ile Pro Leu Gly Ile Gly Ile Ala His Leu Ile Glu Glu Ala
        115                 120                 125

Asp Leu Asn Arg Trp Gly Asn Asn Met Leu Ala Asp Val Leu Leu Thr
    130                 135                 140

Pro Asp Phe Trp Val Phe Gly Val Ala Ala Phe Ala Ser Ala Ser Met
145                 150                 155                 160

Pro Leu Leu Trp Arg Arg Arg Thr Arg Leu Phe Leu Phe Thr Ile Thr
                165                 170                 175

Leu Thr Leu Leu Leu Tyr Thr Gly Thr Leu Ala Asp Val Thr Met Leu
            180                 185                 190

Thr Ala Thr Ile Ile Gly Thr Val Ala Gly Glu Leu Asn Arg His Arg
        195                 200                 205

Lys Thr Pro Gly Gly Arg Trp Leu Pro Gly Ser Leu Thr Val Arg Glu
    210                 215                 220

Ala Arg Ile Met Thr Ala Ile Leu Val Thr Ala Val Ala Ala Gly Pro
225                 230                 235                 240
```

```
Val Leu Ala Ala Leu Asn Pro Leu Thr His Gly Pro Phe Ser Ser Ala
                245                 250                 255

Thr Lys Leu Ile Trp Gln Pro Leu Val Thr Glu Glu His Met His His
            260                 265                 270

Leu Cys His Thr Asp Ser Thr Ser Asp Ala Cys Gln Gly Ala Leu Asp
        275                 280                 285

Gln Leu Gln Gln His Gly Val Gly Pro Ser Val Ala Asn Leu Ile Pro
    290                 295                 300

Leu Ile Leu Thr Val Val Leu Ala Met Gly Leu Ser Arg Gly Arg Arg
305                 310                 315                 320

Leu Ala Trp Ile Leu Ala Val Leu Ala Gln Leu Ile Ser Ile Ala Val
                325                 330                 335

Leu Met Phe Gln Leu Thr Lys Leu Ser Ala Asp Ser Thr Asp Leu Leu
            340                 345                 350

Trp Ser Val Asn Ala Phe Ser Val Ile Val Pro Trp Leu Val Ala Leu
        355                 360                 365

Ala Val Leu Val Phe Ser Arg Arg Ala Phe Gln Val Lys Ile Asp Thr
    370                 375                 380

Thr Arg Ile Ser Lys Ser Leu Gly Ala Leu Met Val Thr Trp Leu Ala
385                 390                 395                 400

Thr Ala Ala Leu Trp Ile Leu Ala Thr Leu Phe Leu Pro His Ala Phe
                405                 410                 415

His Pro His Pro Thr Leu Gly Leu Ala Phe Lys Glu Leu Pro Phe Arg
            420                 425                 430

Tyr Leu Pro Pro Thr Ile Glu Thr Val Leu Ser His Gln Leu Phe Pro
        435                 440                 445

Arg Ser Pro Ala Gly Trp Ala Val Phe Glu Trp Thr Gly Thr Leu Phe
    450                 455                 460

Trp Leu Val Val Ala Ala Thr Leu Tyr His Leu Leu Met Gly Val Pro
465                 470                 475                 480

Ser Asn Lys Ala His Glu Asp Gln Glu Asn Ala Ala Thr Leu Leu Arg
                485                 490                 495

Ser Gly Ser Gly Asp His Leu Ser Trp Met Thr Ile Trp Gly Gly Asn
            500                 505                 510

Thr Tyr Trp Trp Ala Pro Glu Asn Ala Gly Tyr Val Ala Tyr Arg Val
        515                 520                 525

Lys Arg Gly Ile Ala Ile Thr Leu Gly Glu Pro Ile Leu Gly Pro Asp
    530                 535                 540

Ser Ser Val Ser Lys Ala Glu Leu Ala Ala Gln Phe Glu Glu Phe Ala
545                 550                 555                 560

Ser Asn Gln Gly Trp Ile Val Ala Trp Tyr Ser Val Cys Glu Glu Phe
```

```
                565                 570                 575

Ser Lys Glu Arg Ile Asn Ala Gly His His Thr Leu Arg Val Ala Glu
            580                 585                 590

Glu Ala Val Leu Ser Ser Ala Asn Ala Asp Phe Lys Gly Lys His Phe
        595                 600                 605

Gln Asn Val Arg Thr Ala Arg Asn Arg Ala Ala Lys Glu Gly Val Ser
    610                 615                 620

Ser Ile Trp Thr Thr Trp Ala Asp Leu Ser Ala Glu Met Gln His Lys
625                 630                 635                 640

Ile Ile Thr Leu Ser Glu Glu Trp Val Ser Asp Lys Ala Leu Pro Glu
                645                 650                 655

Met Gly Phe Thr Leu Gly Thr Val Asn Glu Leu Ser Asp Pro Asp Thr
            660                 665                 670

Tyr Leu Leu Leu Ala Ile Asp Glu Glu Glu His Leu His Gly Val Thr
        675                 680                 685

Ser Trp Leu Pro Val Tyr Glu Lys Gly Arg Ile Val Gly Tyr Thr Leu
    690                 695                 700

Asp Val Met Arg Arg Asp Pro Gln Gly Phe Lys Ser Val Ile Glu Phe
705                 710                 715                 720

Leu Ile Ser Glu Ala Val Val Ile Ala Arg Asp His Asp Leu Glu Trp
                725                 730                 735

Met Ser Met Ser Gly Ala Pro Leu Ser Thr Pro Pro Gly Val Ala Asp
            740                 745                 750

Asp Gly Thr Ile Gly Gln Ile Leu Glu Leu Leu Gly Arg Ala Met Glu
        755                 760                 765

Pro Phe Tyr Gly Phe Arg Ser Leu Ala Ala Ser Lys Asn Lys Phe His
    770                 775                 780

Pro Glu His His Gly Trp Tyr Leu Cys Tyr Arg Asp Glu Leu Ser Leu
785                 790                 795                 800

Pro Ser Ile Gly Leu Ala Val Ala Ala Cys Tyr Leu Asn Glu Phe Pro
                805                 810                 815

Leu Pro Asn Trp Leu Lys Lys Thr Ala Thr Ser Ala Pro Ser His Ser
            820                 825                 830
```

<210> 357
<211> 2495
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS

<222> (1)..(2472)
<223> FRXA00731

<400> 357

```
tta tta ttc ggt ctg aga tgg ctg ggc agg tcc ctg cgt ttc gca ccg   48
Leu Leu Phe Gly Leu Arg Trp Leu Gly Arg Ser Leu Arg Phe Ala Pro
  1               5                  10                  15

tta agc ctg ctc atg atc gtt gtc atg cgg ggt ttg agg gaa gtg ttt   96
Leu Ser Leu Leu Met Ile Val Val Met Arg Gly Leu Arg Glu Val Phe
             20                  25                  30

ggc gcc gaa gat ccc gca aat agc tct ttg gta gac aac ctt ggg ctc   144
Gly Ala Glu Asp Pro Ala Asn Ser Ser Leu Val Asp Asn Leu Gly Leu
         35                  40                  45

acc ctg ccg tgg tct ctt aat gat ccg cat ttt ctc acc gca ggg ttt   192
Thr Leu Pro Trp Ser Leu Asn Asp Pro His Phe Leu Thr Ala Gly Phe
     50                  55                  60

agc gct tcc acc acc aca gca gcg ctc atg tcc acg ttg tgg atc atc   240
Ser Ala Ser Thr Thr Thr Ala Ala Leu Met Ser Thr Leu Trp Ile Ile
 65                  70                  75                  80

gtg ttt gcg gtg ccc tct gaa cgg att ctg ggc agc ctc aaa ttc gcg   288
Val Phe Ala Val Pro Ser Glu Arg Ile Leu Gly Ser Leu Lys Phe Ala
                 85                  90                  95

atc aca gca gcg ctt atc cac atc act tcc att ccg ctg ggc atc ggc   336
Ile Thr Ala Ala Leu Ile His Ile Thr Ser Ile Pro Leu Gly Ile Gly
            100                 105                 110

atc gcc cac ctc atc gaa gaa gcc gat ctc aac cgc tgg ggc aac aac   384
Ile Ala His Leu Ile Glu Glu Ala Asp Leu Asn Arg Trp Gly Asn Asn
        115                 120                 125

atg ttg gcc gat gtg ctg ctc acc cca gat ttc tgg gtc ttc ggc gtc   432
Met Leu Ala Asp Val Leu Leu Thr Pro Asp Phe Trp Val Phe Gly Val
    130                 135                 140

gcc gct ttc gca tcc gcc tcc atg cca ctg ctc tgg cga cgg cgc acc   480
Ala Ala Phe Ala Ser Ala Ser Met Pro Leu Leu Trp Arg Arg Arg Thr
145                 150                 155                 160

cga ttg ttc ctc ttt act atc acc ttg acg ctg ctg ctt tat acg ggc   528
Arg Leu Phe Leu Phe Thr Ile Thr Leu Thr Leu Leu Leu Tyr Thr Gly
                165                 170                 175

acg ctt gcc gac gtc acc atg ctc acc gcg acc atc atc ggc acc gtt   576
Thr Leu Ala Asp Val Thr Met Leu Thr Ala Thr Ile Ile Gly Thr Val
            180                 185                 190

gcc ggc gag ttg aac agg cat cgg aaa acc cca ggt ggc cgc tgg ctt   624
Ala Gly Glu Leu Asn Arg His Arg Lys Thr Pro Gly Gly Arg Trp Leu
        195                 200                 205

ccc ggt tcc ctc acc gtg cgt gaa gcg cgc att atg acg gcc att ttg   672
Pro Gly Ser Leu Thr Val Arg Glu Ala Arg Ile Met Thr Ala Ile Leu
    210                 215                 220

gtc act gcc gta gca gca ggt cca gtg ctt gct gcg ctt aat cca ctc   720
```

```
Val Thr Ala Val Ala Ala Gly Pro Val Leu Ala Ala Leu Asn Pro Leu
225                 230                 235                 240

acc cac ggc cct ttt tcc agt gca acg aaa ttg atc tgg cag ccc ctt   768
Thr His Gly Pro Phe Ser Ser Ala Thr Lys Leu Ile Trp Gln Pro Leu
                245                 250                 255

gtc act gaa gaa cac atg cat cac ctc tgc cac aca gac agc acc tct   816
Val Thr Glu Glu His Met His His Leu Cys His Thr Asp Ser Thr Ser
            260                 265                 270

gat gca tgc caa ggt gcg ctt gat cag ctc caa cag cac ggt gtt ggc   864
Asp Ala Cys Gln Gly Ala Leu Asp Gln Leu Gln Gln His Gly Val Gly
        275                 280                 285

cct tcc gtt gcc aac ctg att cca ctg atc ctc acc gtg gtc ctt gcg   912
Pro Ser Val Ala Asn Leu Ile Pro Leu Ile Leu Thr Val Val Leu Ala
    290                 295                 300

atg ggg ctt agc cgc gga cgt cga ctt gca tgg att ttg gcg gtt ttg   960
Met Gly Leu Ser Arg Gly Arg Arg Leu Ala Trp Ile Leu Ala Val Leu
305                 310                 315                 320

gcc cag ctc att tcc atc gca gtg ttg atg ttc cag ctg acc aaa cta  1008
Ala Gln Leu Ile Ser Ile Ala Val Leu Met Phe Gln Leu Thr Lys Leu
                325                 330                 335

tcg gct gat tcc acc gat ctt cta tgg tca gtc aat gcc ttt agc gtg  1056
Ser Ala Asp Ser Thr Asp Leu Leu Trp Ser Val Asn Ala Phe Ser Val
            340                 345                 350

atc gtt cct tgg ctg gtg gcg ctc gcc gtc ttg gtg ttt tcc cgc cgt  1104
Ile Val Pro Trp Leu Val Ala Leu Ala Val Leu Val Phe Ser Arg Arg
        355                 360                 365

gca ttc cag gtg aag att gat acc acc cgg att tct aaa tcc tta ggc  1152
Ala Phe Gln Val Lys Ile Asp Thr Thr Arg Ile Ser Lys Ser Leu Gly
    370                 375                 380

gct ctc atg gtt aca tgg ttg gca acg gca gca ttg tgg atc ctt gcc  1200
Ala Leu Met Val Thr Trp Leu Ala Thr Ala Ala Leu Trp Ile Leu Ala
385                 390                 395                 400

aca ttg ttc ctg cca cac gca ttc cac cca cat cca aca ttg ggg ctg  1248
Thr Leu Phe Leu Pro His Ala Phe His Pro His Pro Thr Leu Gly Leu
                405                 410                 415

gct ttc aaa gaa ctc ccc ttc cgc tat ctc cca cca act atc gaa acg  1296
Ala Phe Lys Glu Leu Pro Phe Arg Tyr Leu Pro Pro Thr Ile Glu Thr
            420                 425                 430

gtg tta agc cat caa ctc ttc ccc aga agc cct gct ggg tgg gca gtg  1344
Val Leu Ser His Gln Leu Phe Pro Arg Ser Pro Ala Gly Trp Ala Val
        435                 440                 445

ttt gaa tgg act gga acg cta ttc tgg ctg gtc gta gca gca act ctt  1392
Phe Glu Trp Thr Gly Thr Leu Phe Trp Leu Val Val Ala Ala Thr Leu
    450                 455                 460

tat cat ctg ctc atg ggt gtg ccc agc aac aaa gcg cac gag gac caa  1440
Tyr His Leu Leu Met Gly Val Pro Ser Asn Lys Ala His Glu Asp Gln
```

```
465                 470                 475                 480

gaa aac gca gcg act ctc ctg cgc tct ggc agc ggc gat cac ttg tcc  1488
Glu Asn Ala Ala Thr Leu Leu Arg Ser Gly Ser Gly Asp His Leu Ser
                485                 490                 495

tgg atg acc att tgg ggt ggc aat acg tat tgg tgg gca cca gaa aat  1536
Trp Met Thr Ile Trp Gly Gly Asn Thr Tyr Trp Trp Ala Pro Glu Asn
            500                 505                 510

gca gga tat gtg gcc tac cgc gtg aaa agg ggc atc gca att aca ttg  1584
Ala Gly Tyr Val Ala Tyr Arg Val Lys Arg Gly Ile Ala Ile Thr Leu
        515                 520                 525

ggt gag cct att ctg ggt ccg gat tca tcc gtc tct aaa gca gag ctg  1632
Gly Glu Pro Ile Leu Gly Pro Asp Ser Ser Val Ser Lys Ala Glu Leu
    530                 535                 540

gcc gca cag ttt gaa gaa ttt gcc agc aac caa ggc tgg att gtt gcg  1680
Ala Ala Gln Phe Glu Glu Phe Ala Ser Asn Gln Gly Trp Ile Val Ala
545                 550                 555                 560

tgg tat tcc gtt tgt gaa gaa ttc tca aag gaa cgc atc aac gct ggc  1728
Trp Tyr Ser Val Cys Glu Glu Phe Ser Lys Glu Arg Ile Asn Ala Gly
                565                 570                 575

cac cac aca ctt cgt gtg gct gag gaa gca gtc tta agc tca gct aat  1776
His His Thr Leu Arg Val Ala Glu Glu Ala Val Leu Ser Ser Ala Asn
            580                 585                 590

gcg gat ttc aaa ggt aag cac ttc caa aat gtc cgc acc gcc cga aac  1824
Ala Asp Phe Lys Gly Lys His Phe Gln Asn Val Arg Thr Ala Arg Asn
        595                 600                 605

cgc gcg gcc aaa gag ggc gta agt tcc atc tgg aca acc tgg gct gat  1872
Arg Ala Ala Lys Glu Gly Val Ser Ser Ile Trp Thr Thr Trp Ala Asp
    610                 615                 620

ttg agt gcc gaa atg cag cac aag atc atc acg ctg tcg gaa gaa tgg  1920
Leu Ser Ala Glu Met Gln His Lys Ile Ile Thr Leu Ser Glu Glu Trp
625                 630                 635                 640

gtc tct gat aaa gct ctg ccg gag atg ggc ttc acg ctt ggc act gtc  1968
Val Ser Asp Lys Ala Leu Pro Glu Met Gly Phe Thr Leu Gly Thr Val
                645                 650                 655

aac gag ctc tca gat cca gat acc tat ctt ctt ctc gcg att gat gag  2016
Asn Glu Leu Ser Asp Pro Asp Thr Tyr Leu Leu Leu Ala Ile Asp Glu
            660                 665                 670

gaa gag cat ctg cac ggt gtg acc agt tgg ttg ccg gtc tat gaa aaa  2064
Glu Glu His Leu His Gly Val Thr Ser Trp Leu Pro Val Tyr Glu Lys
        675                 680                 685

gga cgc atc gtc ggc tac aca ctt gat gtg atg cgc cgt gat ccg caa  2112
Gly Arg Ile Val Gly Tyr Thr Leu Asp Val Met Arg Arg Asp Pro Gln
    690                 695                 700

ggc ttt aaa tct gtc atc gag ttt ctc att tcc gag gcc gtc gtt atc  2160
Gly Phe Lys Ser Val Ile Glu Phe Leu Ile Ser Glu Ala Val Val Ile
705                 710                 715                 720
```

```
gca agg gat cac gat ctg gaa tgg atg tcg atg tcc ggc gct cct ttg   2208
Ala Arg Asp His Asp Leu Glu Trp Met Ser Met Ser Gly Ala Pro Leu
                725                 730                 735

agt acg ccc cca ggt gtg gcc gac gac ggc acc atc gga caa att ttg   2256
Ser Thr Pro Pro Gly Val Ala Asp Asp Gly Thr Ile Gly Gln Ile Leu
            740                 745                 750

gag ctt ttg ggc cga gca atg gag ccg ttc tac ggt ttc cgt tcc ctc   2304
Glu Leu Leu Gly Arg Ala Met Glu Pro Phe Tyr Gly Phe Arg Ser Leu
        755                 760                 765

gct gcg tcc aag aac aaa ttc cac cca gaa cac cac ggt tgg tac ttg   2352
Ala Ala Ser Lys Asn Lys Phe His Pro Glu His His Gly Trp Tyr Leu
    770                 775                 780

tgt tac cgc gat gaa tta tcg tta cca agc att ggc ctt gcc gtt gct   2400
Cys Tyr Arg Asp Glu Leu Ser Leu Pro Ser Ile Gly Leu Ala Val Ala
785                 790                 795                 800

gcc tgc tac ctc aac gag ttt ccg ctg ccg aat tgg ctg aaa aag acc   2448
Ala Cys Tyr Leu Asn Glu Phe Pro Leu Pro Asn Trp Leu Lys Lys Thr
                805                 810                 815

gcc act tcc gcc cca agc cac agc tagaaaaacg cgtaaccttg gtg         2495
Ala Thr Ser Ala Pro Ser His Ser
            820
```

<210> 358
<211> 824
<212> PRT
<213> Corynebacterium glutamicum

<400> 358

```
Leu Leu Phe Gly Leu Arg Trp Leu Gly Arg Ser Leu Arg Phe Ala Pro
  1               5                  10                  15

Leu Ser Leu Leu Met Ile Val Val Met Arg Gly Leu Arg Glu Val Phe
             20                  25                  30

Gly Ala Glu Asp Pro Ala Asn Ser Ser Leu Val Asp Asn Leu Gly Leu
         35                  40                  45

Thr Leu Pro Trp Ser Leu Asn Asp Pro His Phe Leu Thr Ala Gly Phe
     50                  55                  60

Ser Ala Ser Thr Thr Thr Ala Ala Leu Met Ser Thr Leu Trp Ile Ile
 65                  70                  75                  80

Val Phe Ala Val Pro Ser Glu Arg Ile Leu Gly Ser Leu Lys Phe Ala
                 85                  90                  95

Ile Thr Ala Ala Leu Ile His Ile Thr Ser Ile Pro Leu Gly Ile Gly
            100                 105                 110

Ile Ala His Leu Ile Glu Glu Ala Asp Leu Asn Arg Trp Gly Asn Asn
        115                 120                 125

Met Leu Ala Asp Val Leu Leu Thr Pro Asp Phe Trp Val Phe Gly Val
```

```
    130                 135                 140

Ala Ala Phe Ala Ser Ala Ser Met Pro Leu Leu Trp Arg Arg Arg Thr
145                 150                 155                 160

Arg Leu Phe Leu Phe Thr Ile Thr Leu Thr Leu Leu Leu Tyr Thr Gly
                165                 170                 175

Thr Leu Ala Asp Val Thr Met Leu Thr Ala Thr Ile Ile Gly Thr Val
            180                 185                 190

Ala Gly Glu Leu Asn Arg His Arg Lys Thr Pro Gly Gly Arg Trp Leu
        195                 200                 205

Pro Gly Ser Leu Thr Val Arg Glu Ala Arg Ile Met Thr Ala Ile Leu
    210                 215                 220

Val Thr Ala Val Ala Ala Gly Pro Val Leu Ala Ala Leu Asn Pro Leu
225                 230                 235                 240

Thr His Gly Pro Phe Ser Ser Ala Thr Lys Leu Ile Trp Gln Pro Leu
                245                 250                 255

Val Thr Glu Glu His Met His His Leu Cys His Thr Asp Ser Thr Ser
            260                 265                 270

Asp Ala Cys Gln Gly Ala Leu Asp Gln Leu Gln Gln His Gly Val Gly
        275                 280                 285

Pro Ser Val Ala Asn Leu Ile Pro Leu Ile Leu Thr Val Val Leu Ala
    290                 295                 300

Met Gly Leu Ser Arg Gly Arg Arg Leu Ala Trp Ile Leu Ala Val Leu
305                 310                 315                 320

Ala Gln Leu Ile Ser Ile Ala Val Leu Met Phe Gln Leu Thr Lys Leu
                325                 330                 335

Ser Ala Asp Ser Thr Asp Leu Leu Trp Ser Val Asn Ala Phe Ser Val
            340                 345                 350

Ile Val Pro Trp Leu Val Ala Leu Ala Val Leu Val Phe Ser Arg Arg
        355                 360                 365

Ala Phe Gln Val Lys Ile Asp Thr Thr Arg Ile Ser Lys Ser Leu Gly
    370                 375                 380

Ala Leu Met Val Thr Trp Leu Ala Thr Ala Ala Leu Trp Ile Leu Ala
385                 390                 395                 400

Thr Leu Phe Leu Pro His Ala Phe His Pro His Pro Thr Leu Gly Leu
                405                 410                 415

Ala Phe Lys Glu Leu Pro Phe Arg Tyr Leu Pro Pro Thr Ile Glu Thr
            420                 425                 430

Val Leu Ser His Gln Leu Phe Pro Arg Ser Pro Ala Gly Trp Ala Val
        435                 440                 445

Phe Glu Trp Thr Gly Thr Leu Phe Trp Leu Val Val Ala Ala Thr Leu
    450                 455                 460
```

```
Tyr His Leu Leu Met Gly Val Pro Ser Asn Lys Ala His Glu Asp Gln
465                 470                 475                 480

Glu Asn Ala Ala Thr Leu Leu Arg Ser Gly Ser Gly Asp His Leu Ser
                485                 490                 495

Trp Met Thr Ile Trp Gly Gly Asn Thr Tyr Trp Trp Ala Pro Glu Asn
            500                 505                 510

Ala Gly Tyr Val Ala Tyr Arg Val Lys Arg Gly Ile Ala Ile Thr Leu
        515                 520                 525

Gly Glu Pro Ile Leu Gly Pro Asp Ser Ser Val Ser Lys Ala Glu Leu
    530                 535                 540

Ala Ala Gln Phe Glu Glu Phe Ala Ser Asn Gln Gly Trp Ile Val Ala
545                 550                 555                 560

Trp Tyr Ser Val Cys Glu Glu Phe Ser Lys Glu Arg Ile Asn Ala Gly
                565                 570                 575

His His Thr Leu Arg Val Ala Glu Glu Ala Val Leu Ser Ser Ala Asn
            580                 585                 590

Ala Asp Phe Lys Gly Lys His Phe Gln Asn Val Arg Thr Ala Arg Asn
        595                 600                 605

Arg Ala Ala Lys Glu Gly Val Ser Ser Ile Trp Thr Thr Trp Ala Asp
    610                 615                 620

Leu Ser Ala Glu Met Gln His Lys Ile Ile Thr Leu Ser Glu Glu Trp
625                 630                 635                 640

Val Ser Asp Lys Ala Leu Pro Glu Met Gly Phe Thr Leu Gly Thr Val
                645                 650                 655

Asn Glu Leu Ser Asp Pro Asp Thr Tyr Leu Leu Leu Ala Ile Asp Glu
            660                 665                 670

Glu Glu His Leu His Gly Val Thr Ser Trp Leu Pro Val Tyr Glu Lys
        675                 680                 685

Gly Arg Ile Val Gly Tyr Thr Leu Asp Val Met Arg Arg Asp Pro Gln
    690                 695                 700

Gly Phe Lys Ser Val Ile Glu Phe Leu Ile Ser Glu Ala Val Val Ile
705                 710                 715                 720

Ala Arg Asp His Asp Leu Glu Trp Met Ser Met Ser Gly Ala Pro Leu
                725                 730                 735

Ser Thr Pro Pro Gly Val Ala Asp Asp Gly Thr Ile Gly Gln Ile Leu
            740                 745                 750

Glu Leu Leu Gly Arg Ala Met Glu Pro Phe Tyr Gly Phe Arg Ser Leu
        755                 760                 765

Ala Ala Ser Lys Asn Lys Phe His Pro Glu His His Gly Trp Tyr Leu
    770                 775                 780
```

```
Cys Tyr Arg Asp Glu Leu Ser Leu Pro Ser Ile Gly Leu Ala Val Ala
785                 790                 795                 800

Ala Cys Tyr Leu Asn Glu Phe Pro Leu Pro Asn Trp Leu Lys Lys Thr
                805                 810                 815

Ala Thr Ser Ala Pro Ser His Ser
            820


<210> 359
<211> 386
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(363)
<223> RXN00738

<400> 359
tgt caa gag gag acg gat ggc ttt ttt gat ttt ggg cgc gat atg cgg   48
Cys Gln Glu Glu Thr Asp Gly Phe Phe Asp Phe Gly Arg Asp Met Arg
  1               5                  10                  15

ccc ggt gag cgc cgg tcg tat ggc act ttg ctt aac gac gcc acg acg   96
Pro Gly Glu Arg Arg Ser Tyr Gly Thr Leu Leu Asn Asp Ala Thr Thr
             20                  25                  30

cag gtg tcg cac atc ctc ggc aat gcc ttc acc cga tct ggg ctc aac   144
Gln Val Ser His Ile Leu Gly Asn Ala Phe Thr Arg Ser Gly Leu Asn
         35                  40                  45

gct gag tac gcg aat ctt tat ggt cag gcg ttg gtg ggc atg gtg tcg   192
Ala Glu Tyr Ala Asn Leu Tyr Gly Gln Ala Leu Val Gly Met Val Ser
     50                  55                  60

atg acg gcg caa tgg tgg ttg gat gag cgc act ccg ccg aag gaa gaa   240
Met Thr Ala Gln Trp Trp Leu Asp Glu Arg Thr Pro Pro Lys Glu Glu
 65                  70                  75                  80

gtt gcc gca cat att gtt aat ctt tgt tgg aat ggt ttg acg ggg atg   288
Val Ala Ala His Ile Val Asn Leu Cys Trp Asn Gly Leu Thr Gly Met
                85                  90                  95

gaa gcc gat ccg aag tta act ccc atc agt tct gct gag ggt gcg att   336
Glu Ala Asp Pro Lys Leu Thr Pro Ile Ser Ser Ala Glu Gly Ala Ile
            100                 105                 110

ttt ggt caa gaa aag gag agt gaa gcg tgacacctat gctcgcgggg         383
Phe Gly Gln Glu Lys Glu Ser Glu Ala
        115                 120

ctg                                                               386


<210> 360
<211> 121
<212> PRT
<213> Corynebacterium glutamicum
```

<400> 360
Cys Gln Glu Glu Thr Asp Gly Phe Phe Asp Phe Gly Arg Asp Met Arg
1 5 10 15

Pro Gly Glu Arg Arg Ser Tyr Gly Thr Leu Leu Asn Asp Ala Thr Thr
20 25 30

Gln Val Ser His Ile Leu Gly Asn Ala Phe Thr Arg Ser Gly Leu Asn
35 40 45

Ala Glu Tyr Ala Asn Leu Tyr Gly Gln Ala Leu Val Gly Met Val Ser
50 55 60

Met Thr Ala Gln Trp Trp Leu Asp Glu Arg Thr Pro Pro Lys Glu Glu
65 70 75 80

Val Ala Ala His Ile Val Asn Leu Cys Trp Asn Gly Leu Thr Gly Met
85 90 95

Glu Ala Asp Pro Lys Leu Thr Pro Ile Ser Ser Ala Glu Gly Ala Ile
100 105 110

Phe Gly Gln Glu Lys Glu Ser Glu Ala
115 120

<210> 361
<211> 388
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (78)..(365)
<223> FRXA00738

<400> 361
catgccccta ttagacggat ggctttttttg attttgggcg cgatatgcgg cccggtgagc 60

gccggtcgta tggcactttg ctt aac gac gcc acg acg cag gtg tcg cac atc 113
Leu Leu Asn Asp Ala Thr Thr Gln Val Ser His Ile
1 5 10

ctc ggc aat gcc ttc acc cga tct ggg ctc aac gct gag tac gcg aat 161
Leu Gly Asn Ala Phe Thr Arg Ser Gly Leu Asn Ala Glu Tyr Ala Asn
15 20 25

ctt tat ggt cag gcg ttg gtg ggc atg gtg tcg atg acg gcg caa tgg 209
Leu Tyr Gly Gln Ala Leu Val Gly Met Val Ser Met Thr Ala Gln Trp
30 35 40

tgg ttg gat gag cgc act ccg ccg aag gaa gaa gtt gcc gca cat att 257
Trp Leu Asp Glu Arg Thr Pro Pro Lys Glu Glu Val Ala Ala His Ile
45 50 55 60

gtt aat ctt tgt tgg aat ggt ttg acg ggg atg gaa gcc gat ccg aag 305
Val Asn Leu Cys Trp Asn Gly Leu Thr Gly Met Glu Ala Asp Pro Lys
65 70 75

tta act ccc atc agt tct gct gag ggt gcg att ttt ggt caa gaa aag 353
Leu Thr Pro Ile Ser Ser Ala Glu Gly Ala Ile Phe Gly Gln Glu Lys

```
            80                  85                  90

gag agt gaa gcg tgacacctat gctcgcgggg ctg                          388
Glu Ser Glu Ala
         95


<210> 362
<211> 96
<212> PRT
<213> Corynebacterium glutamicum

<400> 362
Leu Leu Asn Asp Ala Thr Thr Gln Val Ser His Ile Leu Gly Asn Ala
  1               5                  10                  15

Phe Thr Arg Ser Gly Leu Asn Ala Glu Tyr Ala Asn Leu Tyr Gly Gln
             20                  25                  30

Ala Leu Val Gly Met Val Ser Met Thr Ala Gln Trp Trp Leu Asp Glu
         35                  40                  45

Arg Thr Pro Pro Lys Glu Glu Val Ala Ala His Ile Val Asn Leu Cys
     50                  55                  60

Trp Asn Gly Leu Thr Gly Met Glu Ala Asp Pro Lys Leu Thr Pro Ile
 65                  70                  75                  80

Ser Ser Ala Glu Gly Ala Ile Phe Gly Gln Glu Lys Glu Ser Glu Ala
                 85                  90                  95



<210> 363
<211> 561
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(538)
<223> RXN00750

<400> 363
tttaaacaaa agcgataaca atgaaccgat ggtgtctacg acagaaccga ctcccccacc 60

cactaacacc ccaccagaaa ataacacctc gaccgaacct atg gac tgg tcg atc   115
                                            Met Asp Trp Ser Ile
                                              1               5

att att aat gtg ctt gcc gtt gct act gtc gtg ata ctc acc ctt atc   163
Ile Ile Asn Val Leu Ala Val Ala Thr Val Val Ile Leu Thr Leu Ile
                 10                  15                  20

atc gca gct gca tta tat agg ggt ttc aca cgc aac aaa ata aaa aaa   211
Ile Ala Ala Ala Leu Tyr Arg Gly Phe Thr Arg Asn Lys Ile Lys Lys
             25                  30                  35

ctt gaa gct ata cga gaa gcc cag caa cac gaa cgc gac aat ccc act   259
```

```
Leu Glu Ala Ile Arg Glu Ala Gln Gln His Glu Arg Asp Asn Pro Thr
         40                  45                  50

atc cgc att gct gat ctt cgc ggc atc atg gat act cac cac tac atc   307
Ile Arg Ile Ala Asp Leu Arg Gly Ile Met Asp Thr His His Tyr Ile
     55                  60                  65

tac acc gac gtc atg gtt aca cgt gca cat gaa ctc atg att act gca   355
Tyr Thr Asp Val Met Val Thr Arg Ala His Glu Leu Met Ile Thr Ala
 70                  75                  80                  85

ccc gca ttc ttt gat gtc act ctc ccc gaa gca gtg ctc tac gaa gat   403
Pro Ala Phe Phe Asp Val Thr Leu Pro Glu Ala Val Leu Tyr Glu Asp
                 90                  95                 100

act aaa cgt gct gct cat gat gcc ctt aac ggc tat aaa gac acc act   451
Thr Lys Arg Ala Ala His Asp Ala Leu Asn Gly Tyr Lys Asp Thr Thr
            105                 110                 115

gtc gct agt gca gag aag atc atg ctt gta gat gca gtc acc gca gca   499
Val Ala Ser Ala Glu Lys Ile Met Leu Val Asp Ala Val Thr Ala Ala
        120                 125                 130

tgg act ctc tat tcc aca aaa gca aac acc gga tcc acg tgatccgaga    548
Trp Thr Leu Tyr Ser Thr Lys Ala Asn Thr Gly Ser Thr
    135                 140                 145

gccgagtacc gct                                                   561


<210> 364
<211> 146
<212> PRT
<213> Corynebacterium glutamicum

<400> 364
Met Asp Trp Ser Ile Ile Ile Asn Val Leu Ala Val Ala Thr Val Val
  1               5                  10                  15

Ile Leu Thr Leu Ile Ile Ala Ala Ala Leu Tyr Arg Gly Phe Thr Arg
             20                  25                  30

Asn Lys Ile Lys Lys Leu Glu Ala Ile Arg Glu Ala Gln Gln His Glu
         35                  40                  45

Arg Asp Asn Pro Thr Ile Arg Ile Ala Asp Leu Arg Gly Ile Met Asp
     50                  55                  60

Thr His His Tyr Ile Tyr Thr Asp Val Met Val Thr Arg Ala His Glu
 65                  70                  75                  80

Leu Met Ile Thr Ala Pro Ala Phe Phe Asp Val Thr Leu Pro Glu Ala
                 85                  90                  95

Val Leu Tyr Glu Asp Thr Lys Arg Ala Ala His Asp Ala Leu Asn Gly
            100                 105                 110

Tyr Lys Asp Thr Thr Val Ala Ser Ala Glu Lys Ile Met Leu Val Asp
        115                 120                 125

Ala Val Thr Ala Ala Trp Thr Leu Tyr Ser Thr Lys Ala Asn Thr Gly
```

```
    130                 135                 140

Ser Thr
145


<210> 365
<211> 561
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(538)
<223> FRXA00750

<400> 365
tttaaacaaa agcgataaca atgaaccgat ggtgtctacg acagaaccga ctccccacc 60

cactaacacc ccaccagaaa ataacacctc gaccgaacct atg gac tgg tcg atc   115
                                              Met Asp Trp Ser Ile
                                                1               5

att att aat gtg ctt gcc gtt gct act gtc gtg ata ctc acc ctt atc   163
Ile Ile Asn Val Leu Ala Val Ala Thr Val Val Ile Leu Thr Leu Ile
                10                  15                  20

atc gca gct gca tta tat agg ggt ttc aca cgc aac aaa ata aaa aaa   211
Ile Ala Ala Ala Leu Tyr Arg Gly Phe Thr Arg Asn Lys Ile Lys Lys
            25                  30                  35

ctt gaa gct ata cga gaa gcc cag caa cac gaa cgc gac aat ccc act   259
Leu Glu Ala Ile Arg Glu Ala Gln Gln His Glu Arg Asp Asn Pro Thr
        40                  45                  50

atc cgc att gct gat ctt cgc ggc atc atg gat act cac cac tac atc   307
Ile Arg Ile Ala Asp Leu Arg Gly Ile Met Asp Thr His His Tyr Ile
    55                  60                  65

tac acc gac gtc atg gtt aca cgt gca cat gaa ctc atg att act gca   355
Tyr Thr Asp Val Met Val Thr Arg Ala His Glu Leu Met Ile Thr Ala
70                  75                  80                  85

ccc gca ttc ttt gat gtc act ctc ccc gaa gca gtg ctc tac gaa gat   403
Pro Ala Phe Phe Asp Val Thr Leu Pro Glu Ala Val Leu Tyr Glu Asp
                90                  95                 100

act aaa cgt gct gct cat gat gcc ctt aac ggc tat aaa gac acc act   451
Thr Lys Arg Ala Ala His Asp Ala Leu Asn Gly Tyr Lys Asp Thr Thr
            105                 110                 115

gtc gct agt gca gag aag atc atg ctt gta gat gca gtc acc gca gca   499
Val Ala Ser Ala Glu Lys Ile Met Leu Val Asp Ala Val Thr Ala Ala
        120                 125                 130

tgg act ctc tat tcc aca aaa gca aac acc gga tcc acg tgatccgaga    548
Trp Thr Leu Tyr Ser Thr Lys Ala Asn Thr Gly Ser Thr
    135                 140                 145

gccgagtacc gct                                                   561
```

<210> 366
<211> 146
<212> PRT
<213> Corynebacterium glutamicum

<400> 366
Met Asp Trp Ser Ile Ile Ile Asn Val Leu Ala Val Ala Thr Val Val
1 5 10 15

Ile Leu Thr Leu Ile Ile Ala Ala Ala Leu Tyr Arg Gly Phe Thr Arg
20 25 30

Asn Lys Ile Lys Lys Leu Glu Ala Ile Arg Glu Ala Gln Gln His Glu
35 40 45

Arg Asp Asn Pro Thr Ile Arg Ile Ala Asp Leu Arg Gly Ile Met Asp
50 55 60

Thr His His Tyr Ile Tyr Thr Asp Val Met Val Thr Arg Ala His Glu
65 70 75 80

Leu Met Ile Thr Ala Pro Ala Phe Phe Asp Val Thr Leu Pro Glu Ala
85 90 95

Val Leu Tyr Glu Asp Thr Lys Arg Ala Ala His Asp Ala Leu Asn Gly
100 105 110

Tyr Lys Asp Thr Thr Val Ala Ser Ala Glu Lys Ile Met Leu Val Asp
115 120 125

Ala Val Thr Ala Ala Trp Thr Leu Tyr Ser Thr Lys Ala Asn Thr Gly
130 135 140

Ser Thr
145

<210> 367
<211> 999
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(976)
<223> RXN00762

<400> 367
gatgctgcga tggtcacaag tcgttttctg gatttttcca catctatatc tttaccccac 60

gttcctgcaa gagattcaaa cttggggcta acctggggac atg aat act tcc gat 115
Met Asn Thr Ser Asp
1 5

cgt att aaa agc act caa atc gcg ctg gat cgt gac ctc cgt gag cag 163
Arg Ile Lys Ser Thr Gln Ile Ala Leu Asp Arg Asp Leu Arg Glu Gln
10 15 20

gca cta ttg ctt ttg aag gag gtt cgc gca gtt gat ggc gtg gat gct 211
Ala Leu Leu Leu Leu Lys Glu Val Arg Ala Val Asp Gly Val Asp Ala

```
                25                  30                  35

tta tca gaa caa ttt gtc cgt ggg ctt gca gaa ccc gga ctt gtt cac   259
Leu Ser Glu Gln Phe Val Arg Gly Leu Ala Glu Pro Gly Leu Val His
         40                  45                  50

tcc cat tta ata gtc acg ctc aat agc gag ctg gtt ggc ctc gcg gcc   307
Ser His Leu Ile Val Thr Leu Asn Ser Glu Leu Val Gly Leu Ala Ala
     55                  60                  65

gcg gat gag gaa acc acg gaa ctg gct gtc cac ccg gcg cac agg cgt   355
Ala Asp Glu Glu Thr Thr Glu Leu Ala Val His Pro Ala His Arg Arg
 70                  75                  80                  85

cag gga atc ggt aag gcg ctt atc gac gcc gcc ccc acc tca tca atc   403
Gln Gly Ile Gly Lys Ala Leu Ile Asp Ala Ala Pro Thr Ser Ser Ile
                 90                  95                 100

tgg gcg cat gga aat aca gca ggt gca caa gcg ttg gca tcc acc ctg   451
Trp Ala His Gly Asn Thr Ala Gly Ala Gln Ala Leu Ala Ser Thr Leu
            105                 110                 115

cgt atg aag aag act cgc gag ctt ctg gtg atg gag att tcc gac agg   499
Arg Met Lys Lys Thr Arg Glu Leu Leu Val Met Glu Ile Ser Asp Arg
        120                 125                 130

gcg ctc gat gac tct gca gca tac aaa gat cca gat gga att aca cac   547
Ala Leu Asp Asp Ser Ala Ala Tyr Lys Asp Pro Asp Gly Ile Thr His
    135                 140                 145

agt agt ttg gcg aat gcc cct gtg gag aaa tca gta gct gag gct aaa   595
Ser Ser Leu Ala Asn Ala Pro Val Glu Lys Ser Val Ala Glu Ala Lys
150                 155                 160                 165

tgg ctt caa tcc aac aac gaa gca ttc gac tgg cat ccc gag cag ggc   643
Trp Leu Gln Ser Asn Asn Glu Ala Phe Asp Trp His Pro Glu Gln Gly
                170                 175                 180

gga tgg aca act cat cgg ttg gcg cag gct cag aaa gcc gat tgg tac   691
Gly Trp Thr Thr His Arg Leu Ala Gln Ala Gln Lys Ala Asp Trp Tyr
            185                 190                 195

aag gac tct gac gtg tta ttc ctc tgg gac ggc gaa gag atc gtt ggc   739
Lys Asp Ser Asp Val Leu Phe Leu Trp Asp Gly Glu Glu Ile Val Gly
        200                 205                 210

ttc cac tgg gta aag cag cac agt cca gaa tta caa gag att tac gta   787
Phe His Trp Val Lys Gln His Ser Pro Glu Leu Gln Glu Ile Tyr Val
    215                 220                 225

gtt ggc ctt tct tca gcc tac cgt ggt cgc ggc ttg gga gat ccg ctt   835
Val Gly Leu Ser Ser Ala Tyr Arg Gly Arg Gly Leu Gly Asp Pro Leu
230                 235                 240                 245

gtt cgc ctc gga ctg cat cac atg agg gct cat ggt gct cga aaa gtg   883
Val Arg Leu Gly Leu His His Met Arg Ala His Gly Ala Arg Lys Val
                250                 255                 260

att ctt tat gtg gaa gct ggc aac act ccg gca gtc gcg gca tac gaa   931
Ile Leu Tyr Val Glu Ala Gly Asn Thr Pro Ala Val Ala Ala Tyr Glu
            265                 270                 275
```

aaa ctg gga ttc act gtc gcg gaa agc cac gta gtt tac gaa aag 976
Lys Leu Gly Phe Thr Val Ala Glu Ser His Val Val Tyr Glu Lys
280 285 290

taaaaaagag acttgctaaa aac 999

<210> 368
<211> 292
<212> PRT
<213> Corynebacterium glutamicum

<400> 368
Met Asn Thr Ser Asp Arg Ile Lys Ser Thr Gln Ile Ala Leu Asp Arg
1 5 10 15

Asp Leu Arg Glu Gln Ala Leu Leu Leu Leu Lys Glu Val Arg Ala Val
20 25 30

Asp Gly Val Asp Ala Leu Ser Glu Gln Phe Val Arg Gly Leu Ala Glu
35 40 45

Pro Gly Leu Val His Ser His Leu Ile Val Thr Leu Asn Ser Glu Leu
50 55 60

Val Gly Leu Ala Ala Ala Asp Glu Glu Thr Thr Glu Leu Ala Val His
65 70 75 80

Pro Ala His Arg Arg Gln Gly Ile Gly Lys Ala Leu Ile Asp Ala Ala
85 90 95

Pro Thr Ser Ser Ile Trp Ala His Gly Asn Thr Ala Gly Ala Gln Ala
100 105 110

Leu Ala Ser Thr Leu Arg Met Lys Lys Thr Arg Glu Leu Leu Val Met
115 120 125

Glu Ile Ser Asp Arg Ala Leu Asp Asp Ser Ala Ala Tyr Lys Asp Pro
130 135 140

Asp Gly Ile Thr His Ser Ser Leu Ala Asn Ala Pro Val Glu Lys Ser
145 150 155 160

Val Ala Glu Ala Lys Trp Leu Gln Ser Asn Asn Glu Ala Phe Asp Trp
165 170 175

His Pro Glu Gln Gly Gly Trp Thr Thr His Arg Leu Ala Gln Ala Gln
180 185 190

Lys Ala Asp Trp Tyr Lys Asp Ser Asp Val Leu Phe Leu Trp Asp Gly
195 200 205

Glu Glu Ile Val Gly Phe His Trp Val Lys Gln His Ser Pro Glu Leu
210 215 220

Gln Glu Ile Tyr Val Val Gly Leu Ser Ser Ala Tyr Arg Gly Arg Gly
225 230 235 240

Leu Gly Asp Pro Leu Val Arg Leu Gly Leu His His Met Arg Ala His
245 250 255

```
Gly Ala Arg Lys Val Ile Leu Tyr Val Glu Ala Gly Asn Thr Pro Ala
           260                 265                 270

Val Ala Ala Tyr Glu Lys Leu Gly Phe Thr Val Ala Glu Ser His Val
        275                 280                 285

Val Tyr Glu Lys
    290


<210> 369
<211> 1242
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1219)
<223> RXN00768

<400> 369
tcaagcgcca taacgcctga ttatgcacgg ttaaggcgca tctcgctcac tggtgctaac 60

cacttgcgct tttggaagga ataacccttc ctgtcagatt gtg ggt act atc gaa   115
                                          Val Gly Thr Ile Glu
                                            1               5

gac gtg gct aac gaa caa atc gag gtc gcg aac aac act gat cag att   163
Asp Val Ala Asn Glu Gln Ile Glu Val Ala Asn Asn Thr Asp Gln Ile
                10                  15                  20

cct gca gga tac aag tcc cct ctt ctt tct aga agt ggt gcg gca gaa   211
Pro Ala Gly Tyr Lys Ser Pro Leu Leu Ser Arg Ser Gly Ala Ala Glu
            25                  30                  35

gcg cag ggc gct gct gct caa gca ggt act gaa ggt gtc gcg tgg cat   259
Ala Gln Gly Ala Ala Ala Gln Ala Gly Thr Glu Gly Val Ala Trp His
        40                  45                  50

tac ggt tcc cct ctc gtc gag caa cgc atc ttc gaa act ggc acg ggc   307
Tyr Gly Ser Pro Leu Val Glu Gln Arg Ile Phe Glu Thr Gly Thr Gly
    55                  60                  65

tta gtt gac cgt tct aat cgc aag gtg atc aaa gtc gaa ggg cct gat   355
Leu Val Asp Arg Ser Asn Arg Lys Val Ile Lys Val Glu Gly Pro Asp
70                  75                  80                  85

gcc ccc acg ttc ctc aat aat att ttg tcc caa aag gtt gat tcc gtt   403
Ala Pro Thr Phe Leu Asn Asn Ile Leu Ser Gln Lys Val Asp Ser Val
                90                  95                  100

gaa aac ggc ttt act gcc ggt gcc ctg gat ttg gat gcg cag ggt cgt   451
Glu Asn Gly Phe Thr Ala Gly Ala Leu Asp Leu Asp Ala Gln Gly Arg
            105                 110                 115

att caa cac aca atg cag gta act gtc gtc gat ggg gtt ttc tac ctc   499
Ile Gln His Thr Met Gln Val Thr Val Val Asp Gly Val Phe Tyr Leu
        120                 125                 130

gac acg tcc gcg gcg gag ttt gat acc ctc atc ggt ttc ttg acc aag   547
```

```
Asp Thr Ser Ala Ala Glu Phe Asp Thr Leu Ile Gly Phe Leu Thr Lys
    135                 140                 145

atg att ttc tgg tcg gaa gtc acc gtc cag gaa gcc gat ctg gcg atc   595
Met Ile Phe Trp Ser Glu Val Thr Val Gln Glu Ala Asp Leu Ala Ile
150                 155                 160                 165

atc act ctg ctc ggc cag gaa att gcc ctt ccg gac gcg gtc ttt gcc   643
Ile Thr Leu Leu Gly Gln Glu Ile Ala Leu Pro Asp Ala Val Phe Ala
                170                 175                 180

cgt agg gtc gat tgg aat ggg cca tcg cgt atc gac gtc gcc atc cgg   691
Arg Arg Val Asp Trp Asn Gly Pro Ser Arg Ile Asp Val Ala Ile Arg
            185                 190                 195

cgt gaa aac ctg gag gag ggc gtc gac aag ctc tta gaa gct ggc gca   739
Arg Glu Asn Leu Glu Glu Gly Val Asp Lys Leu Leu Glu Ala Gly Ala
        200                 205                 210

aag ctc acc ggt ctc atg gct tac acg gcc gag cgc gtg aag gcg ttg   787
Lys Leu Thr Gly Leu Met Ala Tyr Thr Ala Glu Arg Val Lys Ala Leu
    215                 220                 225

gag ccc gct gcg ggc gtg gat ttg gat gat aag acc att ccc cat gaa   835
Glu Pro Ala Ala Gly Val Asp Leu Asp Asp Lys Thr Ile Pro His Glu
230                 235                 240                 245

atc ccc cat tgg att ggc cgt ggc gaa cat tta ggc gct gtg cat ttg   883
Ile Pro His Trp Ile Gly Arg Gly Glu His Leu Gly Ala Val His Leu
                250                 255                 260

acc aag ggt tgc tac cgc ggg cag gaa act gtc gcg cgc gtt gat aat   931
Thr Lys Gly Cys Tyr Arg Gly Gln Glu Thr Val Ala Arg Val Asp Asn
            265                 270                 275

ctt ggg cgt tcc ccg cgc gtg ctg gtt ctg ctt cat ctt gac ggt tcc   979
Leu Gly Arg Ser Pro Arg Val Leu Val Leu Leu His Leu Asp Gly Ser
        280                 285                 290

gca ccg ctg gat cct gtg act ggc gct gaa atc aag gcc ggt gcg cgc   1027
Ala Pro Leu Asp Pro Val Thr Gly Ala Glu Ile Lys Ala Gly Ala Arg
    295                 300                 305

acc gtt ggt cgt ctg ggc acc gtt gtc cat gac gcc gat tac ggg ccg   1075
Thr Val Gly Arg Leu Gly Thr Val Val His Asp Ala Asp Tyr Gly Pro
310                 315                 320                 325

atc gct ctc ggg ctg gtt aag cgc agc gct ttg gat aaa gaa ctt cac   1123
Ile Ala Leu Gly Leu Val Lys Arg Ser Ala Leu Asp Lys Glu Leu His
                330                 335                 340

atc gat gat gtc tct gta aac gtc gac cgc gat ctg ctt cct gcg gag   1171
Ile Asp Asp Val Ser Val Asn Val Asp Arg Asp Leu Leu Pro Ala Glu
            345                 350                 355

gaa agt gaa caa cgc gga cgc gca gcg atc aat aag ctc aag ggt ctt   1219
Glu Ser Glu Gln Arg Gly Arg Ala Ala Ile Asn Lys Leu Lys Gly Leu
        360                 365                 370

taactaaaac gatttatagc gaa                                        1242
```

<210> 370
<211> 373
<212> PRT
<213> Corynebacterium glutamicum

<400> 370

```
Val Gly Thr Ile Glu Asp Val Ala Asn Glu Gln Ile Glu Val Ala Asn
  1               5                  10                  15

Asn Thr Asp Gln Ile Pro Ala Gly Tyr Lys Ser Pro Leu Leu Ser Arg
             20                  25                  30

Ser Gly Ala Ala Glu Ala Gln Gly Ala Ala Ala Gln Ala Gly Thr Glu
         35                  40                  45

Gly Val Ala Trp His Tyr Gly Ser Pro Leu Val Glu Gln Arg Ile Phe
     50                  55                  60

Glu Thr Gly Thr Gly Leu Val Asp Arg Ser Asn Arg Lys Val Ile Lys
 65                  70                  75                  80

Val Glu Gly Pro Asp Ala Pro Thr Phe Leu Asn Asn Ile Leu Ser Gln
                 85                  90                  95

Lys Val Asp Ser Val Glu Asn Gly Phe Thr Ala Gly Ala Leu Asp Leu
            100                 105                 110

Asp Ala Gln Gly Arg Ile Gln His Thr Met Gln Val Thr Val Val Asp
        115                 120                 125

Gly Val Phe Tyr Leu Asp Thr Ser Ala Ala Glu Phe Asp Thr Leu Ile
    130                 135                 140

Gly Phe Leu Thr Lys Met Ile Phe Trp Ser Glu Val Thr Val Gln Glu
145                 150                 155                 160

Ala Asp Leu Ala Ile Ile Thr Leu Leu Gly Gln Glu Ile Ala Leu Pro
                165                 170                 175

Asp Ala Val Phe Ala Arg Arg Val Asp Trp Asn Gly Pro Ser Arg Ile
            180                 185                 190

Asp Val Ala Ile Arg Arg Glu Asn Leu Glu Glu Gly Val Asp Lys Leu
        195                 200                 205

Leu Glu Ala Gly Ala Lys Leu Thr Gly Leu Met Ala Tyr Thr Ala Glu
    210                 215                 220

Arg Val Lys Ala Leu Glu Pro Ala Ala Gly Val Asp Leu Asp Asp Lys
225                 230                 235                 240

Thr Ile Pro His Glu Ile Pro His Trp Ile Gly Arg Gly Glu His Leu
                245                 250                 255

Gly Ala Val His Leu Thr Lys Gly Cys Tyr Arg Gly Gln Glu Thr Val
            260                 265                 270

Ala Arg Val Asp Asn Leu Gly Arg Ser Pro Arg Val Leu Val Leu Leu
        275                 280                 285
```

```
His Leu Asp Gly Ser Ala Pro Leu Asp Pro Val Thr Gly Ala Glu Ile
    290                 295                 300

Lys Ala Gly Ala Arg Thr Val Gly Arg Leu Gly Thr Val Val His Asp
305                 310                 315                 320

Ala Asp Tyr Gly Pro Ile Ala Leu Gly Leu Val Lys Arg Ser Ala Leu
                325                 330                 335

Asp Lys Glu Leu His Ile Asp Asp Val Ser Val Asn Val Asp Arg Asp
            340                 345                 350

Leu Leu Pro Ala Glu Glu Ser Glu Gln Arg Gly Arg Ala Ala Ile Asn
        355                 360                 365

Lys Leu Lys Gly Leu
    370
```

<210> 371
<211> 567
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(544)
<223> FRXA00768

<400> 371

```
gacgtcgcca tccggcgtga aaacctggag gagggcgtcg acaagctctt agaagctggc 60

gcaaagctca ccggtctcat ggcttacacg gcccgagcgc gtg aag gcg ttg gag   115
                                            Val Lys Ala Leu Glu
                                              1               5

ccc gct gcg ggc gtg gat ttg gat gat aag acc att ccc cat gaa atc   163
Pro Ala Ala Gly Val Asp Leu Asp Asp Lys Thr Ile Pro His Glu Ile
                10                  15                  20

ccc cat tgg att ggc cgt ggc gaa cat tta ggc gct gtg cat ttg acc   211
Pro His Trp Ile Gly Arg Gly Glu His Leu Gly Ala Val His Leu Thr
            25                  30                  35

aag ggt tgc tac cgc ggg cag gaa act gtc gcg cgc gtt gat aat ctt   259
Lys Gly Cys Tyr Arg Gly Gln Glu Thr Val Ala Arg Val Asp Asn Leu
        40                  45                  50

ggg cgt tcc ccg cgc gtg ctg gtt ctg ctt cat ctt gac ggt tcc gca   307
Gly Arg Ser Pro Arg Val Leu Val Leu Leu His Leu Asp Gly Ser Ala
    55                  60                  65

ccg ctg gat cct gtg act ggc gct gaa atc aag gcc ggt gcg cgc acc   355
Pro Leu Asp Pro Val Thr Gly Ala Glu Ile Lys Ala Gly Ala Arg Thr
70                  75                  80                  85

gtt ggt cgt ctg ggc acc gtt gtc cat gac gcc gat tac ggg ccg atc   403
Val Gly Arg Leu Gly Thr Val Val His Asp Ala Asp Tyr Gly Pro Ile
                90                  95                  100

gct ctc ggg ctg gtt aag cgc agc gct ttg gat aaa gaa ctt cac atc   451
```

```
Ala Leu Gly Leu Val Lys Arg Ser Ala Leu Asp Lys Glu Leu His Ile
            105                 110                 115

gat gat gtc tct gta aac gtc gac cgc gat ctg ctt cct gcg gag gaa   499
Asp Asp Val Ser Val Asn Val Asp Arg Asp Leu Leu Pro Ala Glu Glu
        120                 125                 130

agt gaa caa cgc gga cgc gca gcg atc aat aag ctc aag ggt ctt       544
Ser Glu Gln Arg Gly Arg Ala Ala Ile Asn Lys Leu Lys Gly Leu
    135                 140                 145

taactaaaac gatttatagc gaa                                        567


<210> 372
<211> 148
<212> PRT
<213> Corynebacterium glutamicum

<400> 372
Val Lys Ala Leu Glu Pro Ala Ala Gly Val Asp Leu Asp Asp Lys Thr
  1               5                  10                  15

Ile Pro His Glu Ile Pro His Trp Ile Gly Arg Gly Glu His Leu Gly
            20                  25                  30

Ala Val His Leu Thr Lys Gly Cys Tyr Arg Gly Gln Glu Thr Val Ala
         35                  40                  45

Arg Val Asp Asn Leu Gly Arg Ser Pro Arg Val Leu Val Leu Leu His
     50                  55                  60

Leu Asp Gly Ser Ala Pro Leu Asp Pro Val Thr Gly Ala Glu Ile Lys
 65                  70                  75                  80

Ala Gly Ala Arg Thr Val Gly Arg Leu Gly Thr Val Val His Asp Ala
                 85                  90                  95

Asp Tyr Gly Pro Ile Ala Leu Gly Leu Val Lys Arg Ser Ala Leu Asp
            100                 105                 110

Lys Glu Leu His Ile Asp Asp Val Ser Val Asn Val Asp Arg Asp Leu
        115                 120                 125

Leu Pro Ala Glu Glu Ser Glu Gln Arg Gly Arg Ala Ala Ile Asn Lys
    130                 135                 140

Leu Lys Gly Leu
145


<210> 373
<211> 837
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(814)
<223> FRXA00767
```

<400> 373
tcaagcgcca taacgcctga ttatgcacgg ttaaggcgca tctcgctcac tggtgctaac 60

cacttgcgct tttggaagga ataacccttc ctgtcagatt gtg ggt act atc gaa 115
Val Gly Thr Ile Glu
1 5

gac gtg gct aac gaa caa atc gag gtc gcg aac aac act gat cag att 163
Asp Val Ala Asn Glu Gln Ile Glu Val Ala Asn Asn Thr Asp Gln Ile
10 15 20

cct gca gga tac aag tcc cct ctt ctt tct aga agt ggt gcg gca gaa 211
Pro Ala Gly Tyr Lys Ser Pro Leu Leu Ser Arg Ser Gly Ala Ala Glu
25 30 35

gcg cag ggc gct gct gct caa gca ggt act gaa ggt gtc gcg tgg cat 259
Ala Gln Gly Ala Ala Ala Gln Ala Gly Thr Glu Gly Val Ala Trp His
40 45 50

tac ggt tcc cct ctc gtc gag caa cgc atc ttc gaa act ggc acg ggc 307
Tyr Gly Ser Pro Leu Val Glu Gln Arg Ile Phe Glu Thr Gly Thr Gly
55 60 65

tta gtt gac cgt tct aat cgc aag gtg atc aaa gtc gaa ggg cct gat 355
Leu Val Asp Arg Ser Asn Arg Lys Val Ile Lys Val Glu Gly Pro Asp
70 75 80 85

gcc ccc acg ttc ctc aat aat att ttg tcc caa aag gtt gat tcc gtt 403
Ala Pro Thr Phe Leu Asn Asn Ile Leu Ser Gln Lys Val Asp Ser Val
90 95 100

gaa aac ggc ttt act gcc ggt gcc ctg gat ttg gat gcg cag ggt cgt 451
Glu Asn Gly Phe Thr Ala Gly Ala Leu Asp Leu Asp Ala Gln Gly Arg
105 110 115

att caa cac aca atg cag gta act gtc gtc gat ggg gtt ttc tac ctc 499
Ile Gln His Thr Met Gln Val Thr Val Val Asp Gly Val Phe Tyr Leu
120 125 130

gac acg tcc gcg gcg gag ttt gat acc ctc atc ggt ttc ttg acc aag 547
Asp Thr Ser Ala Ala Glu Phe Asp Thr Leu Ile Gly Phe Leu Thr Lys
135 140 145

atg att ttc tgg tcg gaa gtc acc gtc cag gaa gcc gat ctg gcg atc 595
Met Ile Phe Trp Ser Glu Val Thr Val Gln Glu Ala Asp Leu Ala Ile
150 155 160 165

atc act ctg ctc ggc cag gaa att gcc ctt ccg gac gcg gtc ttt gcc 643
Ile Thr Leu Leu Gly Gln Glu Ile Ala Leu Pro Asp Ala Val Phe Ala
170 175 180

cgt agg gtc gat tgg aat ggg cca tcg cgt atc gac gtc gcc atc cgg 691
Arg Arg Val Asp Trp Asn Gly Pro Ser Arg Ile Asp Val Ala Ile Arg
185 190 195

cgt gaa aac ctg gag gag ggc gtc gac aag ctc tta gaa gct ggc gca 739
Arg Glu Asn Leu Glu Glu Gly Val Asp Lys Leu Leu Glu Ala Gly Ala
200 205 210

aag ctc acc ggt ctc atg gct tac acg gcc cga gcg cgt gaa ggc gtt 787
Lys Leu Thr Gly Leu Met Ala Tyr Thr Ala Arg Ala Arg Glu Gly Val

```
    215                 220                 225

gga gcc cgc tgc ggg cgt gga ttt gga tgataagacc attccccatg          834
Gly Ala Arg Cys Gly Arg Gly Phe Gly
230                 235

aaa                                                                837


<210> 374
<211> 238
<212> PRT
<213> Corynebacterium glutamicum

<400> 374
Val Gly Thr Ile Glu Asp Val Ala Asn Glu Gln Ile Glu Val Ala Asn
  1               5                  10                  15

Asn Thr Asp Gln Ile Pro Ala Gly Tyr Lys Ser Pro Leu Leu Ser Arg
             20                  25                  30

Ser Gly Ala Ala Glu Ala Gln Gly Ala Ala Ala Gln Ala Gly Thr Glu
         35                  40                  45

Gly Val Ala Trp His Tyr Gly Ser Pro Leu Val Glu Gln Arg Ile Phe
     50                  55                  60

Glu Thr Gly Thr Gly Leu Val Asp Arg Ser Asn Arg Lys Val Ile Lys
 65                  70                  75                  80

Val Glu Gly Pro Asp Ala Pro Thr Phe Leu Asn Asn Ile Leu Ser Gln
                 85                  90                  95

Lys Val Asp Ser Val Glu Asn Gly Phe Thr Ala Gly Ala Leu Asp Leu
            100                 105                 110

Asp Ala Gln Gly Arg Ile Gln His Thr Met Gln Val Thr Val Val Asp
        115                 120                 125

Gly Val Phe Tyr Leu Asp Thr Ser Ala Ala Glu Phe Asp Thr Leu Ile
    130                 135                 140

Gly Phe Leu Thr Lys Met Ile Phe Trp Ser Glu Val Thr Val Gln Glu
145                 150                 155                 160

Ala Asp Leu Ala Ile Ile Thr Leu Leu Gly Gln Glu Ile Ala Leu Pro
                165                 170                 175

Asp Ala Val Phe Ala Arg Arg Val Asp Trp Asn Gly Pro Ser Arg Ile
            180                 185                 190

Asp Val Ala Ile Arg Arg Glu Asn Leu Glu Glu Gly Val Asp Lys Leu
        195                 200                 205

Leu Glu Ala Gly Ala Lys Leu Thr Gly Leu Met Ala Tyr Thr Ala Arg
    210                 215                 220

Ala Arg Glu Gly Val Gly Ala Arg Cys Gly Arg Gly Phe Gly
225                 230                 235
```

<210> 375
<211> 336
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(313)
<223> RXN00769

<400> 375
ggctattgtg tctatcagga atacagttaa tacatcttga aaagcccatg ggccatccga 60

attcccagga tcggcccgct cactccaagg gggtcaggca atg ggt cgc ggt cgc 115
Met Gly Arg Gly Arg
1 5

gcg aag gca aaa cag acc aaa gtt gct cgc cag ttg aag tac agc tct 163
Ala Lys Ala Lys Gln Thr Lys Val Ala Arg Gln Leu Lys Tyr Ser Ser
10 15 20

cca gac atg gat ctc gat tcg ctg cag cgg gag ctg gct aac cag tct 211
Pro Asp Met Asp Leu Asp Ser Leu Gln Arg Glu Leu Ala Asn Gln Ser
25 30 35

cct agg cgt tcc tac tcc gat acc cct gat gat gag gac cag tac gca 259
Pro Arg Arg Ser Tyr Ser Asp Thr Pro Asp Asp Glu Asp Gln Tyr Ala
40 45 50

gag tat gcg gac tgg gat gag gac gac acc gac aat cgt gcc tac ggc 307
Glu Tyr Ala Asp Trp Asp Glu Asp Asp Thr Asp Asn Arg Ala Tyr Gly
55 60 65

aca aac tgatttcgtg tgtccttaac tct 336
Thr Asn
70

<210> 376
<211> 71
<212> PRT
<213> Corynebacterium glutamicum

<400> 376
Met Gly Arg Gly Arg Ala Lys Ala Lys Gln Thr Lys Val Ala Arg Gln
1 5 10 15

Leu Lys Tyr Ser Ser Pro Asp Met Asp Leu Asp Ser Leu Gln Arg Glu
20 25 30

Leu Ala Asn Gln Ser Pro Arg Arg Ser Tyr Ser Asp Thr Pro Asp Asp
35 40 45

Glu Asp Gln Tyr Ala Glu Tyr Ala Asp Trp Asp Glu Asp Asp Thr Asp
50 55 60

Asn Arg Ala Tyr Gly Thr Asn
65 70

<210> 377

<211> 336
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(313)
<223> FRXA00769

<400> 377
ggctattgtg tctatcagga atacagttaa tacatcttga aaagcccatg ggccatccga 60

attcccagga tcggcccgct cactccaagg gggtcaggca atg ggt cgc ggt cgc 115
Met Gly Arg Gly Arg
1 5

gcg aag gca aaa cag acc aaa gtt gct cgc cag ttg aag tac agc tct 163
Ala Lys Ala Lys Gln Thr Lys Val Ala Arg Gln Leu Lys Tyr Ser Ser
10 15 20

cca gac atg gat ctc gat tcg ctg cag cgg gag ctg gct aac cag tct 211
Pro Asp Met Asp Leu Asp Ser Leu Gln Arg Glu Leu Ala Asn Gln Ser
25 30 35

cct agg cgt tcc tac tcc gat acc cct gat gat gag gac cag tac gca 259
Pro Arg Arg Ser Tyr Ser Asp Thr Pro Asp Asp Glu Asp Gln Tyr Ala
40 45 50

gag tat gcg gac tgg gat gag gac gac acc gac aat cgt gcc tac ggc 307
Glu Tyr Ala Asp Trp Asp Glu Asp Asp Thr Asp Asn Arg Ala Tyr Gly
55 60 65

aca aac tgatttcgtg tgtccttaac tct 336
Thr Asn
70

<210> 378
<211> 71
<212> PRT
<213> Corynebacterium glutamicum

<400> 378
Met Gly Arg Gly Arg Ala Lys Ala Lys Gln Thr Lys Val Ala Arg Gln
1 5 10 15

Leu Lys Tyr Ser Ser Pro Asp Met Asp Leu Asp Ser Leu Gln Arg Glu
20 25 30

Leu Ala Asn Gln Ser Pro Arg Arg Ser Tyr Ser Asp Thr Pro Asp Asp
35 40 45

Glu Asp Gln Tyr Ala Glu Tyr Ala Asp Trp Asp Glu Asp Asp Thr Asp
50 55 60

Asn Arg Ala Tyr Gly Thr Asn
65 70

<210> 379
<211> 942

<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(919)
<223> RXN00771

<400> 379
```
tacccctgtt ttggagaatg ctccgagcca ggggtacttt tcttttcctc acacacagta 60

gctgctgaga aaaatgaaga ccttttgtta ggttgggagt atg acc aac cca tac   115
                                            Met Thr Asn Pro Tyr
                                              1               5

gag gcc ttc ata ccg ctc aag cat cgt acg ggg att gaa ccc gag cac   163
Glu Ala Phe Ile Pro Leu Lys His Arg Thr Gly Ile Glu Pro Glu His
                 10                  15                  20

acc ttt tgg gaa tgg gaa aac aaa agg gtt cac att gca agg aga cgt   211
Thr Phe Trp Glu Trp Glu Asn Lys Arg Val His Ile Ala Arg Arg Arg
             25                  30                  35

cga gaa gcg ccc gtc cgc gtt atc gtg gtg cat ggg cta ggc acc cat   259
Arg Glu Ala Pro Val Arg Val Ile Val Val His Gly Leu Gly Thr His
         40                  45                  50

agt ggc gcc ctc tgg ccc ctc gtc gcg gcc att gag ggc gcg gac ctc   307
Ser Gly Ala Leu Trp Pro Leu Val Ala Ala Ile Glu Gly Ala Asp Leu
     55                  60                  65

gcc gcg atc gac ctg cct aaa act ccg ctt tac gac gat tgg ctg cgc   355
Ala Ala Ile Asp Leu Pro Lys Thr Pro Leu Tyr Asp Asp Trp Leu Arg
 70                  75                  80                  85

ctt tta gaa tct ttc atc tcg tcc gaa gac gac ggt cgg cca ctc atc   403
Leu Leu Glu Ser Phe Ile Ser Ser Glu Asp Asp Gly Arg Pro Leu Ile
                 90                  95                 100

ctg atc ggt gca ggc acc gga ggc ttg ctt tgc gca gaa gct gca cac   451
Leu Ile Gly Ala Gly Thr Gly Gly Leu Leu Cys Ala Glu Ala Ala His
            105                 110                 115

cgc aca gga ctg gtc gca cac gtc att gcc acc tgc ctg ctc aac ccc   499
Arg Thr Gly Leu Val Ala His Val Ile Ala Thr Cys Leu Leu Asn Pro
        120                 125                 130

tcc gac cag ccg acg cgc cgg gca ctg ttc agg ttt tca ccg ctg act   547
Ser Asp Gln Pro Thr Arg Arg Ala Leu Phe Arg Phe Ser Pro Leu Thr
    135                 140                 145

cgg ttg atc caa ggc cgc ttg cgc aac cgc gaa att ccc gtg acc aga   595
Arg Leu Ile Gln Gly Arg Leu Arg Asn Arg Glu Ile Pro Val Thr Arg
150                 155                 160                 165

gtg ttg aac ttc agc aaa atc agc cgc agc cca gcc ctg agc aaa ttg   643
Val Leu Asn Phe Ser Lys Ile Ser Arg Ser Pro Ala Leu Ser Lys Leu
                170                 175                 180

tgc gcg gcc gat gaa ttt agc gga gca tcc aaa ata acc tgg ggt ttc   691
Cys Ala Ala Asp Glu Phe Ser Gly Ala Ser Lys Ile Thr Trp Gly Phe
```

```
            185                 190                 195

ctc gcg tca tat gtg caa cac aag gcc aaa ctg ggt gca gtt ccc gtc   739
Leu Ala Ser Tyr Val Gln His Lys Ala Lys Leu Gly Ala Val Pro Val
        200                 205                 210

act ctg atg cac cct gac cac gac ctt ctg act ccc gtt gag ctc agt   787
Thr Leu Met His Pro Asp His Asp Leu Leu Thr Pro Val Glu Leu Ser
    215                 220                 225

ctg cgt acg ctt tcg cgc ctc aaa gcg ccc act gac gtg gtt atg ctc   835
Leu Arg Thr Leu Ser Arg Leu Lys Ala Pro Thr Asp Val Val Met Leu
230                 235                 240                 245

aag gac tgc ggg cat ttt ccc atc gaa gaa ccc ggc ttc acc acc atg   883
Lys Asp Cys Gly His Phe Pro Ile Glu Glu Pro Gly Phe Thr Thr Met
                250                 255                 260

ctc gaa acc gtc aca tca gtt atc gcg cgg aat agt tagcgggcgc        929
Leu Glu Thr Val Thr Ser Val Ile Ala Arg Asn Ser
            265                 270

atgtggttgg gat                                                   942


<210> 380
<211> 273
<212> PRT
<213> Corynebacterium glutamicum

<400> 380
Met Thr Asn Pro Tyr Glu Ala Phe Ile Pro Leu Lys His Arg Thr Gly
  1               5                  10                  15

Ile Glu Pro Glu His Thr Phe Trp Glu Trp Glu Asn Lys Arg Val His
             20                  25                  30

Ile Ala Arg Arg Arg Arg Glu Ala Pro Val Arg Val Ile Val Val His
         35                  40                  45

Gly Leu Gly Thr His Ser Gly Ala Leu Trp Pro Leu Val Ala Ala Ile
     50                  55                  60

Glu Gly Ala Asp Leu Ala Ala Ile Asp Leu Pro Lys Thr Pro Leu Tyr
 65                  70                  75                  80

Asp Asp Trp Leu Arg Leu Leu Glu Ser Phe Ile Ser Ser Glu Asp Asp
                85                  90                  95

Gly Arg Pro Leu Ile Leu Ile Gly Ala Gly Thr Gly Gly Leu Leu Cys
            100                 105                 110

Ala Glu Ala Ala His Arg Thr Gly Leu Val Ala His Val Ile Ala Thr
        115                 120                 125

Cys Leu Leu Asn Pro Ser Asp Gln Pro Thr Arg Arg Ala Leu Phe Arg
    130                 135                 140

Phe Ser Pro Leu Thr Arg Leu Ile Gln Gly Arg Leu Arg Asn Arg Glu
145                 150                 155                 160
```

```
Ile Pro Val Thr Arg Val Leu Asn Phe Ser Lys Ile Ser Arg Ser Pro
                165                 170                 175

Ala Leu Ser Lys Leu Cys Ala Ala Asp Glu Phe Ser Gly Ala Ser Lys
            180                 185                 190

Ile Thr Trp Gly Phe Leu Ala Ser Tyr Val Gln His Lys Ala Lys Leu
        195                 200                 205

Gly Ala Val Pro Val Thr Leu Met His Pro Asp His Asp Leu Leu Thr
    210                 215                 220

Pro Val Glu Leu Ser Leu Arg Thr Leu Ser Arg Leu Lys Ala Pro Thr
225                 230                 235                 240

Asp Val Val Met Leu Lys Asp Cys Gly His Phe Pro Ile Glu Glu Pro
                245                 250                 255

Gly Phe Thr Thr Met Leu Glu Thr Val Thr Ser Val Ile Ala Arg Asn
            260                 265                 270

Ser
```

Sequence Listing Free Text

<210> 381
<211> 801
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(778)
<223> FRXA00771

<400> 381

```
tacccctgtt ttggagaatg ctccgagcca ggggtacttt tcttttcctc acacacagta 60

gctgctgaga aaaatgaaga ccttttgtta ggttgggagt atg acc aac cca tac   115
                                              Met Thr Asn Pro Tyr
                                                1               5

gag gcc ttc ata ccg ctc aag cat cgt acg ggg att gaa ccc gag cac   163
Glu Ala Phe Ile Pro Leu Lys His Arg Thr Gly Ile Glu Pro Glu His
                10                  15                  20

acc ttt tgg gaa tgg gaa aac aaa agg gtt cac att gca agg aga cgt   211
Thr Phe Trp Glu Trp Glu Asn Lys Arg Val His Ile Ala Arg Arg Arg
            25                  30                  35

cga gaa gcg ccc gtc cgc gtt atc gtg gtg cat ggg cta ggc acc cat   259
Arg Glu Ala Pro Val Arg Val Ile Val Val His Gly Leu Gly Thr His
        40                  45                  50

agt ggc gcc ctc tgg ccc ctc gtc gcg gcc att gag ggc gcg gac ctc   307
Ser Gly Ala Leu Trp Pro Leu Val Ala Ala Ile Glu Gly Ala Asp Leu
    55                  60                  65

gcc gcg atc gac ctg cct aaa act ccg ctt tac gac gat tgg ctg cgc   355
Ala Ala Ile Asp Leu Pro Lys Thr Pro Leu Tyr Asp Asp Trp Leu Arg
70                  75                  80                  85
```

```
ctt tta gaa tct ttc atc tcg tcc gaa gac gac ggt cgg cca ctc atc   403
Leu Leu Glu Ser Phe Ile Ser Ser Glu Asp Asp Gly Arg Pro Leu Ile
                 90                  95                 100

ctg atc ggt gca ggc acc gga ggc ttg ctt tgc gca gaa gct gca cac   451
Leu Ile Gly Ala Gly Thr Gly Gly Leu Leu Cys Ala Glu Ala Ala His
            105                 110                 115

cgc aca gga ctg gtc gca cac gtc att gcc acc tgc ctg ctc aac ccc   499
Arg Thr Gly Leu Val Ala His Val Ile Ala Thr Cys Leu Leu Asn Pro
        120                 125                 130

tcc gac cag ccg acg cgc cgg gca ctg ttc agg ttt tca ccg ctg act   547
Ser Asp Gln Pro Thr Arg Arg Ala Leu Phe Arg Phe Ser Pro Leu Thr
    135                 140                 145

cgg ttg atc caa ggc cgc ttg cgc aac cgc gaa att ccc gtg acc aga   595
Arg Leu Ile Gln Gly Arg Leu Arg Asn Arg Glu Ile Pro Val Thr Arg
150                 155                 160                 165

gtg ttg aac ttc agc aaa atc agc cgc agc cca gcc ctg agc aaa ttg   643
Val Leu Asn Phe Ser Lys Ile Ser Arg Ser Pro Ala Leu Ser Lys Leu
                170                 175                 180

tgc gcg gcc gat gaa ttt aac gga gca ttc aaa ata acc tgg ggt ttc   691
Cys Ala Ala Asp Glu Phe Asn Gly Ala Phe Lys Ile Thr Trp Gly Phe
            185                 190                 195

ctc gcg tca tat gtg caa cac aag gcc aaa ctg ggt gca gtt ccc ctc   739
Leu Ala Ser Tyr Val Gln His Lys Ala Lys Leu Gly Ala Val Pro Leu
        200                 205                 210

act ctg atg cac cct gac cac gac ctt ttt gac tcc cgt tgagctcaaa    788
Thr Leu Met His Pro Asp His Asp Leu Phe Asp Ser Arg
    215                 220                 225

tctgcgtacg ctt                                                   801


<210> 382
<211> 226
<212> PRT
<213> Corynebacterium glutamicum

<400> 382
Met Thr Asn Pro Tyr Glu Ala Phe Ile Pro Leu Lys His Arg Thr Gly
  1               5                  10                  15

Ile Glu Pro Glu His Thr Phe Trp Glu Trp Glu Asn Lys Arg Val His
             20                  25                  30

Ile Ala Arg Arg Arg Arg Glu Ala Pro Val Arg Val Ile Val Val His
         35                  40                  45

Gly Leu Gly Thr His Ser Gly Ala Leu Trp Pro Leu Val Ala Ala Ile
     50                  55                  60

Glu Gly Ala Asp Leu Ala Ala Ile Asp Leu Pro Lys Thr Pro Leu Tyr
 65                  70                  75                  80
```

```
Asp Asp Trp Leu Arg Leu Leu Glu Ser Phe Ile Ser Ser Glu Asp Asp
                85                  90                  95

Gly Arg Pro Leu Ile Leu Ile Gly Ala Gly Thr Gly Gly Leu Leu Cys
            100                 105                 110

Ala Glu Ala Ala His Arg Thr Gly Leu Val Ala His Val Ile Ala Thr
        115                 120                 125

Cys Leu Leu Asn Pro Ser Asp Gln Pro Thr Arg Arg Ala Leu Phe Arg
    130                 135                 140

Phe Ser Pro Leu Thr Arg Leu Ile Gln Gly Arg Leu Arg Asn Arg Glu
145                 150                 155                 160

Ile Pro Val Thr Arg Val Leu Asn Phe Ser Lys Ile Ser Arg Ser Pro
                165                 170                 175

Ala Leu Ser Lys Leu Cys Ala Ala Asp Glu Phe Asn Gly Ala Phe Lys
            180                 185                 190

Ile Thr Trp Gly Phe Leu Ala Ser Tyr Val Gln His Lys Ala Lys Leu
        195                 200                 205

Gly Ala Val Pro Leu Thr Leu Met His Pro Asp His Asp Leu Phe Asp
    210                 215                 220

Ser Arg
225
```

[illegible]

<210> 383
<211> 680
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(657)
<223> RXN00785

<400> 383

```
atc atc gct act ctc ggt gtg acc ttg ctg gtt gag gcc cgc gga tta   48
Ile Ile Ala Thr Leu Gly Val Thr Leu Leu Val Glu Ala Arg Gly Leu
  1               5                  10                  15

ttc ttg acg gtt gcg tcc att ccc att ctg ttt ggt att ttc aca cca   96
Phe Leu Thr Val Ala Ser Ile Pro Ile Leu Phe Gly Ile Phe Thr Pro
             20                  25                  30

ctg act tcg tgg ttt gtg tcc caa caa ggc gtg gct gcg aat gtg tcc   144
Leu Thr Ser Trp Phe Val Ser Gln Gln Gly Val Ala Ala Asn Val Ser
         35                  40                  45

cct ggt gtt tcc gtc acg gaa atc ctc acg gct gtt tat cct ttg gcg   192
Pro Gly Val Ser Val Thr Glu Ile Leu Thr Ala Val Tyr Pro Leu Ala
     50                  55                  60

cag ttg ttc ccc acc ctg atc atg gtc act ttg gtg gcg gca ttg atc   240
Gln Leu Phe Pro Thr Leu Ile Met Val Thr Leu Val Ala Ala Leu Ile
 65                  70                  75                  80
```

```
gct gtg gtg cgg att att ctg ctg cgc agg aac cag gaa tct cgt cag   288
Ala Val Val Arg Ile Ile Leu Leu Arg Arg Asn Gln Glu Ser Arg Gln
                 85                  90                  95

gtt tct ggg gaa ctt acc cgg cgc gcg cag cgt gag gct gag gaa gct   336
Val Ser Gly Glu Leu Thr Arg Arg Ala Gln Arg Glu Ala Glu Glu Ala
            100                 105                 110

aat cag aat gct gct cgt cgt gct cgc gca cag agc acg agg gta caa   384
Asn Gln Asn Ala Ala Arg Arg Ala Arg Ala Gln Ser Thr Arg Val Gln
        115                 120                 125

agt tct aaa aca cgt aac cgt cgc gcg caa cca acc ggc gat acc ggt   432
Ser Ser Lys Thr Arg Asn Arg Arg Ala Gln Pro Thr Gly Asp Thr Gly
    130                 135                 140

tca caa gtc acg gtt gat gag ttg atc agg cgt agc cag gag cgc cgg   480
Ser Gln Val Thr Val Asp Glu Leu Ile Arg Arg Ser Gln Glu Arg Arg
145                 150                 155                 160

caa act gtt gcg cag cgc caa act gag cgc ggt gtg ccg ttt act cca   528
Gln Thr Val Ala Gln Arg Gln Thr Glu Arg Gly Val Pro Phe Thr Pro
                165                 170                 175

act ccg ggt cct gtg gtg gcc ccc aag ccg cgc ccg agc gcc cct gag   576
Thr Pro Gly Pro Val Val Ala Pro Lys Pro Arg Pro Ser Ala Pro Glu
            180                 185                 190

gcg ccg gct cct acg gat gtg ggt gag cgt cga caa gca gcc cct aaa   624
Ala Pro Ala Pro Thr Asp Val Gly Glu Arg Arg Gln Ala Ala Pro Lys
        195                 200                 205

cgc cgc acc tcg ctc gac gat gat ctg tac agc taaaaaatcc ccgctcatgt 677
Arg Arg Thr Ser Leu Asp Asp Asp Leu Tyr Ser
    210                 215

ggc                                                               680
```

<210> 384
<211> 219
<212> PRT
<213> Corynebacterium glutamicum

<400> 384

```
Ile Ile Ala Thr Leu Gly Val Thr Leu Leu Val Glu Ala Arg Gly Leu
  1               5                  10                  15

Phe Leu Thr Val Ala Ser Ile Pro Ile Leu Phe Gly Ile Phe Thr Pro
             20                  25                  30

Leu Thr Ser Trp Phe Val Ser Gln Gln Gly Val Ala Ala Asn Val Ser
         35                  40                  45

Pro Gly Val Ser Val Thr Glu Ile Leu Thr Ala Val Tyr Pro Leu Ala
     50                  55                  60

Gln Leu Phe Pro Thr Leu Ile Met Val Thr Leu Val Ala Ala Leu Ile
 65                  70                  75                  80
```

```
Ala Val Val Arg Ile Ile Leu Leu Arg Arg Asn Gln Glu Ser Arg Gln
                85                  90                  95

Val Ser Gly Glu Leu Thr Arg Arg Ala Gln Arg Glu Ala Glu Glu Ala
            100                 105                 110

Asn Gln Asn Ala Ala Arg Arg Ala Arg Ala Gln Ser Thr Arg Val Gln
        115                 120                 125

Ser Ser Lys Thr Arg Asn Arg Arg Ala Gln Pro Thr Gly Asp Thr Gly
    130                 135                 140

Ser Gln Val Thr Val Asp Glu Leu Ile Arg Arg Ser Gln Glu Arg Arg
145                 150                 155                 160

Gln Thr Val Ala Gln Arg Gln Thr Glu Arg Gly Val Pro Phe Thr Pro
                165                 170                 175

Thr Pro Gly Pro Val Val Ala Pro Lys Pro Arg Pro Ser Ala Pro Glu
            180                 185                 190

Ala Pro Ala Pro Thr Asp Val Gly Glu Arg Arg Gln Ala Ala Pro Lys
        195                 200                 205

Arg Arg Thr Ser Leu Asp Asp Asp Leu Tyr Ser
    210                 215


<210> 385
<211> 621
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(621)
<223> FRXA00785

<400> 385
atc atc gct act ctc ggt gtg acc ttg ctg gtt gag gcc cgc gga tta   48
Ile Ile Ala Thr Leu Gly Val Thr Leu Leu Val Glu Ala Arg Gly Leu
  1               5                  10                  15

ttc ttg acg gtt gcg tcc att ccc att ctg ttt ggt att ttc aca cca   96
Phe Leu Thr Val Ala Ser Ile Pro Ile Leu Phe Gly Ile Phe Thr Pro
             20                  25                  30

ctg act tcg tgg ttt gtg tcc caa caa ggc gtg gct gcg aat gtg tcc   144
Leu Thr Ser Trp Phe Val Ser Gln Gln Gly Val Ala Ala Asn Val Ser
         35                  40                  45

cct ggt gtt tcc gtc acg gaa atc ctc acg gct gtt tat cct ttg gcg   192
Pro Gly Val Ser Val Thr Glu Ile Leu Thr Ala Val Tyr Pro Leu Ala
     50                  55                  60

cag ttg ttc ccc acc ctg atc atg gtc act ttg gtg gcg gca ttg atc   240
Gln Leu Phe Pro Thr Leu Ile Met Val Thr Leu Val Ala Ala Leu Ile
 65                  70                  75                  80

gct gtg gtg cgg att att ctg ctg cgc agg aac cag gaa tct cgt cag   288
Ala Val Val Arg Ile Ile Leu Leu Arg Arg Asn Gln Glu Ser Arg Gln
```

```
                85                  90                  95

gtt tct ggg gaa ctt acc cgg cgc gcg cag cgt gag gct gag gaa gct   336
Val Ser Gly Glu Leu Thr Arg Arg Ala Gln Arg Glu Ala Glu Glu Ala
            100                 105                 110

aat cag aat gct gct cgt cgt gct cgc gca cag agc acg agg gta caa   384
Asn Gln Asn Ala Ala Arg Arg Ala Arg Ala Gln Ser Thr Arg Val Gln
        115                 120                 125

agt tct aaa aca cgt aac cgt cgc gcg caa cca acc ggc gat acc ggt   432
Ser Ser Lys Thr Arg Asn Arg Arg Ala Gln Pro Thr Gly Asp Thr Gly
    130                 135                 140

tca caa gtc acg gtt gat gag ttg atc agg cgt agc cag gag cgc cgg   480
Ser Gln Val Thr Val Asp Glu Leu Ile Arg Arg Ser Gln Glu Arg Arg
145                 150                 155                 160

caa act gtt gcg cag cgc caa act gag cgc ggt gtg ccg ttt act cca   528
Gln Thr Val Ala Gln Arg Gln Thr Glu Arg Gly Val Pro Phe Thr Pro
                165                 170                 175

act ccg ggt cct gtg gtg gcc ccc aag ccg cgc ccg agc gcc cct gag   576
Thr Pro Gly Pro Val Val Ala Pro Lys Pro Arg Pro Ser Ala Pro Glu
            180                 185                 190

gcg ccg gct cct acg gat gtg ggt gag cgt cga caa gca gcc cct       621
Ala Pro Ala Pro Thr Asp Val Gly Glu Arg Arg Gln Ala Ala Pro
        195                 200                 205


<210> 386
<211> 207
<212> PRT
<213> Corynebacterium glutamicum

<400> 386
Ile Ile Ala Thr Leu Gly Val Thr Leu Leu Val Glu Ala Arg Gly Leu
  1               5                  10                  15

Phe Leu Thr Val Ala Ser Ile Pro Ile Leu Phe Gly Ile Phe Thr Pro
             20                  25                  30

Leu Thr Ser Trp Phe Val Ser Gln Gln Gly Val Ala Ala Asn Val Ser
         35                  40                  45

Pro Gly Val Ser Val Thr Glu Ile Leu Thr Ala Val Tyr Pro Leu Ala
     50                  55                  60

Gln Leu Phe Pro Thr Leu Ile Met Val Thr Leu Val Ala Ala Leu Ile
 65                  70                  75                  80

Ala Val Val Arg Ile Ile Leu Leu Arg Arg Asn Gln Glu Ser Arg Gln
                 85                  90                  95

Val Ser Gly Glu Leu Thr Arg Arg Ala Gln Arg Glu Ala Glu Glu Ala
            100                 105                 110

Asn Gln Asn Ala Ala Arg Arg Ala Arg Ala Gln Ser Thr Arg Val Gln
        115                 120                 125
```

```
Ser Ser Lys Thr Arg Asn Arg Arg Ala Gln Pro Thr Gly Asp Thr Gly
    130                 135                 140

Ser Gln Val Thr Val Asp Glu Leu Ile Arg Arg Ser Gln Glu Arg Arg
145                 150                 155                 160

Gln Thr Val Ala Gln Arg Gln Thr Glu Arg Gly Val Pro Phe Thr Pro
                165                 170                 175

Thr Pro Gly Pro Val Val Ala Pro Lys Pro Arg Pro Ser Ala Pro Glu
            180                 185                 190

Ala Pro Ala Pro Thr Asp Val Gly Glu Arg Arg Gln Ala Ala Pro
        195                 200                 205


<210> 387
<211> 651
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(628)
<223> RXN00795

<400> 387
tttggattct ggacacccaa aaggggttt cgtaccaaac tcgtgacata ctaggcgggt 60

ggctgagaaa cgaccgaaaa tttttgatgg cagtcgagac atg att atc tcg ttg   115
                                            Met Ile Ile Ser Leu
                                              1               5

gta gtc tcc gcg atc atc atg ttg gta gcg gtg gga ttc acg gga atg   163
Val Val Ser Ala Ile Ile Met Leu Val Ala Val Gly Phe Thr Gly Met
                 10                  15                  20

tgt tct ttc aat aca gga tcc cct gaa aat ggg cag gta cct gaa gtt   211
Cys Ser Phe Asn Thr Gly Ser Pro Glu Asn Gly Gln Val Pro Glu Val
             25                  30                  35

gat gct tcc act ttt atg tca atg gaa gcg cgc gca atg act gat cat   259
Asp Ala Ser Thr Phe Met Ser Met Glu Ala Arg Ala Met Thr Asp His
         40                  45                  50

gca act agg ttg ccg gaa act cct gaa ggc tgg acc aca aat tca gct   307
Ala Thr Arg Leu Pro Glu Thr Pro Glu Gly Trp Thr Thr Asn Ser Ala
     55                  60                  65

cga cgc acc atg gtg gat gac acc ccg gca tct gta gtt gga tat gtc   355
Arg Arg Thr Met Val Asp Asp Thr Pro Ala Ser Val Val Gly Tyr Val
 70                  75                  80                  85

acc gca gat gag ggc tat att cag ctc act caa act ggt gaa acc gtt   403
Thr Ala Asp Glu Gly Tyr Ile Gln Leu Thr Gln Thr Gly Glu Thr Val
                 90                  95                 100

gag gat gct gtg gct ggt tat gat act cgc tgg cgt gat ctt tct gag   451
Glu Asp Ala Val Ala Gly Tyr Asp Thr Arg Trp Arg Asp Leu Ser Glu
            105                 110                 115
```

```
tct tat gat ctt gat ggc cac gac gtg gga att tac acc tca cag gaa   499
Ser Tyr Asp Leu Asp Gly His Asp Val Gly Ile Tyr Thr Ser Gln Glu
        120                 125                 130

tct gat gtg cgt gat ctg cgt gtg atg gat ctg ggc gat gcc cgc gtc   547
Ser Asp Val Arg Asp Leu Arg Val Met Asp Leu Gly Asp Ala Arg Val
    135                 140                 145

atg gtc tcg ggt gct gct acc gat gaa gaa ttc aat gat ctg ctt cgc   595
Met Val Ser Gly Ala Ala Thr Asp Glu Glu Phe Asn Asp Leu Leu Arg
150                 155                 160                 165

gca gtt gcg aat tcg gag cca ctg cct acc aat taagaattgg tcgaaccacc 648
Ala Val Ala Asn Ser Glu Pro Leu Pro Thr Asn
                170                 175

aaa                                                              651


<210> 388
<211> 176
<212> PRT
<213> Corynebacterium glutamicum

<400> 388
Met Ile Ile Ser Leu Val Val Ser Ala Ile Ile Met Leu Val Ala Val
  1               5                  10                  15

Gly Phe Thr Gly Met Cys Ser Phe Asn Thr Gly Ser Pro Glu Asn Gly
             20                  25                  30

Gln Val Pro Glu Val Asp Ala Ser Thr Phe Met Ser Met Glu Ala Arg
         35                  40                  45

Ala Met Thr Asp His Ala Thr Arg Leu Pro Glu Thr Pro Glu Gly Trp
     50                  55                  60

Thr Thr Asn Ser Ala Arg Arg Thr Met Val Asp Asp Thr Pro Ala Ser
 65                  70                  75                  80

Val Val Gly Tyr Val Thr Ala Asp Glu Gly Tyr Ile Gln Leu Thr Gln
                 85                  90                  95

Thr Gly Glu Thr Val Glu Asp Ala Val Ala Gly Tyr Asp Thr Arg Trp
            100                 105                 110

Arg Asp Leu Ser Glu Ser Tyr Asp Leu Asp Gly His Asp Val Gly Ile
        115                 120                 125

Tyr Thr Ser Gln Glu Ser Asp Val Arg Asp Leu Arg Val Met Asp Leu
    130                 135                 140

Gly Asp Ala Arg Val Met Val Ser Gly Ala Ala Thr Asp Glu Glu Phe
145                 150                 155                 160

Asn Asp Leu Leu Arg Ala Val Ala Asn Ser Glu Pro Leu Pro Thr Asn
                165                 170                 175
```

<210> 389
<211> 651
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(628)
<223> FRXA00795

<400> 389
tttggattct ggacacccaa aaggggttt cgtaccaaac tcgtgacata ctaggcgggt 60

ggctgagaaa cgaccgaaaa tttttgatgg cagtcgagac atg att atc tcg ttg 115
Met Ile Ile Ser Leu
1 5

gta gtc tcc gcg atc atc atg ttg gta gcg gtg gga ttc acg gga atg 163
Val Val Ser Ala Ile Ile Met Leu Val Ala Val Gly Phe Thr Gly Met
10 15 20

tgt tct ttc aat aca gga tcc cct gaa aat ggg cag gta cct gaa gtt 211
Cys Ser Phe Asn Thr Gly Ser Pro Glu Asn Gly Gln Val Pro Glu Val
25 30 35

gat gct tcc act ttt atg tca atg gaa gcg cgc gca atg act gat cat 259
Asp Ala Ser Thr Phe Met Ser Met Glu Ala Arg Ala Met Thr Asp His
40 45 50

gca act agg ttg ccg gaa act cct gaa ggc tgg acc aca aat tca gct 307
Ala Thr Arg Leu Pro Glu Thr Pro Glu Gly Trp Thr Thr Asn Ser Ala
55 60 65

cga cgc acc atg gtg gat gac acc ccg gca tct gta gtt gga tat gtc 355
Arg Arg Thr Met Val Asp Asp Thr Pro Ala Ser Val Val Gly Tyr Val
70 75 80 85

acc gca gat gag ggc tat att cag ctc act caa act ggt gaa acc gtt 403
Thr Ala Asp Glu Gly Tyr Ile Gln Leu Thr Gln Thr Gly Glu Thr Val
90 95 100

gag gat gct gtg gct ggt tat gat act cgc tgg cgt gat ctt tct gag 451
Glu Asp Ala Val Ala Gly Tyr Asp Thr Arg Trp Arg Asp Leu Ser Glu
105 110 115

tct tat gat ctt gat ggc cac gac gtg gga att tac acc tca cag gaa 499
Ser Tyr Asp Leu Asp Gly His Asp Val Gly Ile Tyr Thr Ser Gln Glu
120 125 130

tct gat gtg cgt gat ctg cgt gtg atg gat ctg ggc gat gcc cgc gtc 547
Ser Asp Val Arg Asp Leu Arg Val Met Asp Leu Gly Asp Ala Arg Val
135 140 145

atg gtc tcg ggt gct gct acc gat gaa gaa ttc aat gat ctg ctt cgc 595
Met Val Ser Gly Ala Ala Thr Asp Glu Glu Phe Asn Asp Leu Leu Arg
150 155 160 165

gca gtt gcg aat tcg gag cca ctg cct acc aat taagaattgg tcgaaccacc 648
Ala Val Ala Asn Ser Glu Pro Leu Pro Thr Asn
170 175

aaa 651

<210> 390
<211> 176
<212> PRT
<213> Corynebacterium glutamicum

<400> 390

```
Met Ile Ile Ser Leu Val Val Ser Ala Ile Ile Met Leu Val Ala Val
  1               5                  10                  15

Gly Phe Thr Gly Met Cys Ser Phe Asn Thr Gly Ser Pro Glu Asn Gly
             20                  25                  30

Gln Val Pro Glu Val Asp Ala Ser Thr Phe Met Ser Met Glu Ala Arg
         35                  40                  45

Ala Met Thr Asp His Ala Thr Arg Leu Pro Glu Thr Pro Glu Gly Trp
     50                  55                  60

Thr Thr Asn Ser Ala Arg Arg Thr Met Val Asp Asp Thr Pro Ala Ser
 65                  70                  75                  80

Val Val Gly Tyr Val Thr Ala Asp Glu Gly Tyr Ile Gln Leu Thr Gln
                 85                  90                  95

Thr Gly Glu Thr Val Glu Asp Ala Val Ala Gly Tyr Asp Thr Arg Trp
            100                 105                 110

Arg Asp Leu Ser Glu Ser Tyr Asp Leu Asp Gly His Asp Val Gly Ile
        115                 120                 125

Tyr Thr Ser Gln Glu Ser Asp Val Arg Asp Leu Arg Val Met Asp Leu
    130                 135                 140

Gly Asp Ala Arg Val Met Val Ser Gly Ala Ala Thr Asp Glu Glu Phe
145                 150                 155                 160

Asn Asp Leu Leu Arg Ala Val Ala Asn Ser Glu Pro Leu Pro Thr Asn
                165                 170                 175
```

<210> 391
<211> 825
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(802)
<223> RXN00831

<400> 391

```
agctccaaga aagtcagtgc tgtgcatggc tcggtgctgc tcatgctttt cggtgtttac 60

atgatgagca tgttcgcctg atttaggtag cctggtggga atg agt gca ctt gag   115
```

```
                                                    Met Ser Ala Leu Glu
                                                      1               5

aca ttg caa tgg cag gac tgg tca agc gtc tta att gtg gta gct cac   163
Thr Leu Gln Trp Gln Asp Trp Ser Ser Val Leu Ile Val Val Ala His
                  10                  15                  20

cca gat gat ccg gag tat ggg ctt tcc gcg gct gtt aaa gaa tgg aca   211
Pro Asp Asp Pro Glu Tyr Gly Leu Ser Ala Ala Val Lys Glu Trp Thr
              25                  30                  35

gac gcc ggg gtg gag gtg tct tac ctg ctg ctc acc cac ggg gag gca   259
Asp Ala Gly Val Glu Val Ser Tyr Leu Leu Leu Thr His Gly Glu Ala
          40                  45                  50

ggt atc caa ggt tta gac cct aaa gaa acc ggg tca ttg cgc gca gcg   307
Gly Ile Gln Gly Leu Asp Pro Lys Glu Thr Gly Ser Leu Arg Ala Ala
      55                  60                  65

gaa cag cgg gct gca tgt gat gtg gta gga gtt aga aat ctc acc att   355
Glu Gln Arg Ala Ala Cys Asp Val Val Gly Val Arg Asn Leu Thr Ile
  70                  75                  80                  85

ttg aat cac cca gat tcc atg ttg gtg tac aat ctg gta ctg cgc aaa   403
Leu Asn His Pro Asp Ser Met Leu Val Tyr Asn Leu Val Leu Arg Lys
                  90                  95                 100

gat att gct cgg gaa atc cgg atc cgt aaa cca aat gct gtg gtg gta   451
Asp Ile Ala Arg Glu Ile Arg Ile Arg Lys Pro Asn Ala Val Val Val
              105                 110                 115

tcc aat ttt gat gta gag gcc tac ggt ggt ttg aac cag gcg gat cac   499
Ser Asn Phe Asp Val Glu Ala Tyr Gly Gly Leu Asn Gln Ala Asp His
          120                 125                 130

cgc gtg gcg gga tta gcc gca att gat gcg acc cgc gat gcc gct aat   547
Arg Val Ala Gly Leu Ala Ala Ile Asp Ala Thr Arg Asp Ala Ala Asn
      135                 140                 145

ccg tgg gcg cag cca gag ctg ttg cag gag gat ctg cag ccg tgg gga   595
Pro Trp Ala Gln Pro Glu Leu Leu Gln Glu Asp Leu Gln Pro Trp Gly
150                 155                 160                 165

gct gaa gtc atc atc att gcc gga cac cca gag ccc acc cac acc atg   643
Ala Glu Val Ile Ile Ile Ala Gly His Pro Glu Pro Thr His Thr Met
                  170                 175                 180

gat ctg gct aaa gat tct gtt gat gcc gga gtt gca tcc ctt caa gct   691
Asp Leu Ala Lys Asp Ser Val Asp Ala Gly Val Ala Ser Leu Gln Ala
              185                 190                 195

cac aag gaa tac ttg gcc gct ctt cca gat ccc ccg aag ccg gag gag   739
His Lys Glu Tyr Leu Ala Ala Leu Pro Asp Pro Pro Lys Pro Glu Glu
          200                 205                 210

ttc att ccg gcg ttt ctc gag gta gag ggc ggt tac gca gcg gcc ttc   787
Phe Ile Pro Ala Phe Leu Glu Val Glu Gly Gly Tyr Ala Ala Ala Phe
      215                 220                 225

cga gtt ttc gga cgg taagcagggc gatacgtgat agg                     825
Arg Val Phe Gly Arg
```

230

<210> 392
<211> 234
<212> PRT
<213> Corynebacterium glutamicum

<400> 392
Met Ser Ala Leu Glu Thr Leu Gln Trp Gln Asp Trp Ser Ser Val Leu
1 5 10 15

Ile Val Val Ala His Pro Asp Asp Pro Glu Tyr Gly Leu Ser Ala Ala
20 25 30

Val Lys Glu Trp Thr Asp Ala Gly Val Glu Val Ser Tyr Leu Leu Leu
35 40 45

Thr His Gly Glu Ala Gly Ile Gln Gly Leu Asp Pro Lys Glu Thr Gly
50 55 60

Ser Leu Arg Ala Ala Glu Gln Arg Ala Ala Cys Asp Val Val Gly Val
65 70 75 80

Arg Asn Leu Thr Ile Leu Asn His Pro Asp Ser Met Leu Val Tyr Asn
85 90 95

Leu Val Leu Arg Lys Asp Ile Ala Arg Glu Ile Arg Ile Arg Lys Pro
100 105 110

Asn Ala Val Val Val Ser Asn Phe Asp Val Glu Ala Tyr Gly Gly Leu
115 120 125

Asn Gln Ala Asp His Arg Val Ala Gly Leu Ala Ala Ile Asp Ala Thr
130 135 140

Arg Asp Ala Ala Asn Pro Trp Ala Gln Pro Glu Leu Leu Gln Glu Asp
145 150 155 160

Leu Gln Pro Trp Gly Ala Glu Val Ile Ile Ala Gly His Pro Glu
165 170 175

Pro Thr His Thr Met Asp Leu Ala Lys Asp Ser Val Asp Ala Gly Val
180 185 190

Ala Ser Leu Gln Ala His Lys Glu Tyr Leu Ala Ala Leu Pro Asp Pro
195 200 205

Pro Lys Pro Glu Glu Phe Ile Pro Ala Phe Leu Glu Val Glu Gly Gly
210 215 220

Tyr Ala Ala Ala Phe Arg Val Phe Gly Arg
225 230

<210> 393
<211> 825
<212> DNA
<213> Corynebacterium glutamicum

<220>

<221> CDS
<222> (101)..(802)
<223> FRXA00831

<400> 393
agctccaaga aagtcagtgc tgtgcatggc tcggtgctgc tcatgctttt cggtgtttac 60

atgatgagca tgttcgcctg atttaggtag cctggtggga atg agt gca ctt gag 115
Met Ser Ala Leu Glu
1 5

aca ttg caa tgg cag gac tgg tca agc gtc tta att gtg gta gct cac 163
Thr Leu Gln Trp Gln Asp Trp Ser Ser Val Leu Ile Val Val Ala His
10 15 20

cca gat gat ccg gag tat ggg ctt tcc gcg gct gtt aaa gaa tgg aca 211
Pro Asp Asp Pro Glu Tyr Gly Leu Ser Ala Ala Val Lys Glu Trp Thr
25 30 35

gac gcc ggg gtg gag gtg tct tac ctg ctg ctc acc cac ggg gag gca 259
Asp Ala Gly Val Glu Val Ser Tyr Leu Leu Leu Thr His Gly Glu Ala
40 45 50

ggt atc caa ggt tta gac cct aaa gaa acc ggg tca ttg cgc gca gcg 307
Gly Ile Gln Gly Leu Asp Pro Lys Glu Thr Gly Ser Leu Arg Ala Ala
55 60 65

gaa cag cgg gct gca tgt gat gtg gta gga gtt aga aat ctc acc att 355
Glu Gln Arg Ala Ala Cys Asp Val Val Gly Val Arg Asn Leu Thr Ile
70 75 80 85

ttg aat cac cca gat tcc atg ttg gtg tac aat ctg gta ctg cgc aaa 403
Leu Asn His Pro Asp Ser Met Leu Val Tyr Asn Leu Val Leu Arg Lys
90 95 100

gat att gct cgg gaa atc cgg atc cgt aaa cca aat gct gtg gtg gta 451
Asp Ile Ala Arg Glu Ile Arg Ile Arg Lys Pro Asn Ala Val Val Val
105 110 115

tcc aat ttt gat gta gag gcc tac ggt ggt ttg aac cag gcg gat cac 499
Ser Asn Phe Asp Val Glu Ala Tyr Gly Gly Leu Asn Gln Ala Asp His
120 125 130

cgc gtg gcg gga tta gcc gca att gat gcg acc cgc gat gcc gct aat 547
Arg Val Ala Gly Leu Ala Ala Ile Asp Ala Thr Arg Asp Ala Ala Asn
135 140 145

ccg tgg gcg cag cca gag ctg ttg cag gag gat ctg cag ccg tgg gga 595
Pro Trp Ala Gln Pro Glu Leu Leu Gln Glu Asp Leu Gln Pro Trp Gly
150 155 160 165

gct gaa gtc atc atc att gcc gga cac cca gag ccc acc cac acc atg 643
Ala Glu Val Ile Ile Ile Ala Gly His Pro Glu Pro Thr His Thr Met
170 175 180

gat ctg gct aaa gat tct gtt gat gcc gga gtt gca tcc ctt caa gct 691
Asp Leu Ala Lys Asp Ser Val Asp Ala Gly Val Ala Ser Leu Gln Ala
185 190 195

cac aag gaa tac ttg gcc gct ctt cca gat ccc ccg aag ccg gag gag 739
His Lys Glu Tyr Leu Ala Ala Leu Pro Asp Pro Pro Lys Pro Glu Glu

```
        200                 205                 210

ttc att ccg gcg ttt ctc gag gta gag ggc ggt tac gca gcg gcc ttc   787
Phe Ile Pro Ala Phe Leu Glu Val Glu Gly Gly Tyr Ala Ala Ala Phe
    215                 220                 225

cga gtt ttc gga cgg taagcagggc gatacgtgat agg                     825
Arg Val Phe Gly Arg
230
```

<210> 394
<211> 234
<212> PRT
<213> Corynebacterium glutamicum

<400> 394

```
Met Ser Ala Leu Glu Thr Leu Gln Trp Gln Asp Trp Ser Ser Val Leu
  1               5                  10                  15

Ile Val Val Ala His Pro Asp Asp Pro Glu Tyr Gly Leu Ser Ala Ala
             20                  25                  30

Val Lys Glu Trp Thr Asp Ala Gly Val Glu Val Ser Tyr Leu Leu Leu
         35                  40                  45

Thr His Gly Glu Ala Gly Ile Gln Gly Leu Asp Pro Lys Glu Thr Gly
     50                  55                  60

Ser Leu Arg Ala Ala Glu Gln Arg Ala Ala Cys Asp Val Val Gly Val
 65                  70                  75                  80

Arg Asn Leu Thr Ile Leu Asn His Pro Asp Ser Met Leu Val Tyr Asn
                 85                  90                  95

Leu Val Leu Arg Lys Asp Ile Ala Arg Glu Ile Arg Ile Arg Lys Pro
            100                 105                 110

Asn Ala Val Val Val Ser Asn Phe Asp Val Glu Ala Tyr Gly Gly Leu
        115                 120                 125

Asn Gln Ala Asp His Arg Val Ala Gly Leu Ala Ala Ile Asp Ala Thr
    130                 135                 140

Arg Asp Ala Ala Asn Pro Trp Ala Gln Pro Glu Leu Leu Gln Glu Asp
145                 150                 155                 160

Leu Gln Pro Trp Gly Ala Glu Val Ile Ile Ile Ala Gly His Pro Glu
                165                 170                 175

Pro Thr His Thr Met Asp Leu Ala Lys Asp Ser Val Asp Ala Gly Val
            180                 185                 190

Ala Ser Leu Gln Ala His Lys Glu Tyr Leu Ala Ala Leu Pro Asp Pro
        195                 200                 205

Pro Lys Pro Glu Glu Phe Ile Pro Ala Phe Leu Glu Val Glu Gly Gly
    210                 215                 220

Tyr Ala Ala Ala Phe Arg Val Phe Gly Arg
225                 230
```

<210> 395
<211> 1077
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1054)
<223> RXN00835

<400> 395
actgcaccag cgccaacgat cgcaattttc atacctgcta tcttgcctga gcacagataa 60

gatttgtaag cactacccct tctctacaaa ggagtcatca atg gcc ggt gga ttg 115
Met Ala Gly Gly Leu
1 5

gca gca cta tta gac gat gtc gca gca att act cga gcg gct gca gcc 163
Ala Ala Leu Leu Asp Asp Val Ala Ala Ile Thr Arg Ala Ala Ala Ala
10 15 20

agc ctc gat gat gtc acg gcg atg gct gga aaa acc agc gtt aaa gcc 211
Ser Leu Asp Asp Val Thr Ala Met Ala Gly Lys Thr Ser Val Lys Ala
25 30 35

gca ggc gtg gtt gta gat gac acg gca gtt acc ccg caa tat gtt caa 259
Ala Gly Val Val Val Asp Asp Thr Ala Val Thr Pro Gln Tyr Val Gln
40 45 50

ggt gtc aaa cct gca cgc gaa ctg ccc atg att tgg cgg atc gct aag 307
Gly Val Lys Pro Ala Arg Glu Leu Pro Met Ile Trp Arg Ile Ala Lys
55 60 65

ggc tct ttg gta aac aag atc atc atc att ttg ccc atc gcg ttg ctt 355
Gly Ser Leu Val Asn Lys Ile Ile Ile Ile Leu Pro Ile Ala Leu Leu
70 75 80 85

ctt tcc gcg ttt gct ccg tgg gct ctc aca cca att ttg atg ctg ggc 403
Leu Ser Ala Phe Ala Pro Trp Ala Leu Thr Pro Ile Leu Met Leu Gly
90 95 100

ggc tcc tac ctg tgc ttc gaa ggt gca gaa aag atc tgg cac tcc ctc 451
Gly Ser Tyr Leu Cys Phe Glu Gly Ala Glu Lys Ile Trp His Ser Leu
105 110 115

cac agg cgc atc aaa ggt gaa cag cac agc acc gaa ccc aag tcg cag 499
His Arg Arg Ile Lys Gly Glu Gln His Ser Thr Glu Pro Lys Ser Gln
120 125 130

gaa agc cca aag tca gag gat cag ctg gtc aaa agt gcc atc aca act 547
Glu Ser Pro Lys Ser Glu Asp Gln Leu Val Lys Ser Ala Ile Thr Thr
135 140 145

gac ctc atc ctt tcc gca gag atc atg gtt att tca ctc aat cag att 595
Asp Leu Ile Leu Ser Ala Glu Ile Met Val Ile Ser Leu Asn Gln Ile
150 155 160 165

gca gat caa act atc tgg atg cag gct gcg gtt ctt ttc gtc gta ggt 643
Ala Asp Gln Thr Ile Trp Met Gln Ala Ala Val Leu Phe Val Val Gly

```
                170                 175                 180

att ggc atc acc gcg ctc gtg tac ggc gta gtc ggt gtt ctt gtg aaa   691
Ile Gly Ile Thr Ala Leu Val Tyr Gly Val Val Gly Val Leu Val Lys
            185                 190                 195

atg gat gac gtc gga ctt aca ctt tca aag cgt gac tcc gca ggt atc   739
Met Asp Asp Val Gly Leu Thr Leu Ser Lys Arg Asp Ser Ala Gly Ile
        200                 205                 210

cag aaa ttt ggc cgc ggc ttg gtc aaa gcg atg ccc atc gtt ctt caa   787
Gln Lys Phe Gly Arg Gly Leu Val Lys Ala Met Pro Ile Val Leu Gln
    215                 220                 225

gtt att tct gtt gtc ggc gtt ttt gcc atg ctg tgg gtt ggt ggc cac   835
Val Ile Ser Val Val Gly Val Phe Ala Met Leu Trp Val Gly Gly His
230                 235                 240                 245

atc atg gtc gtt gga act gaa gag tta gga tgg gaa ctt ccc tac cac   883
Ile Met Val Val Gly Thr Glu Glu Leu Gly Trp Glu Leu Pro Tyr His
                250                 255                 260

ctt gtt cac gga cta gag tcc tgg gct aac ggt atc gga ggc agt gct   931
Leu Val His Gly Leu Glu Ser Trp Ala Asn Gly Ile Gly Gly Ser Ala
            265                 270                 275

ctg gga tgg gtt ggc aat act ttc ggg tca ctt gtg ttc ggc ctc att   979
Leu Gly Trp Val Gly Asn Thr Phe Gly Ser Leu Val Phe Gly Leu Ile
        280                 285                 290

tgg ggc gcg att atc acc gtt gtg gtc agt gtg atc aag aag ttc att   1027
Trp Gly Ala Ile Ile Thr Val Val Val Ser Val Ile Lys Lys Phe Ile
    295                 300                 305

cca cag cgt gcg caa aac tcg tct cat tagtggagag ttgttcgctg         1074
Pro Gln Arg Ala Gln Asn Ser Ser His
310                 315

taa                                                               1077
```

<210> 396
<211> 318
<212> PRT
<213> Corynebacterium glutamicum

<400> 396

```
Met Ala Gly Gly Leu Ala Ala Leu Leu Asp Asp Val Ala Ala Ile Thr
  1               5                  10                  15

Arg Ala Ala Ala Ala Ser Leu Asp Asp Val Thr Ala Met Ala Gly Lys
             20                  25                  30

Thr Ser Val Lys Ala Ala Gly Val Val Val Asp Asp Thr Ala Val Thr
         35                  40                  45

Pro Gln Tyr Val Gln Gly Val Lys Pro Ala Arg Glu Leu Pro Met Ile
     50                  55                  60

Trp Arg Ile Ala Lys Gly Ser Leu Val Asn Lys Ile Ile Ile Ile Leu
 65                  70                  75                  80
```

```
Pro Ile Ala Leu Leu Leu Ser Ala Phe Ala Pro Trp Ala Leu Thr Pro
                85                  90                  95

Ile Leu Met Leu Gly Gly Ser Tyr Leu Cys Phe Glu Gly Ala Glu Lys
            100                 105                 110

Ile Trp His Ser Leu His Arg Arg Ile Lys Gly Glu Gln His Ser Thr
        115                 120                 125

Glu Pro Lys Ser Gln Glu Ser Pro Lys Ser Glu Asp Gln Leu Val Lys
    130                 135                 140

Ser Ala Ile Thr Thr Asp Leu Ile Leu Ser Ala Glu Ile Met Val Ile
145                 150                 155                 160

Ser Leu Asn Gln Ile Ala Asp Gln Thr Ile Trp Met Gln Ala Ala Val
                165                 170                 175

Leu Phe Val Val Gly Ile Gly Ile Thr Ala Leu Val Tyr Gly Val Val
            180                 185                 190

Gly Val Leu Val Lys Met Asp Asp Val Gly Leu Thr Leu Ser Lys Arg
        195                 200                 205

Asp Ser Ala Gly Ile Gln Lys Phe Gly Arg Gly Leu Val Lys Ala Met
    210                 215                 220

Pro Ile Val Leu Gln Val Ile Ser Val Val Gly Val Phe Ala Met Leu
225                 230                 235                 240

Trp Val Gly Gly His Ile Met Val Val Gly Thr Glu Glu Leu Gly Trp
                245                 250                 255

Glu Leu Pro Tyr His Leu Val His Gly Leu Glu Ser Trp Ala Asn Gly
            260                 265                 270

Ile Gly Gly Ser Ala Leu Gly Trp Val Gly Asn Thr Phe Gly Ser Leu
        275                 280                 285

Val Phe Gly Leu Ile Trp Gly Ala Ile Ile Thr Val Val Val Ser Val
    290                 295                 300

Ile Lys Lys Phe Ile Pro Gln Arg Ala Gln Asn Ser Ser His
305                 310                 315
```

<210> 397
<211> 713
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(690)
<223> FRXA00835

<400> 397

```
ttt gct ccg tgg gct ctc aca cca att ttg atg ctg ggc ggc tcc tac   48
Phe Ala Pro Trp Ala Leu Thr Pro Ile Leu Met Leu Gly Gly Ser Tyr
  1               5                  10                  15
```

```
ctg tgc ttc gaa ggt gca gaa aag atc tgg cac tcc ctc cac agg cgc   96
Leu Cys Phe Glu Gly Ala Glu Lys Ile Trp His Ser Leu His Arg Arg
            20                  25                  30

atc aaa ggt gaa cag cac agc acc gaa ccc aag tcg cag gaa agc cca   144
Ile Lys Gly Glu Gln His Ser Thr Glu Pro Lys Ser Gln Glu Ser Pro
        35                  40                  45

aag tca gag gat cag ctg gtc aaa agt gcc atc aca act gac ctc atc   192
Lys Ser Glu Asp Gln Leu Val Lys Ser Ala Ile Thr Thr Asp Leu Ile
    50                  55                  60

ctt tcc gca gag atc atg gtt att tca ctc aat cag att gca gat caa   240
Leu Ser Ala Glu Ile Met Val Ile Ser Leu Asn Gln Ile Ala Asp Gln
65                  70                  75                  80

act atc tgg atg cag gct gcg gtt ctt ttc gtc gta ggt att ggc atc   288
Thr Ile Trp Met Gln Ala Ala Val Leu Phe Val Val Gly Ile Gly Ile
                85                  90                  95

acc gcg ctc gtg tac ggc gta gtc ggt gtt ctt gtg aaa atg gat gac   336
Thr Ala Leu Val Tyr Gly Val Val Gly Val Leu Val Lys Met Asp Asp
            100                 105                 110

gtc gga ctt aca ctt tca aag cgt gac tcc gca ggt atc cag aaa ttt   384
Val Gly Leu Thr Leu Ser Lys Arg Asp Ser Ala Gly Ile Gln Lys Phe
        115                 120                 125

ggc cgc ggc ttg gtc aaa gcg atg ccc atc gtt ctt caa gtt att tct   432
Gly Arg Gly Leu Val Lys Ala Met Pro Ile Val Leu Gln Val Ile Ser
    130                 135                 140

gtt gtc ggc gtt ttt gcc atg ctg tgg gtt ggt ggc cac atc atg gtc   480
Val Val Gly Val Phe Ala Met Leu Trp Val Gly Gly His Ile Met Val
145                 150                 155                 160

gtt gga act gaa gag tta gga tgg gaa ctt ccc tac cac ctt gtt cac   528
Val Gly Thr Glu Glu Leu Gly Trp Glu Leu Pro Tyr His Leu Val His
                165                 170                 175

gga cta gag tcc tgg gct aac ggt atc gga ggc agt gct ctg gga tgg   576
Gly Leu Glu Ser Trp Ala Asn Gly Ile Gly Gly Ser Ala Leu Gly Trp
            180                 185                 190

gtt ggc aat act ttc ggg tca ctt gtg ttc ggc ctc att tgg ggc gcg   624
Val Gly Asn Thr Phe Gly Ser Leu Val Phe Gly Leu Ile Trp Gly Ala
        195                 200                 205

att atc acc gtt gtg gtc agt gtg atc aag aag ttc att cca cag cgt   672
Ile Ile Thr Val Val Val Ser Val Ile Lys Lys Phe Ile Pro Gln Arg
    210                 215                 220

gcg caa aac tcg tct cat tagtggagag ttgttcgctg taa                713
Ala Gln Asn Ser Ser His
225                 230
```

<210> 398
<211> 230
<212> PRT

<213> Corynebacterium glutamicum

<400> 398

```
Phe Ala Pro Trp Ala Leu Thr Pro Ile Leu Met Leu Gly Gly Ser Tyr
  1               5                  10                  15

Leu Cys Phe Glu Gly Ala Glu Lys Ile Trp His Ser Leu His Arg Arg
             20                  25                  30

Ile Lys Gly Glu Gln His Ser Thr Glu Pro Lys Ser Gln Glu Ser Pro
         35                  40                  45

Lys Ser Glu Asp Gln Leu Val Lys Ser Ala Ile Thr Thr Asp Leu Ile
     50                  55                  60

Leu Ser Ala Glu Ile Met Val Ile Ser Leu Asn Gln Ile Ala Asp Gln
 65                  70                  75                  80

Thr Ile Trp Met Gln Ala Ala Val Leu Phe Val Val Gly Ile Gly Ile
                 85                  90                  95

Thr Ala Leu Val Tyr Gly Val Val Gly Val Leu Val Lys Met Asp Asp
            100                 105                 110

Val Gly Leu Thr Leu Ser Lys Arg Asp Ser Ala Gly Ile Gln Lys Phe
        115                 120                 125

Gly Arg Gly Leu Val Lys Ala Met Pro Ile Val Leu Gln Val Ile Ser
    130                 135                 140

Val Val Gly Val Phe Ala Met Leu Trp Val Gly Gly His Ile Met Val
145                 150                 155                 160

Val Gly Thr Glu Glu Leu Gly Trp Glu Leu Pro Tyr His Leu Val His
                165                 170                 175

Gly Leu Glu Ser Trp Ala Asn Gly Ile Gly Gly Ser Ala Leu Gly Trp
            180                 185                 190

Val Gly Asn Thr Phe Gly Ser Leu Val Phe Gly Leu Ile Trp Gly Ala
        195                 200                 205

Ile Ile Thr Val Val Val Ser Val Ile Lys Lys Phe Ile Pro Gln Arg
    210                 215                 220

Ala Gln Asn Ser Ser His
225                 230
```

<210> 399
<211> 1816
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1816)
<223> RXN00836

<400> 399

```
ggagagttgt tcgctgtaat ttcgctgtac agttaatatg acttttttact gtctcaatca 60
```

```
attcacaagt ttgcacgaaa tttaaggaaa ggagtgccca atg tat acc cat tca   115
                                             Met Tyr Thr His Ser
                                               1               5

aca ggc act cct cag ctt gat ttc gac ggt gac atc tat ccc ctt cac   163
Thr Gly Thr Pro Gln Leu Asp Phe Asp Gly Asp Ile Tyr Pro Leu His
                  10                  15                  20

ctc ttc ttc tct gca cag act gcc caa cat ttc gct ctc gag cgc gtc   211
Leu Phe Phe Ser Ala Gln Thr Ala Gln His Phe Ala Leu Glu Arg Val
              25                  30                  35

aat tgg cat gtc tta cgc gct att gtg aaa cct gag caa ggc gaa ctc   259
Asn Trp His Val Leu Arg Ala Ile Val Lys Pro Glu Gln Gly Glu Leu
          40                  45                  50

atc gtc gaa gcg ctt ctc gca cca ata gaa tcc gca aca aaa atc ggt   307
Ile Val Glu Ala Leu Leu Ala Pro Ile Glu Ser Ala Thr Lys Ile Gly
      55                  60                  65

gtt tgg gtt caa gat gaa ttt ctc ggg gtg att gca gag tcc cag ttc   355
Val Trp Val Gln Asp Glu Phe Leu Gly Val Ile Ala Glu Ser Gln Phe
  70                  75                  80                  85

ctg ttg aat tct caa ttg tct cga att ttt gcc tct ggc cac ctg att   403
Leu Leu Asn Ser Gln Leu Ser Arg Ile Phe Ala Ser Gly His Leu Ile
                  90                  95                 100

tcc agc caa cta ctt ctc aca ccg agt aaa gga tct ctc gct tca gtt   451
Ser Ser Gln Leu Leu Leu Thr Pro Ser Lys Gly Ser Leu Ala Ser Val
             105                 110                 115

ctt ctt cca aac cta aaa ttc ggg ctc atc agc aat gat cct cca cga   499
Leu Leu Pro Asn Leu Lys Phe Gly Leu Ile Ser Asn Asp Pro Pro Arg
         120                 125                 130

gct gat tcc cac ctc tta ccg cta ggc aga atg tgg cgc gtt gag ccc   547
Ala Asp Ser His Leu Leu Pro Leu Gly Arg Met Trp Arg Val Glu Pro
     135                 140                 145

acc gtt cat gct ctg ttt gag gat ttc tca ctt ggc tcc acg att ctt   595
Thr Val His Ala Leu Phe Glu Asp Phe Ser Leu Gly Ser Thr Ile Leu
150                 155                 160                 165

ttt ggg ctg agg ctt gat tta gaa gcc cta att gtc tcc tat aac gga   643
Phe Gly Leu Arg Leu Asp Leu Glu Ala Leu Ile Val Ser Tyr Asn Gly
                 170                 175                 180

ata gaa tgt ggc atc tta aac ttt gat gac gcc tca gca cta agc tct   691
Ile Glu Cys Gly Ile Leu Asn Phe Asp Asp Ala Ser Ala Leu Ser Ser
             185                 190                 195

gct gtg aaa ttc tca aat gca aat ggt ctc acc ccc acg gtg ctc ggc   739
Ala Val Lys Phe Ser Asn Ala Asn Gly Leu Thr Pro Thr Val Leu Gly
         200                 205                 210

cac gta gtc cgg gag aac ggt gaa aca tcc ttc gag att gac gtt ctc   787
His Val Val Arg Glu Asn Gly Glu Thr Ser Phe Glu Ile Asp Val Leu
     215                 220                 225
```

```
cca ctg gag ttg tgg tcg aag aag cag cat cgc ctt gag gtt tta aaa   835
Pro Leu Glu Leu Trp Ser Lys Lys Gln His Arg Leu Glu Val Leu Lys
230                 235                 240                 245

atc cct cgg ttg ata cct aaa gag gca gat tcc caa aat tat gtg aag   883
Ile Pro Arg Leu Ile Pro Lys Glu Ala Asp Ser Gln Asn Tyr Val Lys
                250                 255                 260

gcg aca gcg ctc ctt tca gac gag att ctg cga cca caa acg ctg tcc   931
Ala Thr Ala Leu Leu Ser Asp Glu Ile Leu Arg Pro Gln Thr Leu Ser
            265                 270                 275

aaa aag gca ctg tct ttg tcg gac acc gca gtt aag tac agc cct cat   979
Lys Lys Ala Leu Ser Leu Ser Asp Thr Ala Val Lys Tyr Ser Pro His
        280                 285                 290

gtt gct tgt ggc gtg ggg atg ttt agt ctt ttc gcc gtt att ccc ttt   1027
Val Ala Cys Gly Val Gly Met Phe Ser Leu Phe Ala Val Ile Pro Phe
    295                 300                 305

gac aag ttg agt gat cat agt gcg atg ctg ctc gca gtc att agc ttg   1075
Asp Lys Leu Ser Asp His Ser Ala Met Leu Leu Ala Val Ile Ser Leu
310                 315                 320                 325

atg ctt ttt gtg ctg gca tta gta att ctt ttc aag aga att cag tca   1123
Met Leu Phe Val Leu Ala Leu Val Ile Leu Phe Lys Arg Ile Gln Ser
                330                 335                 340

act aat act cag cgt tgg aac ttg gcc tcg tca gtc gga tta ctc gcg   1171
Thr Asn Thr Gln Arg Trp Asn Leu Ala Ser Ser Val Gly Leu Leu Ala
            345                 350                 355

aca ctt ccg att atc ata ttc ctg gtt gct gat aca ttg att cct cag   1219
Thr Leu Pro Ile Ile Ile Phe Leu Val Ala Asp Thr Leu Ile Pro Gln
        360                 365                 370

ggc agc ctg gaa aac cat gct caa ccc gac gta cag gta aca acg tta   1267
Gly Ser Leu Glu Asn His Ala Gln Pro Asp Val Gln Val Thr Thr Leu
    375                 380                 385

gct aac agg cgg cca agt tca cct acc tca ctg gac tca cta ggc gca   1315
Ala Asn Arg Arg Pro Ser Ser Pro Thr Ser Leu Asp Ser Leu Gly Ala
390                 395                 400                 405

ctg aat tca cca agt tcg ccg aat tcc ccg agc tca tca atg ctg caa   1363
Leu Asn Ser Pro Ser Ser Pro Asn Ser Pro Ser Ser Ser Met Leu Gln
                410                 415                 420

aac tct gaa atg ttc gcc tca cca ccg atc gcc tct ggg cag tca ccg   1411
Asn Ser Glu Met Phe Ala Ser Pro Pro Ile Ala Ser Gly Gln Ser Pro
            425                 430                 435

gtt tcg acg ttc cgc tca tgg cta gat cga tcc att ctg cca ctc aca   1459
Val Ser Thr Phe Arg Ser Trp Leu Asp Arg Ser Ile Leu Pro Leu Thr
        440                 445                 450

cga gaa aat tcc gct tca gaa agc gca gtg aca gct ctt gga ccg tcg   1507
Arg Glu Asn Ser Ala Ser Glu Ser Ala Val Thr Ala Leu Gly Pro Ser
    455                 460                 465

ata gtg cag cct gca tct gaa tcg att aca act cca gct caa acg tcg   1555
```

```
Ile Val Gln Pro Ala Ser Glu Ser Ile Thr Thr Pro Ala Gln Thr Ser
470                 475                 480                 485

caa agt cgc cac gca att gac gat ggt gac gac agt aaa acc tca acg   1603
Gln Ser Arg His Ala Ile Asp Asp Gly Asp Asp Ser Lys Thr Ser Thr
                490                 495                 500

gga aga cca gct ccc act act aac tcg ccg atc att gct ctt ccc cca   1651
Gly Arg Pro Ala Pro Thr Thr Asn Ser Pro Ile Ile Ala Leu Pro Pro
            505                 510                 515

acg tgg att atc ggg ccg gaa gat cca gaa tcc acc gac cct aca gca   1699
Thr Trp Ile Ile Gly Pro Glu Asp Pro Glu Ser Thr Asp Pro Thr Ala
        520                 525                 530

cca acc gag ccc acc gag cca agc gaa cct gtc gca acc gac gaa ccc   1747
Pro Thr Glu Pro Thr Glu Pro Ser Glu Pro Val Ala Thr Asp Glu Pro
    535                 540                 545

tca gag acc tct gaa caa act tca cct ctc tta gct cgc gac acc ccc   1795
Ser Glu Thr Ser Glu Gln Thr Ser Pro Leu Leu Ala Arg Asp Thr Pro
550                 555                 560                 565

gaa ctg aac cgg aaa caa ctg                                      1816
Glu Leu Asn Arg Lys Gln Leu
                570
```

<210> 400
<211> 572
<212> PRT
<213> Corynebacterium glutamicum

<400> 400

```
Met Tyr Thr His Ser Thr Gly Thr Pro Gln Leu Asp Phe Asp Gly Asp
  1               5                  10                  15

Ile Tyr Pro Leu His Leu Phe Phe Ser Ala Gln Thr Ala Gln His Phe
             20                  25                  30

Ala Leu Glu Arg Val Asn Trp His Val Leu Arg Ala Ile Val Lys Pro
         35                  40                  45

Glu Gln Gly Glu Leu Ile Val Glu Ala Leu Leu Ala Pro Ile Glu Ser
     50                  55                  60

Ala Thr Lys Ile Gly Val Trp Val Gln Asp Glu Phe Leu Gly Val Ile
 65                  70                  75                  80

Ala Glu Ser Gln Phe Leu Leu Asn Ser Gln Leu Ser Arg Ile Phe Ala
                 85                  90                  95

Ser Gly His Leu Ile Ser Ser Gln Leu Leu Leu Thr Pro Ser Lys Gly
            100                 105                 110

Ser Leu Ala Ser Val Leu Leu Pro Asn Leu Lys Phe Gly Leu Ile Ser
        115                 120                 125

Asn Asp Pro Pro Arg Ala Asp Ser His Leu Leu Pro Leu Gly Arg Met
    130                 135                 140
```

```
Trp Arg Val Glu Pro Thr Val His Ala Leu Phe Glu Asp Phe Ser Leu
145                 150                 155                 160

Gly Ser Thr Ile Leu Phe Gly Leu Arg Leu Asp Leu Glu Ala Leu Ile
                165                 170                 175

Val Ser Tyr Asn Gly Ile Glu Cys Gly Ile Leu Asn Phe Asp Asp Ala
            180                 185                 190

Ser Ala Leu Ser Ser Ala Val Lys Phe Ser Asn Ala Asn Gly Leu Thr
        195                 200                 205

Pro Thr Val Leu Gly His Val Val Arg Glu Asn Gly Glu Thr Ser Phe
    210                 215                 220

Glu Ile Asp Val Leu Pro Leu Glu Leu Trp Ser Lys Lys Gln His Arg
225                 230                 235                 240

Leu Glu Val Leu Lys Ile Pro Arg Leu Ile Pro Lys Glu Ala Asp Ser
                245                 250                 255

Gln Asn Tyr Val Lys Ala Thr Ala Leu Leu Ser Asp Glu Ile Leu Arg
            260                 265                 270

Pro Gln Thr Leu Ser Lys Lys Ala Leu Ser Leu Ser Asp Thr Ala Val
        275                 280                 285

Lys Tyr Ser Pro His Val Ala Cys Gly Val Gly Met Phe Ser Leu Phe
    290                 295                 300

Ala Val Ile Pro Phe Asp Lys Leu Ser Asp His Ser Ala Met Leu Leu
305                 310                 315                 320

Ala Val Ile Ser Leu Met Leu Phe Val Leu Ala Leu Val Ile Leu Phe
                325                 330                 335

Lys Arg Ile Gln Ser Thr Asn Thr Gln Arg Trp Asn Leu Ala Ser Ser
            340                 345                 350

Val Gly Leu Leu Ala Thr Leu Pro Ile Ile Ile Phe Leu Val Ala Asp
        355                 360                 365

Thr Leu Ile Pro Gln Gly Ser Leu Glu Asn His Ala Gln Pro Asp Val
    370                 375                 380

Gln Val Thr Thr Leu Ala Asn Arg Arg Pro Ser Ser Pro Thr Ser Leu
385                 390                 395                 400

Asp Ser Leu Gly Ala Leu Asn Ser Pro Ser Ser Pro Asn Ser Pro Ser
                405                 410                 415

Ser Ser Met Leu Gln Asn Ser Glu Met Phe Ala Ser Pro Pro Ile Ala
            420                 425                 430

Ser Gly Gln Ser Pro Val Ser Thr Phe Arg Ser Trp Leu Asp Arg Ser
        435                 440                 445

Ile Leu Pro Leu Thr Arg Glu Asn Ser Ala Ser Glu Ser Ala Val Thr
    450                 455                 460

Ala Leu Gly Pro Ser Ile Val Gln Pro Ala Ser Glu Ser Ile Thr Thr
```

```
465                 470                 475                 480

Pro Ala Gln Thr Ser Gln Ser Arg His Ala Ile Asp Asp Gly Asp Asp
                485                 490                 495

Ser Lys Thr Ser Thr Gly Arg Pro Ala Pro Thr Thr Asn Ser Pro Ile
            500                 505                 510

Ile Ala Leu Pro Pro Thr Trp Ile Ile Gly Pro Glu Asp Pro Glu Ser
        515                 520                 525

Thr Asp Pro Thr Ala Pro Thr Glu Pro Thr Glu Pro Ser Glu Pro Val
    530                 535                 540

Ala Thr Asp Glu Pro Ser Glu Thr Ser Glu Gln Thr Ser Pro Leu Leu
545                 550                 555                 560

Ala Arg Asp Thr Pro Glu Leu Asn Arg Lys Gln Leu
                565                 570
```

<210> 401
<211> 1771
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1771)
<223> FRXA00836

<400> 401

```
ggagagttgt tcgctgtaat ttcgctgtac agttaatatg acttttttact gtctcaatca 60

attcacaagt ttgcacgaaa tttaaggaaa ggagtgccca atg tat acc cat tca   115
                                              Met Tyr Thr His Ser
                                                1               5

aca ggc act cct cag ctt gat ttc gac ggt gac atc tat ccc ctt cac   163
Thr Gly Thr Pro Gln Leu Asp Phe Asp Gly Asp Ile Tyr Pro Leu His
                10                  15                  20

ctc ttc ttc tct gca cag act gcc caa cat ttc gct ctc gag cgc gtc   211
Leu Phe Phe Ser Ala Gln Thr Ala Gln His Phe Ala Leu Glu Arg Val
            25                  30                  35

aat tgg cat gtc tta cgc gct att gtg aaa cct gag caa ggc gaa ctc   259
Asn Trp His Val Leu Arg Ala Ile Val Lys Pro Glu Gln Gly Glu Leu
        40                  45                  50

atc gtc gaa gcg ctt ctc gca cca ata gaa tcc gca aca aaa atc ggt   307
Ile Val Glu Ala Leu Leu Ala Pro Ile Glu Ser Ala Thr Lys Ile Gly
    55                  60                  65

gtt tgg gtt caa gat gaa ttt ctc ggg gtg att gca gag tcc cag ttc   355
Val Trp Val Gln Asp Glu Phe Leu Gly Val Ile Ala Glu Ser Gln Phe
70                  75                  80                  85

ctg ttg aat tct caa ttg tct cga att ttt gcc tct ggc cac ctg att   403
Leu Leu Asn Ser Gln Leu Ser Arg Ile Phe Ala Ser Gly His Leu Ile
                90                  95                  100
```

```
tcc agc caa cta ctt ctc aca ccg agt aaa gga tct ctc gct tca gtt   451
Ser Ser Gln Leu Leu Leu Thr Pro Ser Lys Gly Ser Leu Ala Ser Val
            105                 110                 115

ctt ctt cca aac cta aaa ttc ggg ctc atc agc aat gat cct cca cga   499
Leu Leu Pro Asn Leu Lys Phe Gly Leu Ile Ser Asn Asp Pro Pro Arg
        120                 125                 130

gct gat tcc cac ctc tta ccg cta ggc aga atg tgg cgc gtt gag ccc   547
Ala Asp Ser His Leu Leu Pro Leu Gly Arg Met Trp Arg Val Glu Pro
    135                 140                 145

acc gtt cat gct ctg ttt gag gat ttc tca ctt ggc tcc acg att ctt   595
Thr Val His Ala Leu Phe Glu Asp Phe Ser Leu Gly Ser Thr Ile Leu
150                 155                 160                 165

ttt ggg ctg agg ctt gat tta gaa gcc cta att gtc tcc tat aac gga   643
Phe Gly Leu Arg Leu Asp Leu Glu Ala Leu Ile Val Ser Tyr Asn Gly
                170                 175                 180

ata gaa tgt ggc atc tta aac ttt gat gac gcc tca gca cta agc tct   691
Ile Glu Cys Gly Ile Leu Asn Phe Asp Asp Ala Ser Ala Leu Ser Ser
            185                 190                 195

gct gtg aaa ttc tca aat gca aat ggt ctc acc ccc acg gtg ctc ggc   739
Ala Val Lys Phe Ser Asn Ala Asn Gly Leu Thr Pro Thr Val Leu Gly
        200                 205                 210

cac gta gtc cgg gag aac ggt gaa aca tcc ttc gag att gac gtt ctc   787
His Val Val Arg Glu Asn Gly Glu Thr Ser Phe Glu Ile Asp Val Leu
    215                 220                 225

cca ctg gag ttg tgg tcg aag aag cag cat cgc ctt gag gtt tta aaa   835
Pro Leu Glu Leu Trp Ser Lys Lys Gln His Arg Leu Glu Val Leu Lys
230                 235                 240                 245

atc cct cgg ttg ata cct aaa gag gca gat tcc caa aat tat gtg aag   883
Ile Pro Arg Leu Ile Pro Lys Glu Ala Asp Ser Gln Asn Tyr Val Lys
                250                 255                 260

gcg aca gcg ctc ctt tca gac gag att ctg cga cca caa acg ctg tcc   931
Ala Thr Ala Leu Leu Ser Asp Glu Ile Leu Arg Pro Gln Thr Leu Ser
            265                 270                 275

aaa aag gca ctg tct ttg tcg gac acc gca gtt aag tac agc cct cat   979
Lys Lys Ala Leu Ser Leu Ser Asp Thr Ala Val Lys Tyr Ser Pro His
        280                 285                 290

gtt gct tgt ggc gtg ggg atg ttt agt ctt ttc gcc gtt att ccc ttt   1027
Val Ala Cys Gly Val Gly Met Phe Ser Leu Phe Ala Val Ile Pro Phe
    295                 300                 305

gac aag ttg agt gat cat agt gcg atg ctg ctc gca gtc att agc ttg   1075
Asp Lys Leu Ser Asp His Ser Ala Met Leu Leu Ala Val Ile Ser Leu
310                 315                 320                 325

atg ctt ttt gtg ctg gca tta gta att ctt ttc aag aga att cag tca   1123
Met Leu Phe Val Leu Ala Leu Val Ile Leu Phe Lys Arg Ile Gln Ser
                330                 335                 340
```

```
act aat act cag cgt tgg aac ttg gcc tcg tca gtc gga tta ctc gcg   1171
Thr Asn Thr Gln Arg Trp Asn Leu Ala Ser Ser Val Gly Leu Leu Ala
            345                 350                 355

aca ctt ccg att atc ata ttc ctg gtt gct gat aca ttg att cct cag   1219
Thr Leu Pro Ile Ile Ile Phe Leu Val Ala Asp Thr Leu Ile Pro Gln
        360                 365                 370

ggc agc ctg gaa aac cat gct caa ccc gac gta cag gta aca acg tta   1267
Gly Ser Leu Glu Asn His Ala Gln Pro Asp Val Gln Val Thr Thr Leu
    375                 380                 385

gct aac agg cgg cca agt tca cct acc tca ctg gac tca cta ggc gca   1315
Ala Asn Arg Arg Pro Ser Ser Pro Thr Ser Leu Asp Ser Leu Gly Ala
390                 395                 400                 405

ctg aat tca cca agt tcg ccg aat tcc ccg agc tca tca atg ctg caa   1363
Leu Asn Ser Pro Ser Ser Pro Asn Ser Pro Ser Ser Ser Met Leu Gln
                410                 415                 420

aac tct gaa atg ttc gcc tca cca ccg atc gcc tct ggg cag tca ccg   1411
Asn Ser Glu Met Phe Ala Ser Pro Pro Ile Ala Ser Gly Gln Ser Pro
            425                 430                 435

gtt tcg acg ttc cgc tca tgg cta gat cga tcc att ctg cca ctc aca   1459
Val Ser Thr Phe Arg Ser Trp Leu Asp Arg Ser Ile Leu Pro Leu Thr
        440                 445                 450

cga gaa aat tcc gct tca gaa agc gca gtg aca gct ctt gga ccg tcg   1507
Arg Glu Asn Ser Ala Ser Glu Ser Ala Val Thr Ala Leu Gly Pro Ser
    455                 460                 465

ata gtg cag cct gca tct gaa tcg att aca act cca gct caa acg tcg   1555
Ile Val Gln Pro Ala Ser Glu Ser Ile Thr Thr Pro Ala Gln Thr Ser
470                 475                 480                 485

caa agt cgc cac gca att gac gat ggt gac gac agt aaa acc tca acg   1603
Gln Ser Arg His Ala Ile Asp Asp Gly Asp Asp Ser Lys Thr Ser Thr
                490                 495                 500

gga aga cca gct ccc act act aac tcg ccg atc att gct ctt ccc cca   1651
Gly Arg Pro Ala Pro Thr Thr Asn Ser Pro Ile Ile Ala Leu Pro Pro
            505                 510                 515

acg tgg att atc ggg ccg gaa gat cca gaa tcc acc gac cct aca gca   1699
Thr Trp Ile Ile Gly Pro Glu Asp Pro Glu Ser Thr Asp Pro Thr Ala
        520                 525                 530

cca acc gag ccc acc gag cca agc gaa cct gtc gca acc gac gaa ccc   1747
Pro Thr Glu Pro Thr Glu Pro Ser Glu Pro Val Ala Thr Asp Glu Pro
    535                 540                 545

tca gag acc tct gaa caa act tca                                  1771
Ser Glu Thr Ser Glu Gln Thr Ser
550                 555
```

<210> 402
<211> 557
<212> PRT
<213> Corynebacterium glutamicum

<400> 402

```
Met Tyr Thr His Ser Thr Gly Thr Pro Gln Leu Asp Phe Asp Gly Asp
 1               5                  10                  15

Ile Tyr Pro Leu His Leu Phe Phe Ser Ala Gln Thr Ala Gln His Phe
            20                  25                  30

Ala Leu Glu Arg Val Asn Trp His Val Leu Arg Ala Ile Val Lys Pro
        35                  40                  45

Glu Gln Gly Glu Leu Ile Val Glu Ala Leu Leu Ala Pro Ile Glu Ser
    50                  55                  60

Ala Thr Lys Ile Gly Val Trp Val Gln Asp Glu Phe Leu Gly Val Ile
65                  70                  75                  80

Ala Glu Ser Gln Phe Leu Leu Asn Ser Gln Leu Ser Arg Ile Phe Ala
                85                  90                  95

Ser Gly His Leu Ile Ser Ser Gln Leu Leu Leu Thr Pro Ser Lys Gly
            100                 105                 110

Ser Leu Ala Ser Val Leu Leu Pro Asn Leu Lys Phe Gly Leu Ile Ser
        115                 120                 125

Asn Asp Pro Pro Arg Ala Asp Ser His Leu Leu Pro Leu Gly Arg Met
    130                 135                 140

Trp Arg Val Glu Pro Thr Val His Ala Leu Phe Glu Asp Phe Ser Leu
145                 150                 155                 160

Gly Ser Thr Ile Leu Phe Gly Leu Arg Leu Asp Leu Glu Ala Leu Ile
                165                 170                 175

Val Ser Tyr Asn Gly Ile Glu Cys Gly Ile Leu Asn Phe Asp Asp Ala
            180                 185                 190

Ser Ala Leu Ser Ser Ala Val Lys Phe Ser Asn Ala Asn Gly Leu Thr
        195                 200                 205

Pro Thr Val Leu Gly His Val Val Arg Glu Asn Gly Glu Thr Ser Phe
    210                 215                 220

Glu Ile Asp Val Leu Pro Leu Glu Leu Trp Ser Lys Lys Gln His Arg
225                 230                 235                 240

Leu Glu Val Leu Lys Ile Pro Arg Leu Ile Pro Lys Glu Ala Asp Ser
                245                 250                 255

Gln Asn Tyr Val Lys Ala Thr Ala Leu Leu Ser Asp Glu Ile Leu Arg
            260                 265                 270

Pro Gln Thr Leu Ser Lys Lys Ala Leu Ser Leu Ser Asp Thr Ala Val
        275                 280                 285

Lys Tyr Ser Pro His Val Ala Cys Gly Val Gly Met Phe Ser Leu Phe
    290                 295                 300

Ala Val Ile Pro Phe Asp Lys Leu Ser Asp His Ser Ala Met Leu Leu
305                 310                 315                 320
```

Ala Val Ile Ser Leu Met Leu Phe Val Leu Ala Leu Val Ile Leu Phe
325 330 335

Lys Arg Ile Gln Ser Thr Asn Thr Gln Arg Trp Asn Leu Ala Ser Ser
340 345 350

Val Gly Leu Leu Ala Thr Leu Pro Ile Ile Ile Phe Leu Val Ala Asp
355 360 365

Thr Leu Ile Pro Gln Gly Ser Leu Glu Asn His Ala Gln Pro Asp Val
370 375 380

Gln Val Thr Thr Leu Ala Asn Arg Arg Pro Ser Ser Pro Thr Ser Leu
385 390 395 400

Asp Ser Leu Gly Ala Leu Asn Ser Pro Ser Ser Pro Asn Ser Pro Ser
405 410 415

Ser Ser Met Leu Gln Asn Ser Glu Met Phe Ala Ser Pro Pro Ile Ala
420 425 430

Ser Gly Gln Ser Pro Val Ser Thr Phe Arg Ser Trp Leu Asp Arg Ser
435 440 445

Ile Leu Pro Leu Thr Arg Glu Asn Ser Ala Ser Glu Ser Ala Val Thr
450 455 460

Ala Leu Gly Pro Ser Ile Val Gln Pro Ala Ser Glu Ser Ile Thr Thr
465 470 475 480

Pro Ala Gln Thr Ser Gln Ser Arg His Ala Ile Asp Asp Gly Asp Asp
485 490 495

Ser Lys Thr Ser Thr Gly Arg Pro Ala Pro Thr Thr Asn Ser Pro Ile
500 505 510

Ile Ala Leu Pro Pro Thr Trp Ile Ile Gly Pro Glu Asp Pro Glu Ser
515 520 525

Thr Asp Pro Thr Ala Pro Thr Glu Pro Thr Glu Pro Ser Glu Pro Val
530 535 540

Ala Thr Asp Glu Pro Ser Glu Thr Ser Glu Gln Thr Ser
545 550 555

<210> 403
<211> 837
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(814)
<223> RXN00840

<400> 403
gcgattaatg tgacaggagg aaaagaagtt aactgaagtt actaatgtga ctaaagttgt 60

tccctccgca ttgtctcgtt gaaaggtaag taaaactcaa gtg aca aag aca ctc 115

```
                                                    Val Thr Lys Thr Leu
                                                      1               5

ccc cga ctg ctt aca gtc gct gcc gct cta gcc att gca ctc ccg gca   163
Pro Arg Leu Leu Thr Val Ala Ala Ala Leu Ala Ile Ala Leu Pro Ala
                10                  15                  20

acc ccg gta gca tcg gct gtc aca cca gtt gaa caa gct ttc aac gcc   211
Thr Pro Val Ala Ser Ala Val Thr Pro Val Glu Gln Ala Phe Asn Ala
            25                  30                  35

tca tcg aat ctc tcc agc ggt ctc ccc gta gac caa tgg gga cgc ccc   259
Ser Ser Asn Leu Ser Ser Gly Leu Pro Val Asp Gln Trp Gly Arg Pro
        40                  45                  50

aac gag cag ttc cgc caa caa atc gaa cag gca gta aac caa ccg tgg   307
Asn Glu Gln Phe Arg Gln Gln Ile Glu Gln Ala Val Asn Gln Pro Trp
    55                  60                  65

gtc ccg cag gaa atc aag aac atc gtt tct cag gcc atg ggt ttt atc   355
Val Pro Gln Glu Ile Lys Asn Ile Val Ser Gln Ala Met Gly Phe Ile
70                  75                  80                  85

acc ggt gac ggc agc gaa ggt ggg gac att gaa atc ccc gac aac gca   403
Thr Gly Asp Gly Ser Glu Gly Gly Asp Ile Glu Ile Pro Asp Asn Ala
                90                  95                  100

cca cgc atc gcg cag ttc ttc tgg ccc acc cga tca gaa aac tgc atc   451
Pro Arg Ile Ala Gln Phe Phe Trp Pro Thr Arg Ser Glu Asn Cys Ile
            105                 110                 115

aac gga aat tct gca gcc gta gga tct gcc ttc gca gtt cca gga cca   499
Asn Gly Asn Ser Ala Ala Val Gly Ser Ala Phe Ala Val Pro Gly Pro
        120                 125                 130

gca gat ctc ccc ctc ccc ggc gca ggt gtc ggc caa acc tcc ttc gtg   547
Ala Asp Leu Pro Leu Pro Gly Ala Gly Val Gly Gln Thr Ser Phe Val
    135                 140                 145

ttc acc gca ctg gga act ggc ccc ctc gca gaa cag caa agc acc gca   595
Phe Thr Ala Leu Gly Thr Gly Pro Leu Ala Glu Gln Gln Ser Thr Ala
150                 155                 160                 165

atg act gtt caa tgg gca aac tta agc aac ttc acc cat ggc acc acg   643
Met Thr Val Gln Trp Ala Asn Leu Ser Asn Phe Thr His Gly Thr Thr
                170                 175                 180

acg ttg agc aac acc gga atc aac ccc gat ggc ccc tca acg att tcc   691
Thr Leu Ser Asn Thr Gly Ile Asn Pro Asp Gly Pro Ser Thr Ile Ser
            185                 190                 195

ggt gtg gca gac aca gga cgc ggc atc atc gtc gcc tcc atg tca ggc   739
Gly Val Ala Asp Thr Gly Arg Gly Ile Ile Val Ala Ser Met Ser Gly  .
        200                 205                 210

ggc ctc acc aca tcc acc gaa aac ggt tca gcg aac tgt aat ttc atc   787
Gly Leu Thr Thr Ser Thr Glu Asn Gly Ser Ala Asn Cys Asn Phe Ile
    215                 220                 225

ccg act gcc gtc gta ttc gat gtg agg taagaaaaca atgactgatc         834
Pro Thr Ala Val Val Phe Asp Val Arg
```

230 235

ttc 837

<210> 404
<211> 238
<212> PRT
<213> Corynebacterium glutamicum

<400> 404
Val Thr Lys Thr Leu Pro Arg Leu Leu Thr Val Ala Ala Ala Leu Ala
1 5 10 15

Ile Ala Leu Pro Ala Thr Pro Val Ala Ser Ala Val Thr Pro Val Glu
20 25 30

Gln Ala Phe Asn Ala Ser Ser Asn Leu Ser Ser Gly Leu Pro Val Asp
35 40 45

Gln Trp Gly Arg Pro Asn Glu Gln Phe Arg Gln Gln Ile Glu Gln Ala
50 55 60

Val Asn Gln Pro Trp Val Pro Gln Glu Ile Lys Asn Ile Val Ser Gln
65 70 75 80

Ala Met Gly Phe Ile Thr Gly Asp Gly Ser Glu Gly Gly Asp Ile Glu
85 90 95

Ile Pro Asp Asn Ala Pro Arg Ile Ala Gln Phe Phe Trp Pro Thr Arg
100 105 110

Ser Glu Asn Cys Ile Asn Gly Asn Ser Ala Ala Val Gly Ser Ala Phe
115 120 125

Ala Val Pro Gly Pro Ala Asp Leu Pro Leu Pro Gly Ala Gly Val Gly
130 135 140

Gln Thr Ser Phe Val Phe Thr Ala Leu Gly Thr Gly Pro Leu Ala Glu
145 150 155 160

Gln Gln Ser Thr Ala Met Thr Val Gln Trp Ala Asn Leu Ser Asn Phe
165 170 175

Thr His Gly Thr Thr Thr Leu Ser Asn Thr Gly Ile Asn Pro Asp Gly
180 185 190

Pro Ser Thr Ile Ser Gly Val Ala Asp Thr Gly Arg Gly Ile Ile Val
195 200 205

Ala Ser Met Ser Gly Gly Leu Thr Thr Ser Thr Glu Asn Gly Ser Ala
210 215 220

Asn Cys Asn Phe Ile Pro Thr Ala Val Val Phe Asp Val Arg
225 230 235

<210> 405
<211> 837
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(814)
<223> FRXA00840

<400> 405
gcgattaatg tgacaggagg aaaagaagtt aactgaagtt actaatgtga ctaaagttgt 60

tccctccgca ttgtctcgtt gaaaggtaag taaaactcaa gtg aca aag aca ctc 115
Val Thr Lys Thr Leu
1 5

ccc cga ctg ctt aca gtc gct gcc gct cta gcc att gca ctc ccg gca 163
Pro Arg Leu Leu Thr Val Ala Ala Ala Leu Ala Ile Ala Leu Pro Ala
10 15 20

acc ccg gta gca tcg gct gtc aca cca gtt gaa caa gct ttc aac gcc 211
Thr Pro Val Ala Ser Ala Val Thr Pro Val Glu Gln Ala Phe Asn Ala
25 30 35

tca tcg aat ctc tcc agc ggt ctc ccc gta gac caa tgg gga cgc ccc 259
Ser Ser Asn Leu Ser Ser Gly Leu Pro Val Asp Gln Trp Gly Arg Pro
40 45 50

aac gag cag ttc cgc caa caa atc gaa cag gca gta aac caa ccg tgg 307
Asn Glu Gln Phe Arg Gln Gln Ile Glu Gln Ala Val Asn Gln Pro Trp
55 60 65

gtc ccg cag gaa atc aag aac atc gtt tct cag gcc atg ggt ttt atc 355
Val Pro Gln Glu Ile Lys Asn Ile Val Ser Gln Ala Met Gly Phe Ile
70 75 80 85

acc ggt gac ggc agc gaa ggt ggg gac att gaa atc ccc gac aac gca 403
Thr Gly Asp Gly Ser Glu Gly Gly Asp Ile Glu Ile Pro Asp Asn Ala
90 95 100

cca cgc atc gcg cag ttc ttc tgg ccc acc cga tca gaa aac tgc atc 451
Pro Arg Ile Ala Gln Phe Phe Trp Pro Thr Arg Ser Glu Asn Cys Ile
105 110 115

aac gga aat tct gca gcc gta gga tct gcc ttc gca gtt cca gga cca 499
Asn Gly Asn Ser Ala Ala Val Gly Ser Ala Phe Ala Val Pro Gly Pro
120 125 130

gca gat ctc ccc ctc ccc ggc gca ggt gtc ggc caa acc tcc ttc gtg 547
Ala Asp Leu Pro Leu Pro Gly Ala Gly Val Gly Gln Thr Ser Phe Val
135 140 145

ttc acc gca ctg gga act ggc ccc ctc gca gaa cag caa agc acc gca 595
Phe Thr Ala Leu Gly Thr Gly Pro Leu Ala Glu Gln Gln Ser Thr Ala
150 155 160 165

atg act gtt caa tgg gca aac tta agc aac ttc acc cat ggc acc acg 643
Met Thr Val Gln Trp Ala Asn Leu Ser Asn Phe Thr His Gly Thr Thr
170 175 180

acg ttg agc aac acc gga atc aac ccc gat ggc ccc tca acg att tcc 691
Thr Leu Ser Asn Thr Gly Ile Asn Pro Asp Gly Pro Ser Thr Ile Ser
185 190 195

```
ggt gtg gca gac aca gga cgc ggc atc atc gtc gcc tcc atg tca ggc   739
Gly Val Ala Asp Thr Gly Arg Gly Ile Ile Val Ala Ser Met Ser Gly
        200                 205                 210

ggc ctc acc aca tcc acc gaa aac ggt tca gcg aac tgt aat ttc atc   787
Gly Leu Thr Thr Ser Thr Glu Asn Gly Ser Ala Asn Cys Asn Phe Ile
    215                 220                 225

ccg act gcc gtc gta ttc gat gtg agg taagaaaaca atgactgatc        834
Pro Thr Ala Val Val Phe Asp Val Arg
230                 235

ttc                                                              837


<210> 406
<211> 238
<212> PRT
<213> Corynebacterium glutamicum

<400> 406
Val Thr Lys Thr Leu Pro Arg Leu Leu Thr Val Ala Ala Ala Leu Ala
  1               5                  10                  15

Ile Ala Leu Pro Ala Thr Pro Val Ala Ser Ala Val Thr Pro Val Glu
             20                  25                  30

Gln Ala Phe Asn Ala Ser Ser Asn Leu Ser Ser Gly Leu Pro Val Asp
         35                  40                  45

Gln Trp Gly Arg Pro Asn Glu Gln Phe Arg Gln Gln Ile Glu Gln Ala
     50                  55                  60

Val Asn Gln Pro Trp Val Pro Gln Glu Ile Lys Asn Ile Val Ser Gln
 65                  70                  75                  80

Ala Met Gly Phe Ile Thr Gly Asp Gly Ser Glu Gly Gly Asp Ile Glu
                 85                  90                  95

Ile Pro Asp Asn Ala Pro Arg Ile Ala Gln Phe Phe Trp Pro Thr Arg
            100                 105                 110

Ser Glu Asn Cys Ile Asn Gly Asn Ser Ala Ala Val Gly Ser Ala Phe
        115                 120                 125

Ala Val Pro Gly Pro Ala Asp Leu Pro Leu Pro Gly Ala Gly Val Gly
    130                 135                 140

Gln Thr Ser Phe Val Phe Thr Ala Leu Gly Thr Gly Pro Leu Ala Glu
145                 150                 155                 160

Gln Gln Ser Thr Ala Met Thr Val Gln Trp Ala Asn Leu Ser Asn Phe
                165                 170                 175

Thr His Gly Thr Thr Thr Leu Ser Asn Thr Gly Ile Asn Pro Asp Gly
            180                 185                 190

Pro Ser Thr Ile Ser Gly Val Ala Asp Thr Gly Arg Gly Ile Ile Val
        195                 200                 205

Ala Ser Met Ser Gly Gly Leu Thr Thr Ser Thr Glu Asn Gly Ser Ala
```

```
    210                 215                 220

Asn Cys Asn Phe Ile Pro Thr Ala Val Val Phe Asp Val Arg
225                 230                 235


<210> 407
<211> 660
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(637)
<223> RXN00841

<400> 407
gcctccatgt caggcggcct caccacatcc accgaaaacg gttcagcgaa ctgtaatttc 60

atcccgactg ccgtcgtatt cgatgtgagg taagaaaaca atg act gat ctt cat   115
                                            Met Thr Asp Leu His
                                              1               5


ccc gta aag cag gaa att ttc aac act gct gaa tcc ata aac aca gat   163
Pro Val Lys Gln Glu Ile Phe Asn Thr Ala Glu Ser Ile Asn Thr Asp
                 10                  15                  20

ccc aag ggg ttt ctc cgc gag gta gac acc ttc aaa gta acc gac ttc   211
Pro Lys Gly Phe Leu Arg Glu Val Asp Thr Phe Lys Val Thr Asp Phe
             25                  30                  35

ggc ctg tac atg gct cgt ggt gca aac cac ccc aag ttc gga tac ttg   259
Gly Leu Tyr Met Ala Arg Gly Ala Asn His Pro Lys Phe Gly Tyr Leu
         40                  45                  50

gaa agc tgg ctc ctc cca gaa ctt gga ttg cgt gcc aac att ttc cac   307
Glu Ser Trp Leu Leu Pro Glu Leu Gly Leu Arg Ala Asn Ile Phe His
     55                  60                  65

ttc cgc aaa ggc gtg gat gaa cgt cag gat tac tac atc gat gtc gct   355
Phe Arg Lys Gly Val Asp Glu Arg Gln Asp Tyr Tyr Ile Asp Val Ala
 70                  75                  80                  85

gaa att cgc gtc gaa gac aac atc tgg acc acc cgc gac ctc tac gtg   403
Glu Ile Arg Val Glu Asp Asn Ile Trp Thr Thr Arg Asp Leu Tyr Val
                 90                  95                 100

gat ctc atc tct gtc tgc gga gaa cca gta aca gtc atg gac atc gac   451
Asp Leu Ile Ser Val Cys Gly Glu Pro Val Thr Val Met Asp Ile Asp
             105                 110                 115

gaa cta gct gca gca acc tca gca ggg ctt atc act gca gat gac gct   499
Glu Leu Ala Ala Ala Thr Ser Ala Gly Leu Ile Thr Ala Asp Asp Ala
         120                 125                 130

gag cgc gca att gat gcc acc ttg aat gct gtt gaa gga atc acc cgc   547
Glu Arg Ala Ile Asp Ala Thr Leu Asn Ala Val Glu Gly Ile Thr Arg
     135                 140                 145

cac ggc gac gat cct atg cag tgg ctg cgc tcc aag gga atc gaa ctc   595
His Gly Asp Asp Pro Met Gln Trp Leu Arg Ser Lys Gly Ile Glu Leu
```

```
150                 155                 160                 165

acc tgg gct gac gcc agc cag gta gag ctc gtc cct gca gag          637
Thr Trp Ala Asp Ala Ser Gln Val Glu Leu Val Pro Ala Glu
                170                 175

taactacttc ctaaccgctg ctt                                        660


<210> 408
<211> 179
<212> PRT
<213> Corynebacterium glutamicum

<400> 408
Met Thr Asp Leu His Pro Val Lys Gln Glu Ile Phe Asn Thr Ala Glu
  1               5                  10                  15

Ser Ile Asn Thr Asp Pro Lys Gly Phe Leu Arg Glu Val Asp Thr Phe
             20                  25                  30

Lys Val Thr Asp Phe Gly Leu Tyr Met Ala Arg Gly Ala Asn His Pro
         35                  40                  45

Lys Phe Gly Tyr Leu Glu Ser Trp Leu Leu Pro Glu Leu Gly Leu Arg
     50                  55                  60

Ala Asn Ile Phe His Phe Arg Lys Gly Val Asp Glu Arg Gln Asp Tyr
 65                  70                  75                  80

Tyr Ile Asp Val Ala Glu Ile Arg Val Glu Asp Asn Ile Trp Thr Thr
                 85                  90                  95

Arg Asp Leu Tyr Val Asp Leu Ile Ser Val Cys Gly Glu Pro Val Thr
            100                 105                 110

Val Met Asp Ile Asp Glu Leu Ala Ala Ala Thr Ser Ala Gly Leu Ile
        115                 120                 125

Thr Ala Asp Asp Ala Glu Arg Ala Ile Asp Ala Thr Leu Asn Ala Val
    130                 135                 140

Glu Gly Ile Thr Arg His Gly Asp Asp Pro Met Gln Trp Leu Arg Ser
145                 150                 155                 160

Lys Gly Ile Glu Leu Thr Trp Ala Asp Ala Ser Gln Val Glu Leu Val
                165                 170                 175

Pro Ala Glu


<210> 409
<211> 660
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(637)
<223> FRXA00841
```

<400> 409
gcctccatgt caggcggcct caccacatcc accgaaaacg gttcagcgaa ctgtaatttc 60

atcccgactg ccgtcgtatt cgatgtgagg taagaaaaca atg act gat ctt cat 115
Met Thr Asp Leu His
1 5

ccc gta aag cag gaa att ttc aac act gct gaa tcc ata aac aca gat 163
Pro Val Lys Gln Glu Ile Phe Asn Thr Ala Glu Ser Ile Asn Thr Asp
10 15 20

ccc aag ggg ttt ctc cgc gag gta gac acc ttc aaa gta acc gac ttc 211
Pro Lys Gly Phe Leu Arg Glu Val Asp Thr Phe Lys Val Thr Asp Phe
25 30 35

ggc ctg tac atg gct cgt ggt gca aac cac ccc aag ttc gga tac ttg 259
Gly Leu Tyr Met Ala Arg Gly Ala Asn His Pro Lys Phe Gly Tyr Leu
40 45 50

gaa agc tgg ctc ctc cca gaa ctt gga ttg cgt gcc aac att ttc cac 307
Glu Ser Trp Leu Leu Pro Glu Leu Gly Leu Arg Ala Asn Ile Phe His
55 60 65

ttc cgc aaa ggc gtg gat gaa cgt cag gat tac tac atc gat gtc gct 355
Phe Arg Lys Gly Val Asp Glu Arg Gln Asp Tyr Tyr Ile Asp Val Ala
70 75 80 85

gaa att cgc gtc gaa gac aac atc tgg acc acc cgc gac ctc tac gtg 403
Glu Ile Arg Val Glu Asp Asn Ile Trp Thr Thr Arg Asp Leu Tyr Val
90 95 100

gat ctc atc tct gtc tgc gga gaa cca gta aca gtc atg gac atc gac 451
Asp Leu Ile Ser Val Cys Gly Glu Pro Val Thr Val Met Asp Ile Asp
105 110 115

gaa cta gct gca gca acc tca gca ggg ctt atc act gca gat gac gct 499
Glu Leu Ala Ala Ala Thr Ser Ala Gly Leu Ile Thr Ala Asp Asp Ala
120 125 130

gag cgc gca att gat gcc acc ttg aat gct gtt gaa gga atc acc cgc 547
Glu Arg Ala Ile Asp Ala Thr Leu Asn Ala Val Glu Gly Ile Thr Arg
135 140 145

cac ggc gac gat cct atg cag tgg ctg cgc tcc aag gga atc gaa ctc 595
His Gly Asp Asp Pro Met Gln Trp Leu Arg Ser Lys Gly Ile Glu Leu
150 155 160 165

acc tgg gct gac gcc agc cag gta gag ctc gtc cct gca gag 637
Thr Trp Ala Asp Ala Ser Gln Val Glu Leu Val Pro Ala Glu
170 175

taactacttc ctaaccgctg ctt 660

<210> 410
<211> 179
<212> PRT
<213> Corynebacterium glutamicum

<400> 410

```
Met Thr Asp Leu His Pro Val Lys Gln Glu Ile Phe Asn Thr Ala Glu
 1               5                  10                  15

Ser Ile Asn Thr Asp Pro Lys Gly Phe Leu Arg Glu Val Asp Thr Phe
            20                  25                  30

Lys Val Thr Asp Phe Gly Leu Tyr Met Ala Arg Gly Ala Asn His Pro
        35                  40                  45

Lys Phe Gly Tyr Leu Glu Ser Trp Leu Leu Pro Glu Leu Gly Leu Arg
    50                  55                  60

Ala Asn Ile Phe His Phe Arg Lys Gly Val Asp Glu Arg Gln Asp Tyr
65                  70                  75                  80

Tyr Ile Asp Val Ala Glu Ile Arg Val Glu Asp Asn Ile Trp Thr Thr
                85                  90                  95

Arg Asp Leu Tyr Val Asp Leu Ile Ser Val Cys Gly Glu Pro Val Thr
            100                 105                 110

Val Met Asp Ile Asp Glu Leu Ala Ala Ala Thr Ser Ala Gly Leu Ile
        115                 120                 125

Thr Ala Asp Asp Ala Glu Arg Ala Ile Asp Ala Thr Leu Asn Ala Val
    130                 135                 140

Glu Gly Ile Thr Arg His Gly Asp Asp Pro Met Gln Trp Leu Arg Ser
145                 150                 155                 160

Lys Gly Ile Glu Leu Thr Trp Ala Asp Ala Ser Gln Val Glu Leu Val
                165                 170                 175

Pro Ala Glu
```

Replacement Sheet

<210> 411
<211> 993
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(970)
<223> RXN00846

<400> 411
ctgcgggaga ctcgggtaga agcgaaaaat aacggtatcc tcggggctgc ggatggctgg 60

cctgggggaa tttcaagtgc tgcaagttgg aggaaaaacg atg ttg aag aat gat 115
                                            Met Leu Lys Asn Asp
                                              1   5

ctg tct ggt gct cga gtt gta gct gtg cat gcg cac cct gac gat gag 163
Leu Ser Gly Ala Arg Val Val Ala Val His Ala His Pro Asp Asp Glu
                10   15   20

gcg att acc acc ggt ggt gtg ctt gcg gat ctt gct gct cgt ggc gcc 211
Ala Ile Thr Thr Gly Gly Val Leu Ala Asp Leu Ala Ala Arg Gly Ala
            25   30   35

```
gat gtc acg gta att acc tgc acg ttg ggc gag cag ggt gag gtt atc   259
Asp Val Thr Val Ile Thr Cys Thr Leu Gly Glu Gln Gly Glu Val Ile
         40                  45                  50

ggt gag aca ttc gcg cag cta gtc aac ggt gat gcg gat cag ctt ggc   307
Gly Glu Thr Phe Ala Gln Leu Val Asn Gly Asp Ala Asp Gln Leu Gly
     55                  60                  65

ggg ttt agg atc cat gag ctt tac gcc tcg ctg gag att ctg ggc gtg   355
Gly Phe Arg Ile His Glu Leu Tyr Ala Ser Leu Glu Ile Leu Gly Val
 70                  75                  80                  85

cgt ggc att cat ctg ggt ggc gct ggc tgc tgg agg gat tcc ggt atg   403
Arg Gly Ile His Leu Gly Gly Ala Gly Cys Trp Arg Asp Ser Gly Met
                 90                  95                 100

gtt ggt gat cct gca aat gag cat ccg cgt gcg ttt att cac tct ggt   451
Val Gly Asp Pro Ala Asn Glu His Pro Arg Ala Phe Ile His Ser Gly
            105                 110                 115

gac cgt gca gtg gag caa ttg aaa gaa ctt ctt gcg gaa ttg aag cca   499
Asp Arg Ala Val Glu Gln Leu Lys Glu Leu Leu Ala Glu Leu Lys Pro
        120                 125                 130

cat ctt ttg atc acc tat ggc cct gac ggc ggc tat ggg cac ccc gat   547
His Leu Leu Ile Thr Tyr Gly Pro Asp Gly Gly Tyr Gly His Pro Asp
    135                 140                 145

cac att cgt gcg cat gaa atc acc cac gca gca gcc ggc gag caa cgc   595
His Ile Arg Ala His Glu Ile Thr His Ala Ala Ala Gly Glu Gln Arg
150                 155                 160                 165

att ctg tgg gct gtg agc gac cgt gag gag ctc gag gac ggt cta aag   643
Ile Leu Trp Ala Val Ser Asp Arg Glu Glu Leu Glu Asp Gly Leu Lys
                170                 175                 180

gca atc act ggg ctt cct gaa ggt tgg ggc agg gga gag ctc tct gcg   691
Ala Ile Thr Gly Leu Pro Glu Gly Trp Gly Arg Gly Glu Leu Ser Ala
            185                 190                 195

gtc gat tcc gtg gac ctc tct gtt gag ctg aac gat gaa gtg tat gcc   739
Val Asp Ser Val Asp Leu Ser Val Glu Leu Asn Asp Glu Val Tyr Ala
        200                 205                 210

acc aag gtg gaa tcc atg cgc gcg cat gcg aca caa ttg tgg atc gct   787
Thr Lys Val Glu Ser Met Arg Ala His Ala Thr Gln Leu Trp Ile Ala
    215                 220                 225

gac ggt tcc gta tct cgc acc aac ccg gtt gcc gca cac gca gtg aca   835
Asp Gly Ser Val Ser Arg Thr Asn Pro Val Ala Ala His Ala Val Thr
230                 235                 240                 245

cag cag gac aat gtg aag gtg tgg gcg cta tct aat ttg att gca caa   883
Gln Gln Asp Asn Val Lys Val Trp Ala Leu Ser Asn Leu Ile Ala Gln
                250                 255                 260

ccc atc atg cgc cac gag cac tac caa ctc ggc gcc gga aca cca ctg   931
Pro Ile Met Arg His Glu His Tyr Gln Leu Gly Ala Gly Thr Pro Leu
            265                 270                 275
```

```
cct gaa ggt gca act gga gtg ctt gac gga ctg gag ttc tgacacggtt    980
Pro Glu Gly Ala Thr Gly Val Leu Asp Gly Leu Glu Phe
        280                 285                 290

atggcagaat cta                                                   993


<210> 412
<211> 290
<212> PRT
<213> Corynebacterium glutamicum

<400> 412
Met Leu Lys Asn Asp Leu Ser Gly Ala Arg Val Val Ala Val His Ala
  1               5                  10                  15

His Pro Asp Asp Glu Ala Ile Thr Thr Gly Gly Val Leu Ala Asp Leu
             20                  25                  30

Ala Ala Arg Gly Ala Asp Val Thr Val Ile Thr Cys Thr Leu Gly Glu
         35                  40                  45

Gln Gly Glu Val Ile Gly Glu Thr Phe Ala Gln Leu Val Asn Gly Asp
     50                  55                  60

Ala Asp Gln Leu Gly Gly Phe Arg Ile His Glu Leu Tyr Ala Ser Leu
 65                  70                  75                  80

Glu Ile Leu Gly Val Arg Gly Ile His Leu Gly Gly Ala Gly Cys Trp
                 85                  90                  95

Arg Asp Ser Gly Met Val Gly Asp Pro Ala Asn Glu His Pro Arg Ala
            100                 105                 110

Phe Ile His Ser Gly Asp Arg Ala Val Glu Gln Leu Lys Glu Leu Leu
        115                 120                 125

Ala Glu Leu Lys Pro His Leu Leu Ile Thr Tyr Gly Pro Asp Gly Gly
    130                 135                 140

Tyr Gly His Pro Asp His Ile Arg Ala His Glu Ile Thr His Ala Ala
145                 150                 155                 160

Ala Gly Glu Gln Arg Ile Leu Trp Ala Val Ser Asp Arg Glu Glu Leu
                165                 170                 175

Glu Asp Gly Leu Lys Ala Ile Thr Gly Leu Pro Glu Gly Trp Gly Arg
            180                 185                 190

Gly Glu Leu Ser Ala Val Asp Ser Val Asp Leu Ser Val Glu Leu Asn
        195                 200                 205

Asp Glu Val Tyr Ala Thr Lys Val Glu Ser Met Arg Ala His Ala Thr
    210                 215                 220

Gln Leu Trp Ile Ala Asp Gly Ser Val Ser Arg Thr Asn Pro Val Ala
225                 230                 235                 240

Ala His Ala Val Thr Gln Gln Asp Asn Val Lys Val Trp Ala Leu Ser
                245                 250                 255
```

```
Asn Leu Ile Ala Gln Pro Ile Met Arg His Glu His Tyr Gln Leu Gly
            260                 265                 270

Ala Gly Thr Pro Leu Pro Glu Gly Ala Thr Gly Val Leu Asp Gly Leu
        275                 280                 285

Glu Phe
    290
```

<210> 413
<211> 487
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(487)
<223> FRXA00846

<400> 413

```
ctgcgggaga ctcgggtaga agcgaaaaat aacggtatcc tcggggctgc ggatggctgg 60

cctgggggaa tttcaagtgc tgcaagttgg aggaaaaacg atg ttg aag aat gat   115
                                            Met Leu Lys Asn Asp
                                              1               5

ctg tct ggt gct cga gtt gta gct gtg cat gcg cac cct gac gat gag   163
Leu Ser Gly Ala Arg Val Val Ala Val His Ala His Pro Asp Asp Glu
                 10                  15                  20

gcg att acc acc ggt ggt gtg ctt gcg gat ctt gct gct cgt ggc gcc   211
Ala Ile Thr Thr Gly Gly Val Leu Ala Asp Leu Ala Ala Arg Gly Ala
             25                  30                  35

gat gtc acg gta att acc tgc acg ttg ggc gag cag ggt gag gtt atc   259
Asp Val Thr Val Ile Thr Cys Thr Leu Gly Glu Gln Gly Glu Val Ile
         40                  45                  50

ggt gag aca ttc gcg cag cta gtc aac ggt gat gcg gat cag ctt ggc   307
Gly Glu Thr Phe Ala Gln Leu Val Asn Gly Asp Ala Asp Gln Leu Gly
     55                  60                  65

ggg ttt agg atc cat gag ctt tac gcc tcg ctg gag att ctg ggc gtg   355
Gly Phe Arg Ile His Glu Leu Tyr Ala Ser Leu Glu Ile Leu Gly Val
 70                  75                  80                  85

cgt ggc att cat ctg ggt ggc gct ggc tgc tgg agg gat tcc ggt atg   403
Arg Gly Ile His Leu Gly Gly Ala Gly Cys Trp Arg Asp Ser Gly Met
                 90                  95                 100

gtt ggt gat cct gca aat gag cat ccg cgt gcg ttt att cac tct ggt   451
Val Gly Asp Pro Ala Asn Glu His Pro Arg Ala Phe Ile His Ser Gly
             105                 110                 115

gac cgt gca gtg gag caa ttg aaa gaa ctt ctt gcg                   487
Asp Arg Ala Val Glu Gln Leu Lys Glu Leu Leu Ala
         120                 125
```

<210> 414

<211> 129
<212> PRT
<213> Corynebacterium glutamicum

<400> 414
Met Leu Lys Asn Asp Leu Ser Gly Ala Arg Val Val Ala Val His Ala
1 5 10 15

His Pro Asp Asp Glu Ala Ile Thr Thr Gly Gly Val Leu Ala Asp Leu
20 25 30

Ala Ala Arg Gly Ala Asp Val Thr Val Ile Thr Cys Thr Leu Gly Glu
35 40 45

Gln Gly Glu Val Ile Gly Glu Thr Phe Ala Gln Leu Val Asn Gly Asp
50 55 60

Ala Asp Gln Leu Gly Gly Phe Arg Ile His Glu Leu Tyr Ala Ser Leu
65 70 75 80

Glu Ile Leu Gly Val Arg Gly Ile His Leu Gly Gly Ala Gly Cys Trp
85 90 95

Arg Asp Ser Gly Met Val Gly Asp Pro Ala Asn Glu His Pro Arg Ala
100 105 110

Phe Ile His Ser Gly Asp Arg Ala Val Glu Gln Leu Lys Glu Leu Leu
115 120 125

Ala

<210> 415
<211> 951
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(928)
<223> RXN00850

<400> 415
ggcagttgtg ccggtatacg tggcgtcatg gataatgatc gcataaatga atacagcgaa 60

attacctgtt tcagatattt aggaaggctc acttttcaac atg gct aat cca ttc 115
Met Ala Asn Pro Phe
1 5

tcc aag gca tgg aag tac ctc atg gcg ttg ttc gac tcc aag att gag 163
Ser Lys Ala Trp Lys Tyr Leu Met Ala Leu Phe Asp Ser Lys Ile Glu
10 15 20

gag aac gcg gat cct aag gta cag atc cag caa gcc atc gaa gat gct 211
Glu Asn Ala Asp Pro Lys Val Gln Ile Gln Gln Ala Ile Glu Asp Ala
25 30 35

cag cgc cag cat cag gag ctc tcc cag cag gca gca gct gtt att ggt 259
Gln Arg Gln His Gln Glu Leu Ser Gln Gln Ala Ala Ala Val Ile Gly
40 45 50

```
aac cag cgt cag ctt gaa atg cag ctg aac cgc cgt ctg gct gaa att   307
Asn Gln Arg Gln Leu Glu Met Gln Leu Asn Arg Arg Leu Ala Glu Ile
     55                  60                  65

gag aag ctg cag ggc aac acc cgc cag gct atc cag ctg gct gac aag   355
Glu Lys Leu Gln Gly Asn Thr Arg Gln Ala Ile Gln Leu Ala Asp Lys
 70                  75                  80                  85

gct cgc gct gac ggt gat gtc aag aag gct act gag tac gaa aac gcc   403
Ala Arg Ala Asp Gly Asp Val Lys Lys Ala Thr Glu Tyr Glu Asn Ala
                 90                  95                 100

gct gag gct ttc gct gca cag ctg gtt act gct gag cag tcc gtt gaa   451
Ala Glu Ala Phe Ala Ala Gln Leu Val Thr Ala Glu Gln Ser Val Glu
            105                 110                 115

gat acc aag cag ctc cac gac cag gct ctg cag cag gct gat cag gct   499
Asp Thr Lys Gln Leu His Asp Gln Ala Leu Gln Gln Ala Asp Gln Ala
        120                 125                 130

aag aag gct gtg gag cgt aac tcc atg gct ttg cag cag aag gtt gct   547
Lys Lys Ala Val Glu Arg Asn Ser Met Ala Leu Gln Gln Lys Val Ala
    135                 140                 145

gag cgc acc aag ctt ctg agc cag ctg gag cag gcg aag atg cag gaa   595
Glu Arg Thr Lys Leu Leu Ser Gln Leu Glu Gln Ala Lys Met Gln Glu
150                 155                 160                 165

aag gtt tcc gag tcc ctg aag tcc atg gat tct ttg acc tcc ggc agc   643
Lys Val Ser Glu Ser Leu Lys Ser Met Asp Ser Leu Thr Ser Gly Ser
                170                 175                 180

act cct aac ctg gat caa gtt cgt gag aag att gag cgt cgt tac gct   691
Thr Pro Asn Leu Asp Gln Val Arg Glu Lys Ile Glu Arg Arg Tyr Ala
            185                 190                 195

aac gcg ctt ggc cag gct gag ctt gcg tcc aac tct gtt gag ggc cgc   739
Asn Ala Leu Gly Gln Ala Glu Leu Ala Ser Asn Ser Val Glu Gly Arg
        200                 205                 210

atg gct gag gtt gag cag gct ggc gtt cag atg gct gga cac tcc cgc   787
Met Ala Glu Val Glu Gln Ala Gly Val Gln Met Ala Gly His Ser Arg
    215                 220                 225

ctt gag cag atc cgc gct gag atg gct ggt ggt tcc ctg acc gct ggt   835
Leu Glu Gln Ile Arg Ala Glu Met Ala Gly Gly Ser Leu Thr Ala Gly
230                 235                 240                 245

aac aag cag gag tcc att gag gct cct gca gcg ggc aac aac gtc act   883
Asn Lys Gln Glu Ser Ile Glu Ala Pro Ala Ala Gly Asn Asn Val Thr
                250                 255                 260

gat gac gca gtt gca cag cgc atg cgt gag ctg cgc ggc gag gct       928
Asp Asp Ala Val Ala Gln Arg Met Arg Glu Leu Arg Gly Glu Ala
            265                 270                 275

taaacctgcc acagcagact aaa                                        951
```

<210> 416

<211> 276
<212> PRT
<213> Corynebacterium glutamicum

<400> 416

```
Met Ala Asn Pro Phe Ser Lys Ala Trp Lys Tyr Leu Met Ala Leu Phe
  1               5                  10                  15

Asp Ser Lys Ile Glu Glu Asn Ala Asp Pro Lys Val Gln Ile Gln Gln
             20                  25                  30

Ala Ile Glu Asp Ala Gln Arg Gln His Gln Glu Leu Ser Gln Gln Ala
         35                  40                  45

Ala Ala Val Ile Gly Asn Gln Arg Gln Leu Glu Met Gln Leu Asn Arg
     50                  55                  60

Arg Leu Ala Glu Ile Glu Lys Leu Gln Gly Asn Thr Arg Gln Ala Ile
 65                  70                  75                  80

Gln Leu Ala Asp Lys Ala Arg Ala Asp Gly Asp Val Lys Lys Ala Thr
                 85                  90                  95

Glu Tyr Glu Asn Ala Ala Glu Ala Phe Ala Ala Gln Leu Val Thr Ala
            100                 105                 110

Glu Gln Ser Val Glu Asp Thr Lys Gln Leu His Asp Gln Ala Leu Gln
        115                 120                 125

Gln Ala Asp Gln Ala Lys Lys Ala Val Glu Arg Asn Ser Met Ala Leu
    130                 135                 140

Gln Gln Lys Val Ala Glu Arg Thr Lys Leu Leu Ser Gln Leu Glu Gln
145                 150                 155                 160

Ala Lys Met Gln Glu Lys Val Ser Glu Ser Leu Lys Ser Met Asp Ser
                165                 170                 175

Leu Thr Ser Gly Ser Thr Pro Asn Leu Asp Gln Val Arg Glu Lys Ile
            180                 185                 190

Glu Arg Arg Tyr Ala Asn Ala Leu Gly Gln Ala Glu Leu Ala Ser Asn
        195                 200                 205

Ser Val Glu Gly Arg Met Ala Glu Val Glu Gln Ala Gly Val Gln Met
    210                 215                 220

Ala Gly His Ser Arg Leu Glu Gln Ile Arg Ala Glu Met Ala Gly Gly
225                 230                 235                 240

Ser Leu Thr Ala Gly Asn Lys Gln Glu Ser Ile Glu Ala Pro Ala Ala
                245                 250                 255

Gly Asn Asn Val Thr Asp Asp Ala Val Ala Gln Arg Met Arg Glu Leu
            260                 265                 270

Arg Gly Glu Ala
        275
```

<210> 417

<211> 336
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(313)
<223> RXN00854

<400> 417
ttcatccgcc ctggaagacg gtcatgacgg ggacccttct tagggtcgct gtcggagatt 60

ggacacgtaa cttctgtgct tgcgctgtat tatcgtcccc atg cgt tta tcg gag 115
Met Arg Leu Ser Glu
1 5

ttt cgg caa ctc att gaa gat gaa ttc gga gaa gcc aaa ggg gag tgg 163
Phe Arg Gln Leu Ile Glu Asp Glu Phe Gly Glu Ala Lys Gly Glu Trp
10 15 20

att gca cac tcg cat gtg att ggt gcc ctc ggc gtc act gca gat gtt 211
Ile Ala His Ser His Val Ile Gly Ala Leu Gly Val Thr Ala Asp Val
25 30 35

gca gta gat acc ggg gtt gat ctg cgc gat gta tgg gaa caa ctg tgc 259
Ala Val Asp Thr Gly Val Asp Leu Arg Asp Val Trp Glu Gln Leu Cys
40 45 50

att gat ttc agt gtt ccc gaa gag cga cga ctt ggt aaa gat gaa cca 307
Ile Asp Phe Ser Val Pro Glu Glu Arg Arg Leu Gly Lys Asp Glu Pro
55 60 65

ggg ttc tagcttgttc gaggggttc gca 336
Gly Phe
70

<210> 418
<211> 71
<212> PRT
<213> Corynebacterium glutamicum

<400> 418
Met Arg Leu Ser Glu Phe Arg Gln Leu Ile Glu Asp Glu Phe Gly Glu
1 5 10 15

Ala Lys Gly Glu Trp Ile Ala His Ser His Val Ile Gly Ala Leu Gly
20 25 30

Val Thr Ala Asp Val Ala Val Asp Thr Gly Val Asp Leu Arg Asp Val
35 40 45

Trp Glu Gln Leu Cys Ile Asp Phe Ser Val Pro Glu Glu Arg Arg Leu
50 55 60

Gly Lys Asp Glu Pro Gly Phe
65 70

<210> 419
<211> 336

<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(313)
<223> FRXA00854

<400> 419
ttcatccgcc ctggaagacg gtcatgacgg ggacccttct tagggtcgct gtcggagatt 60

ggacacgtaa cttctgtgct tgcgctgtat tatcgtcccc atg cgt tta tcg gag 115
Met Arg Leu Ser Glu
1 5

ttt cgg caa ctc att gaa gat gaa ttc gga gaa gcc aaa ggg gag tgg 163
Phe Arg Gln Leu Ile Glu Asp Glu Phe Gly Glu Ala Lys Gly Glu Trp
10 15 20

att gca cac tcg cat gtg att ggt gcc ctc ggc gtc act gca gat gtt 211
Ile Ala His Ser His Val Ile Gly Ala Leu Gly Val Thr Ala Asp Val
25 30 35

gca gta gat acc ggg gtt gat ctg cgc gat gta tgg gaa caa ctg tgc 259
Ala Val Asp Thr Gly Val Asp Leu Arg Asp Val Trp Glu Gln Leu Cys
40 45 50

att gat ttc agt gtt ccc gaa gag cga cga ctt ggt aaa gat gaa cca 307
Ile Asp Phe Ser Val Pro Glu Glu Arg Arg Leu Gly Lys Asp Glu Pro
55 60 65

ggg ttc tagcttgttc gaggggggttc gca 336
Gly Phe
70

<210> 420
<211> 71
<212> PRT
<213> Corynebacterium glutamicum

<400> 420
Met Arg Leu Ser Glu Phe Arg Gln Leu Ile Glu Asp Glu Phe Gly Glu
1 5 10 15

Ala Lys Gly Glu Trp Ile Ala His Ser His Val Ile Gly Ala Leu Gly
20 25 30

Val Thr Ala Asp Val Ala Val Asp Thr Gly Val Asp Leu Arg Asp Val
35 40 45

Trp Glu Gln Leu Cys Ile Asp Phe Ser Val Pro Glu Glu Arg Arg Leu
50 55 60

Gly Lys Asp Glu Pro Gly Phe
65 70

<210> 421
<211> 408
<212> DNA

<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(385)
<223> RXN00855

<400> 421
taaaaacctc tcgacggacg aagcgccaca aaagcaagag aagaatataa gtgaaccaaa 60

ttccgtttag tgtacgtcta gacgcctaaa cttacctgtt atg act tat ttt gcc 115
Met Thr Tyr Phe Ala
1 5

gtg ctt tac aca tac aac cca gac agc gag aaa gtc gct gaa gtt cgt 163
Val Leu Tyr Thr Tyr Asn Pro Asp Ser Glu Lys Val Ala Glu Val Arg
10 15 20

acc gtc cac cgc gag ttc att gcc aac ctt cat gcg gag ggc aaa atc 211
Thr Val His Arg Glu Phe Ile Ala Asn Leu His Ala Glu Gly Lys Ile
25 30 35

gtt ggc tcc ggt cct ttc gtg gac ggc gac ggt ggc gcg ctg att gtc 259
Val Gly Ser Gly Pro Phe Val Asp Gly Asp Gly Gly Ala Leu Ile Val
40 45 50

atc aag ttg gaa gaa ggc tcc aac ctt gtt gat gct gaa acc ctg atg 307
Ile Lys Leu Glu Glu Gly Ser Asn Leu Val Asp Ala Glu Thr Leu Met
55 60 65

aac aat gat cca ttc cac gta gaa aac gtg ctg gac aac cgc gtc atc 355
Asn Asn Asp Pro Phe His Val Glu Asn Val Leu Asp Asn Arg Val Ile
70 75 80 85

cgt agc tgg aac cct gtg acc aaa gat ttc taggcaactt tttctttaac 405
Arg Ser Trp Asn Pro Val Thr Lys Asp Phe
90 95

aat 408

<210> 422
<211> 95
<212> PRT
<213> Corynebacterium glutamicum

<400> 422
Met Thr Tyr Phe Ala Val Leu Tyr Thr Tyr Asn Pro Asp Ser Glu Lys
1 5 10 15

Val Ala Glu Val Arg Thr Val His Arg Glu Phe Ile Ala Asn Leu His
20 25 30

Ala Glu Gly Lys Ile Val Gly Ser Gly Pro Phe Val Asp Gly Asp Gly
35 40 45

Gly Ala Leu Ile Val Ile Lys Leu Glu Glu Gly Ser Asn Leu Val Asp
50 55 60

Ala Glu Thr Leu Met Asn Asn Asp Pro Phe His Val Glu Asn Val Leu
65 70 75 80

```
Asp Asn Arg Val Ile Arg Ser Trp Asn Pro Val Thr Lys Asp Phe
                 85                  90                  95


<210> 423
<211> 408
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(385)
<223> FRXA00855

<400> 423
taaaaacctc tcgacggacg aagcgccaca aaagcaagag aagaatataa gtgaaccaaa 60

ttccgtttag tgtacgtcta gacgcctaaa cttacctgtt atg act tat ttt gcc   115
                                            Met Thr Tyr Phe Ala
                                              1               5

gtg ctt tac aca tac aac cca gac agc gag aaa gtc gct gaa gtt cgt   163
Val Leu Tyr Thr Tyr Asn Pro Asp Ser Glu Lys Val Ala Glu Val Arg
                10                  15                  20

acc gtc cac cgc gag ttc att gcc aac ctt cat gcg gag ggc aaa atc   211
Thr Val His Arg Glu Phe Ile Ala Asn Leu His Ala Glu Gly Lys Ile
            25                  30                  35

gtt ggc tcc ggt cct ttc gtg gac ggc gac ggt ggc gcg ctg att gtc   259
Val Gly Ser Gly Pro Phe Val Asp Gly Asp Gly Gly Ala Leu Ile Val
        40                  45                  50

atc aag ttg gaa gaa ggc tcc aac ctt gtt gat gct gaa acc ctg atg   307
Ile Lys Leu Glu Glu Gly Ser Asn Leu Val Asp Ala Glu Thr Leu Met
    55                  60                  65

aac aat gat cca ttc cac gta gaa aac gtg ctg gac aac cgc gtc atc   355
Asn Asn Asp Pro Phe His Val Glu Asn Val Leu Asp Asn Arg Val Ile
70                  75                  80                  85

cgt agc tgg aac cct gtg acc aaa gat ttc taggcaactt tttctttaac     405
Arg Ser Trp Asn Pro Val Thr Lys Asp Phe
                90                  95

aat                                                               408


<210> 424
<211> 95
<212> PRT
<213> Corynebacterium glutamicum

<400> 424
Met Thr Tyr Phe Ala Val Leu Tyr Thr Tyr Asn Pro Asp Ser Glu Lys
  1               5                  10                  15

Val Ala Glu Val Arg Thr Val His Arg Glu Phe Ile Ala Asn Leu His
            20                  25                  30
```

```
Ala Glu Gly Lys Ile Val Gly Ser Gly Pro Phe Val Asp Gly Asp Gly
         35                  40                  45

Gly Ala Leu Ile Val Ile Lys Leu Glu Glu Gly Ser Asn Leu Val Asp
     50                  55                  60

Ala Glu Thr Leu Met Asn Asn Asp Pro Phe His Val Glu Asn Val Leu
 65                  70                  75                  80

Asp Asn Arg Val Ile Arg Ser Trp Asn Pro Val Thr Lys Asp Phe
                 85                  90                  95


<210> 425
<211> 1044
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1021)
<223> RXN00869

<400> 425
gccaacaccg cgggtgcgct tgtggcgtcc cgtcttgaat gctccaccgc aatgcctact 60

accgatgagg tggaagcctc cctcaaccag aaagtctgat atg act cct ccg att   115
                                            Met Thr Pro Pro Ile
                                              1               5

atc tcc cca gag agc ttt gaa gcc cta agg cgg atg cgt gcg gct gaa   163
Ile Ser Pro Glu Ser Phe Glu Ala Leu Arg Arg Met Arg Ala Ala Glu
                 10                  15                  20

ccc acg atg gtg gcg gaa cgt ttc aag cag cgc cgt aag cgt gaa ctg   211
Pro Thr Met Val Ala Glu Arg Phe Lys Gln Arg Arg Lys Arg Glu Leu
             25                  30                  35

ctc ggt gag gac ggc aag ctg ttt atc gtg gct gcc gac cac cca gcg   259
Leu Gly Glu Asp Gly Lys Leu Phe Ile Val Ala Ala Asp His Pro Ala
         40                  45                  50

cgc ggc gca ctt gct gtt ggc gac aat gaa acc gcc atg gct aac cgc   307
Arg Gly Ala Leu Ala Val Gly Asp Asn Glu Thr Ala Met Ala Asn Arg
     55                  60                  65

tat gaa ctg ctc gaa cgc atg gct atc gca ctg tct cgc ccg ggt gtg   355
Tyr Glu Leu Leu Glu Arg Met Ala Ile Ala Leu Ser Arg Pro Gly Val
 70                  75                  80                  85

gat ggt gtg ctg gga act cca gac atc att gat gat ctg gcg gcg ctc   403
Asp Gly Val Leu Gly Thr Pro Asp Ile Ile Asp Asp Leu Ala Ala Leu
                 90                  95                 100

gga ctg ctc gat gac aag atc gtg gtt ggc tcc atg aac cgt ggt ggc   451
Gly Leu Leu Asp Asp Lys Ile Val Val Gly Ser Met Asn Arg Gly Gly
            105                 110                 115

ctg cgt ggc gct tcc ttt gaa atg gat gat cgc tac acc ggc tac aac   499
Leu Arg Gly Ala Ser Phe Glu Met Asp Asp Arg Tyr Thr Gly Tyr Asn
        120                 125                 130
```

```
gtg tcc tcc atg gtt gat cgt ggc gtg gat ttc gcg aaa acc cta gtg   547
Val Ser Ser Met Val Asp Arg Gly Val Asp Phe Ala Lys Thr Leu Val
    135                 140                 145

cgc atc aac ttg agc gac gcc gga acc gcc ccg acc ttg gaa gcc acc   595
Arg Ile Asn Leu Ser Asp Ala Gly Thr Ala Pro Thr Leu Glu Ala Thr
150                 155                 160                 165

gcg cat gca gtc aat gag gct gca gca gca cag ctg ccc atc atg ctc   643
Ala His Ala Val Asn Glu Ala Ala Ala Gln Leu Pro Ile Met Leu
                170                 175                 180

gag ccg ttc atg agt aac tgg gta aac ggc aag gtg gtc aat gat ctt   691
Glu Pro Phe Met Ser Asn Trp Val Asn Gly Lys Val Val Asn Asp Leu
            185                 190                 195

tcc acc gat gca gtt atc caa tct gtc gcc att gct gct ggt ctg ggc   739
Ser Thr Asp Ala Val Ile Gln Ser Val Ala Ile Ala Ala Gly Leu Gly
        200                 205                 210

aat gat tct tcc tat acc tgg atg aag ctt cca gtg gtg gag gag atg   787
Asn Asp Ser Ser Tyr Thr Trp Met Lys Leu Pro Val Val Glu Glu Met
    215                 220                 225

gag cgc gtc atg gaa tcc acc acc atg cca acc ctg ttg ttg ggc ggc   835
Glu Arg Val Met Glu Ser Thr Thr Met Pro Thr Leu Leu Leu Gly Gly
230                 235                 240                 245

gaa ggc ggc aac gat cca gat gcc acc ttc gca tcc tgg gag cat gca   883
Glu Gly Gly Asn Asp Pro Asp Ala Thr Phe Ala Ser Trp Glu His Ala
                250                 255                 260

ctc acc ctg ccg ggt gtg cgt ggc ctg acc gtg gga cgc act ctg ctg   931
Leu Thr Leu Pro Gly Val Arg Gly Leu Thr Val Gly Arg Thr Leu Leu
            265                 270                 275

tat ccg caa gac ggc gat gtc gcc gcc gct gtt gat acc gca gcg cga   979
Tyr Pro Gln Asp Gly Asp Val Ala Ala Ala Val Asp Thr Ala Ala Arg
        280                 285                 290

ctt gtt cac aca gat att caa caa ttc act tcg cag agc att          1021
Leu Val His Thr Asp Ile Gln Gln Phe Thr Ser Gln Ser Ile
    295                 300                 305

taaggaattt acacacatgt ctg                                       1044
```

<210> 426
<211> 307
<212> PRT
<213> Corynebacterium glutamicum

<400> 426

```
Met Thr Pro Pro Ile Ile Ser Pro Glu Ser Phe Glu Ala Leu Arg Arg
  1               5                  10                  15

Met Arg Ala Ala Glu Pro Thr Met Val Ala Glu Arg Phe Lys Gln Arg
             20                  25                  30

Arg Lys Arg Glu Leu Leu Gly Glu Asp Gly Lys Leu Phe Ile Val Ala
```

```
         35                  40                  45

Ala Asp His Pro Ala Arg Gly Ala Leu Ala Val Gly Asp Asn Glu Thr
     50                  55                  60

Ala Met Ala Asn Arg Tyr Glu Leu Leu Glu Arg Met Ala Ile Ala Leu
 65                  70                  75                  80

Ser Arg Pro Gly Val Asp Gly Val Leu Gly Thr Pro Asp Ile Ile Asp
                 85                  90                  95

Asp Leu Ala Ala Leu Gly Leu Leu Asp Asp Lys Ile Val Val Gly Ser
            100                 105                 110

Met Asn Arg Gly Gly Leu Arg Gly Ala Ser Phe Glu Met Asp Asp Arg
        115                 120                 125

Tyr Thr Gly Tyr Asn Val Ser Ser Met Val Asp Arg Gly Val Asp Phe
    130                 135                 140

Ala Lys Thr Leu Val Arg Ile Asn Leu Ser Asp Ala Gly Thr Ala Pro
145                 150                 155                 160

Thr Leu Glu Ala Thr Ala His Ala Val Asn Glu Ala Ala Ala Ala Gln
                165                 170                 175

Leu Pro Ile Met Leu Glu Pro Phe Met Ser Asn Trp Val Asn Gly Lys
            180                 185                 190

Val Val Asn Asp Leu Ser Thr Asp Ala Val Ile Gln Ser Val Ala Ile
        195                 200                 205

Ala Ala Gly Leu Gly Asn Asp Ser Ser Tyr Thr Trp Met Lys Leu Pro
    210                 215                 220

Val Val Glu Glu Met Glu Arg Val Met Glu Ser Thr Thr Met Pro Thr
225                 230                 235                 240

Leu Leu Leu Gly Gly Glu Gly Gly Asn Asp Pro Asp Ala Thr Phe Ala
                245                 250                 255

Ser Trp Glu His Ala Leu Thr Leu Pro Gly Val Arg Gly Leu Thr Val
            260                 265                 270

Gly Arg Thr Leu Leu Tyr Pro Gln Asp Gly Asp Val Ala Ala Ala Val
        275                 280                 285

Asp Thr Ala Ala Arg Leu Val His Thr Asp Ile Gln Gln Phe Thr Ser
    290                 295                 300

Gln Ser Ile
305
```

<210> 427
<211> 815
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS

<222> (1)..(792)
<223> FRXA00869

<400> 427

```
ctg ttt atc gtg gct gcc gac cac cca gcg cgc ggc gca ctt gct gtt   48
Leu Phe Ile Val Ala Ala Asp His Pro Ala Arg Gly Ala Leu Ala Val
  1               5                  10                  15

ggc gac aat gaa ccc gcc atg gct aac cgc tat gaa ctg ctc gaa cgc   96
Gly Asp Asn Glu Pro Ala Met Ala Asn Arg Tyr Glu Leu Leu Glu Arg
             20                  25                  30

atg gct atc gca ctg tct cgc ccg ggt gtg gat ggt gtg ctg gga act   144
Met Ala Ile Ala Leu Ser Arg Pro Gly Val Asp Gly Val Leu Gly Thr
         35                  40                  45

cca gac atc att gat gat ctg gcg gcg ctc gga ctg ctc gat gac aag   192
Pro Asp Ile Ile Asp Asp Leu Ala Ala Leu Gly Leu Leu Asp Asp Lys
     50                  55                  60

atc gtg gtt ggc tcc atg aac cgt ggt ggc ctg cgt ggc gct tcc ttt   240
Ile Val Val Gly Ser Met Asn Arg Gly Gly Leu Arg Gly Ala Ser Phe
 65                  70                  75                  80

gaa atg gat gat cgc tac acc ggc tac aac gtg tcc tcc atg gtt gat   288
Glu Met Asp Asp Arg Tyr Thr Gly Tyr Asn Val Ser Ser Met Val Asp
                 85                  90                  95

cgt ggc gtg gat ttc gcg aaa acc cta gtg cgc atc aac ttg agc gac   336
Arg Gly Val Asp Phe Ala Lys Thr Leu Val Arg Ile Asn Leu Ser Asp
            100                 105                 110

gcc gga acc gcc ccg acc ttg gaa gcc acc gcg cat gca gtc aat gag   384
Ala Gly Thr Ala Pro Thr Leu Glu Ala Thr Ala His Ala Val Asn Glu
        115                 120                 125

gct gca gca gca cag ctg ccc atc atg ctc gag ccg ttc atg agt aac   432
Ala Ala Ala Ala Gln Leu Pro Ile Met Leu Glu Pro Phe Met Ser Asn
    130                 135                 140

tgg gta aac ggc aag gtg gtc aat gat ctt tcc acc gat gca gtt atc   480
Trp Val Asn Gly Lys Val Val Asn Asp Leu Ser Thr Asp Ala Val Ile
145                 150                 155                 160

caa tct gtc gcc att gct gct ggt ctg ggc aat gat tct tcc tat acc   528
Gln Ser Val Ala Ile Ala Ala Gly Leu Gly Asn Asp Ser Ser Tyr Thr
                165                 170                 175

tgg atg aag ctt cca gtg gtg gag gag atg gag cgc gtc atg gaa tcc   576
Trp Met Lys Leu Pro Val Val Glu Glu Met Glu Arg Val Met Glu Ser
            180                 185                 190

acc acc atg cca acc ctg ttg ttg ggc ggc gaa ggc ggc aac gat cca   624
Thr Thr Met Pro Thr Leu Leu Leu Gly Gly Glu Gly Gly Asn Asp Pro
        195                 200                 205

gat gcc acc ttc gca tcc tgg gag cat gca ctc acc ctg ccg ggt gtg   672
Asp Ala Thr Phe Ala Ser Trp Glu His Ala Leu Thr Leu Pro Gly Val
    210                 215                 220

cgt ggc ctg acc gtg gga cgc act ctg ctg tat ccg caa gac ggc gat   720
```

```
Arg Gly Leu Thr Val Gly Arg Thr Leu Leu Tyr Pro Gln Asp Gly Asp
225                 230                 235                 240

gtc gcc gcc gct gtt gat acc gca gcg cga ctt gtt cac aca gat att   768
Val Ala Ala Ala Val Asp Thr Ala Ala Arg Leu Val His Thr Asp Ile
                245                 250                 255

caa caa ttc act tcg cag agc att taaggaattt acacacatgt ctg         815
Gln Gln Phe Thr Ser Gln Ser Ile
            260


<210> 428
<211> 264
<212> PRT
<213> Corynebacterium glutamicum

<400> 428
Leu Phe Ile Val Ala Ala Asp His Pro Ala Arg Gly Ala Leu Ala Val
  1               5                  10                  15

Gly Asp Asn Glu Pro Ala Met Ala Asn Arg Tyr Glu Leu Leu Glu Arg
             20                  25                  30

Met Ala Ile Ala Leu Ser Arg Pro Gly Val Asp Gly Val Leu Gly Thr
         35                  40                  45

Pro Asp Ile Ile Asp Asp Leu Ala Ala Leu Gly Leu Leu Asp Asp Lys
     50                  55                  60

Ile Val Val Gly Ser Met Asn Arg Gly Gly Leu Arg Gly Ala Ser Phe
 65                  70                  75                  80

Glu Met Asp Asp Arg Tyr Thr Gly Tyr Asn Val Ser Ser Met Val Asp
                 85                  90                  95

Arg Gly Val Asp Phe Ala Lys Thr Leu Val Arg Ile Asn Leu Ser Asp
            100                 105                 110

Ala Gly Thr Ala Pro Thr Leu Glu Ala Thr Ala His Ala Val Asn Glu
        115                 120                 125

Ala Ala Ala Ala Gln Leu Pro Ile Met Leu Glu Pro Phe Met Ser Asn
    130                 135                 140

Trp Val Asn Gly Lys Val Val Asn Asp Leu Ser Thr Asp Ala Val Ile
145                 150                 155                 160

Gln Ser Val Ala Ile Ala Ala Gly Leu Gly Asn Asp Ser Ser Tyr Thr
                165                 170                 175

Trp Met Lys Leu Pro Val Val Glu Glu Met Glu Arg Val Met Glu Ser
            180                 185                 190

Thr Thr Met Pro Thr Leu Leu Leu Gly Gly Glu Gly Gly Asn Asp Pro
        195                 200                 205

Asp Ala Thr Phe Ala Ser Trp Glu His Ala Leu Thr Leu Pro Gly Val
    210                 215                 220

Arg Gly Leu Thr Val Gly Arg Thr Leu Leu Tyr Pro Gln Asp Gly Asp
```

```
225                 230                 235                 240

Val Ala Ala Ala Val Asp Thr Ala Ala Arg Leu Val His Thr Asp Ile
                245                 250                 255

Gln Gln Phe Thr Ser Gln Ser Ile
            260
```

<210> 429
<211> 753
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(730)
<223> RXN00915

<400> 429

```
cttggctgca ggtccaccat cagcacaggt ctttgacatg aacgtagctc gccgcgacgt 60

ttcttcagga ccttctctac ctggtgaggg tgagttctaa atg tcc gcc gcc tat   115
                                              Met Ser Ala Ala Tyr
                                                1               5

tcg cag gac acc att ttg acg gtg ttt ctg ggg agg ggt ctg acc gct   163
Ser Gln Asp Thr Ile Leu Thr Val Phe Leu Gly Arg Gly Leu Thr Ala
                10                  15                  20

gaa ggg atc cga cag acc cta gaa gac ttc gca gaa acc ggc cta gtc   211
Glu Gly Ile Arg Gln Thr Leu Glu Asp Phe Ala Glu Thr Gly Leu Val
            25                  30                  35

cgc aac ctg gtg tgg att gat gcc gat agt ttc cac gag tct tca tct   259
Arg Asn Leu Val Trp Ile Asp Ala Asp Ser Phe His Glu Ser Ser Ser
        40                  45                  50

gaa gtc acc cac ttg gca acc aac caa gac ggt ctt ccg gag ctt cag   307
Glu Val Thr His Leu Ala Thr Asn Gln Asp Gly Leu Pro Glu Leu Gln
    55                  60                  65

cga cga cct ttc aat gag ttg gtg tcc cgg tca cga acc acc aag ctt   355
Arg Arg Pro Phe Asn Glu Leu Val Ser Arg Ser Arg Thr Thr Lys Leu
70                  75                  80                  85

cac atc ggt gtc atc aac gtc att gat ggc agc gaa ggc atg ctt cat   403
His Ile Gly Val Ile Asn Val Ile Asp Gly Ser Glu Gly Met Leu His
                90                  95                  100

gca gaa gaa ctc aac cca ttg gtt ggg atc atc gac agt gtc tgt tca   451
Ala Glu Glu Leu Asn Pro Leu Val Gly Ile Ile Asp Ser Val Cys Ser
            105                 110                 115

cac cac caa att cac cga tcc aac gtg atg atc ggt gcg gtg gct gcc   499
His His Gln Ile His Arg Ser Asn Val Met Ile Gly Ala Val Ala Ala
        120                 125                 130

aca ctt gat gag gaa ctt cca att ctt cgt ggt tat gtg aac ctg atg   547
Thr Leu Asp Glu Glu Leu Pro Ile Leu Arg Gly Tyr Val Asn Leu Met
    135                 140                 145
```

```
ctg gca cct gaa gat agc cac agc cca ggc acc gca aca gtg acc tac   595
Leu Ala Pro Glu Asp Ser His Ser Pro Gly Thr Ala Thr Val Thr Tyr
150                 155                 160                 165

cgt cat ggt ttc agc gat cac cgt tta ccc tgc act gcg tgg cta ata   643
Arg His Gly Phe Ser Asp His Arg Leu Pro Cys Thr Ala Trp Leu Ile
                170                 175                 180

tcg cca gct tgt acg gac tgt ggg aag gca gca cat cca cac caa tcg   691
Ser Pro Ala Cys Thr Asp Cys Gly Lys Ala Ala His Pro His Gln Ser
            185                 190                 195

aac agc tcg tac ctg cga aag gtt cca gct ttc gtt tgg tgaggtcttt    740
Asn Ser Ser Tyr Leu Arg Lys Val Pro Ala Phe Val Trp
        200                 205                 210

ttacaggcga att                                                   753


<210> 430
<211> 210
<212> PRT
<213> Corynebacterium glutamicum

<400> 430
Met Ser Ala Ala Tyr Ser Gln Asp Thr Ile Leu Thr Val Phe Leu Gly
  1               5                  10                  15

Arg Gly Leu Thr Ala Glu Gly Ile Arg Gln Thr Leu Glu Asp Phe Ala
             20                  25                  30

Glu Thr Gly Leu Val Arg Asn Leu Val Trp Ile Asp Ala Asp Ser Phe
         35                  40                  45

His Glu Ser Ser Ser Glu Val Thr His Leu Ala Thr Asn Gln Asp Gly
     50                  55                  60

Leu Pro Glu Leu Gln Arg Arg Pro Phe Asn Glu Leu Val Ser Arg Ser
 65                  70                  75                  80

Arg Thr Thr Lys Leu His Ile Gly Val Ile Asn Val Ile Asp Gly Ser
                 85                  90                  95

Glu Gly Met Leu His Ala Glu Glu Leu Asn Pro Leu Val Gly Ile Ile
            100                 105                 110

Asp Ser Val Cys Ser His His Gln Ile His Arg Ser Asn Val Met Ile
        115                 120                 125

Gly Ala Val Ala Ala Thr Leu Asp Glu Glu Leu Pro Ile Leu Arg Gly
    130                 135                 140

Tyr Val Asn Leu Met Leu Ala Pro Glu Asp Ser His Ser Pro Gly Thr
145                 150                 155                 160

Ala Thr Val Thr Tyr Arg His Gly Phe Ser Asp His Arg Leu Pro Cys
                165                 170                 175

Thr Ala Trp Leu Ile Ser Pro Ala Cys Thr Asp Cys Gly Lys Ala Ala
            180                 185                 190
```

```
His Pro His Gln Ser Asn Ser Ser Tyr Leu Arg Lys Val Pro Ala Phe
        195                 200                 205

Val Trp
    210


<210> 431
<211> 610
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(610)
<223> FRXA00915

<400> 431
cttggctgca ggtccaccat cagcacaggt ctttgacatg aacgtagctc gccgcgacgt 60

ttcttcagga ccttctctac ctggtgaggg tgagttctaa atg tcc gcc gcc tat   115
                                            Met Ser Ala Ala Tyr
                                              1               5

tcg cag gac acc att ttg acg gtg ttt ctg ggg agg ggt ctg acc gct   163
Ser Gln Asp Thr Ile Leu Thr Val Phe Leu Gly Arg Gly Leu Thr Ala
                10                  15                  20

gaa ggg atc cga cag acc cta gaa gac ttc gca gaa acc ggc cta gtc   211
Glu Gly Ile Arg Gln Thr Leu Glu Asp Phe Ala Glu Thr Gly Leu Val
            25                  30                  35

cgc aac ctg gtg tgg att gat gcc gat agt ttc cac gag tct tca tct   259
Arg Asn Leu Val Trp Ile Asp Ala Asp Ser Phe His Glu Ser Ser Ser
        40                  45                  50

gaa gtc acc cac ttg gca acc aac caa gac ggt ctt ccg gag ctt cag   307
Glu Val Thr His Leu Ala Thr Asn Gln Asp Gly Leu Pro Glu Leu Gln
    55                  60                  65

cga cga cct ttc aat gag ttg gtg tcc cgg tca cga acc acc aag ctt   355
Arg Arg Pro Phe Asn Glu Leu Val Ser Arg Ser Arg Thr Thr Lys Leu
70                  75                  80                  85

cac atc ggt gtc atc aac gtc att gat ggc agc gaa ggc atg ctt cat   403
His Ile Gly Val Ile Asn Val Ile Asp Gly Ser Glu Gly Met Leu His
                90                  95                  100

gca gaa gaa ctc aac cca ttg gtt ggg atc atc gac agt gtc tgt tca   451
Ala Glu Glu Leu Asn Pro Leu Val Gly Ile Ile Asp Ser Val Cys Ser
            105                 110                 115

cac cac caa att cac cga tcc aac gtg atg atc ggt gcg gtg gct gcc   499
His His Gln Ile His Arg Ser Asn Val Met Ile Gly Ala Val Ala Ala
        120                 125                 130

aca ctt gat gag gaa ctt cca att ctt cgt ggt tat gtg aac ctg atg   547
Thr Leu Asp Glu Glu Leu Pro Ile Leu Arg Gly Tyr Val Asn Leu Met
    135                 140                 145
```

```
ctg gca cct gaa gat agc cac agc cca ggc acc gca aca gtg acc tac   595
Leu Ala Pro Glu Asp Ser His Ser Pro Gly Thr Ala Thr Val Thr Tyr
150                 155                 160                 165

cgt cat ggt ttc agc                                           610
Arg His Gly Phe Ser
               170
```

<210> 432
<211> 170
<212> PRT
<213> Corynebacterium glutamicum

<400> 432

```
Met Ser Ala Ala Tyr Ser Gln Asp Thr Ile Leu Thr Val Phe Leu Gly
  1               5                  10                  15

Arg Gly Leu Thr Ala Glu Gly Ile Arg Gln Thr Leu Glu Asp Phe Ala
             20                  25                  30

Glu Thr Gly Leu Val Arg Asn Leu Val Trp Ile Asp Ala Asp Ser Phe
         35                  40                  45

His Glu Ser Ser Ser Glu Val Thr His Leu Ala Thr Asn Gln Asp Gly
     50                  55                  60

Leu Pro Glu Leu Gln Arg Arg Pro Phe Asn Glu Leu Val Ser Arg Ser
 65                  70                  75                  80

Arg Thr Thr Lys Leu His Ile Gly Val Ile Asn Val Ile Asp Gly Ser
                 85                  90                  95

Glu Gly Met Leu His Ala Glu Glu Leu Asn Pro Leu Val Gly Ile Ile
            100                 105                 110

Asp Ser Val Cys Ser His His Gln Ile His Arg Ser Asn Val Met Ile
        115                 120                 125

Gly Ala Val Ala Ala Thr Leu Asp Glu Glu Leu Pro Ile Leu Arg Gly
    130                 135                 140

Tyr Val Asn Leu Met Leu Ala Pro Glu Asp Ser His Ser Pro Gly Thr
145                 150                 155                 160

Ala Thr Val Thr Tyr Arg His Gly Phe Ser
                165                 170
```

<210> 433
<211> 2802
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2779)
<223> RXN00917

<400> 433

```
tgccgtggaa gaaagcgctc tttactgcga cagccgtcct attggtgttt gctgttgtgt 60
```

```
ggtcggcctt ggatattgcc ctgtgggtag gaaagcagtc atg gtg aac acg ttg   115
                                              Met Val Asn Thr Leu
                                                1               5

aac tct aaa acc gtg aat gta ccc cgt ttt gcc aga ggc gtt gtt gct   163
Asn Ser Lys Thr Val Asn Val Pro Arg Phe Ala Arg Gly Val Val Ala
                  10                  15                  20

gca gcc aca gcg cta ttt ttt ggc gct ttg gta agc ctc gcg cct agt   211
Ala Ala Thr Ala Leu Phe Phe Gly Ala Leu Val Ser Leu Ala Pro Ser
              25                  30                  35

gcg ttg gcg cag gaa cca cct gca gtt gag gcc gga gcg tca ggt tct   259
Ala Leu Ala Gln Glu Pro Pro Ala Val Glu Ala Gly Ala Ser Gly Ser
          40                  45                  50

ttg agc aac ctg ggt gcc tgc atc gct gat aaa ggc act ctt gat gtc   307
Leu Ser Asn Leu Gly Ala Cys Ile Ala Asp Lys Gly Thr Leu Asp Val
      55                  60                  65

atc atc atg atc gat gag aca gaa tcc ttg atc cat gaa gct cgt gac   355
Ile Ile Met Ile Asp Glu Thr Glu Ser Leu Ile His Glu Ala Arg Asp
  70                  75                  80                  85

ggc gtg gtc aac gcc aat gaa cca ggc gcg gac gca cag cac cac cgt   403
Gly Val Val Asn Ala Asn Glu Pro Gly Ala Asp Ala Gln His His Arg
                  90                  95                 100

gtt cct gca gca cag agc ttt gtg gat gag ctt cta gcc aag caa agc   451
Val Pro Ala Ala Gln Ser Phe Val Asp Glu Leu Leu Ala Lys Gln Ser
             105                 110                 115

gat ggt gat ctg aac acc cgc atc cgt gtt gct ggt ttc ggc cag acg   499
Asp Gly Asp Leu Asn Thr Arg Ile Arg Val Ala Gly Phe Gly Gln Thr
         120                 125                 130

tac aaa tct ggt gcc act gat cca gac aat tac gga gca tgg acg caa   547
Tyr Lys Ser Gly Ala Thr Asp Pro Asp Asn Tyr Gly Ala Trp Thr Gln
     135                 140                 145

cta gat gcc tcc acc gtt ggc gga gta caa gat gaa atc tcc cgc ttc   595
Leu Asp Ala Ser Thr Val Gly Gly Val Gln Asp Glu Ile Ser Arg Phe
150                 155                 160                 165

gct gac cgc acc cag gag cag tac acc aac tac gcc tcc gcg att gag   643
Ala Asp Arg Thr Gln Glu Gln Tyr Thr Asn Tyr Ala Ser Ala Ile Glu
                 170                 175                 180

ggc gct tac cag gac ttc act agg tcc ggc tct gag gac gcc tgc cgc   691
Gly Ala Tyr Gln Asp Phe Thr Arg Ser Gly Ser Glu Asp Ala Cys Arg
             185                 190                 195

atg ctg gtg acc ttc acc gac ggc gca ctg acc gct caa gaa ggc gcc   739
Met Leu Val Thr Phe Thr Asp Gly Ala Leu Thr Ala Gln Glu Gly Ala
         200                 205                 210

gat gtt gca gaa gca gca ctg tgc gcg ccg ggt ggc gtc acc gat cga   787
Asp Val Ala Glu Ala Ala Leu Cys Ala Pro Gly Gly Val Thr Asp Arg
     215                 220                 225
```

```
ctg cgc agt gct ggc atc acc cac atc ggc atc ggt tta tcg gca cct   835
Leu Arg Ser Ala Gly Ile Thr His Ile Gly Ile Gly Leu Ser Ala Pro
230                 235                 240                 245

acc aac cca tct gat ttc agc ctg ctg cgc gga acc acc gca ggt ggc   883
Thr Asn Pro Ser Asp Phe Ser Leu Leu Arg Gly Thr Thr Ala Gly Gly
                250                 255                 260

gga aca tgt ggt gtc gaa cca gct aac ggt gca ttc ttc cca gca gat   931
Gly Thr Cys Gly Val Glu Pro Ala Asn Gly Ala Phe Phe Pro Ala Asp
            265                 270                 275

aac gtg ggc gga ctt ttc gca gca ttc cgt gaa gcc ctt gcg att ggt   979
Asn Val Gly Gly Leu Phe Ala Ala Phe Arg Glu Ala Leu Ala Ile Gly
        280                 285                 290

ggt gaa aca att ggt gaa acc cga gct ggt gat cct ttc agc ttc acc   1027
Gly Glu Thr Ile Gly Glu Thr Arg Ala Gly Asp Pro Phe Ser Phe Thr
    295                 300                 305

ctg gac aac tcg gtg aac tct gtg cgt ttc acc gcg atc gcc aag gat   1075
Leu Asp Asn Ser Val Asn Ser Val Arg Phe Thr Ala Ile Ala Lys Asp
310                 315                 320                 325

gat ctc ggc ccg aac gcc cac ttg gtg ctc acc gca ccc aac ggc gaa   1123
Asp Leu Gly Pro Asn Ala His Leu Val Leu Thr Ala Pro Asn Gly Glu
                330                 335                 340

acg gtt gag ctc aaa gat tct gga agc agc gtc gcc aac agc act gac   1171
Thr Val Glu Leu Lys Asp Ser Gly Ser Ser Val Ala Asn Ser Thr Asp
            345                 350                 355

gtg agt tgg gaa gcc gaa agc agc cca gta aaa atg gct gat ggt tcc   1219
Val Ser Trp Glu Ala Glu Ser Ser Pro Val Lys Met Ala Asp Gly Ser
        360                 365                 370

ctc aac ctg cag caa ggt ggg gat tgg aag ggt gtc tgg cag att cag   1267
Leu Asn Leu Gln Gln Gly Gly Asp Trp Lys Gly Val Trp Gln Ile Gln
    375                 380                 385

ttc caa gga att gat cct gca gcg gtt gat gga cgc gta ttc aac tca   1315
Phe Gln Gly Ile Asp Pro Ala Ala Val Asp Gly Arg Val Phe Asn Ser
390                 395                 400                 405

gtg gag atc cag cct gac ctc cag ctt gtg ttc agt ggc ggt gat tcg   1363
Val Glu Ile Gln Pro Asp Leu Gln Leu Val Phe Ser Gly Gly Asp Ser
                410                 415                 420

acg tca ggt gca ctt aac ctt cgc gat gat cag cag ctg aat atg cag   1411
Thr Ser Gly Ala Leu Asn Leu Arg Asp Asp Gln Gln Leu Asn Met Gln
            425                 430                 435

ctg gtg ggc cgt gat ggt cag cca cgc atc ctt gag ggg tcc gcg ctg   1459
Leu Val Gly Arg Asp Gly Gln Pro Arg Ile Leu Glu Gly Ser Ala Leu
        440                 445                 450

gtc gat ctt ggt ttc acc cgc gca gat acc ggc gag ttc gcc cct ttg   1507
Val Asp Leu Gly Phe Thr Arg Ala Asp Thr Gly Glu Phe Ala Pro Leu
    455                 460                 465

gct caa gga att gat att tct ggc ggc gaa tta agc ttc ccg ctg gat   1555
```

```
Ala Gln Gly Ile Asp Ile Ser Gly Gly Glu Leu Ser Phe Pro Leu Asp
470                 475                 480                 485

acg att tcg cag ctc cca gcc atc ggc acg gtg gaa gcg cgt acc acg   1603
Thr Ile Ser Gln Leu Pro Ala Ile Gly Thr Val Glu Ala Arg Thr Thr
                490                 495                 500

atc acc acc gca ggc gtc gat gat ctc ccc ggc acc acg ttg agc cca   1651
Ile Thr Thr Ala Gly Val Asp Asp Leu Pro Gly Thr Thr Leu Ser Pro
            505                 510                 515

att ctc aac acc acg cgc atc acc atc act cag cgc gat atg cct cag   1699
Ile Leu Asn Thr Thr Arg Ile Thr Ile Thr Gln Arg Asp Met Pro Gln
        520                 525                 530

ctg cca gcg tcg gtt cgc ttc aca gcg gat gag gac gtt gtt acc gta   1747
Leu Pro Ala Ser Val Arg Phe Thr Ala Asp Glu Asp Val Val Thr Val
    535                 540                 545

gac atc ccc atc acc ggc ccc ggc aag gta tgg att gca ccg gga acc   1795
Asp Ile Pro Ile Thr Gly Pro Gly Lys Val Trp Ile Ala Pro Gly Thr
550                 555                 560                 565

cag ctc agc gga gtg ctt cca gac ggc gtg gac ggc att gca gca tca   1843
Gln Leu Ser Gly Val Leu Pro Asp Gly Val Asp Gly Ile Ala Ala Ser
                570                 575                 580

agt act ttc gac agc cca gat aat gct ttg gtg ctc gga ctg gat gag   1891
Ser Thr Phe Asp Ser Pro Asp Asn Ala Leu Val Leu Gly Leu Asp Glu
            585                 590                 595

cag ggc acg att cct gtt gaa cta acc gtg agc gat ctt cgt gac gga   1939
Gln Gly Thr Ile Pro Val Glu Leu Thr Val Ser Asp Leu Arg Asp Gly
        600                 605                 610

ctg gtc aac ggc tcg att cca ctc cag atc tcc aac gct gag ggc gcc   1987
Leu Val Asn Gly Ser Ile Pro Leu Gln Ile Ser Asn Ala Glu Gly Ala
    615                 620                 625

aat gaa acc agc gtg gat ctg ccg aca gaa ggc acg ttg agc gtt ccc   2035
Asn Glu Thr Ser Val Asp Leu Pro Thr Glu Gly Thr Leu Ser Val Pro
630                 635                 640                 645

att aac gcc tcc act ttc gca ttg gca ttc att ttg gcc ctt gtg ctt   2083
Ile Asn Ala Ser Thr Phe Ala Leu Ala Phe Ile Leu Ala Leu Val Leu
                650                 655                 660

tcc ctc ctg att ccg ctg ctc att ttg tat att gtg cgt ttc ctc tcc   2131
Ser Leu Leu Ile Pro Leu Leu Ile Leu Tyr Ile Val Arg Phe Leu Ser
            665                 670                 675

gca aag gtt ccg tcc tct gcg atg agt ggc gtg cgc att cca gtg gaa   2179
Ala Lys Val Pro Ser Ser Ala Met Ser Gly Val Arg Ile Pro Val Glu
        680                 685                 690

ttc tcc ggt gaa gct ctg cgc tat gcg ggc agc act atg cct gat ctc   2227
Phe Ser Gly Glu Ala Leu Arg Tyr Ala Gly Ser Thr Met Pro Asp Leu
    695                 700                 705

gca tcg caa acc acc gcc acc aag cag gtc gtt gtt cat gga gac acc   2275
Ala Ser Gln Thr Thr Ala Thr Lys Gln Val Val Val His Gly Asp Thr
```

```
710                 715                 720                 725

ttc aat gtg gaa ggc cac aaa ctt aaa gtc cag cgc ttc cag ctg aac   2323
Phe Asn Val Glu Gly His Lys Leu Lys Val Gln Arg Phe Gln Leu Asn
                730                 735                 740

ccg att gcg tct cct gca gtg atc gtg cag acc gac ccg tcg atc agc   2371
Pro Ile Ala Ser Pro Ala Val Ile Val Gln Thr Asp Pro Ser Ile Ser
            745                 750                 755

ttc gac ggc aaa caa aag ggc aca caa gct aaa ctc ccg ctg gcg gtc   2419
Phe Asp Gly Lys Gln Lys Gly Thr Gln Ala Lys Leu Pro Leu Ala Val
        760                 765                 770

caa ggc agt tgg ttc ctc act gca agc ggc gct gac cct tcc aag atg   2467
Gln Gly Ser Trp Phe Leu Thr Ala Ser Gly Ala Asp Pro Ser Lys Met
    775                 780                 785

gaa ctc atc gcc ctg aca aac ctg ccg ctc gag cag ggc caa atc gac   2515
Glu Leu Ile Ala Leu Thr Asn Leu Pro Leu Glu Gln Gly Gln Ile Asp
790                 795                 800                 805

cgc atg atc gca ggt atc acc agc aaa gcc cct gat agg gca cgc gaa   2563
Arg Met Ile Ala Gly Ile Thr Ser Lys Ala Pro Asp Arg Ala Arg Glu
                810                 815                 820

cta caa aaa ttg ctt gac gac gcc gcg acc tcc cag ccc gca aag gtt   2611
Leu Gln Lys Leu Leu Asp Asp Ala Ala Thr Ser Gln Pro Ala Lys Val
            825                 830                 835

cca ccg cgc gcc cca gcc gcg cag ggc cac gtc gaa aag caa gct cct   2659
Pro Pro Arg Ala Pro Ala Ala Gln Gly His Val Glu Lys Gln Ala Pro
        840                 845                 850

agt ttt ggc act ggt tcc ggt ggt ggt ttc ggc tcc agc aat ggt gga   2707
Ser Phe Gly Thr Gly Ser Gly Gly Gly Phe Gly Ser Ser Asn Gly Gly
    855                 860                 865

ggc ttt ggc tcc ggt agc gga tcc aac gac aca aat ggt gga ttt ggt   2755
Gly Phe Gly Ser Gly Ser Gly Ser Asn Asp Thr Asn Gly Gly Phe Gly
870                 875                 880                 885

tcc agc ggc ggc ttc ggc gcg cga taacctgtaa cttgcgatta aaa         2802
Ser Ser Gly Gly Phe Gly Ala Arg
                890
```

<210> 434
<211> 893
<212> PRT
<213> Corynebacterium glutamicum

<400> 434

```
Met Val Asn Thr Leu Asn Ser Lys Thr Val Asn Val Pro Arg Phe Ala
  1               5                  10                  15

Arg Gly Val Val Ala Ala Ala Thr Ala Leu Phe Phe Gly Ala Leu Val
             20                  25                  30

Ser Leu Ala Pro Ser Ala Leu Ala Gln Glu Pro Pro Ala Val Glu Ala
         35                  40                  45
```

```
Gly Ala Ser Gly Ser Leu Ser Asn Leu Gly Ala Cys Ile Ala Asp Lys
     50                  55                  60

Gly Thr Leu Asp Val Ile Ile Met Ile Asp Glu Thr Glu Ser Leu Ile
 65                  70                  75                  80

His Glu Ala Arg Asp Gly Val Val Asn Ala Asn Glu Pro Gly Ala Asp
                85                  90                  95

Ala Gln His His Arg Val Pro Ala Ala Gln Ser Phe Val Asp Glu Leu
            100                 105                 110

Leu Ala Lys Gln Ser Asp Gly Asp Leu Asn Thr Arg Ile Arg Val Ala
        115                 120                 125

Gly Phe Gly Gln Thr Tyr Lys Ser Gly Ala Thr Asp Pro Asp Asn Tyr
    130                 135                 140

Gly Ala Trp Thr Gln Leu Asp Ala Ser Thr Val Gly Gly Val Gln Asp
145                 150                 155                 160

Glu Ile Ser Arg Phe Ala Asp Arg Thr Gln Glu Gln Tyr Thr Asn Tyr
                165                 170                 175

Ala Ser Ala Ile Glu Gly Ala Tyr Gln Asp Phe Thr Arg Ser Gly Ser
            180                 185                 190

Glu Asp Ala Cys Arg Met Leu Val Thr Phe Thr Asp Gly Ala Leu Thr
        195                 200                 205

Ala Gln Glu Gly Ala Asp Val Ala Glu Ala Ala Leu Cys Ala Pro Gly
    210                 215                 220

Gly Val Thr Asp Arg Leu Arg Ser Ala Gly Ile Thr His Ile Gly Ile
225                 230                 235                 240

Gly Leu Ser Ala Pro Thr Asn Pro Ser Asp Phe Ser Leu Leu Arg Gly
                245                 250                 255

Thr Thr Ala Gly Gly Gly Thr Cys Gly Val Glu Pro Ala Asn Gly Ala
            260                 265                 270

Phe Phe Pro Ala Asp Asn Val Gly Gly Leu Phe Ala Ala Phe Arg Glu
        275                 280                 285

Ala Leu Ala Ile Gly Gly Glu Thr Ile Gly Glu Thr Arg Ala Gly Asp
    290                 295                 300

Pro Phe Ser Phe Thr Leu Asp Asn Ser Val Asn Ser Val Arg Phe Thr
305                 310                 315                 320

Ala Ile Ala Lys Asp Asp Leu Gly Pro Asn Ala His Leu Val Leu Thr
                325                 330                 335

Ala Pro Asn Gly Glu Thr Val Glu Leu Lys Asp Ser Gly Ser Ser Val
            340                 345                 350

Ala Asn Ser Thr Asp Val Ser Trp Glu Ala Glu Ser Ser Pro Val Lys
        355                 360                 365
```

```
Met Ala Asp Gly Ser Leu Asn Leu Gln Gln Gly Gly Asp Trp Lys Gly
    370                 375                 380

Val Trp Gln Ile Gln Phe Gln Gly Ile Asp Pro Ala Ala Val Asp Gly
385                 390                 395                 400

Arg Val Phe Asn Ser Val Glu Ile Gln Pro Asp Leu Gln Leu Val Phe
                405                 410                 415

Ser Gly Gly Asp Ser Thr Ser Gly Ala Leu Asn Leu Arg Asp Asp Gln
            420                 425                 430

Gln Leu Asn Met Gln Leu Val Gly Arg Asp Gly Gln Pro Arg Ile Leu
        435                 440                 445

Glu Gly Ser Ala Leu Val Asp Leu Gly Phe Thr Arg Ala Asp Thr Gly
    450                 455                 460

Glu Phe Ala Pro Leu Ala Gln Gly Ile Asp Ile Ser Gly Gly Glu Leu
465                 470                 475                 480

Ser Phe Pro Leu Asp Thr Ile Ser Gln Leu Pro Ala Ile Gly Thr Val
                485                 490                 495

Glu Ala Arg Thr Thr Ile Thr Thr Ala Gly Val Asp Asp Leu Pro Gly
            500                 505                 510

Thr Thr Leu Ser Pro Ile Leu Asn Thr Thr Arg Ile Thr Ile Thr Gln
        515                 520                 525

Arg Asp Met Pro Gln Leu Pro Ala Ser Val Arg Phe Thr Ala Asp Glu
    530                 535                 540

Asp Val Val Thr Val Asp Ile Pro Ile Thr Gly Pro Gly Lys Val Trp
545                 550                 555                 560

Ile Ala Pro Gly Thr Gln Leu Ser Gly Val Leu Pro Asp Gly Val Asp
                565                 570                 575

Gly Ile Ala Ala Ser Ser Thr Phe Asp Ser Pro Asp Asn Ala Leu Val
            580                 585                 590

Leu Gly Leu Asp Glu Gln Gly Thr Ile Pro Val Glu Leu Thr Val Ser
        595                 600                 605

Asp Leu Arg Asp Gly Leu Val Asn Gly Ser Ile Pro Leu Gln Ile Ser
    610                 615                 620

Asn Ala Glu Gly Ala Asn Glu Thr Ser Val Asp Leu Pro Thr Glu Gly
625                 630                 635                 640

Thr Leu Ser Val Pro Ile Asn Ala Ser Thr Phe Ala Leu Ala Phe Ile
                645                 650                 655

Leu Ala Leu Val Leu Ser Leu Leu Ile Pro Leu Leu Ile Leu Tyr Ile
            660                 665                 670

Val Arg Phe Leu Ser Ala Lys Val Pro Ser Ser Ala Met Ser Gly Val
        675                 680                 685

Arg Ile Pro Val Glu Phe Ser Gly Glu Ala Leu Arg Tyr Ala Gly Ser
```

```
    690                 695                 700

Thr Met Pro Asp Leu Ala Ser Gln Thr Thr Ala Thr Lys Gln Val Val
705                 710                 715                 720

Val His Gly Asp Thr Phe Asn Val Glu Gly His Lys Leu Lys Val Gln
                725                 730                 735

Arg Phe Gln Leu Asn Pro Ile Ala Ser Pro Ala Val Ile Val Gln Thr
            740                 745                 750

Asp Pro Ser Ile Ser Phe Asp Gly Lys Gln Lys Gly Thr Gln Ala Lys
        755                 760                 765

Leu Pro Leu Ala Val Gln Gly Ser Trp Phe Leu Thr Ala Ser Gly Ala
    770                 775                 780

Asp Pro Ser Lys Met Glu Leu Ile Ala Leu Thr Asn Leu Pro Leu Glu
785                 790                 795                 800

Gln Gly Gln Ile Asp Arg Met Ile Ala Gly Ile Thr Ser Lys Ala Pro
                805                 810                 815

Asp Arg Ala Arg Glu Leu Gln Lys Leu Leu Asp Asp Ala Ala Thr Ser
            820                 825                 830

Gln Pro Ala Lys Val Pro Pro Arg Ala Pro Ala Ala Gln Gly His Val
        835                 840                 845

Glu Lys Gln Ala Pro Ser Phe Gly Thr Gly Ser Gly Gly Gly Phe Gly
    850                 855                 860

Ser Ser Asn Gly Gly Gly Phe Gly Ser Gly Ser Gly Ser Asn Asp Thr
865                 870                 875                 880

Asn Gly Gly Phe Gly Ser Ser Gly Gly Phe Gly Ala Arg
                885                 890


<210> 435
<211> 1406
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1383)
<223> FRXA00917

<400> 435
cag ctg aat atg cag ctg gtg ggc cgt gat ggt cag cca cgc atc ctt   48
Gln Leu Asn Met Gln Leu Val Gly Arg Asp Gly Gln Pro Arg Ile Leu
  1               5                  10                  15

gag ggg tcc gcg ctg gtc gat ctt ggt ttc acc cgc gca gat acc ggc   96
Glu Gly Ser Ala Leu Val Asp Leu Gly Phe Thr Arg Ala Asp Thr Gly
             20                  25                  30

gag ttc gcc cct ttg gct caa gga att gat att tct ggc ggc gaa tta   144
Glu Phe Ala Pro Leu Ala Gln Gly Ile Asp Ile Ser Gly Gly Glu Leu
         35                  40                  45
```

```
agc ttc ccg ctg gat acg att tcg cag ctc cca gcc atc ggc acg gtg   192
Ser Phe Pro Leu Asp Thr Ile Ser Gln Leu Pro Ala Ile Gly Thr Val
     50                  55                  60

gaa gcg cgt acc acg atc acc acc gca ggc gtc gat gat ctc ccc ggc   240
Glu Ala Arg Thr Thr Ile Thr Thr Ala Gly Val Asp Asp Leu Pro Gly
 65                  70                  75                  80

acc acg ttg agc cca att ctc aac acc acg cgc atc acc atc act cag   288
Thr Thr Leu Ser Pro Ile Leu Asn Thr Thr Arg Ile Thr Ile Thr Gln
                 85                  90                  95

cgc gat atg cct cag ctg cca gcg tcg gtt cgc ttc aca gcg gat gag   336
Arg Asp Met Pro Gln Leu Pro Ala Ser Val Arg Phe Thr Ala Asp Glu
            100                 105                 110

gac gtt gtt acc gta gac atc ccc atc acc ggc ccc ggc aag gta tgg   384
Asp Val Val Thr Val Asp Ile Pro Ile Thr Gly Pro Gly Lys Val Trp
        115                 120                 125

att gca ccg gga acc cag ctc agc gga gtg ctt cca gac ggc gtg gac   432
Ile Ala Pro Gly Thr Gln Leu Ser Gly Val Leu Pro Asp Gly Val Asp
    130                 135                 140

ggc att gca gca tca agt act ttc gac agc cca gat aat gct ttg gtg   480
Gly Ile Ala Ala Ser Ser Thr Phe Asp Ser Pro Asp Asn Ala Leu Val
145                 150                 155                 160

ctc gga ctg gat gag cag ggc acg att cct gtt gaa cta acc gtg agc   528
Leu Gly Leu Asp Glu Gln Gly Thr Ile Pro Val Glu Leu Thr Val Ser
                165                 170                 175

gat ctt cgt gac gga ctg gtc aac ggc tcg att cca ctc cag atc tcc   576
Asp Leu Arg Asp Gly Leu Val Asn Gly Ser Ile Pro Leu Gln Ile Ser
            180                 185                 190

aac gct gag ggc gcc aat gaa acc agc gtg gat ctg ccg aca gaa ggc   624
Asn Ala Glu Gly Ala Asn Glu Thr Ser Val Asp Leu Pro Thr Glu Gly
        195                 200                 205

acg ttg agc gtt ccc att aac gcc tcc act ttc gca ttg gca ttc att   672
Thr Leu Ser Val Pro Ile Asn Ala Ser Thr Phe Ala Leu Ala Phe Ile
    210                 215                 220

ttg gcc ctt gtg ctt tcc ctc ctg att ccg ctg ctc att ttg tat att   720
Leu Ala Leu Val Leu Ser Leu Leu Ile Pro Leu Leu Ile Leu Tyr Ile
225                 230                 235                 240

gtg cgt ttc ctc tcc gca aag gtt ccg tcc tct gcg atg agt ggc gtg   768
Val Arg Phe Leu Ser Ala Lys Val Pro Ser Ser Ala Met Ser Gly Val
                245                 250                 255

cgc att cca gtg gaa ttc tcc ggt gaa gct ctg cgc tat gcg ggc agc   816
Arg Ile Pro Val Glu Phe Ser Gly Glu Ala Leu Arg Tyr Ala Gly Ser
            260                 265                 270

act atg cct gat ctc gca tcg caa acc acc gcc acc aag cag gtc gtt   864
Thr Met Pro Asp Leu Ala Ser Gln Thr Thr Ala Thr Lys Gln Val Val
        275                 280                 285
```

```
gtt cat gga gac acc ttc aat gtg gaa ggc cac aaa ctt aaa gtc cag   912
Val His Gly Asp Thr Phe Asn Val Glu Gly His Lys Leu Lys Val Gln
    290                 295                 300

cgc ttc cag ctg aac ccg att gcg tct cct gca gtg atc gtg cag acc   960
Arg Phe Gln Leu Asn Pro Ile Ala Ser Pro Ala Val Ile Val Gln Thr
305                 310                 315                 320

gac ccg tcg atc agc ttc gac ggc aaa caa aag ggc aca caa gct aaa   1008
Asp Pro Ser Ile Ser Phe Asp Gly Lys Gln Lys Gly Thr Gln Ala Lys
                325                 330                 335

ctc ccg ctg gcg gtc caa ggc agt tgg ttc ctc act gca agc ggc gct   1056
Leu Pro Leu Ala Val Gln Gly Ser Trp Phe Leu Thr Ala Ser Gly Ala
            340                 345                 350

gac cct tcc aag atg gaa ctc atc gcc ctg aca aac ctg ccg ctc gag   1104
Asp Pro Ser Lys Met Glu Leu Ile Ala Leu Thr Asn Leu Pro Leu Glu
        355                 360                 365

cag ggc caa atc gac cgc atg atc gca ggt atc acc agc aaa gcc cct   1152
Gln Gly Gln Ile Asp Arg Met Ile Ala Gly Ile Thr Ser Lys Ala Pro
    370                 375                 380

gat agg gca cgc gaa cta caa aaa ttg ctt gac gac gcc gcg acc tcc   1200
Asp Arg Ala Arg Glu Leu Gln Lys Leu Leu Asp Asp Ala Ala Thr Ser
385                 390                 395                 400

cag ccc gca aag gtt cca ccg cgc gcc cca gcc gcg cag ggc cac gtc   1248
Gln Pro Ala Lys Val Pro Pro Arg Ala Pro Ala Ala Gln Gly His Val
                405                 410                 415

gaa aag caa gct cct agt ttt ggc act ggt tcc ggt ggt ggt ttc ggc   1296
Glu Lys Gln Ala Pro Ser Phe Gly Thr Gly Ser Gly Gly Gly Phe Gly
            420                 425                 430

tcc agc aat ggt gga ggc ttt ggc tcc ggt agc gga tcc aac gac aca   1344
Ser Ser Asn Gly Gly Gly Phe Gly Ser Gly Ser Gly Ser Asn Asp Thr
        435                 440                 445

aat ggt gga ttt ggt tcc agc ggc ggc ttc ggc gcg cga taacctgtaa   1393
Asn Gly Gly Phe Gly Ser Ser Gly Gly Phe Gly Ala Arg
    450                 455                 460

cttgcgatta aaa                                                  1406


<210> 436
<211> 461
<212> PRT
<213> Corynebacterium glutamicum

<400> 436
Gln Leu Asn Met Gln Leu Val Gly Arg Asp Gly Gln Pro Arg Ile Leu
  1               5                  10                  15

Glu Gly Ser Ala Leu Val Asp Leu Gly Phe Thr Arg Ala Asp Thr Gly
             20                  25                  30

Glu Phe Ala Pro Leu Ala Gln Gly Ile Asp Ile Ser Gly Gly Glu Leu
         35                  40                  45
```

```
Ser Phe Pro Leu Asp Thr Ile Ser Gln Leu Pro Ala Ile Gly Thr Val
     50                  55                  60

Glu Ala Arg Thr Thr Ile Thr Thr Ala Gly Val Asp Asp Leu Pro Gly
 65                  70                  75                  80

Thr Thr Leu Ser Pro Ile Leu Asn Thr Thr Arg Ile Thr Ile Thr Gln
                 85                  90                  95

Arg Asp Met Pro Gln Leu Pro Ala Ser Val Arg Phe Thr Ala Asp Glu
            100                 105                 110

Asp Val Val Thr Val Asp Ile Pro Ile Thr Gly Pro Gly Lys Val Trp
        115                 120                 125

Ile Ala Pro Gly Thr Gln Leu Ser Gly Val Leu Pro Asp Gly Val Asp
    130                 135                 140

Gly Ile Ala Ala Ser Ser Thr Phe Asp Ser Pro Asp Asn Ala Leu Val
145                 150                 155                 160

Leu Gly Leu Asp Glu Gln Gly Thr Ile Pro Val Glu Leu Thr Val Ser
                165                 170                 175

Asp Leu Arg Asp Gly Leu Val Asn Gly Ser Ile Pro Leu Gln Ile Ser
            180                 185                 190

Asn Ala Glu Gly Ala Asn Glu Thr Ser Val Asp Leu Pro Thr Glu Gly
        195                 200                 205

Thr Leu Ser Val Pro Ile Asn Ala Ser Thr Phe Ala Leu Ala Phe Ile
    210                 215                 220

Leu Ala Leu Val Leu Ser Leu Leu Ile Pro Leu Leu Ile Leu Tyr Ile
225                 230                 235                 240

Val Arg Phe Leu Ser Ala Lys Val Pro Ser Ser Ala Met Ser Gly Val
                245                 250                 255

Arg Ile Pro Val Glu Phe Ser Gly Glu Ala Leu Arg Tyr Ala Gly Ser
            260                 265                 270

Thr Met Pro Asp Leu Ala Ser Gln Thr Thr Ala Thr Lys Gln Val Val
        275                 280                 285

Val His Gly Asp Thr Phe Asn Val Glu Gly His Lys Leu Lys Val Gln
    290                 295                 300

Arg Phe Gln Leu Asn Pro Ile Ala Ser Pro Ala Val Ile Val Gln Thr
305                 310                 315                 320

Asp Pro Ser Ile Ser Phe Asp Gly Lys Gln Lys Gly Thr Gln Ala Lys
                325                 330                 335

Leu Pro Leu Ala Val Gln Gly Ser Trp Phe Leu Thr Ala Ser Gly Ala
            340                 345                 350

Asp Pro Ser Lys Met Glu Leu Ile Ala Leu Thr Asn Leu Pro Leu Glu
        355                 360                 365
```

```
Gln Gly Gln Ile Asp Arg Met Ile Ala Gly Ile Thr Ser Lys Ala Pro
    370                 375                 380

Asp Arg Ala Arg Glu Leu Gln Lys Leu Leu Asp Asp Ala Ala Thr Ser
385                 390                 395                 400

Gln Pro Ala Lys Val Pro Pro Arg Ala Pro Ala Ala Gln Gly His Val
                405                 410                 415

Glu Lys Gln Ala Pro Ser Phe Gly Thr Gly Ser Gly Gly Gly Phe Gly
            420                 425                 430

Ser Ser Asn Gly Gly Gly Phe Gly Ser Gly Ser Gly Ser Asn Asp Thr
        435                 440                 445

Asn Gly Gly Phe Gly Ser Ser Gly Gly Phe Gly Ala Arg
    450                 455                 460


<210> 437
<211> 536
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(513)
<223> RXN00921

<400> 437
cct gcg gca atc ctc ttg gac cat atc gtt ccg aac ttc agc aga gat   48
Pro Ala Ala Ile Leu Leu Asp His Ile Val Pro Asn Phe Ser Arg Asp
  1               5                  10                  15

cgg tct ttg cca gac atc gaa gac tgg acg aga agc gat gaa gct cag   96
Arg Ser Leu Pro Asp Ile Glu Asp Trp Thr Arg Ser Asp Glu Ala Gln
             20                  25                  30

cag atc ttt gca gga atc att gcg ggt gcg tct gtt caa act ggt aga   144
Gln Ile Phe Ala Gly Ile Ile Ala Gly Ala Ser Val Gln Thr Gly Arg
         35                  40                  45

agc cac ttc atg tgg gat ctt ttg cgg gcg tat ttt gga gtc gct ttg   192
Ser His Phe Met Trp Asp Leu Leu Arg Ala Tyr Phe Gly Val Ala Leu
     50                  55                  60

atc ggc gac gaa gat acc tac agg gct ttt act act ctc acg gtc gat   240
Ile Gly Asp Glu Asp Thr Tyr Arg Ala Phe Thr Thr Leu Thr Val Asp
 65                  70                  75                  80

tct gtt ctt agt ttc gtg cag tta act ctt caa gag ggc aga acg gaa   288
Ser Val Leu Ser Phe Val Gln Leu Thr Leu Gln Glu Gly Arg Thr Glu
                 85                  90                  95

gac att aga cga ttc gag aaa tat ggt gag cag att gcc cga gag gat   336
Asp Ile Arg Arg Phe Glu Lys Tyr Gly Glu Gln Ile Ala Arg Glu Asp
            100                 105                 110

ttg ccg tcg att ctc acc aat gct cga gca gta cag caa tat ctc ggc   384
Leu Pro Ser Ile Leu Thr Asn Ala Arg Ala Val Gln Gln Tyr Leu Gly
        115                 120                 125
```

```
tat atc gac caa gat atc atc aat aag aaa gtg tcc cgg tct agg gat   432
Tyr Ile Asp Gln Asp Ile Ile Asn Lys Lys Val Ser Arg Ser Arg Asp
    130                 135                 140

gtt aac cag att ttt act gag atg gcg cgc gct atc atc aga gca att   480
Val Asn Gln Ile Phe Thr Glu Met Ala Arg Ala Ile Ile Arg Ala Ile
145                 150                 155                 160

agc cgg aat aat att gga aag gac atg cgg tca tgaacgtgat tcgactggat 533
Ser Arg Asn Asn Ile Gly Lys Asp Met Arg Ser
                165                 170

tcc                                                               536
```

<210> 438
<211> 171
<212> PRT
<213> Corynebacterium glutamicum

<400> 438

```
Pro Ala Ala Ile Leu Leu Asp His Ile Val Pro Asn Phe Ser Arg Asp
  1               5                  10                  15

Arg Ser Leu Pro Asp Ile Glu Asp Trp Thr Arg Ser Asp Glu Ala Gln
             20                  25                  30

Gln Ile Phe Ala Gly Ile Ile Ala Gly Ala Ser Val Gln Thr Gly Arg
         35                  40                  45

Ser His Phe Met Trp Asp Leu Leu Arg Ala Tyr Phe Gly Val Ala Leu
     50                  55                  60

Ile Gly Asp Glu Asp Thr Tyr Arg Ala Phe Thr Thr Leu Thr Val Asp
 65                  70                  75                  80

Ser Val Leu Ser Phe Val Gln Leu Thr Leu Gln Glu Gly Arg Thr Glu
                 85                  90                  95

Asp Ile Arg Arg Phe Glu Lys Tyr Gly Glu Gln Ile Ala Arg Glu Asp
            100                 105                 110

Leu Pro Ser Ile Leu Thr Asn Ala Arg Ala Val Gln Gln Tyr Leu Gly
        115                 120                 125

Tyr Ile Asp Gln Asp Ile Ile Asn Lys Lys Val Ser Arg Ser Arg Asp
    130                 135                 140

Val Asn Gln Ile Phe Thr Glu Met Ala Arg Ala Ile Ile Arg Ala Ile
145                 150                 155                 160

Ser Arg Asn Asn Ile Gly Lys Asp Met Arg Ser
                165                 170
```

<210> 439
<211> 2022
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1999)
<223> FRXA00921

<400> 439
tctgggaacg tggattggtg gaagcaggtg agttgcccgt ggccttgaga tggactcatg 60

tcacctacgc gtcctttaga ggaactgcag gtaggggtgg gtg gaa ggt gga act 115
Val Glu Gly Gly Thr
1 5

tgg tct gct cag gcc act aaa gaa gac ctc caa ttt atc gcg gag gtt 163
Trp Ser Ala Gln Ala Thr Lys Glu Asp Leu Gln Phe Ile Ala Glu Val
10 15 20

gcg ccc act cat att gaa acg gtg acc cct ttt gat gat ttc atc tca 211
Ala Pro Thr His Ile Glu Thr Val Thr Pro Phe Asp Asp Phe Ile Ser
25 30 35

tca gaa gat atc gat gcg ttg ccg agg agg ttt gag tac cgt cct ttg 259
Ser Glu Asp Ile Asp Ala Leu Pro Arg Arg Phe Glu Tyr Arg Pro Leu
40 45 50

gca ggc cga tcg ttg atc atg cag tct gtt cct gca ggt aaa gat gcc 307
Ala Gly Arg Ser Leu Ile Met Gln Ser Val Pro Ala Gly Lys Asp Ala
55 60 65

act gga cgt cca ggg aat gtg ttc acc cat gca gta ttt gat ggg gat 355
Thr Gly Arg Pro Gly Asn Val Phe Thr His Ala Val Phe Asp Gly Asp
70 75 80 85

cta gaa agc cca ctg gag tct gtt tat ccc att tcc ctg tac cgt tca 403
Leu Glu Ser Pro Leu Glu Ser Val Tyr Pro Ile Ser Leu Tyr Arg Ser
90 95 100

cct gat ttg ctg acc cct ttt cgt gca gcc gcg gtc aac gct gcc gag 451
Pro Asp Leu Leu Thr Pro Phe Arg Ala Ala Ala Val Asn Ala Ala Glu
105 110 115

ctc cct ttg gat gca ggc gag ccg aga att ggc ccc atc act gat ctg 499
Leu Pro Leu Asp Ala Gly Glu Pro Arg Ile Gly Pro Ile Thr Asp Leu
120 125 130

tcc ttg tcg tgg atg atg atc gac agc atg ttt ggc gat cgc aga cag 547
Ser Leu Ser Trp Met Met Ile Asp Ser Met Phe Gly Asp Arg Arg Gln
135 140 145

cag ttc tac cag ctt caa gat gct ctc caa gct gga gat aaa gct act 595
Gln Phe Tyr Gln Leu Gln Asp Ala Leu Gln Ala Gly Asp Lys Ala Thr
150 155 160 165

gtt ttg gtt ctg aac agc act aac gag gca gca tat tgg ctt caa gcg 643
Val Leu Val Leu Asn Ser Thr Asn Glu Ala Ala Tyr Trp Leu Gln Ala
170 175 180

ttg tct tct aca ttg act ccg aat gaa gcc cgg cgt ctg ttg cac ttc 691
Leu Ser Ser Thr Leu Thr Pro Asn Glu Ala Arg Arg Leu Leu His Phe
185 190 195

tca acc ttt gag cgt gct gct acc ttg cca gct cca gat aaa tca atg 739

```
Ser Thr Phe Glu Arg Ala Ala Thr Leu Pro Ala Pro Asp Lys Ser Met
        200                 205                 210

gag gct cgt tct ctg ttt gtg gtc cca gga att gat cgt gaa ttg ttg   787
Glu Ala Arg Ser Leu Phe Val Val Pro Gly Ile Asp Arg Glu Leu Leu
    215                 220                 225

gcg gag cat tca ggg att gtg att atc gat ccg gag att cca cag agc   835
Ala Glu His Ser Gly Ile Val Ile Ile Asp Pro Glu Ile Pro Gln Ser
230                 235                 240                 245

caa cct ttc ggc ccg cag gga tcc tgg tcc cga atg aca gaa ggg ctc   883
Gln Pro Phe Gly Pro Gln Gly Ser Trp Ser Arg Met Thr Glu Gly Leu
                250                 255                 260

ttc tcc gac ggt ttt gat gct gat gaa ctt gtc gca ggg ctg att cgt   931
Phe Ser Asp Gly Phe Asp Ala Asp Glu Leu Val Ala Gly Leu Ile Arg
            265                 270                 275

gcc aac gag aac ctg gat aat agc caa aag gaa ctc gct caa ttt gga   979
Ala Asn Glu Asn Leu Asp Asn Ser Gln Lys Glu Leu Ala Gln Phe Gly
        280                 285                 290

gac ggt tta gcg cga ttt atc cgg aat ggc cgt ttt tcc ggc acg cac  1027
Asp Gly Leu Ala Arg Phe Ile Arg Asn Gly Arg Phe Ser Gly Thr His
    295                 300                 305

ccg ctt cgc gta ctt gct gat cag cat atg ttt gga aag gtg cca gac  1075
Pro Leu Arg Val Leu Ala Asp Gln His Met Phe Gly Lys Val Pro Asp
310                 315                 320                 325

aag cca gca cct aag gtg gag cct gtc gct ccg gca cca aac ccc aat  1123
Lys Pro Ala Pro Lys Val Glu Pro Val Ala Pro Ala Pro Asn Pro Asn
                330                 335                 340

gca att tgg gcg cgt gca tct gag gta gtt cac aat cct cgg aga gca  1171
Ala Ile Trp Ala Arg Ala Ser Glu Val Val His Asn Pro Arg Arg Ala
            345                 350                 355

tca gaa tca caa gat tgg cca agt ctg agg cga ttg ccg gat agt cgg  1219
Ser Glu Ser Gln Asp Trp Pro Ser Leu Arg Arg Leu Pro Asp Ser Arg
        360                 365                 370

cgc agg atc atc aat atg tca gag cag gcg atc aac agc att gag aag  1267
Arg Arg Ile Ile Asn Met Ser Glu Gln Ala Ile Asn Ser Ile Glu Lys
    375                 380                 385

ctt cat gat tcg ccg gca cag gat ctt gtt gcc tat ttg gat ttc ctt  1315
Leu His Asp Ser Pro Ala Gln Asp Leu Val Ala Tyr Leu Asp Phe Leu
390                 395                 400                 405

ttg aaa act gag ctt gcg aca agc att aat gct tcg gat ccc ttt ttt  1363
Leu Lys Thr Glu Leu Ala Thr Ser Ile Asn Ala Ser Asp Pro Phe Phe
                410                 415                 420

cgg agt agt ttt tca gac ttt cca gcg atg gac aac tgg cga cac att  1411
Arg Ser Ser Phe Ser Asp Phe Pro Ala Met Asp Asn Trp Arg His Ile
            425                 430                 435

aag ttc acc gag gat gcg cac cct cgc ttg agg gaa cta ctc gtg gac  1459
Lys Phe Thr Glu Asp Ala His Pro Arg Leu Arg Glu Leu Leu Val Asp
```

```
        440                 445                 450

gca gaa cgc gat gct agg aac aga gca cct gcg gca atc gtc ttg gac   1507
Ala Glu Arg Asp Ala Arg Asn Arg Ala Pro Ala Ala Ile Val Leu Asp
    455                 460                 465

cat atc gtt ccg aac ttc agc aga gat cgg tct ttg cca gac atc gaa   1555
His Ile Val Pro Asn Phe Ser Arg Asp Arg Ser Leu Pro Asp Ile Glu
470                 475                 480                 485

gac tgg acg aga agc gat gaa gct cag cag atc ttt gca gga atc att   1603
Asp Trp Thr Arg Ser Asp Glu Ala Gln Gln Ile Phe Ala Gly Ile Ile
                490                 495                 500

gcg ggt gcg tct gtt caa act ggt aga agc cac ttc atg tgg gat ctt   1651
Ala Gly Ala Ser Val Gln Thr Gly Arg Ser His Phe Met Trp Asp Leu
            505                 510                 515

ttg cgg gcg tat ttt gga gtc gct ttg atc ggc gac gaa gat acc tac   1699
Leu Arg Ala Tyr Phe Gly Val Ala Leu Ile Gly Asp Glu Asp Thr Tyr
        520                 525                 530

agg gct ttt act act ctc acg gtc gat tct gtt ctt agt ttc gtg cag   1747
Arg Ala Phe Thr Thr Leu Thr Val Asp Ser Val Leu Ser Phe Val Gln
    535                 540                 545

tta act ctt caa gag ggc aga acg gaa gac att aga cga ttc gag aaa   1795
Leu Thr Leu Gln Glu Gly Arg Thr Glu Asp Ile Arg Arg Phe Glu Lys
550                 555                 560                 565

tat ggt gag cag att gcc cga gag gat ttg ccg tcg att ctc acc aat   1843
Tyr Gly Glu Gln Ile Ala Arg Glu Asp Leu Pro Ser Ile Leu Thr Asn
                570                 575                 580

gct cga gca gta cag caa tat ctc ggc tat atc gac caa gat atc atc   1891
Ala Arg Ala Val Gln Gln Tyr Leu Gly Tyr Ile Asp Gln Asp Ile Ile
            585                 590                 595

aat aag aaa gtg tcc cgg tct agg gat gtt aac cag att ttt act gag   1939
Asn Lys Lys Val Ser Arg Ser Arg Asp Val Asn Gln Ile Phe Thr Glu
        600                 605                 610

atg gcg cgc gct atc atc aga gca att agc cgg aat aat att gga aag   1987
Met Ala Arg Ala Ile Ile Arg Ala Ile Ser Arg Asn Asn Ile Gly Lys
    615                 620                 625

gac atg cgg tca tgaacgtgat tcgactggat tcc                        2022
Asp Met Arg Ser
630
```

<210> 440
<211> 633
<212> PRT
<213> Corynebacterium glutamicum

<400> 440

```
Val Glu Gly Gly Thr Trp Ser Ala Gln Ala Thr Lys Glu Asp Leu Gln
  1               5                  10                  15

Phe Ile Ala Glu Val Ala Pro Thr His Ile Glu Thr Val Thr Pro Phe
```

```
             20                  25                  30

Asp Asp Phe Ile Ser Ser Glu Asp Ile Asp Ala Leu Pro Arg Arg Phe
         35                  40                  45

Glu Tyr Arg Pro Leu Ala Gly Arg Ser Leu Ile Met Gln Ser Val Pro
     50                  55                  60

Ala Gly Lys Asp Ala Thr Gly Arg Pro Gly Asn Val Phe Thr His Ala
 65                  70                  75                  80

Val Phe Asp Gly Asp Leu Glu Ser Pro Leu Glu Ser Val Tyr Pro Ile
                 85                  90                  95

Ser Leu Tyr Arg Ser Pro Asp Leu Leu Thr Pro Phe Arg Ala Ala Ala
            100                 105                 110

Val Asn Ala Ala Glu Leu Pro Leu Asp Ala Gly Glu Pro Arg Ile Gly
        115                 120                 125

Pro Ile Thr Asp Leu Ser Leu Ser Trp Met Met Ile Asp Ser Met Phe
    130                 135                 140

Gly Asp Arg Arg Gln Gln Phe Tyr Gln Leu Gln Asp Ala Leu Gln Ala
145                 150                 155                 160

Gly Asp Lys Ala Thr Val Leu Val Leu Asn Ser Thr Asn Glu Ala Ala
                165                 170                 175

Tyr Trp Leu Gln Ala Leu Ser Ser Thr Leu Thr Pro Asn Glu Ala Arg
            180                 185                 190

Arg Leu Leu His Phe Ser Thr Phe Glu Arg Ala Ala Thr Leu Pro Ala
        195                 200                 205

Pro Asp Lys Ser Met Glu Ala Arg Ser Leu Phe Val Val Pro Gly Ile
    210                 215                 220

Asp Arg Glu Leu Leu Ala Glu His Ser Gly Ile Val Ile Ile Asp Pro
225                 230                 235                 240

Glu Ile Pro Gln Ser Gln Pro Phe Gly Pro Gln Gly Ser Trp Ser Arg
                245                 250                 255

Met Thr Glu Gly Leu Phe Ser Asp Gly Phe Asp Ala Asp Glu Leu Val
            260                 265                 270

Ala Gly Leu Ile Arg Ala Asn Glu Asn Leu Asp Asn Ser Gln Lys Glu
        275                 280                 285

Leu Ala Gln Phe Gly Asp Gly Leu Ala Arg Phe Ile Arg Asn Gly Arg
    290                 295                 300

Phe Ser Gly Thr His Pro Leu Arg Val Leu Ala Asp Gln His Met Phe
305                 310                 315                 320

Gly Lys Val Pro Asp Lys Pro Ala Pro Lys Val Glu Pro Val Ala Pro
                325                 330                 335

Ala Pro Asn Pro Asn Ala Ile Trp Ala Arg Ala Ser Glu Val Val His
            340                 345                 350
```

```
Asn Pro Arg Arg Ala Ser Glu Ser Gln Asp Trp Pro Ser Leu Arg Arg
        355                 360                 365

Leu Pro Asp Ser Arg Arg Arg Ile Ile Asn Met Ser Glu Gln Ala Ile
    370                 375                 380

Asn Ser Ile Glu Lys Leu His Asp Ser Pro Ala Gln Asp Leu Val Ala
385                 390                 395                 400

Tyr Leu Asp Phe Leu Leu Lys Thr Glu Leu Ala Thr Ser Ile Asn Ala
                405                 410                 415

Ser Asp Pro Phe Phe Arg Ser Ser Phe Ser Asp Phe Pro Ala Met Asp
            420                 425                 430

Asn Trp Arg His Ile Lys Phe Thr Glu Asp Ala His Pro Arg Leu Arg
        435                 440                 445

Glu Leu Leu Val Asp Ala Glu Arg Asp Ala Arg Asn Arg Ala Pro Ala
    450                 455                 460

Ala Ile Val Leu Asp His Ile Val Pro Asn Phe Ser Arg Asp Arg Ser
465                 470                 475                 480

Leu Pro Asp Ile Glu Asp Trp Thr Arg Ser Asp Glu Ala Gln Gln Ile
                485                 490                 495

Phe Ala Gly Ile Ile Ala Gly Ala Ser Val Gln Thr Gly Arg Ser His
            500                 505                 510

Phe Met Trp Asp Leu Leu Arg Ala Tyr Phe Gly Val Ala Leu Ile Gly
        515                 520                 525

Asp Glu Asp Thr Tyr Arg Ala Phe Thr Thr Leu Thr Val Asp Ser Val
    530                 535                 540

Leu Ser Phe Val Gln Leu Thr Leu Gln Glu Gly Arg Thr Glu Asp Ile
545                 550                 555                 560

Arg Arg Phe Glu Lys Tyr Gly Glu Gln Ile Ala Arg Glu Asp Leu Pro
                565                 570                 575

Ser Ile Leu Thr Asn Ala Arg Ala Val Gln Gln Tyr Leu Gly Tyr Ile
            580                 585                 590

Asp Gln Asp Ile Ile Asn Lys Lys Val Ser Arg Ser Arg Asp Val Asn
        595                 600                 605

Gln Ile Phe Thr Glu Met Ala Arg Ala Ile Ile Arg Ala Ile Ser Arg
    610                 615                 620

Asn Asn Ile Gly Lys Asp Met Arg Ser
625                 630
```

<210> 441
<211> 1035
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1012)
<223> RXN00943

<400> 441
taggtacgat cggacgagga gaaaaaatct gaaaacaatc cagtggccca cctcggctta 60

taaaactgga caacagtatt ttgattggag catcaccata atg atc cgc aaa ctt 115
Met Ile Arg Lys Leu
1 5

gct cga cca atg ctt gca tcg gtc tac gtc gca gat ggc gca gaa aca 163
Ala Arg Pro Met Leu Ala Ser Val Tyr Val Ala Asp Gly Ala Glu Thr
10 15 20

gta ttg aac acc agc gca cac gtc gaa ggc act cag gta gtt ctg gat 211
Val Leu Asn Thr Ser Ala His Val Glu Gly Thr Gln Val Val Leu Asp
25 30 35

cgt atc cgt tat gtg ctg ccc cgt aag tac gca aag cgc att tcc aga 259
Arg Ile Arg Tyr Val Leu Pro Arg Lys Tyr Ala Lys Arg Ile Ser Arg
40 45 50

gat cca gaa ttg gtc acc cgc gtc att ggc ggc acc aaa gtc ggt gcg 307
Asp Pro Glu Leu Val Thr Arg Val Ile Gly Gly Thr Lys Val Gly Ala
55 60 65

ggt tct ttg cta gct att ggt cgt gca cca cgc acc tct gca gct acc 355
Gly Ser Leu Leu Ala Ile Gly Arg Ala Pro Arg Thr Ser Ala Ala Thr
70 75 80 85

ctc gca atc ctg act atc cct aac atc ctg gct cgc aat gcg ttc tgg 403
Leu Ala Ile Leu Thr Ile Pro Asn Ile Leu Ala Arg Asn Ala Phe Trp
90 95 100

gaa acc cag gat gcg gat gaa aag cgt aac cgc cgc aac ggt ttc ctc 451
Glu Thr Gln Asp Ala Asp Glu Lys Arg Asn Arg Arg Asn Gly Phe Leu
105 110 115

acc aac att gcc ctg ctt ggt ggc ctg ttt atc act tct gtt gat act 499
Thr Asn Ile Ala Leu Leu Gly Gly Leu Phe Ile Thr Ser Val Asp Thr
120 125 130

gag ggc aag cct ggc gtg aag tgg cgt gca acc aat gct aca aag cgt 547
Glu Gly Lys Pro Gly Val Lys Trp Arg Ala Thr Asn Ala Thr Lys Arg
135 140 145

ggc aag aag cag ctg cag cag gca ctt cca acc aaa tct gag act gaa 595
Gly Lys Lys Gln Leu Gln Gln Ala Leu Pro Thr Lys Ser Glu Thr Glu
150 155 160 165

aag ttc ggt gag aag gcc tct gat tgg ttc aac gat act tct gac aag 643
Lys Phe Gly Glu Lys Ala Ser Asp Trp Phe Asn Asp Thr Ser Asp Lys
170 175 180

gtc acc gag tac gcg tac acc gct cag gat ttt gtc ggt gag aac aag 691
Val Thr Glu Tyr Ala Tyr Thr Ala Gln Asp Phe Val Gly Glu Asn Lys
185 190 195

gat gac tgg atc aag tcc gca acc gag act gct cac aag gtc gct gat 739

```
Asp Asp Trp Ile Lys Ser Ala Thr Glu Thr Ala His Lys Val Ala Asp
        200                 205                 210

act gtg agc gat tac gct cac aag gct acc tct tac ctt gag gag aac   787
Thr Val Ser Asp Tyr Ala His Lys Ala Thr Ser Tyr Leu Glu Glu Asn
    215                 220                 225

agc ggt gac tgg ctt gag gct gcg cag gct aac gcc aag act gct cgt   835
Ser Gly Asp Trp Leu Glu Ala Ala Gln Ala Asn Ala Lys Thr Ala Arg
230                 235                 240                 245

aag tct gca gtg aag gct gcc ggc aag gct cag gaa aag gct aac ttt   883
Lys Ser Ala Val Lys Ala Ala Gly Lys Ala Gln Glu Lys Ala Asn Phe
                250                 255                 260

gct ctt cag gtc gca gag gaa acc tct ggt cgc gcc aac aag aag gca   931
Ala Leu Gln Val Ala Glu Glu Thr Ser Gly Arg Ala Asn Lys Lys Ala
            265                 270                 275

act aag agc tac gac aag ctt cag aag cag gct gat aag gcc atc gat   979
Thr Lys Ser Tyr Asp Lys Leu Gln Lys Gln Ala Asp Lys Ala Ile Asp
        280                 285                 290

cgt gca cag aag aag ctg aag ggc atc gaa ctt taagtaactt cttcctgatt 1032
Arg Ala Gln Lys Lys Leu Lys Gly Ile Glu Leu
    295                 300

gag                                                               1035


<210> 442
<211> 304
<212> PRT
<213> Corynebacterium glutamicum

<400> 442
Met Ile Arg Lys Leu Ala Arg Pro Met Leu Ala Ser Val Tyr Val Ala
  1               5                  10                  15

Asp Gly Ala Glu Thr Val Leu Asn Thr Ser Ala His Val Glu Gly Thr
             20                  25                  30

Gln Val Val Leu Asp Arg Ile Arg Tyr Val Leu Pro Arg Lys Tyr Ala
         35                  40                  45

Lys Arg Ile Ser Arg Asp Pro Glu Leu Val Thr Arg Val Ile Gly Gly
     50                  55                  60

Thr Lys Val Gly Ala Gly Ser Leu Leu Ala Ile Gly Arg Ala Pro Arg
 65                  70                  75                  80

Thr Ser Ala Ala Thr Leu Ala Ile Leu Thr Ile Pro Asn Ile Leu Ala
                 85                  90                  95

Arg Asn Ala Phe Trp Glu Thr Gln Asp Ala Asp Glu Lys Arg Asn Arg
            100                 105                 110

Arg Asn Gly Phe Leu Thr Asn Ile Ala Leu Leu Gly Gly Leu Phe Ile
        115                 120                 125

Thr Ser Val Asp Thr Glu Gly Lys Pro Gly Val Lys Trp Arg Ala Thr
```

```
    130                 135                 140

Asn Ala Thr Lys Arg Gly Lys Lys Gln Leu Gln Gln Ala Leu Pro Thr
145                 150                 155                 160

Lys Ser Glu Thr Glu Lys Phe Gly Glu Lys Ala Ser Asp Trp Phe Asn
                165                 170                 175

Asp Thr Ser Asp Lys Val Thr Glu Tyr Ala Tyr Thr Ala Gln Asp Phe
            180                 185                 190

Val Gly Glu Asn Lys Asp Asp Trp Ile Lys Ser Ala Thr Glu Thr Ala
        195                 200                 205

His Lys Val Ala Asp Thr Val Ser Asp Tyr Ala His Lys Ala Thr Ser
    210                 215                 220

Tyr Leu Glu Glu Asn Ser Gly Asp Trp Leu Glu Ala Ala Gln Ala Asn
225                 230                 235                 240

Ala Lys Thr Ala Arg Lys Ser Ala Val Lys Ala Ala Gly Lys Ala Gln
                245                 250                 255

Glu Lys Ala Asn Phe Ala Leu Gln Val Ala Glu Glu Thr Ser Gly Arg
            260                 265                 270

Ala Asn Lys Lys Ala Thr Lys Ser Tyr Asp Lys Leu Gln Lys Gln Ala
        275                 280                 285

Asp Lys Ala Ile Asp Arg Ala Gln Lys Lys Leu Lys Gly Ile Glu Leu
    290                 295                 300
```

Application Filed Electronically

<210> 443
<211> 530
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(507)
<223> FRXA00943

<400> 443

```
aag cct ggc gtg aag tgg cgt gca acc aat gct aca aag cgt ggc aag   48
Lys Pro Gly Val Lys Trp Arg Ala Thr Asn Ala Thr Lys Arg Gly Lys
  1               5                  10                  15

aag cag ctg cag cag gca ctt tca acc aaa tct gag act gaa aag ttc   96
Lys Gln Leu Gln Gln Ala Leu Ser Thr Lys Ser Glu Thr Glu Lys Phe
             20                  25                  30

ggt gag aag gcc tct gat tgg ttc aac gat act tct gac aag gtc acc   144
Gly Glu Lys Ala Ser Asp Trp Phe Asn Asp Thr Ser Asp Lys Val Thr
         35                  40                  45

gag tac gcg tac acc gct cag gat ttt gtc ggt gag aac aag gat gac   192
Glu Tyr Ala Tyr Thr Ala Gln Asp Phe Val Gly Glu Asn Lys Asp Asp
```

```
     50                  55                  60

tgg atc aag tcc gca acc gag act gct cac aag gtc gct gat act gtg   240
Trp Ile Lys Ser Ala Thr Glu Thr Ala His Lys Val Ala Asp Thr Val
 65                  70                  75                  80

agc gat tac gct cac aag gct acc tct tac ctt gag gag aac agc ggt   288
Ser Asp Tyr Ala His Lys Ala Thr Ser Tyr Leu Glu Glu Asn Ser Gly
                85                  90                  95

gac tgg ctt gag gct gcg cag gct aac gcc aag act gct cgt aag tct   336
Asp Trp Leu Glu Ala Ala Gln Ala Asn Ala Lys Thr Ala Arg Lys Ser
            100                 105                 110

gca gtg aag gct gcc ggc aag gct cac gaa aag gct aac ttt gct ctt   384
Ala Val Lys Ala Ala Gly Lys Ala His Glu Lys Ala Asn Phe Ala Leu
        115                 120                 125

cag gtc gca gag gaa acc tct ggt cgc gcc aac aag aag gca act aag   432
Gln Val Ala Glu Glu Thr Ser Gly Arg Ala Asn Lys Lys Ala Thr Lys
    130                 135                 140

agc tac gac aag ctt cag aag cag gct gat aag gcc atc gat cgt gca   480
Ser Tyr Asp Lys Leu Gln Lys Gln Ala Asp Lys Ala Ile Asp Arg Ala
145                 150                 155                 160

cag aag aag ctg aag ggc atc gaa ctt taagtaactt cttcctgatt         527
Gln Lys Lys Leu Lys Gly Ile Glu Leu
                165

gag                                                               530


<210> 444
<211> 169
<212> PRT
<213> Corynebacterium glutamicum

<400> 444
Lys Pro Gly Val Lys Trp Arg Ala Thr Asn Ala Thr Lys Arg Gly Lys
  1               5                  10                  15

Lys Gln Leu Gln Gln Ala Leu Ser Thr Lys Ser Glu Thr Glu Lys Phe
             20                  25                  30

Gly Glu Lys Ala Ser Asp Trp Phe Asn Asp Thr Ser Asp Lys Val Thr
         35                  40                  45

Glu Tyr Ala Tyr Thr Ala Gln Asp Phe Val Gly Glu Asn Lys Asp Asp
     50                  55                  60

Trp Ile Lys Ser Ala Thr Glu Thr Ala His Lys Val Ala Asp Thr Val
 65                  70                  75                  80

Ser Asp Tyr Ala His Lys Ala Thr Ser Tyr Leu Glu Glu Asn Ser Gly
                85                  90                  95

Asp Trp Leu Glu Ala Ala Gln Ala Asn Ala Lys Thr Ala Arg Lys Ser
            100                 105                 110

Ala Val Lys Ala Ala Gly Lys Ala His Glu Lys Ala Asn Phe Ala Leu
```

```
        115                 120                 125

Gln Val Ala Glu Glu Thr Ser Gly Arg Ala Asn Lys Lys Ala Thr Lys
    130                 135                 140

Ser Tyr Asp Lys Leu Gln Lys Gln Ala Asp Lys Ala Ile Asp Arg Ala
145                 150                 155                 160

Gln Lys Lys Leu Lys Gly Ile Glu Leu
                165
```

<210> 445
<211> 316
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(316)
<223> FRXA02423

<400> 445
taggtacgat cggacgagga gaaaaaatct gaaaacaatc cagtggccca cctcggctta 60

taaaactgga caacagtatt ttgattggag catcaccata atg atc cgc aaa ctt 115
                                            Met Ile Arg Lys Leu
                                              1   5

gct cga cca atg ctt gca tcg gtc tac gtc gca gat ggc gca gaa aca 163
Ala Arg Pro Met Leu Ala Ser Val Tyr Val Ala Asp Gly Ala Glu Thr
                10   15   20

gta ttg aac acc agc gca cac gtc gaa ggc act cag gta gtt ctg gat 211
Val Leu Asn Thr Ser Ala His Val Glu Gly Thr Gln Val Val Leu Asp
            25   30   35

cgt atc cgt tat gtg ctg ccc cgt aag tac gca aag cgc att tcc aga 259
Arg Ile Arg Tyr Val Leu Pro Arg Lys Tyr Ala Lys Arg Ile Ser Arg
        40   45   50

gat cca gaa ttg gtc acc cgc gtc att ggc ggc acc aaa gtc tgt gcg 307
Asp Pro Glu Leu Val Thr Arg Val Ile Gly Gly Thr Lys Val Cys Ala
    55   60   65

ggt tct tgt   316
Gly Ser Cys
 70

<210> 446
<211> 72
<212> PRT
<213> Corynebacterium glutamicum

<400> 446
Met Ile Arg Lys Leu Ala Arg Pro Met Leu Ala Ser Val Tyr Val Ala
  1   5   10   15

Asp Gly Ala Glu Thr Val Leu Asn Thr Ser Ala His Val Glu Gly Thr
            20   25   30
```
```

```
Gln Val Val Leu Asp Arg Ile Arg Tyr Val Leu Pro Arg Lys Tyr Ala
         35                  40                  45

Lys Arg Ile Ser Arg Asp Pro Glu Leu Val Thr Arg Val Ile Gly Gly
     50                  55                  60

Thr Lys Val Cys Ala Gly Ser Cys
 65                  70


<210> 447
<211> 1095
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1072)
<223> RXN00945

<400> 447
tcacagtacc acccacaagc cacaaggagg gtatggaggt gggcgtctaa agccaaattt 60

ttcccggtgt ttgaggcgat tgcaccgtac actaatgtgc atg ctt gaa cgc ctc   115
                                        Met Leu Glu Arg Leu
                                          1               5

aaa cgc cta gat ccg ctc att gtc ctc att gtg ctg gct gtc att gtg   163
Lys Arg Leu Asp Pro Leu Ile Val Leu Ile Val Leu Ala Val Ile Val
                 10                  15                  20

gcg atc atc att cca gtt cgc ggg gtt gct gcg gat tgg ttt gat gtc   211
Ala Ile Ile Ile Pro Val Arg Gly Val Ala Ala Asp Trp Phe Asp Val
             25                  30                  35

gcc gtc aag att gcc att gcg ctg ctg ttt ttt ctt tat ggt gcc cgc   259
Ala Val Lys Ile Ala Ile Ala Leu Leu Phe Phe Leu Tyr Gly Ala Arg
         40                  45                  50

cta tcc acc caa gag gcg ctg aat ggt ctg aag cac tgg agg ctt cac   307
Leu Ser Thr Gln Glu Ala Leu Asn Gly Leu Lys His Trp Arg Leu His
     55                  60                  65

ctg act att ttg gcg atc act ttc gga ata ttc cca ctt atc ggc att   355
Leu Thr Ile Leu Ala Ile Thr Phe Gly Ile Phe Pro Leu Ile Gly Ile
 70                  75                  80                  85

ggg ctc gag ccg atg act gca ttt gtg tcg gaa gat att tat cgg gga   403
Gly Leu Glu Pro Met Thr Ala Phe Val Ser Glu Asp Ile Tyr Arg Gly
                 90                  95                 100

att ttg ttc ctc acg ctc gtt ccg tcc acc gtg cag tca tcg gtg gcg   451
Ile Leu Phe Leu Thr Leu Val Pro Ser Thr Val Gln Ser Ser Val Ala
             105                 110                 115

ttt acc tcg atc gct aaa ggc aac gta gct ggt gcg att gtg tcg gca   499
Phe Thr Ser Ile Ala Lys Gly Asn Val Ala Gly Ala Ile Val Ser Ala
         120                 125                 130

tcg ctc tcc aac ctt gcg ggt gtt ttc ctc act ccg ctg ctg gtc atg   547
```

```
Ser Leu Ser Asn Leu Ala Gly Val Phe Leu Thr Pro Leu Leu Val Met
    135                 140                 145

ctc atc atg tct gcg ggc ggg gga gtt cac gtg gat tcc cag gtc ttc   595
Leu Ile Met Ser Ala Gly Gly Gly Val His Val Asp Ser Gln Val Phe
150                 155                 160                 165

ctc gac att gcg att cag ctt ctg ctg ccg ttc atc ctc ggc cag gta   643
Leu Asp Ile Ala Ile Gln Leu Leu Leu Pro Phe Ile Leu Gly Gln Val
                170                 175                 180

tgt agg cgt tgg gtg aag aat ttt gcg gcc aac aaa gca aca aaa atc   691
Cys Arg Arg Trp Val Lys Asn Phe Ala Ala Asn Lys Ala Thr Lys Ile
            185                 190                 195

gtg gac cgc ggc tcg atc gcg atg gtc gtg tac tcc gcg ttt tct gcc   739
Val Asp Arg Gly Ser Ile Ala Met Val Val Tyr Ser Ala Phe Ser Ala
        200                 205                 210

ggc atg gtg gct ggc att tgg tcc act gtg agc gtt cta gag att atc   787
Gly Met Val Ala Gly Ile Trp Ser Thr Val Ser Val Leu Glu Ile Ile
    215                 220                 225

tac ctc att gtt ttc gct att ctg ctg gtg atg gcc atg ctg tgg ttc   835
Tyr Leu Ile Val Phe Ala Ile Leu Leu Val Met Ala Met Leu Trp Phe
230                 235                 240                 245

acg ctg ttc atg gct aca cgc ctt gga ttt aac cgg gca gat tcc atc   883
Thr Leu Phe Met Ala Thr Arg Leu Gly Phe Asn Arg Ala Asp Ser Ile
                250                 255                 260

gct att cag ttc tgc gga acc aag aaa tcc ctg gcc aca ggc ctc cca   931
Ala Ile Gln Phe Cys Gly Thr Lys Lys Ser Leu Ala Thr Gly Leu Pro
            265                 270                 275

atg gcg gca gtc atc ttc ggt ggc gcc aat atc ggc ctg ctc atc ttg   979
Met Ala Ala Val Ile Phe Gly Gly Ala Asn Ile Gly Leu Leu Ile Leu
        280                 285                 290

ccg ttg atg atc ttc cac caa gtc cag ctg atg att tgt gca tgg ctt   1027
Pro Leu Met Ile Phe His Gln Val Gln Leu Met Ile Cys Ala Trp Leu
    295                 300                 305

gca gct cgt tat ggt cgt gat gcg cag gaa cag aaa gcc aac gcc       1072
Ala Ala Arg Tyr Gly Arg Asp Ala Gln Glu Gln Lys Ala Asn Ala
310                 315                 320

taaaagtcct cagtagctag cca                                       1095


<210> 448
<211> 324
<212> PRT
<213> Corynebacterium glutamicum

<400> 448
Met Leu Glu Arg Leu Lys Arg Leu Asp Pro Leu Ile Val Leu Ile Val
  1               5                  10                  15

Leu Ala Val Ile Val Ala Ile Ile Ile Pro Val Arg Gly Val Ala Ala
             20                  25                  30
```

```
Asp Trp Phe Asp Val Ala Val Lys Ile Ala Ile Ala Leu Leu Phe Phe
         35                  40                  45

Leu Tyr Gly Ala Arg Leu Ser Thr Gln Glu Ala Leu Asn Gly Leu Lys
     50                  55                  60

His Trp Arg Leu His Leu Thr Ile Leu Ala Ile Thr Phe Gly Ile Phe
 65                  70                  75                  80

Pro Leu Ile Gly Ile Gly Leu Glu Pro Met Thr Ala Phe Val Ser Glu
                 85                  90                  95

Asp Ile Tyr Arg Gly Ile Leu Phe Leu Thr Leu Val Pro Ser Thr Val
            100                 105                 110

Gln Ser Ser Val Ala Phe Thr Ser Ile Ala Lys Gly Asn Val Ala Gly
        115                 120                 125

Ala Ile Val Ser Ala Ser Leu Ser Asn Leu Ala Gly Val Phe Leu Thr
    130                 135                 140

Pro Leu Leu Val Met Leu Ile Met Ser Ala Gly Gly Gly Val His Val
145                 150                 155                 160

Asp Ser Gln Val Phe Leu Asp Ile Ala Ile Gln Leu Leu Leu Pro Phe
                165                 170                 175

Ile Leu Gly Gln Val Cys Arg Arg Trp Val Lys Asn Phe Ala Ala Asn
            180                 185                 190

Lys Ala Thr Lys Ile Val Asp Arg Gly Ser Ile Ala Met Val Val Tyr
        195                 200                 205

Ser Ala Phe Ser Ala Gly Met Val Ala Gly Ile Trp Ser Thr Val Ser
    210                 215                 220

Val Leu Glu Ile Ile Tyr Leu Ile Val Phe Ala Ile Leu Leu Val Met
225                 230                 235                 240

Ala Met Leu Trp Phe Thr Leu Phe Met Ala Thr Arg Leu Gly Phe Asn
                245                 250                 255

Arg Ala Asp Ser Ile Ala Ile Gln Phe Cys Gly Thr Lys Lys Ser Leu
            260                 265                 270

Ala Thr Gly Leu Pro Met Ala Ala Val Ile Phe Gly Gly Ala Asn Ile
        275                 280                 285

Gly Leu Leu Ile Leu Pro Leu Met Ile Phe His Gln Val Gln Leu Met
    290                 295                 300

Ile Cys Ala Trp Leu Ala Ala Arg Tyr Gly Arg Asp Ala Gln Glu Gln
305                 310                 315                 320

Lys Ala Asn Ala
```

<210> 449
<211> 897

<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(874)
<223> RXN00946

<400> 449
gggccggtgt gaataaaaca ccttccccaa atagacagca tggtctagat tagcttgaaa 60

cgaaagcgta cattcgcagc aactaacgga aagcacactc atg act cac act ctg 115
Met Thr His Thr Leu
1 5

cag gca act aat ccc ctt gat caa acc gct tgg cac gct tgg cat ttc 163
Gln Ala Thr Asn Pro Leu Asp Gln Thr Ala Trp His Ala Trp His Phe
10 15 20

tcc cga aac aaa gag gcc atc agc cgc acc ggc gcc acc agc ctg agt 211
Ser Arg Asn Lys Glu Ala Ile Ser Arg Thr Gly Ala Thr Ser Leu Ser
25 30 35

gcc aca gag tgg att agc gcc acc aca ctc aag gac gcg cac act ttt 259
Ala Thr Glu Trp Ile Ser Ala Thr Thr Leu Lys Asp Ala His Thr Phe
40 45 50

cct tca ctt ccc ggg cga tgg tat aaa cga ggc ggc ggg gta gtg gga 307
Pro Ser Leu Pro Gly Arg Trp Tyr Lys Arg Gly Gly Gly Val Val Gly
55 60 65

gca cat tta cca cca gct ttc gca aca act gga acg gtg caa ctg cgc 355
Ala His Leu Pro Pro Ala Phe Ala Thr Thr Gly Thr Val Gln Leu Arg
70 75 80 85

ccc ggt gag ctc ttg ata gcg gaa gat ttc acc ctc acc gtc att gaa 403
Pro Gly Glu Leu Leu Ile Ala Glu Asp Phe Thr Leu Thr Val Ile Glu
90 95 100

cgg ctt gga cag ttt gca ctt cag gtt ttt gat gca cgc aat ccg aag 451
Arg Leu Gly Gln Phe Ala Leu Gln Val Phe Asp Ala Arg Asn Pro Lys
105 110 115

cgt ttt gaa ttc cac tcc atc gca gct ttc cca ccg tcc gag gaa tgg 499
Arg Phe Glu Phe His Ser Ile Ala Ala Phe Pro Pro Ser Glu Glu Trp
120 125 130

cgg att gag gct cgc ttc ttc ccg gaa cct gac act gtt aac acc gct 547
Arg Ile Glu Ala Arg Phe Phe Pro Glu Pro Asp Thr Val Asn Thr Ala
135 140 145

gca gct gat gga gtt atc gtt gcc acg cct act gcg ggt tgg gtg cac 595
Ala Ala Asp Gly Val Ile Val Ala Thr Pro Thr Ala Gly Trp Val His
150 155 160 165

ttt ttg aag ggc cgt ctg gat tac cgt ctt cgt gta acc gtt cag aaa 643
Phe Leu Lys Gly Arg Leu Asp Tyr Arg Leu Arg Val Thr Val Gln Lys
170 175 180

aat aat cta cgg gca cta ttt agc gac aat tcc tcg acg ttg ggc gtt 691
Asn Asn Leu Arg Ala Leu Phe Ser Asp Asn Ser Ser Thr Leu Gly Val

```
            185                 190                 195

tat cag cat cgt ttt gtc gac atc cca cgc cct gat gcc gag gga aac   739
Tyr Gln His Arg Phe Val Asp Ile Pro Arg Pro Asp Ala Glu Gly Asn
        200                 205                 210

acc atc att gat ttc aac cgc gct tat ctt ccc cca aag gca ttg aac   787
Thr Ile Ile Asp Phe Asn Arg Ala Tyr Leu Pro Pro Lys Ala Leu Asn
    215                 220                 225

cga aag ttc ctg tgc cca tcg ccc agc ctg aac aac cac ctc aat ctc   835
Arg Lys Phe Leu Cys Pro Ser Pro Ser Leu Asn Asn His Leu Asn Leu
230                 235                 240                 245

acc gtg gag gca ggg gag aag tgg gtg gtt gct gga gga taatacttgc    884
Thr Val Glu Ala Gly Glu Lys Trp Val Val Ala Gly Gly
                250                 255

taaccgtcct aaa                                                   897


<210> 450
<211> 258
<212> PRT
<213> Corynebacterium glutamicum

<400> 450
Met Thr His Thr Leu Gln Ala Thr Asn Pro Leu Asp Gln Thr Ala Trp
  1               5                  10                  15

His Ala Trp His Phe Ser Arg Asn Lys Glu Ala Ile Ser Arg Thr Gly
             20                  25                  30

Ala Thr Ser Leu Ser Ala Thr Glu Trp Ile Ser Ala Thr Thr Leu Lys
         35                  40                  45

Asp Ala His Thr Phe Pro Ser Leu Pro Gly Arg Trp Tyr Lys Arg Gly
     50                  55                  60

Gly Gly Val Val Gly Ala His Leu Pro Pro Ala Phe Ala Thr Thr Gly
 65                  70                  75                  80

Thr Val Gln Leu Arg Pro Gly Glu Leu Leu Ile Ala Glu Asp Phe Thr
                 85                  90                  95

Leu Thr Val Ile Glu Arg Leu Gly Gln Phe Ala Leu Gln Val Phe Asp
            100                 105                 110

Ala Arg Asn Pro Lys Arg Phe Glu Phe His Ser Ile Ala Ala Phe Pro
        115                 120                 125

Pro Ser Glu Glu Trp Arg Ile Glu Ala Arg Phe Phe Pro Glu Pro Asp
    130                 135                 140

Thr Val Asn Thr Ala Ala Ala Asp Gly Val Ile Val Ala Thr Pro Thr
145                 150                 155                 160

Ala Gly Trp Val His Phe Leu Lys Gly Arg Leu Asp Tyr Arg Leu Arg
                165                 170                 175

Val Thr Val Gln Lys Asn Asn Leu Arg Ala Leu Phe Ser Asp Asn Ser
```

```
            180                 185                 190

Ser Thr Leu Gly Val Tyr Gln His Arg Phe Val Asp Ile Pro Arg Pro
        195                 200                 205

Asp Ala Glu Gly Asn Thr Ile Ile Asp Phe Asn Arg Ala Tyr Leu Pro
    210                 215                 220

Pro Lys Ala Leu Asn Arg Lys Phe Leu Cys Pro Ser Pro Ser Leu Asn
225                 230                 235                 240

Asn His Leu Asn Leu Thr Val Glu Ala Gly Glu Lys Trp Val Val Ala
                245                 250                 255

Gly Gly
```

Sequence Listing

<210> 451
<211> 897
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(874)
<223> FRXA00946

<400> 451

```
gggccggtgt gaataaaaca ccttccccaa atagacagca tggtctagat tagcttgaaa 60

cgaaagcgta cattcgcagc aactaacgga aagcacactc atg act cac act ctg   115
                                              Met Thr His Thr Leu
                                                1               5

cag gca act aat ccc ctt gat caa acc gct tgg cac gct tgg cat ttc   163
Gln Ala Thr Asn Pro Leu Asp Gln Thr Ala Trp His Ala Trp His Phe
                10                  15                  20

tcc cga aac aaa gag gcc atc agc cgc acc ggc gcc acc agc ctg agt   211
Ser Arg Asn Lys Glu Ala Ile Ser Arg Thr Gly Ala Thr Ser Leu Ser
            25                  30                  35

gcc aca gag tgg att agc gcc acc aca ctc aag gac gcg cac act ttt   259
Ala Thr Glu Trp Ile Ser Ala Thr Thr Leu Lys Asp Ala His Thr Phe
        40                  45                  50

cct tca ctt ccc ggg cga tgg tat aaa cga ggc ggc ggg gta gtg gga   307
Pro Ser Leu Pro Gly Arg Trp Tyr Lys Arg Gly Gly Gly Val Val Gly
    55                  60                  65

gca cat tta cca cca gct ttc gca aca act gga acg gtg caa ctg cgc   355
Ala His Leu Pro Pro Ala Phe Ala Thr Thr Gly Thr Val Gln Leu Arg
70                  75                  80                  85

ccc ggt gag ctc ttg ata gcg gaa gat ttc acc ctc acc gtc att gaa   403
Pro Gly Glu Leu Leu Ile Ala Glu Asp Phe Thr Leu Thr Val Ile Glu
                90                  95                  100

cgg ctt gga cag ttt gca ctt cag gtt ttt gat gca cgc aat ccg aag   451
Arg Leu Gly Gln Phe Ala Leu Gln Val Phe Asp Ala Arg Asn Pro Lys
```

```
            105                 110                 115

cgt ttt gaa ttc cac tcc atc gca gct ttc cca ccg tcc gag gaa tgg   499
Arg Phe Glu Phe His Ser Ile Ala Ala Phe Pro Pro Ser Glu Glu Trp
        120                 125                 130

cgg att gag gct cgc ttc ttc ccg gaa cct gac act gtt aac acc gct   547
Arg Ile Glu Ala Arg Phe Phe Pro Glu Pro Asp Thr Val Asn Thr Ala
    135                 140                 145

gca gct gat gga gtt atc gtt gcc acg cct act gcg ggt tgg gtg cac   595
Ala Ala Asp Gly Val Ile Val Ala Thr Pro Thr Ala Gly Trp Val His
150                 155                 160                 165

ttt ttg aag ggc cgt ctg gat tac cgt ctt cgt gta acc gtt cag aaa   643
Phe Leu Lys Gly Arg Leu Asp Tyr Arg Leu Arg Val Thr Val Gln Lys
                170                 175                 180

aat aat cta cgg gca cta ttt agc gac aat tcc tcg acg ttg ggc gtt   691
Asn Asn Leu Arg Ala Leu Phe Ser Asp Asn Ser Ser Thr Leu Gly Val
            185                 190                 195

tat cag cat cgt ttt gtc gac atc cca cgc cct gat gcc gag gga aac   739
Tyr Gln His Arg Phe Val Asp Ile Pro Arg Pro Asp Ala Glu Gly Asn
        200                 205                 210

acc atc att gat ttc aac cgc gct tat ctt ccc cca aag gca ttg aac   787
Thr Ile Ile Asp Phe Asn Arg Ala Tyr Leu Pro Pro Lys Ala Leu Asn
    215                 220                 225

cga aag ttc ctg tgc cca tcg ccc agc ctg aac aac cac ctc aat ctc   835
Arg Lys Phe Leu Cys Pro Ser Pro Ser Leu Asn Asn His Leu Asn Leu
230                 235                 240                 245

acc gtg gag gca ggg gag aag tgg gtg gtt gct gga gga taatacttgc    884
Thr Val Glu Ala Gly Glu Lys Trp Val Val Ala Gly Gly
                250                 255

taaccgtcct aaa                                                   897


<210> 452
<211> 258
<212> PRT
<213> Corynebacterium glutamicum

<400> 452
Met Thr His Thr Leu Gln Ala Thr Asn Pro Leu Asp Gln Thr Ala Trp
  1               5                  10                  15

His Ala Trp His Phe Ser Arg Asn Lys Glu Ala Ile Ser Arg Thr Gly
             20                  25                  30

Ala Thr Ser Leu Ser Ala Thr Glu Trp Ile Ser Ala Thr Thr Leu Lys
         35                  40                  45

Asp Ala His Thr Phe Pro Ser Leu Pro Gly Arg Trp Tyr Lys Arg Gly
     50                  55                  60

Gly Gly Val Val Gly Ala His Leu Pro Pro Ala Phe Ala Thr Thr Gly
 65                  70                  75                  80
```

```
Thr Val Gln Leu Arg Pro Gly Glu Leu Leu Ile Ala Glu Asp Phe Thr
                 85                  90                  95

Leu Thr Val Ile Glu Arg Leu Gly Gln Phe Ala Leu Gln Val Phe Asp
            100                 105                 110

Ala Arg Asn Pro Lys Arg Phe Glu Phe His Ser Ile Ala Ala Phe Pro
        115                 120                 125

Pro Ser Glu Glu Trp Arg Ile Glu Ala Arg Phe Phe Pro Glu Pro Asp
    130                 135                 140

Thr Val Asn Thr Ala Ala Ala Asp Gly Val Ile Val Ala Thr Pro Thr
145                 150                 155                 160

Ala Gly Trp Val His Phe Leu Lys Gly Arg Leu Asp Tyr Arg Leu Arg
                165                 170                 175

Val Thr Val Gln Lys Asn Asn Leu Arg Ala Leu Phe Ser Asp Asn Ser
            180                 185                 190

Ser Thr Leu Gly Val Tyr Gln His Arg Phe Val Asp Ile Pro Arg Pro
        195                 200                 205

Asp Ala Glu Gly Asn Thr Ile Ile Asp Phe Asn Arg Ala Tyr Leu Pro
    210                 215                 220

Pro Lys Ala Leu Asn Arg Lys Phe Leu Cys Pro Ser Pro Ser Leu Asn
225                 230                 235                 240

Asn His Leu Asn Leu Thr Val Glu Ala Gly Glu Lys Trp Val Val Ala
                245                 250                 255

Gly Gly
```

<210> 453
<211> 789
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (14)..(766)
<223> RXN00953

<400> 453

```
cttgcattcc ccaatg gcg cca cca acg gta ggc aac tac atc atg cag tcc 52
               Met Ala Pro Pro Thr Val Gly Asn Tyr Ile Met Gln Ser
                 1               5                  10

ttc act caa ggt ctg cag ttc ggc gtt gca gtt gcc gtg att ctc ttt   100
Phe Thr Gln Gly Leu Gln Phe Gly Val Ala Val Ala Val Ile Leu Phe
     15                  20                  25

ggt gtc cgc acc att ctt ggt gaa ctg gtc ccc gca ttc caa ggt att   148
Gly Val Arg Thr Ile Leu Gly Glu Leu Val Pro Ala Phe Gln Gly Ile
 30                  35                  40                  45
```

```
gct gcg aag gtt gtt ccc gga gct atc ccc gca ttg gat gca ccg atc   196
Ala Ala Lys Val Val Pro Gly Ala Ile Pro Ala Leu Asp Ala Pro Ile
                50                  55                  60

gtg ttc ccc tac gcg cag aac gcc gtt ctc att ggt ttc ttg tct tcc   244
Val Phe Pro Tyr Ala Gln Asn Ala Val Leu Ile Gly Phe Leu Ser Ser
            65                  70                  75

ttc gtc ggt ggc ttg gtt ggc ctg act gtt ctt gca tcg tgg ctg aac   292
Phe Val Gly Gly Leu Val Gly Leu Thr Val Leu Ala Ser Trp Leu Asn
        80                  85                  90

cca gct ttt ggt gtc gcg ttg att ctg cct ggt ttg gtc ccc cac ttc   340
Pro Ala Phe Gly Val Ala Leu Ile Leu Pro Gly Leu Val Pro His Phe
    95                  100                 105

ttc act ggt ggc gcg gcg ggc gtt tac ggt aat gcc acg ggt ggt cgt   388
Phe Thr Gly Gly Ala Ala Gly Val Tyr Gly Asn Ala Thr Gly Gly Arg
110                 115                 120                 125

cga gga gca gta ttt ggc gcc ttt gcc aac ggt ctt ctg att acc ttc   436
Arg Gly Ala Val Phe Gly Ala Phe Ala Asn Gly Leu Leu Ile Thr Phe
                130                 135                 140

ctc cct gct ttc ctg ctt ggt gtg ctt ggt tcc ttc ggg tca gag aac   484
Leu Pro Ala Phe Leu Leu Gly Val Leu Gly Ser Phe Gly Ser Glu Asn
            145                 150                 155

acc act ttc ggt gat gcg gac ttt ggt tgg ttc gga atc gtt gtt ggt   532
Thr Thr Phe Gly Asp Ala Asp Phe Gly Trp Phe Gly Ile Val Val Gly
        160                 165                 170

tct gca gcc aag gtg gaa ggt gct ggc ggg ctc atc ttg ttg ctc atc   580
Ser Ala Ala Lys Val Glu Gly Ala Gly Gly Leu Ile Leu Leu Leu Ile
    175                 180                 185

atc gca gcg gtt ctt ctg ggt ggc gcg atg gtc ttc cag aag cgc gtc   628
Ile Ala Ala Val Leu Leu Gly Gly Ala Met Val Phe Gln Lys Arg Val
190                 195                 200                 205

gtg aat ggg cac tgg gat cca gct ccc aac cgt gag cgc gtg gag aag   676
Val Asn Gly His Trp Asp Pro Ala Pro Asn Arg Glu Arg Val Glu Lys
                210                 215                 220

gcg gaa gct gat gcc act cca acg gct ggg gct cgg acc tac cct aag   724
Ala Glu Ala Asp Ala Thr Pro Thr Ala Gly Ala Arg Thr Tyr Pro Lys
            225                 230                 235

att gct cct ccg gcg ggc gct cct acc cca ccg gct cga agc           766
Ile Ala Pro Pro Ala Gly Ala Pro Thr Pro Pro Ala Arg Ser
        240                 245                 250

taagatctcc aaaaccctga gat                                        789
```

<210> 454
<211> 251
<212> PRT
<213> Corynebacterium glutamicum

<400> 454

```
Met Ala Pro Pro Thr Val Gly Asn Tyr Ile Met Gln Ser Phe Thr Gln
 1               5                  10                  15

Gly Leu Gln Phe Gly Val Ala Val Ala Val Ile Leu Phe Gly Val Arg
            20                  25                  30

Thr Ile Leu Gly Glu Leu Val Pro Ala Phe Gln Gly Ile Ala Ala Lys
        35                  40                  45

Val Val Pro Gly Ala Ile Pro Ala Leu Asp Ala Pro Ile Val Phe Pro
    50                  55                  60

Tyr Ala Gln Asn Ala Val Leu Ile Gly Phe Leu Ser Ser Phe Val Gly
65                  70                  75                  80

Gly Leu Val Gly Leu Thr Val Leu Ala Ser Trp Leu Asn Pro Ala Phe
                85                  90                  95

Gly Val Ala Leu Ile Leu Pro Gly Leu Val Pro His Phe Phe Thr Gly
            100                 105                 110

Gly Ala Ala Gly Val Tyr Gly Asn Ala Thr Gly Gly Arg Arg Gly Ala
        115                 120                 125

Val Phe Gly Ala Phe Ala Asn Gly Leu Leu Ile Thr Phe Leu Pro Ala
    130                 135                 140

Phe Leu Leu Gly Val Leu Gly Ser Phe Gly Ser Glu Asn Thr Thr Phe
145                 150                 155                 160

Gly Asp Ala Asp Phe Gly Trp Phe Gly Ile Val Val Gly Ser Ala Ala
                165                 170                 175

Lys Val Glu Gly Ala Gly Gly Leu Ile Leu Leu Leu Ile Ile Ala Ala
            180                 185                 190

Val Leu Leu Gly Gly Ala Met Val Phe Gln Lys Arg Val Val Asn Gly
        195                 200                 205

His Trp Asp Pro Ala Pro Asn Arg Glu Arg Val Glu Lys Ala Glu Ala
    210                 215                 220

Asp Ala Thr Pro Thr Ala Gly Ala Arg Thr Tyr Pro Lys Ile Ala Pro
225                 230                 235                 240

Pro Ala Gly Ala Pro Thr Pro Pro Ala Arg Ser
                245                 250
```

<210> 455
<211> 579
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(556)
<223> RXN00959

<400> 455
tttggaggcg gagcatcata ccttttaatg tcaggatcgt gcagtgaaga attcaggatg 60

```
aattactcgc tggaatattg gtggggatag agttgttgtt atg acg gtg atc gga   115
                                           Met Thr Val Ile Gly
                                             1               5

att att ctt ggc agc ctt ttt ggc gtt ctt gca gtc ctt ctc atc gtg   163
Ile Ile Leu Gly Ser Leu Phe Gly Val Leu Ala Val Leu Leu Ile Val
                10                  15                  20

gtt ggt gct ttg ggg tgg gcg gct aag ctc cct ggc aac ccg gtt gtg   211
Val Gly Ala Leu Gly Trp Ala Ala Lys Leu Pro Gly Asn Pro Val Val
            25                  30                  35

ggc att cgt gtc cct gag gtg cgt aaa tcc caa gaa ttg tgg gat atg   259
Gly Ile Arg Val Pro Glu Val Arg Lys Ser Gln Glu Leu Trp Asp Met
        40                  45                  50

gcg cac cgt gtc gct ggc ccg ttg tgg gtg ctg tcg gga gtt tcc ttt   307
Ala His Arg Val Ala Gly Pro Leu Trp Val Leu Ser Gly Val Ser Phe
    55                  60                  65

gtt att gca tcg cta gtt gcg ttt gtt gct tct ggt tgg atg tgg ctt   355
Val Ile Ala Ser Leu Val Ala Phe Val Ala Ser Gly Trp Met Trp Leu
70                  75                  80                  85

gtt gtg gcg ttg ggt gtt gag gct gcc atc gcg ttc att ggt atg ggt   403
Val Val Ala Leu Gly Val Glu Ala Ala Ile Ala Phe Ile Gly Met Gly
                90                  95                  100

gcg ggt atg gct gca cat act gtt gcg atg gtt gac gcg aag cgc att   451
Ala Gly Met Ala Ala His Thr Val Ala Met Val Asp Ala Lys Arg Ile
            105                 110                 115

cgc gaa acc ccg cag gcg cct gtt tcc gct gaa att gaa gag gcc ggt   499
Arg Glu Thr Pro Gln Ala Pro Val Ser Ala Glu Ile Glu Glu Ala Gly
        120                 125                 130

ggt gtg act att acc tct gcc gat tat caa caa gac tcc gct gaa tgc   547
Gly Val Thr Ile Thr Ser Ala Asp Tyr Gln Gln Asp Ser Ala Glu Cys
    135                 140                 145

ccc caa gat tgacttggat gcagtgcgta gag                             579
Pro Gln Asp
150
```

<210> 456
<211> 152
<212> PRT
<213> Corynebacterium glutamicum

<400> 456

```
Met Thr Val Ile Gly Ile Ile Leu Gly Ser Leu Phe Gly Val Leu Ala
  1               5                  10                  15

Val Leu Leu Ile Val Val Gly Ala Leu Gly Trp Ala Ala Lys Leu Pro
            20                  25                  30

Gly Asn Pro Val Val Gly Ile Arg Val Pro Glu Val Arg Lys Ser Gln
        35                  40                  45
```

```
Glu Leu Trp Asp Met Ala His Arg Val Ala Gly Pro Leu Trp Val Leu
     50                  55                  60

Ser Gly Val Ser Phe Val Ile Ala Ser Leu Val Ala Phe Val Ala Ser
 65                  70                  75                  80

Gly Trp Met Trp Leu Val Val Ala Leu Gly Val Glu Ala Ala Ile Ala
                85                  90                  95

Phe Ile Gly Met Gly Ala Gly Met Ala Ala His Thr Val Ala Met Val
            100                 105                 110

Asp Ala Lys Arg Ile Arg Glu Thr Pro Gln Ala Pro Val Ser Ala Glu
        115                 120                 125

Ile Glu Glu Ala Gly Gly Val Thr Ile Thr Ser Ala Asp Tyr Gln Gln
    130                 135                 140

Asp Ser Ala Glu Cys Pro Gln Asp
145                 150
```

<210> 457
<211> 427
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(427)
<223> FRXA00959

<400> 457

```
tttggaggcg gagcatcata ccttttaatg tcaggatcgt gcagtgaaga attcaggatg 60

aattactcgc tggaatattg gtggggatag agttgttgtt atg acg gtg atc gga   115
                                            Met Thr Val Ile Gly
                                              1               5

att att ctt ggc agc ctt ttt ggc gtt ctt gca gtc ctt ctc atc gtg   163
Ile Ile Leu Gly Ser Leu Phe Gly Val Leu Ala Val Leu Leu Ile Val
                10                  15                  20

gtt ggt gct ttg ggg tgg gcg gct aag ctc cct ggc aac ccg gtt gtg   211
Val Gly Ala Leu Gly Trp Ala Ala Lys Leu Pro Gly Asn Pro Val Val
            25                  30                  35

ggc att cgt gtc cct gag gtg cgt aaa tcc caa gaa ttg tgg gat atg   259
Gly Ile Arg Val Pro Glu Val Arg Lys Ser Gln Glu Leu Trp Asp Met
        40                  45                  50

gcg cac cgt gtc gct ggc ccg ttg tgg gtg ctg tcg gga gtt tcc ttt   307
Ala His Arg Val Ala Gly Pro Leu Trp Val Leu Ser Gly Val Ser Phe
    55                  60                  65

gtt att gca tcg cta gtt gcg ttt gtt gct tct ggt tgg atg tgg ctt   355
Val Ile Ala Ser Leu Val Ala Phe Val Ala Ser Gly Trp Met Trp Leu
70                  75                  80                  85

gtt gtg gcg ttg ggt gtt gag gct gcc atc gcg ttc att ggt atg ggt   403
Val Val Ala Leu Gly Val Glu Ala Ala Ile Ala Phe Ile Gly Met Gly
```

```
                90                  95                  100

gcg ggt atg gct gcg cat act ggt                                    427
Ala Gly Met Ala Ala His Thr Gly
            105


<210> 458
<211> 109
<212> PRT
<213> Corynebacterium glutamicum

<400> 458
Met Thr Val Ile Gly Ile Ile Leu Gly Ser Leu Phe Gly Val Leu Ala
  1               5                  10                  15

Val Leu Leu Ile Val Val Gly Ala Leu Gly Trp Ala Ala Lys Leu Pro
             20                  25                  30

Gly Asn Pro Val Val Gly Ile Arg Val Pro Glu Val Arg Lys Ser Gln
         35                  40                  45

Glu Leu Trp Asp Met Ala His Arg Val Ala Gly Pro Leu Trp Val Leu
     50                  55                  60

Ser Gly Val Ser Phe Val Ile Ala Ser Leu Val Ala Phe Val Ala Ser
 65                  70                  75                  80

Gly Trp Met Trp Leu Val Val Ala Leu Gly Val Glu Ala Ala Ile Ala
                 85                  90                  95

Phe Ile Gly Met Gly Ala Gly Met Ala Ala His Thr Gly
            100                 105


<210> 459
<211> 960
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(937)
<223> RXN00963

<400> 459
ctggctctga cggcgtcgac ttgttctgct tctctgatac accaattttc gaggccctta 60

acctcgcacg tacttttact ccggaaggaa tctagaactt atg cgt ctt gca aca   115
                                          Met Arg Leu Ala Thr
                                            1               5

atc cgc acc aac ggc acc acc att gct gct cgt gtt gaa tct gaa aac   163
Ile Arg Thr Asn Gly Thr Thr Ile Ala Ala Arg Val Glu Ser Glu Asn
                10                  15                  20

acc gct acc acc atc gag ggc ttt gcc aac gtc ggt gaa tta ctc cag   211
Thr Ala Thr Thr Ile Glu Gly Phe Ala Asn Val Gly Glu Leu Leu Gln
            25                  30                  35

gaa tcc aac tgg cgc gag ctg gca gaa aac gct gct ggt gag gct gtg   259
```

```
Glu Ser Asn Trp Arg Glu Leu Ala Glu Asn Ala Ala Gly Glu Ala Val
         40                  45                  50

acc ttt gaa aac aag gag cta gat gca gta gtt cca gca cct aag aag   307
Thr Phe Glu Asn Lys Glu Leu Asp Ala Val Val Pro Ala Pro Lys Lys
     55                  60                  65

att gtg tgc gtc ggc ctt aac tac gcc aac cac att aaa gaa atg ggc   355
Ile Val Cys Val Gly Leu Asn Tyr Ala Asn His Ile Lys Glu Met Gly
 70                  75                  80                  85

cgc gac ctc cct gat acc cca acc ctt ttt gtt aag ttc cct gac gcg   403
Arg Asp Leu Pro Asp Thr Pro Thr Leu Phe Val Lys Phe Pro Asp Ala
                 90                  95                 100

ctc atc gga cct ttc gat gat gtt gtc gtt cca gag tgg gct aac aag   451
Leu Ile Gly Pro Phe Asp Asp Val Val Val Pro Glu Trp Ala Asn Lys
            105                 110                 115

gct ctc gac tgg gaa ggc gag atg gca gtt atc att ggc aag cgc gca   499
Ala Leu Asp Trp Glu Gly Glu Met Ala Val Ile Ile Gly Lys Arg Ala
        120                 125                 130

cgc cgt gtc aag cag gcc gat gct gct gag tac atc gct ggc tac gca   547
Arg Arg Val Lys Gln Ala Asp Ala Ala Glu Tyr Ile Ala Gly Tyr Ala
    135                 140                 145

gtg atg aac gat tac acc acc cgc gat ttc cag tac gca gca cct gca   595
Val Met Asn Asp Tyr Thr Thr Arg Asp Phe Gln Tyr Ala Ala Pro Ala
150                 155                 160                 165

aag act cca cag tgg cac cag ggc aag tct ttg gaa aag tcc gct ggc   643
Lys Thr Pro Gln Trp His Gln Gly Lys Ser Leu Glu Lys Ser Ala Gly
                170                 175                 180

ttc ggg cct tgg atg act acc cca gat tct ttt gag ttc ggc ggc gag   691
Phe Gly Pro Trp Met Thr Thr Pro Asp Ser Phe Glu Phe Gly Gly Glu
            185                 190                 195

ctg gca acc tac ctc gag ggc gag aag gta cag tcc acc cct acc aat   739
Leu Ala Thr Tyr Leu Glu Gly Glu Lys Val Gln Ser Thr Pro Thr Asn
        200                 205                 210

gac ctg gtc ttt agc cca gaa aag ctc atc gaa tac atc acc cac atc   787
Asp Leu Val Phe Ser Pro Glu Lys Leu Ile Glu Tyr Ile Thr His Ile
    215                 220                 225

tac cca ttg gat gct ggc gac gtc att gtc acc ggt acc cca ggc ggc   835
Tyr Pro Leu Asp Ala Gly Asp Val Ile Val Thr Gly Thr Pro Gly Gly
230                 235                 240                 245

gtt ggc cac gca cgt aac cca cag cgc tac atc ggt gac ggc gaa acc   883
Val Gly His Ala Arg Asn Pro Gln Arg Tyr Ile Gly Asp Gly Glu Thr
                250                 255                 260

gta aag gtt gag att gcg ggc ctc ggc ttc att gaa aac aag acg gtg   931
Val Lys Val Glu Ile Ala Gly Leu Gly Phe Ile Glu Asn Lys Thr Val
            265                 270                 275

ttt gaa taaatgacaa ctttccacga tct                                960
Phe Glu
```

<210> 460
<211> 279
<212> PRT
<213> Corynebacterium glutamicum

<400> 460
Met Arg Leu Ala Thr Ile Arg Thr Asn Gly Thr Thr Ile Ala Ala Arg
1 5 10 15

Val Glu Ser Glu Asn Thr Ala Thr Thr Ile Glu Gly Phe Ala Asn Val
20 25 30

Gly Glu Leu Leu Gln Glu Ser Asn Trp Arg Glu Leu Ala Glu Asn Ala
35 40 45

Ala Gly Glu Ala Val Thr Phe Glu Asn Lys Glu Leu Asp Ala Val Val
50 55 60

Pro Ala Pro Lys Lys Ile Val Cys Val Gly Leu Asn Tyr Ala Asn His
65 70 75 80

Ile Lys Glu Met Gly Arg Asp Leu Pro Asp Thr Pro Thr Leu Phe Val
85 90 95

Lys Phe Pro Asp Ala Leu Ile Gly Pro Phe Asp Asp Val Val Val Pro
100 105 110

Glu Trp Ala Asn Lys Ala Leu Asp Trp Glu Gly Glu Met Ala Val Ile
115 120 125

Ile Gly Lys Arg Ala Arg Arg Val Lys Gln Ala Asp Ala Ala Glu Tyr
130 135 140

Ile Ala Gly Tyr Ala Val Met Asn Asp Tyr Thr Thr Arg Asp Phe Gln
145 150 155 160

Tyr Ala Ala Pro Ala Lys Thr Pro Gln Trp His Gln Gly Lys Ser Leu
165 170 175

Glu Lys Ser Ala Gly Phe Gly Pro Trp Met Thr Thr Pro Asp Ser Phe
180 185 190

Glu Phe Gly Gly Glu Leu Ala Thr Tyr Leu Glu Gly Glu Lys Val Gln
195 200 205

Ser Thr Pro Thr Asn Asp Leu Val Phe Ser Pro Glu Lys Leu Ile Glu
210 215 220

Tyr Ile Thr His Ile Tyr Pro Leu Asp Ala Gly Asp Val Ile Val Thr
225 230 235 240

Gly Thr Pro Gly Gly Val Gly His Ala Arg Asn Pro Gln Arg Tyr Ile
245 250 255

Gly Asp Gly Glu Thr Val Lys Val Glu Ile Ala Gly Leu Gly Phe Ile
260 265 270

Glu Asn Lys Thr Val Phe Glu

275

<210> 461
<211> 538
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(538)
<223> FRXA00963

<400> 461
ctggctctga cggcgtcgac ttgttctgct tctctgatac accaattttc gaggccctta 60

acctcgcacg tacttttact ccggaaggaa tctagaactt atg cgt ctt gca aca 115
Met Arg Leu Ala Thr
1 5

atc cgc acc aac ggc acc acc att gct gct cgt gtt gaa tct gaa aac 163
Ile Arg Thr Asn Gly Thr Thr Ile Ala Ala Arg Val Glu Ser Glu Asn
10 15 20

acc gct acc acc atc gag ggc ttt gcc aac gtc ggt gaa tta ctc cag 211
Thr Ala Thr Thr Ile Glu Gly Phe Ala Asn Val Gly Glu Leu Leu Gln
25 30 35

gaa tcc aac tgg cgc gag ctg gca gaa aac gct gct ggt gag gct gtg 259
Glu Ser Asn Trp Arg Glu Leu Ala Glu Asn Ala Ala Gly Glu Ala Val
40 45 50

acc ttt gaa aac aag gag cta gat gca gta gtt cca gca cct aag aag 307
Thr Phe Glu Asn Lys Glu Leu Asp Ala Val Val Pro Ala Pro Lys Lys
55 60 65

att gtg tgc gtc ggc ctt aac tac gcc aac cac att aaa gaa atg ggc 355
Ile Val Cys Val Gly Leu Asn Tyr Ala Asn His Ile Lys Glu Met Gly
70 75 80 85

cgc gac ctc cct gat acc cca acc ctt ttt gtt aag ttc cct gac gcg 403
Arg Asp Leu Pro Asp Thr Pro Thr Leu Phe Val Lys Phe Pro Asp Ala
90 95 100

ctc atc gga cct ttc gat gat gtt gtc gtt cca gag tgg gct aac aag 451
Leu Ile Gly Pro Phe Asp Asp Val Val Val Pro Glu Trp Ala Asn Lys
105 110 115

gct ctc gac tgg gaa ggc gag atg gca gtt atc att ggc aag cgc gca 499
Ala Leu Asp Trp Glu Gly Glu Met Ala Val Ile Ile Gly Lys Arg Ala
120 125 130

cgc cgt gtc aag cag gcc gat gct gct gag tac atc gct 538
Arg Arg Val Lys Gln Ala Asp Ala Ala Glu Tyr Ile Ala
135 140 145

<210> 462
<211> 146
<212> PRT
<213> Corynebacterium glutamicum

<400> 462
Met Arg Leu Ala Thr Ile Arg Thr Asn Gly Thr Thr Ile Ala Ala Arg
1 5 10 15

Val Glu Ser Glu Asn Thr Ala Thr Thr Ile Glu Gly Phe Ala Asn Val
20 25 30

Gly Glu Leu Leu Gln Glu Ser Asn Trp Arg Glu Leu Ala Glu Asn Ala
35 40 45

Ala Gly Glu Ala Val Thr Phe Glu Asn Lys Glu Leu Asp Ala Val Val
50 55 60

Pro Ala Pro Lys Lys Ile Val Cys Val Gly Leu Asn Tyr Ala Asn His
65 70 75 80

Ile Lys Glu Met Gly Arg Asp Leu Pro Asp Thr Pro Thr Leu Phe Val
85 90 95

Lys Phe Pro Asp Ala Leu Ile Gly Pro Phe Asp Asp Val Val Val Pro
100 105 110

Glu Trp Ala Asn Lys Ala Leu Asp Trp Glu Gly Glu Met Ala Val Ile
115 120 125

Ile Gly Lys Arg Ala Arg Arg Val Lys Gln Ala Asp Ala Ala Glu Tyr
130 135 140

Ile Ala
145

<210> 463
<211> 341
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(318)
<223> RXN00971

<400> 463
aaa gca ctt tcc atc gga acc cag tgg gca caa gtc atg ggc att aac 48
Lys Ala Leu Ser Ile Gly Thr Gln Trp Ala Gln Val Met Gly Ile Asn
1 5 10 15

cac gcc gaa gcc gaa gaa ctc gac gaa gcc ctc tcc ccg ctc att aac 96
His Ala Glu Ala Glu Glu Leu Asp Glu Ala Leu Ser Pro Leu Ile Asn
20 25 30

cgc ctc cgc gaa atg ggc ttt gac ccc acc gaa acc gaa gaa gca aac 144
Arg Leu Arg Glu Met Gly Phe Asp Pro Thr Glu Thr Glu Glu Ala Asn
35 40 45

tcc ctc gct cta cac agc tgc cca ttt gtg gtc aac gac aaa cgc cca 192
Ser Leu Ala Leu His Ser Cys Pro Phe Val Val Asn Asp Lys Arg Pro
50 55 60

tca gcc ttc gtc tgc gcc atc cac gcc gga ttc atc caa gaa agc ctc 240

```
Ser Ala Phe Val Cys Ala Ile His Ala Gly Phe Ile Gln Glu Ser Leu
 65                  70                  75                  80

ggt gaa aac aac cgc atc cag ctg gaa ctc aaa cca ctc aac gcg ccg   288
Gly Glu Asn Asn Arg Ile Gln Leu Glu Leu Lys Pro Leu Asn Ala Pro
                85                  90                  95

ggc acc tgt aag gtt cac gtg ttc agc gaa taattgctgc actaataagg     338
Gly Thr Cys Lys Val His Val Phe Ser Glu
            100                 105

ccc                                                              341


<210> 464
<211> 106
<212> PRT
<213> Corynebacterium glutamicum

<400> 464
Lys Ala Leu Ser Ile Gly Thr Gln Trp Ala Gln Val Met Gly Ile Asn
  1               5                  10                  15

His Ala Glu Ala Glu Glu Leu Asp Glu Ala Leu Ser Pro Leu Ile Asn
            20                  25                  30

Arg Leu Arg Glu Met Gly Phe Asp Pro Thr Glu Thr Glu Glu Ala Asn
         35                  40                  45

Ser Leu Ala Leu His Ser Cys Pro Phe Val Val Asn Asp Lys Arg Pro
     50                  55                  60

Ser Ala Phe Val Cys Ala Ile His Ala Gly Phe Ile Gln Glu Ser Leu
 65                  70                  75                  80

Gly Glu Asn Asn Arg Ile Gln Leu Glu Leu Lys Pro Leu Asn Ala Pro
                85                  90                  95

Gly Thr Cys Lys Val His Val Phe Ser Glu
            100                 105


<210> 465
<211> 296
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(273)
<223> FRXA00971

<400> 465
aac cac gcc gaa gcc gaa gaa ctc gac gaa gcc ctc tcc ccg ctc att   48
Asn His Ala Glu Ala Glu Glu Leu Asp Glu Ala Leu Ser Pro Leu Ile
  1               5                  10                  15

aac cgc ctc cgc gaa atg ggc ttt gac ccc acc gaa acc gaa gaa gca   96
Asn Arg Leu Arg Glu Met Gly Phe Asp Pro Thr Glu Thr Glu Glu Ala
            20                  25                  30
```

```
aac tcc ctc gct cta cac agc tgc cca ttt gtg gtc aac gac aaa cgc   144
Asn Ser Leu Ala Leu His Ser Cys Pro Phe Val Val Asn Asp Lys Arg
         35                  40                  45

cca tca gcc ttc gtc tgc gcc atc cac gcc gga ttc atc caa gaa agc   192
Pro Ser Ala Phe Val Cys Ala Ile His Ala Gly Phe Ile Gln Glu Ser
     50                  55                  60

ctc ggt gaa aac aac cgc atc cag ctg gaa ctc aaa cca ctc aac gcg   240
Leu Gly Glu Asn Asn Arg Ile Gln Leu Glu Leu Lys Pro Leu Asn Ala
 65                  70                  75                  80

ccg ggc acc tgt aag gtt cac gtg ttc agc gaa taattgctgc actaataagg 293
Pro Gly Thr Cys Lys Val His Val Phe Ser Glu
                85                  90

ccc                                                               296


<210> 466
<211> 91
<212> PRT
<213> Corynebacterium glutamicum

<400> 466
Asn His Ala Glu Ala Glu Glu Leu Asp Glu Ala Leu Ser Pro Leu Ile
  1               5                  10                  15

Asn Arg Leu Arg Glu Met Gly Phe Asp Pro Thr Glu Thr Glu Glu Ala
             20                  25                  30

Asn Ser Leu Ala Leu His Ser Cys Pro Phe Val Val Asn Asp Lys Arg
         35                  40                  45

Pro Ser Ala Phe Val Cys Ala Ile His Ala Gly Phe Ile Gln Glu Ser
     50                  55                  60

Leu Gly Glu Asn Asn Arg Ile Gln Leu Glu Leu Lys Pro Leu Asn Ala
 65                  70                  75                  80

Pro Gly Thr Cys Lys Val His Val Phe Ser Glu
                85                  90


<210> 467
<211> 1503
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1480)
<223> RXN00991

<400> 467
acttcaagga aagacggtcc caagagctaa aactccccca cggcacgcga agctgaacag 60

gctttcaccg cttctaaggg caacagctta aaccacgcta atg gac ata ctc ata   115
                                                Met Asp Ile Leu Ile
                                                  1               5
```

```
agc atc ctc tca ctg cta ggc ttc gtg ctt ctt acc gcg agc acc gga   163
Ser Ile Leu Ser Leu Leu Gly Phe Val Leu Leu Thr Ala Ser Thr Gly
                10                  15                  20

cta ttc gtg gcc att gag ttc gca ctc acc ggc tta gaa aaa tcc act   211
Leu Phe Val Ala Ile Glu Phe Ala Leu Thr Gly Leu Glu Lys Ser Thr
            25                  30                  35

gta gaa aca cat gtg aag caa aaa ggc gac agc agc gcc cgc gca gtg   259
Val Glu Thr His Val Lys Gln Lys Gly Asp Ser Ser Ala Arg Ala Val
        40                  45                  50

cag agg gat cat caa aat ctg tcg ttc gtg ctc tct ggt gcc cag ctg   307
Gln Arg Asp His Gln Asn Leu Ser Phe Val Leu Ser Gly Ala Gln Leu
    55                  60                  65

ggc atc acg atc acg aca ctt gcc aca ggc ttc ctc gca gag ccg gtt   355
Gly Ile Thr Ile Thr Thr Leu Ala Thr Gly Phe Leu Ala Glu Pro Val
70                  75                  80                  85

ttg gcc aaa ttc ttc acc cca gca ctt gag ctg gtg gga tta aat gaa   403
Leu Ala Lys Phe Phe Thr Pro Ala Leu Glu Leu Val Gly Leu Asn Glu
                90                  95                  100

tca gca agc tcc gca gta gcc ctc atc atc gca ctg ttg gtg gca act   451
Ser Ala Ser Ser Ala Val Ala Leu Ile Ile Ala Leu Leu Val Ala Thr
            105                 110                 115

acc ctc tcc atg gtt ttt ggt gag ttg gtt ccc aaa aac tgg gcg atc   499
Thr Leu Ser Met Val Phe Gly Glu Leu Val Pro Lys Asn Trp Ala Ile
        120                 125                 130

acc aac ccg ttg ggc gtg gca cgt ttt gtt gtc cac cct gtc aat tgg   547
Thr Asn Pro Leu Gly Val Ala Arg Phe Val Val His Pro Val Asn Trp
    135                 140                 145

ttc aac atg gtt ctc aag ccg ttt att aac ggc atg aac aag tct gca   595
Phe Asn Met Val Leu Lys Pro Phe Ile Asn Gly Met Asn Lys Ser Ala
150                 155                 160                 165

aac ttt att gtc cgc aaa ctt ggt att gaa cca gcc gaa gag ctt gcc   643
Asn Phe Ile Val Arg Lys Leu Gly Ile Glu Pro Ala Glu Glu Leu Ala
                170                 175                 180

tct gcc cgt tcc tcc caa gag ctc acc gcc ttg gta cgc agc tcc gcg   691
Ser Ala Arg Ser Ser Gln Glu Leu Thr Ala Leu Val Arg Ser Ser Ala
            185                 190                 195

gaa agc ggc gga ctg gat caa aac acc gca gcg gtg atc aac cga tcc   739
Glu Ser Gly Gly Leu Asp Gln Asn Thr Ala Ala Val Ile Asn Arg Ser
        200                 205                 210

ctg cag ttc ggt gac gcc acc gct gat gaa ttc atg aca cct cgc tcc   787
Leu Gln Phe Gly Asp Ala Thr Ala Asp Glu Phe Met Thr Pro Arg Ser
    215                 220                 225

acc att gaa tca ttg cgt gcc aca gac acc gtc aat gat ttg atc gag   835
Thr Ile Glu Ser Leu Arg Ala Thr Asp Thr Val Asn Asp Leu Ile Glu
230                 235                 240                 245

ctt gcc ctg gaa acg ggt cac tcc cgc ttc cca gtc acc gaa ggc gac   883
```

```
Leu Ala Leu Glu Thr Gly His Ser Arg Phe Pro Val Thr Glu Gly Asp
                250                 255                 260

ttg gat gaa acc atc ggc atg gtc cac atc aag gac gca ttc tct gta   931
Leu Asp Glu Thr Ile Gly Met Val His Ile Lys Asp Ala Phe Ser Val
            265                 270                 275

gtg cag gca gaa cgc gcc acc acc atg gtg cgc gat cta gcc cgc aaa   979
Val Gln Ala Glu Arg Ala Thr Thr Met Val Arg Asp Leu Ala Arg Lys
        280                 285                 290

att cct gtg gta cca gcc agc ctt gac ggc gac tct gtc ctc aac gct   1027
Ile Pro Val Val Pro Ala Ser Leu Asp Gly Asp Ser Val Leu Asn Ala
    295                 300                 305

gtc cgc tcc gcc ggc tcc caa gtt att ttg gtt gcc gat gaa tac ggc   1075
Val Arg Ser Ala Gly Ser Gln Val Ile Leu Val Ala Asp Glu Tyr Gly
310                 315                 320                 325

gga acc gca ggc atg gtc acc atc gaa gac gtc gtg gag gaa atc ctc   1123
Gly Thr Ala Gly Met Val Thr Ile Glu Asp Val Val Glu Glu Ile Leu
                330                 335                 340

ggc gaa atc cac gat gag cac gac gac tcc gac gcc gaa cgc gat ttc   1171
Gly Glu Ile His Asp Glu His Asp Asp Ser Asp Ala Glu Arg Asp Phe
            345                 350                 355

caa caa ttc ggc gcc agc tgg gaa gtc tcc ggc ctg gtc cgc atc gat   1219
Gln Gln Phe Gly Ala Ser Trp Glu Val Ser Gly Leu Val Arg Ile Asp
        360                 365                 370

gaa ctc gaa aaa cgc gtc ggg tac gtc tcc cct gac ggc ccc tac gaa   1267
Glu Leu Glu Lys Arg Val Gly Tyr Val Ser Pro Asp Gly Pro Tyr Glu
    375                 380                 385

acc ctc ggc ggc ttg atc atg tac aca gtc ggc gcc att cct cgc gtc   1315
Thr Leu Gly Gly Leu Ile Met Tyr Thr Val Gly Ala Ile Pro Arg Val
390                 395                 400                 405

ggc gat gtc gcc cta ctc cca ctg acc gat acc cca acc atg gat gaa   1363
Gly Asp Val Ala Leu Leu Pro Leu Thr Asp Thr Pro Thr Met Asp Glu
                410                 415                 420

ttc gaa tcc ggc ttc tcc gga cgc tgg atc gca cga gta acg gtc atg   1411
Phe Glu Ser Gly Phe Ser Gly Arg Trp Ile Ala Arg Val Thr Val Met
            425                 430                 435

gaa gat cga cgc atc gac aaa gcc gtt ctc acc ccc atc acc cat gaa   1459
Glu Asp Arg Arg Ile Asp Lys Ala Val Leu Thr Pro Ile Thr His Glu
        440                 445                 450

gaa gca aag gag tac gaa aag tgagtatttg ggcaactgtc ctt             1503
Glu Ala Lys Glu Tyr Glu Lys
    455                 460
```

<210> 468
<211> 460
<212> PRT
<213> Corynebacterium glutamicum

<400> 468

```
Met Asp Ile Leu Ile Ser Ile Leu Ser Leu Leu Gly Phe Val Leu Leu
 1               5                  10                  15

Thr Ala Ser Thr Gly Leu Phe Val Ala Ile Glu Phe Ala Leu Thr Gly
            20                  25                  30

Leu Glu Lys Ser Thr Val Glu Thr His Val Lys Gln Lys Gly Asp Ser
        35                  40                  45

Ser Ala Arg Ala Val Gln Arg Asp His Gln Asn Leu Ser Phe Val Leu
    50                  55                  60

Ser Gly Ala Gln Leu Gly Ile Thr Ile Thr Thr Leu Ala Thr Gly Phe
65                  70                  75                  80

Leu Ala Glu Pro Val Leu Ala Lys Phe Phe Thr Pro Ala Leu Glu Leu
                85                  90                  95

Val Gly Leu Asn Glu Ser Ala Ser Ser Ala Val Ala Leu Ile Ile Ala
            100                 105                 110

Leu Leu Val Ala Thr Thr Leu Ser Met Val Phe Gly Glu Leu Val Pro
        115                 120                 125

Lys Asn Trp Ala Ile Thr Asn Pro Leu Gly Val Ala Arg Phe Val Val
    130                 135                 140

His Pro Val Asn Trp Phe Asn Met Val Leu Lys Pro Phe Ile Asn Gly
145                 150                 155                 160

Met Asn Lys Ser Ala Asn Phe Ile Val Arg Lys Leu Gly Ile Glu Pro
                165                 170                 175

Ala Glu Glu Leu Ala Ser Ala Arg Ser Ser Gln Glu Leu Thr Ala Leu
            180                 185                 190

Val Arg Ser Ser Ala Glu Ser Gly Gly Leu Asp Gln Asn Thr Ala Ala
        195                 200                 205

Val Ile Asn Arg Ser Leu Gln Phe Gly Asp Ala Thr Ala Asp Glu Phe
    210                 215                 220

Met Thr Pro Arg Ser Thr Ile Glu Ser Leu Arg Ala Thr Asp Thr Val
225                 230                 235                 240

Asn Asp Leu Ile Glu Leu Ala Leu Glu Thr Gly His Ser Arg Phe Pro
                245                 250                 255

Val Thr Glu Gly Asp Leu Asp Glu Thr Ile Gly Met Val His Ile Lys
            260                 265                 270

Asp Ala Phe Ser Val Val Gln Ala Glu Arg Ala Thr Thr Met Val Arg
        275                 280                 285

Asp Leu Ala Arg Lys Ile Pro Val Val Pro Ala Ser Leu Asp Gly Asp
    290                 295                 300

Ser Val Leu Asn Ala Val Arg Ser Ala Gly Ser Gln Val Ile Leu Val
305                 310                 315                 320
```

```
Ala Asp Glu Tyr Gly Gly Thr Ala Gly Met Val Thr Ile Glu Asp Val
                325                 330                 335

Val Glu Glu Ile Leu Gly Glu Ile His Asp Glu His Asp Asp Ser Asp
            340                 345                 350

Ala Glu Arg Asp Phe Gln Gln Phe Gly Ala Ser Trp Glu Val Ser Gly
        355                 360                 365

Leu Val Arg Ile Asp Glu Leu Glu Lys Arg Val Gly Tyr Val Ser Pro
    370                 375                 380

Asp Gly Pro Tyr Glu Thr Leu Gly Gly Leu Ile Met Tyr Thr Val Gly
385                 390                 395                 400

Ala Ile Pro Arg Val Gly Asp Val Ala Leu Leu Pro Leu Thr Asp Thr
                405                 410                 415

Pro Thr Met Asp Glu Phe Glu Ser Gly Phe Ser Gly Arg Trp Ile Ala
            420                 425                 430

Arg Val Thr Val Met Glu Asp Arg Arg Ile Asp Lys Ala Val Leu Thr
        435                 440                 445

Pro Ile Thr His Glu Glu Ala Lys Glu Tyr Glu Lys
    450                 455                 460


<210> 469
<211> 1185
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1162)
<223> RXN01004

<400> 469
ccggacgctg gatcgcacga gtaacggtca tggaagatcg acgcatcgac aaagccgttc 60

tcacccccat cacccatgaa gaagcaaagg agtacgaaaa gtg agt att tgg gca   115
                                            Val Ser Ile Trp Ala
                                              1               5

act gtc ctt cta att atc gtc ctt ctt tcc gcc aac gcc ttc ttc gtg   163
Thr Val Leu Leu Ile Ile Val Leu Leu Ser Ala Asn Ala Phe Phe Val
                 10                  15                  20

gcc gcg gag ttc gca ctg att tcc tcg cgc cgg gac cgc ctg gat tcc   211
Ala Ala Glu Phe Ala Leu Ile Ser Ser Arg Arg Asp Arg Leu Asp Ser
             25                  30                  35

ctg gta tcc cag ggt aaa aag gga gct gaa aag gtt ctc tac gca acc   259
Leu Val Ser Gln Gly Lys Lys Gly Ala Glu Lys Val Leu Tyr Ala Thr
         40                  45                  50

gag cac ctc tcc atc atg ttg gcg ggc gct cag ttc ggt att acg gtc   307
Glu His Leu Ser Ile Met Leu Ala Gly Ala Gln Phe Gly Ile Thr Val
     55                  60                  65
```

```
tgt tct ctg att ctg ggt aaa gtc gca gaa cct gcg atc gcc cac ttc   355
Cys Ser Leu Ile Leu Gly Lys Val Ala Glu Pro Ala Ile Ala His Phe
 70                  75                  80                  85

att gag gtg cct ttc acc tcc tgg ggt gtt cca aat gat ttg atc cac   403
Ile Glu Val Pro Phe Thr Ser Trp Gly Val Pro Asn Asp Leu Ile His
                90                  95                 100

cca att tcc ttc gtc atc gca ctg gcg atc atc acc tgg ttg cac att   451
Pro Ile Ser Phe Val Ile Ala Leu Ala Ile Ile Thr Trp Leu His Ile
            105                 110                 115

ctc ttt ggt gaa atg gtg cca aag aac atc gct att gct ggc cct gaa   499
Leu Phe Gly Glu Met Val Pro Lys Asn Ile Ala Ile Ala Gly Pro Glu
        120                 125                 130

acc tta ggc atg tgg ctt gct cca gtg ctc att gcg ttt gtg aag att   547
Thr Leu Gly Met Trp Leu Ala Pro Val Leu Ile Ala Phe Val Lys Ile
    135                 140                 145

acc cgc ccg ttg atc gag ttc atg aac tgg atc gcc cgt ctg acc ctt   595
Thr Arg Pro Leu Ile Glu Phe Met Asn Trp Ile Ala Arg Leu Thr Leu
150                 155                 160                 165

cgc gcc ttt ggt gtg gag caa aaa aac gag ctg gat tcc acc gtg gac   643
Arg Ala Phe Gly Val Glu Gln Lys Asn Glu Leu Asp Ser Thr Val Asp
                170                 175                 180

cca gag cag ctg gca tca atg att tcc gag tcc cgt tcc gaa ggc ctc   691
Pro Glu Gln Leu Ala Ser Met Ile Ser Glu Ser Arg Ser Glu Gly Leu
            185                 190                 195

ctt gat gct gaa gag cac gcc cgc ctg tcc aag gcg ctg cgc tct gag   739
Leu Asp Ala Glu Glu His Ala Arg Leu Ser Lys Ala Leu Arg Ser Glu
        200                 205                 210

cag cgt tcc atc aag gaa ctg gtg att aag gat gag gac gtg cgc acg   787
Gln Arg Ser Ile Lys Glu Leu Val Ile Lys Asp Glu Asp Val Arg Thr
    215                 220                 225

ctg gcg ttc ggt aaa tct ggc ccg acc ttg cac cag ttg gag gaa gca   835
Leu Ala Phe Gly Lys Ser Gly Pro Thr Leu His Gln Leu Glu Glu Ala
230                 235                 240                 245

gtc cgc gag acc ggt ttc tcc cgc ttc cct gtc acc ggc cgc gat gga   883
Val Arg Glu Thr Gly Phe Ser Arg Phe Pro Val Thr Gly Arg Asp Gly
                250                 255                 260

tcc tac ttg ggt tat atc cac atc aag gat att ttg cct cgt ctg gct   931
Ser Tyr Leu Gly Tyr Ile His Ile Lys Asp Ile Leu Pro Arg Leu Ala
            265                 270                 275

gat cct gag atg gat ccc tcc gag acc att ccg cgt tct gca ctg cgc   979
Asp Pro Glu Met Asp Pro Ser Glu Thr Ile Pro Arg Ser Ala Leu Arg
        280                 285                 290

cct ttg agc aat gtg gat gcc gac ggc ctc atg gat gac gtc ttg gat   1027
Pro Leu Ser Asn Val Asp Ala Asp Gly Leu Met Asp Asp Val Leu Asp
    295                 300                 305

ttt atg cac tac cgc tcc gcg cac atg gct cag gtt cgc ctc aaa ggt   1075
```

```
Phe Met His Tyr Arg Ser Ala His Met Ala Gln Val Arg Leu Lys Gly
310                 315                 320                 325

gag ctt ctc ggc gtg att acg ctg gag gat ctc atc gaa gaa tac gtg   1123
Glu Leu Leu Gly Val Ile Thr Leu Glu Asp Leu Ile Glu Glu Tyr Val
                330                 335                 340

ggc acc gtc aac gat tgg act cac gaa agc tcc gac gac tagaaatagt    1172
Gly Thr Val Asn Asp Trp Thr His Glu Ser Ser Asp Asp
            345                 350

aactgtgttg gac                                                   1185


<210> 470
<211> 354
<212> PRT
<213> Corynebacterium glutamicum

<400> 470
Val Ser Ile Trp Ala Thr Val Leu Leu Ile Ile Val Leu Leu Ser Ala
  1               5                  10                  15

Asn Ala Phe Phe Val Ala Ala Glu Phe Ala Leu Ile Ser Ser Arg Arg
             20                  25                  30

Asp Arg Leu Asp Ser Leu Val Ser Gln Gly Lys Lys Gly Ala Glu Lys
         35                  40                  45

Val Leu Tyr Ala Thr Glu His Leu Ser Ile Met Leu Ala Gly Ala Gln
     50                  55                  60

Phe Gly Ile Thr Val Cys Ser Leu Ile Leu Gly Lys Val Ala Glu Pro
 65                  70                  75                  80

Ala Ile Ala His Phe Ile Glu Val Pro Phe Thr Ser Trp Gly Val Pro
                 85                  90                  95

Asn Asp Leu Ile His Pro Ile Ser Phe Val Ile Ala Leu Ala Ile Ile
            100                 105                 110

Thr Trp Leu His Ile Leu Phe Gly Glu Met Val Pro Lys Asn Ile Ala
        115                 120                 125

Ile Ala Gly Pro Glu Thr Leu Gly Met Trp Leu Ala Pro Val Leu Ile
    130                 135                 140

Ala Phe Val Lys Ile Thr Arg Pro Leu Ile Glu Phe Met Asn Trp Ile
145                 150                 155                 160

Ala Arg Leu Thr Leu Arg Ala Phe Gly Val Glu Gln Lys Asn Glu Leu
                165                 170                 175

Asp Ser Thr Val Asp Pro Glu Gln Leu Ala Ser Met Ile Ser Glu Ser
            180                 185                 190

Arg Ser Glu Gly Leu Leu Asp Ala Glu Glu His Ala Arg Leu Ser Lys
        195                 200                 205

Ala Leu Arg Ser Glu Gln Arg Ser Ile Lys Glu Leu Val Ile Lys Asp
    210                 215                 220
```

```
Glu Asp Val Arg Thr Leu Ala Phe Gly Lys Ser Gly Pro Thr Leu His
225                 230                 235                 240

Gln Leu Glu Glu Ala Val Arg Glu Thr Gly Phe Ser Arg Phe Pro Val
                245                 250                 255

Thr Gly Arg Asp Gly Ser Tyr Leu Gly Tyr Ile His Ile Lys Asp Ile
            260                 265                 270

Leu Pro Arg Leu Ala Asp Pro Glu Met Asp Pro Ser Glu Thr Ile Pro
        275                 280                 285

Arg Ser Ala Leu Arg Pro Leu Ser Asn Val Asp Ala Asp Gly Leu Met
    290                 295                 300

Asp Asp Val Leu Asp Phe Met His Tyr Arg Ser Ala His Met Ala Gln
305                 310                 315                 320

Val Arg Leu Lys Gly Glu Leu Leu Gly Val Ile Thr Leu Glu Asp Leu
                325                 330                 335

Ile Glu Glu Tyr Val Gly Thr Val Asn Asp Trp Thr His Glu Ser Ser
            340                 345                 350

Asp Asp
```

Application Filed with the EPO - 22 Dec 2005 - 22 Dec 2005

<210> 471
<211> 771
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(748)
<223> RXN01016

<400> 471

```
tgcccgtcga ggtgaacgcc caagaatagt tctctttcgt cgacttctca cgttgatacc 60

gctcggcatc atccaccaaa ttctccagcc gggtgaagca ttg ttg ccg tat gca   115
                                              Leu Leu Pro Tyr Ala
                                                1               5

ata gtc ggc ctg gtc att ttg ctg cca tcc tcc tgg ttg cct cgt tgg   163
Ile Val Gly Leu Val Ile Leu Leu Pro Ser Ser Trp Leu Pro Arg Trp
                10                  15                  20

gct gtc gca gtc ctt ggc gaa gtg tcg ctt gtg cca gcg gtg gtt ttc   211
Ala Val Ala Val Leu Gly Glu Val Ser Leu Val Pro Ala Val Val Phe
            25                  30                  35

ggt ggc ggg ttc ctg ctt atc ccc tca atg ttc ctg atc ggt tca gcg   259
Gly Gly Gly Phe Leu Leu Ile Pro Ser Met Phe Leu Ile Gly Ser Ala
        40                  45                  50

ctc gtt agg tat gga gta gtc gat cgg gca gag aac gca ccg cgg gct   307
Leu Val Arg Tyr Gly Val Val Asp Arg Ala Glu Asn Ala Pro Arg Ala
    55                  60                  65
```

```
atg gga gtc ttt ttc gcc gta agc gca gca atc gct ata cct acg ctg   355
Met Gly Val Phe Phe Ala Val Ser Ala Ala Ile Ala Ile Pro Thr Leu
 70                  75                  80                  85

atc atc cag gca cgt gac atc act tct tca ggc ttc tcg atc gtt tcc   403
Ile Ile Gln Ala Arg Asp Ile Thr Ser Ser Gly Phe Ser Ile Val Ser
                90                  95                 100

aca gtg gcg gga ctc gcg ctt ggc ggc gtc tac att tct tta gtg ttg   451
Thr Val Ala Gly Leu Ala Leu Gly Gly Val Tyr Ile Ser Leu Val Leu
            105                 110                 115

ctg gcc ttg cat aca ccg att cgc ggt gca ctc gct gca gtt ttc gca   499
Leu Ala Leu His Thr Pro Ile Arg Gly Ala Leu Ala Ala Val Phe Ala
        120                 125                 130

cct tta ggg cgt atg gcg cta acc aac tac att ggt gca acg atc ctc   547
Pro Leu Gly Arg Met Ala Leu Thr Asn Tyr Ile Gly Ala Thr Ile Leu
    135                 140                 145

atg ctc att ggc ggg cta atc gtg gat ctt cca cac agc aca tca tgg   595
Met Leu Ile Gly Gly Leu Ile Val Asp Leu Pro His Ser Thr Ser Trp
150                 155                 160                 165

aca gct acg gtg ctc cta gct gcg ggt att ctc att att caa gag cta   643
Thr Ala Thr Val Leu Leu Ala Ala Gly Ile Leu Ile Ile Gln Glu Leu
                170                 175                 180

ctt tct gct tta tgg ttg cgc cac tac aca cag ggg cca ctt ggg tat   691
Leu Ser Ala Leu Trp Leu Arg His Tyr Thr Gln Gly Pro Leu Gly Tyr
            185                 190                 195

cta tgg cgt tgg gtg act tgg gga agc cgt tcc ccc ttc ctt acc cgt   739
Leu Trp Arg Trp Val Thr Trp Gly Ser Arg Ser Pro Phe Leu Thr Arg
        200                 205                 210

tcc gca tca tgacaggtac ggaagtgtcc tac                            771
Ser Ala Ser
    215
```

<210> 472
<211> 216
<212> PRT
<213> Corynebacterium glutamicum

<400> 472

```
Leu Leu Pro Tyr Ala Ile Val Gly Leu Val Ile Leu Leu Pro Ser Ser
  1               5                  10                  15

Trp Leu Pro Arg Trp Ala Val Ala Val Leu Gly Glu Val Ser Leu Val
             20                  25                  30

Pro Ala Val Val Phe Gly Gly Gly Phe Leu Leu Ile Pro Ser Met Phe
         35                  40                  45

Leu Ile Gly Ser Ala Leu Val Arg Tyr Gly Val Val Asp Arg Ala Glu
     50                  55                  60

Asn Ala Pro Arg Ala Met Gly Val Phe Phe Ala Val Ser Ala Ala Ile
```

```
 65                  70                  75                  80

Ala Ile Pro Thr Leu Ile Ile Gln Ala Arg Asp Ile Thr Ser Ser Gly
                85                  90                  95

Phe Ser Ile Val Ser Thr Val Ala Gly Leu Ala Leu Gly Gly Val Tyr
            100                 105                 110

Ile Ser Leu Val Leu Leu Ala Leu His Thr Pro Ile Arg Gly Ala Leu
        115                 120                 125

Ala Ala Val Phe Ala Pro Leu Gly Arg Met Ala Leu Thr Asn Tyr Ile
    130                 135                 140

Gly Ala Thr Ile Leu Met Leu Ile Gly Gly Leu Ile Val Asp Leu Pro
145                 150                 155                 160

His Ser Thr Ser Trp Thr Ala Thr Val Leu Leu Ala Ala Gly Ile Leu
                165                 170                 175

Ile Ile Gln Glu Leu Leu Ser Ala Leu Trp Leu Arg His Tyr Thr Gln
            180                 185                 190

Gly Pro Leu Gly Tyr Leu Trp Arg Trp Val Thr Trp Gly Ser Arg Ser
        195                 200                 205

Pro Phe Leu Thr Arg Ser Ala Ser
    210                 215


<210> 473
<211> 771
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(748)
<223> FRXA01016

<400> 473
tgcccgtcga ggtgaacgcc caagaatagt tctctttcgt cgacttctca cgttgatacc 60

gctcggcatc atccaccaaa ttctccagcc gggtgaagca ttg ttg ccg tat gca   115
                                              Leu Leu Pro Tyr Ala
                                                1               5

ata gtc ggc ctg gtc att ttg ctg cca tcc tcc tgg ttg cct cgt tgg   163
Ile Val Gly Leu Val Ile Leu Leu Pro Ser Ser Trp Leu Pro Arg Trp
                10                  15                  20

gct gtc gca gtc ctt ggc gaa gtg tcg ctt gtg cca gcg gtg gtt ttc   211
Ala Val Ala Val Leu Gly Glu Val Ser Leu Val Pro Ala Val Val Phe
            25                  30                  35

ggt ggc ggg ttc ctg ctt atc ccc tca atg ttc ctg atc ggt tca gcg   259
Gly Gly Gly Phe Leu Leu Ile Pro Ser Met Phe Leu Ile Gly Ser Ala
        40                  45                  50

ctc gtt agg tat gga gta gtc gat cgg gca gag aac gca ccg cgg gct   307
Leu Val Arg Tyr Gly Val Val Asp Arg Ala Glu Asn Ala Pro Arg Ala
```

```
     55                  60                  65

atg gga gtc ttt ttc gcc gta agc gca gca atc gct ata cct acg ctg   355
Met Gly Val Phe Phe Ala Val Ser Ala Ala Ile Ala Ile Pro Thr Leu
 70                  75                  80                  85

atc atc cag gca cgt gac atc act tct tca ggc ttc tcg atc gtt tcc   403
Ile Ile Gln Ala Arg Asp Ile Thr Ser Ser Gly Phe Ser Ile Val Ser
                90                  95                 100

aca gtg gcg gga ctc gcg ctt ggc ggc gtc tac att tct tta gtg ttg   451
Thr Val Ala Gly Leu Ala Leu Gly Gly Val Tyr Ile Ser Leu Val Leu
            105                 110                 115

ctg gcc ttg cat aca ccg att cgc ggt gca ctc gct gca gtt ttc gca   499
Leu Ala Leu His Thr Pro Ile Arg Gly Ala Leu Ala Ala Val Phe Ala
        120                 125                 130

cct tta ggg cgt atg gcg cta acc aac tac att ggt gca acg atc ctc   547
Pro Leu Gly Arg Met Ala Leu Thr Asn Tyr Ile Gly Ala Thr Ile Leu
    135                 140                 145

atg ctc att ggc ggg cta atc gtg gat ctt cca cac agc aca tca tgg   595
Met Leu Ile Gly Gly Leu Ile Val Asp Leu Pro His Ser Thr Ser Trp
150                 155                 160                 165

aca gct acg gtg ctc cta gct gcg ggt att ctc att att caa gag cta   643
Thr Ala Thr Val Leu Leu Ala Ala Gly Ile Leu Ile Ile Gln Glu Leu
                170                 175                 180

ctt tct gct tta tgg ttg cgc cac tac aca cag ggg cca ctt ggg tat   691
Leu Ser Ala Leu Trp Leu Arg His Tyr Thr Gln Gly Pro Leu Gly Tyr
            185                 190                 195

cta tgg cgt tgg gtg act tgg gga agc cgt tcc ccc ttc ctt acc cgt   739
Leu Trp Arg Trp Val Thr Trp Gly Ser Arg Ser Pro Phe Leu Thr Arg
        200                 205                 210

tcc gca tca tgacaggtac ggaagtgtcc tac                            771
Ser Ala Ser
    215
```

Doc 2 of 3 - 2 pages

<210> 474
<211> 216
<212> PRT
<213> Corynebacterium glutamicum

<400> 474

```
Leu Leu Pro Tyr Ala Ile Val Gly Leu Val Ile Leu Leu Pro Ser Ser
  1               5                  10                  15

Trp Leu Pro Arg Trp Ala Val Ala Val Leu Gly Glu Val Ser Leu Val
             20                  25                  30

Pro Ala Val Val Phe Gly Gly Gly Phe Leu Leu Ile Pro Ser Met Phe
         35                  40                  45

Leu Ile Gly Ser Ala Leu Val Arg Tyr Gly Val Val Asp Arg Ala Glu
     50                  55                  60
```

```
Asn Ala Pro Arg Ala Met Gly Val Phe Phe Ala Val Ser Ala Ala Ile
 65                  70                  75                  80

Ala Ile Pro Thr Leu Ile Ile Gln Ala Arg Asp Ile Thr Ser Ser Gly
                85                  90                  95

Phe Ser Ile Val Ser Thr Val Ala Gly Leu Ala Leu Gly Gly Val Tyr
            100                 105                 110

Ile Ser Leu Val Leu Leu Ala Leu His Thr Pro Ile Arg Gly Ala Leu
        115                 120                 125

Ala Ala Val Phe Ala Pro Leu Gly Arg Met Ala Leu Thr Asn Tyr Ile
    130                 135                 140

Gly Ala Thr Ile Leu Met Leu Ile Gly Gly Leu Ile Val Asp Leu Pro
145                 150                 155                 160

His Ser Thr Ser Trp Thr Ala Thr Val Leu Leu Ala Ala Gly Ile Leu
                165                 170                 175

Ile Ile Gln Glu Leu Leu Ser Ala Leu Trp Leu Arg His Tyr Thr Gln
            180                 185                 190

Gly Pro Leu Gly Tyr Leu Trp Arg Trp Val Thr Trp Gly Ser Arg Ser
        195                 200                 205

Pro Phe Leu Thr Arg Ser Ala Ser
    210                 215


<210> 475
<211> 1101
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1078)
<223> RXN01023

<400> 475
aagcgaatcc gggaatgaaa gtgagtgcgc caaagtcaac tccttggttc aagtgtcagt 60

atttttctag tctatcgccc cacaggtagg ctcaggacac atg agt gcc gtg aac   115
                                              Met Ser Ala Val Asn
                                                1               5

agt gct ggt cgc cca gcc aac ggg gga att aac aaa acc ccc atg att   163
Ser Ala Gly Arg Pro Ala Asn Gly Gly Ile Asn Lys Thr Pro Met Ile
                10                  15                  20

att gcc cta gtg tta tct att gtg ttg gtt ttg gcg gtg ctg ttc ggc   211
Ile Ala Leu Val Leu Ser Ile Val Leu Val Leu Ala Val Leu Phe Gly
            25                  30                  35

gcc cga gtc ctc ctt ggc ccc gcc ggc cag caa cag ata gcc atg agt   259
Ala Arg Val Leu Leu Gly Pro Ala Gly Gln Gln Gln Ile Ala Met Ser
        40                  45                  50

ggg ctt ccc gcc cca gac gca gaa tct gct gag tgc gcc gca tta ctc   307
```

```
Gly Leu Pro Ala Pro Asp Ala Glu Ser Ala Glu Cys Ala Ala Leu Leu
 55                  60                  65

gag gat ctc ccc ggc gag gcc ttc ggg cac acc cgt gca gaa atc atg   355
Glu Asp Leu Pro Gly Glu Ala Phe Gly His Thr Arg Ala Glu Ile Met
 70                  75                  80                  85

gat cct gtt cca ccg ggc gct gcc gcc tgg tcc acc tca gac ctc gag   403
Asp Pro Val Pro Pro Gly Ala Ala Ala Trp Ser Thr Ser Asp Leu Glu
                 90                  95                 100

cgt gtg acg ctg cgt tgt ggc gtc gat atg cca ttc cag tac acc gcg   451
Arg Val Thr Leu Arg Cys Gly Val Asp Met Pro Phe Gln Tyr Thr Ala
            105                 110                 115

ctc gcc aac acc gtc gac gtc gac ggc acc acc tgg cta cct gtc tcc   499
Leu Ala Asn Thr Val Asp Val Asp Gly Thr Thr Trp Leu Pro Val Ser
        120                 125                 130

gac atg acc ccc ggc tcc tcc ctg gag acc tgg tac tcc gtc aac cgc   547
Asp Met Thr Pro Gly Ser Ser Leu Glu Thr Trp Tyr Ser Val Asn Arg
    135                 140                 145

ttc ccc gtc gtc gcc atc acc gcc gat gac atc agc acc gac agc gcc   595
Phe Pro Val Val Ala Ile Thr Ala Asp Asp Ile Ser Thr Asp Ser Ala
150                 155                 160                 165

gac aac ccc gtc gcc ccc ttc agc agc gcc gtc gac aag cta gaa aag   643
Asp Asn Pro Val Ala Pro Phe Ser Ser Ala Val Asp Lys Leu Glu Lys
                170                 175                 180

cgc gac ggc cag ccc ttc gac gcc cca ctt acc ggc ttg agc tca gcc   691
Arg Asp Gly Gln Pro Phe Asp Ala Pro Leu Thr Gly Leu Ser Ser Ala
            185                 190                 195

ggc acc aca tgc act tcg ctt ttc gac gcc ctc ccc cgc caa ctc gaa   739
Gly Thr Thr Cys Thr Ser Leu Phe Asp Ala Leu Pro Arg Gln Leu Glu
        200                 205                 210

gtc ggc ggc gac gac ggc aca acg tac gaa cgc atc gag gag gac cgc   787
Val Gly Gly Asp Asp Gly Thr Thr Tyr Glu Arg Ile Glu Glu Asp Arg
    215                 220                 225

atg cag gcc gcc gga tac tcc gac gac gca gtc gcg tgg gac acg ccg   835
Met Gln Ala Ala Gly Tyr Ser Asp Asp Ala Val Ala Trp Asp Thr Pro
230                 235                 240                 245

gga tta gaa ccc att gtg atc cgt tgc ggc gtg gag cct tct gag aac   883
Gly Leu Glu Pro Ile Val Ile Arg Cys Gly Val Glu Pro Ser Glu Asn
                250                 255                 260

tac gca gcc ggt gcc atg ttg cag cag atc gat gac atc ccg tgg ttc   931
Tyr Ala Ala Gly Ala Met Leu Gln Gln Ile Asp Asp Ile Pro Trp Phe
            265                 270                 275

gag gac acc att ttg gcc tcc ggt acc acc tcg tct acc tgg tat gcc   979
Glu Asp Thr Ile Leu Ala Ser Gly Thr Thr Ser Ser Thr Trp Tyr Ala
        280                 285                 290

ctt gga cgc gag atc gac atc gcc gtg tct ctg cct cag gct gct tcc  1027
Leu Gly Arg Glu Ile Asp Ile Ala Val Ser Leu Pro Gln Ala Ala Ser
```

295 300 305

tct tcc ctg att act atc tcc ggt ttc att gaa gac acg gtt cct gcg 1075
Ser Ser Leu Ile Thr Ile Ser Gly Phe Ile Glu Asp Thr Val Pro Ala
310 315 320 325

gaa taagacataa aaaatcgccc cac 1101
Glu

<210> 476
<211> 326
<212> PRT
<213> Corynebacterium glutamicum

<400> 476
Met Ser Ala Val Asn Ser Ala Gly Arg Pro Ala Asn Gly Gly Ile Asn
1 5 10 15

Lys Thr Pro Met Ile Ile Ala Leu Val Leu Ser Ile Val Leu Val Leu
20 25 30

Ala Val Leu Phe Gly Ala Arg Val Leu Leu Gly Pro Ala Gly Gln Gln
35 40 45

Gln Ile Ala Met Ser Gly Leu Pro Ala Pro Asp Ala Glu Ser Ala Glu
50 55 60

Cys Ala Ala Leu Leu Glu Asp Leu Pro Gly Glu Ala Phe Gly His Thr
65 70 75 80

Arg Ala Glu Ile Met Asp Pro Val Pro Pro Gly Ala Ala Ala Trp Ser
85 90 95

Thr Ser Asp Leu Glu Arg Val Thr Leu Arg Cys Gly Val Asp Met Pro
100 105 110

Phe Gln Tyr Thr Ala Leu Ala Asn Thr Val Asp Val Asp Gly Thr Thr
115 120 125

Trp Leu Pro Val Ser Asp Met Thr Pro Gly Ser Ser Leu Glu Thr Trp
130 135 140

Tyr Ser Val Asn Arg Phe Pro Val Val Ala Ile Thr Ala Asp Asp Ile
145 150 155 160

Ser Thr Asp Ser Ala Asp Asn Pro Val Ala Pro Phe Ser Ser Ala Val
165 170 175

Asp Lys Leu Glu Lys Arg Asp Gly Gln Pro Phe Asp Ala Pro Leu Thr
180 185 190

Gly Leu Ser Ser Ala Gly Thr Thr Cys Thr Ser Leu Phe Asp Ala Leu
195 200 205

Pro Arg Gln Leu Glu Val Gly Gly Asp Asp Gly Thr Thr Tyr Glu Arg
210 215 220

Ile Glu Glu Asp Arg Met Gln Ala Ala Gly Tyr Ser Asp Asp Ala Val
225 230 235 240

```
Ala Trp Asp Thr Pro Gly Leu Glu Pro Ile Val Ile Arg Cys Gly Val
                245                 250                 255

Glu Pro Ser Glu Asn Tyr Ala Ala Gly Ala Met Leu Gln Gln Ile Asp
            260                 265                 270

Asp Ile Pro Trp Phe Glu Asp Thr Ile Leu Ala Ser Gly Thr Thr Ser
        275                 280                 285

Ser Thr Trp Tyr Ala Leu Gly Arg Glu Ile Asp Ile Ala Val Ser Leu
    290                 295                 300

Pro Gln Ala Ala Ser Ser Ser Leu Ile Thr Ile Ser Gly Phe Ile Glu
305                 310                 315                 320

Asp Thr Val Pro Ala Glu
                325
```

<210> 477
<211> 974
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(951)
<223> FRXA01023

<400> 477

```
cca gcc aac ggg gga att aac aaa acc ccc atg att att gcc cta gtg   48
Pro Ala Asn Gly Gly Ile Asn Lys Thr Pro Met Ile Ile Ala Leu Val
  1               5                  10                  15

tta tct att gtg ttg gtt ttg gcg gtg ctg ttc ggc gcc cga gtc ctc   96
Leu Ser Ile Val Leu Val Leu Ala Val Leu Phe Gly Ala Arg Val Leu
             20                  25                  30

ctt ggc ccc gcc ggc cag caa cag ata gcc atg agt ggg ctt ccc gcc   144
Leu Gly Pro Ala Gly Gln Gln Gln Ile Ala Met Ser Gly Leu Pro Ala
         35                  40                  45

cca gac gca gaa tct gct gag tgc gcc gca tta ctc gag gat ctc ccc   192
Pro Asp Ala Glu Ser Ala Glu Cys Ala Ala Leu Leu Glu Asp Leu Pro
     50                  55                  60

ggc gag gcc ttc ggg cac acc cgt gca gaa atc atg gat cct gtt cca   240
Gly Glu Ala Phe Gly His Thr Arg Ala Glu Ile Met Asp Pro Val Pro
 65                  70                  75                  80

ccg ggc gct gcc gcc tgg tcc acc tca gac ctc gag cgt gtg acg ctg   288
Pro Gly Ala Ala Ala Trp Ser Thr Ser Asp Leu Glu Arg Val Thr Leu
                 85                  90                  95

cgt tgt ggc gtc gat atg cca ttc cag tac acc gcg ctc gcc aac acc   336
Arg Cys Gly Val Asp Met Pro Phe Gln Tyr Thr Ala Leu Ala Asn Thr
            100                 105                 110

gtc gac gtc gac ggc acc acc tgg cta cct gtc tcc gac atg acc ccc   384
Val Asp Val Asp Gly Thr Thr Trp Leu Pro Val Ser Asp Met Thr Pro
```

```
        115                 120                 125

ggc tcc tcc ctg gag acc tgg tac tcc gtc aac cgc ttc ccc gtc gtc   432
Gly Ser Ser Leu Glu Thr Trp Tyr Ser Val Asn Arg Phe Pro Val Val
    130                 135                 140

gcc atc acc gcc gat gac atc agc acc gac agc gcc gac aac ccc gtc   480
Ala Ile Thr Ala Asp Asp Ile Ser Thr Asp Ser Ala Asp Asn Pro Val
145                 150                 155                 160

gac ccc ttc agc agc gcc gtc gac aag cta gaa aag cgc gac ggc cag   528
Asp Pro Phe Ser Ser Ala Val Asp Lys Leu Glu Lys Arg Asp Gly Gln
                165                 170                 175

ccc ttc gac gcc cca ctt acc ggc ttg agc tca gcc ggc acc aca tgc   576
Pro Phe Asp Ala Pro Leu Thr Gly Leu Ser Ser Ala Gly Thr Thr Cys
            180                 185                 190

act tcg ctt ttc gac gcc ctc ccc cgc caa ctc gaa gtc ggc ggc gac   624
Thr Ser Leu Phe Asp Ala Leu Pro Arg Gln Leu Glu Val Gly Gly Asp
        195                 200                 205

gac ggc aca acg tac gaa cgc atc gag gag gac cgc atg cag gcc gcc   672
Asp Gly Thr Thr Tyr Glu Arg Ile Glu Glu Asp Arg Met Gln Ala Ala
    210                 215                 220

gga tac tcc gac gac gca gtc gcg tgg gac acg ccg gga tta gaa ccc   720
Gly Tyr Ser Asp Asp Ala Val Ala Trp Asp Thr Pro Gly Leu Glu Pro
225                 230                 235                 240

att gtg atc cgt tgc ggc gtg gag cct tct gag aac tac gca gcc ggt   768
Ile Val Ile Arg Cys Gly Val Glu Pro Ser Glu Asn Tyr Ala Ala Gly
                245                 250                 255

gcc atg ttg cag cag atc gat gac atc ccg tgg ttc gag gac acc att   816
Ala Met Leu Gln Gln Ile Asp Asp Ile Pro Trp Phe Glu Asp Thr Ile
            260                 265                 270

ttg gcc tcc ggt acc acc tcg tct acc tgg tat gcc ctt gga cgc gag   864
Leu Ala Ser Gly Thr Thr Ser Ser Thr Trp Tyr Ala Leu Gly Arg Glu
        275                 280                 285

atc gac atc gcc gtg tct ctg cct cag gct gct tcc tct tcc ctg att   912
Ile Asp Ile Ala Val Ser Leu Pro Gln Ala Ala Ser Ser Ser Leu Ile
    290                 295                 300

act atc tcc ggt ttc att gaa gac acg gtt cct gcg gaa taagacataa   961
Thr Ile Ser Gly Phe Ile Glu Asp Thr Val Pro Ala Glu
305                 310                 315

aaaatcgccc cac                                                   974
```

<210> 478
<211> 317
<212> PRT
<213> Corynebacterium glutamicum

<400> 478

```
Pro Ala Asn Gly Gly Ile Asn Lys Thr Pro Met Ile Ile Ala Leu Val
  1               5                  10                  15
```

```
Leu Ser Ile Val Leu Val Leu Ala Val Leu Phe Gly Ala Arg Val Leu
            20                  25                  30

Leu Gly Pro Ala Gly Gln Gln Gln Ile Ala Met Ser Gly Leu Pro Ala
        35                  40                  45

Pro Asp Ala Glu Ser Ala Glu Cys Ala Ala Leu Leu Glu Asp Leu Pro
    50                  55                  60

Gly Glu Ala Phe Gly His Thr Arg Ala Glu Ile Met Asp Pro Val Pro
65                  70                  75                  80

Pro Gly Ala Ala Ala Trp Ser Thr Ser Asp Leu Glu Arg Val Thr Leu
                85                  90                  95

Arg Cys Gly Val Asp Met Pro Phe Gln Tyr Thr Ala Leu Ala Asn Thr
            100                 105                 110

Val Asp Val Asp Gly Thr Thr Trp Leu Pro Val Ser Asp Met Thr Pro
        115                 120                 125

Gly Ser Ser Leu Glu Thr Trp Tyr Ser Val Asn Arg Phe Pro Val Val
    130                 135                 140

Ala Ile Thr Ala Asp Asp Ile Ser Thr Asp Ser Ala Asp Asn Pro Val
145                 150                 155                 160

Asp Pro Phe Ser Ser Ala Val Asp Lys Leu Glu Lys Arg Asp Gly Gln
                165                 170                 175

Pro Phe Asp Ala Pro Leu Thr Gly Leu Ser Ser Ala Gly Thr Thr Cys
            180                 185                 190

Thr Ser Leu Phe Asp Ala Leu Pro Arg Gln Leu Glu Val Gly Gly Asp
        195                 200                 205

Asp Gly Thr Thr Tyr Glu Arg Ile Glu Glu Asp Arg Met Gln Ala Ala
    210                 215                 220

Gly Tyr Ser Asp Asp Ala Val Ala Trp Asp Thr Pro Gly Leu Glu Pro
225                 230                 235                 240

Ile Val Ile Arg Cys Gly Val Glu Pro Ser Glu Asn Tyr Ala Ala Gly
                245                 250                 255

Ala Met Leu Gln Gln Ile Asp Asp Ile Pro Trp Phe Glu Asp Thr Ile
            260                 265                 270

Leu Ala Ser Gly Thr Thr Ser Ser Thr Trp Tyr Ala Leu Gly Arg Glu
        275                 280                 285

Ile Asp Ile Ala Val Ser Leu Pro Gln Ala Ala Ser Ser Ser Leu Ile
    290                 295                 300

Thr Ile Ser Gly Phe Ile Glu Asp Thr Val Pro Ala Glu
305                 310                 315
```

<210> 479
<211> 2172

<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2149)
<223> RXN01028

<400> 479
cgcaagcagc tgcactatat tcaggcattt taccgtgcct gggacccatc aacgccgctt 60

caatgacgct gacccagcgg tgacccatcc gcatctcaca gtg atc tac cca ccg 115
Val Ile Tyr Pro Pro
1 5

ctc acc cct gca tcc gaa gag aaa ttc aac aag atc acc tca gtc gct 163
Leu Thr Pro Ala Ser Glu Glu Lys Phe Asn Lys Ile Thr Ser Val Ala
10 15 20

gct gtg agc aag cgc cca acc acc ctg ccg tat ttc cgt gca gat ggt 211
Ala Val Ser Lys Arg Pro Thr Thr Leu Pro Tyr Phe Arg Ala Asp Gly
25 30 35

tca cct act cgt ggc ttt gct aac ttc tcc aca gga ggt att cac ggt 259
Ser Pro Thr Arg Gly Phe Ala Asn Phe Ser Thr Gly Gly Ile His Gly
40 45 50

gcg gaa tac aac gaa gat cgt ttt gac cat gat caa gat cta cac aca 307
Ala Glu Tyr Asn Glu Asp Arg Phe Asp His Asp Gln Asp Leu His Thr
55 60 65

gtg gca acc cgt gaa ttc ttc gcc att ctt gat gcg aca tta gcg gct 355
Val Ala Thr Arg Glu Phe Phe Ala Ile Leu Asp Ala Thr Leu Ala Ala
70 75 80 85

ctc tac gca gcc cac caa gcc gaa cct gaa tcg gcg gac tac cag att 403
Leu Tyr Ala Ala His Gln Ala Glu Pro Glu Ser Ala Asp Tyr Gln Ile
90 95 100

gca caa gac gca ctc gcc tgg gca aag aat gta ctt agc gat caa aaa 451
Ala Gln Asp Ala Leu Ala Trp Ala Lys Asn Val Leu Ser Asp Gln Lys
105 110 115

ctc atc gct aag tcg cct cag tta tac aac ccc gaa acc ggg gtc acc 499
Leu Ile Ala Lys Ser Pro Gln Leu Tyr Asn Pro Glu Thr Gly Val Thr
120 125 130

tat gag tgg gag ttt gtc gct caa gca gca tgg tgg att cgc aac aaa 547
Tyr Glu Trp Glu Phe Val Ala Gln Ala Ala Trp Trp Ile Arg Asn Lys
135 140 145

ccg gtt gag gtt att tta cca aca ggt gaa tca atg acc gta aaa cac 595
Pro Val Glu Val Ile Leu Pro Thr Gly Glu Ser Met Thr Val Lys His
150 155 160 165

aaa tct gta ttg gca tct gcg tcc tac cca ctc cga gac aac gtg gcg 643
Lys Ser Val Leu Ala Ser Ala Ser Tyr Pro Leu Arg Asp Asn Val Ala
170 175 180

tac tgg cgt agc gaa ccc aaa aca cca cag ctg ttt ccc gta gca aaa 691
Tyr Trp Arg Ser Glu Pro Lys Thr Pro Gln Leu Phe Pro Val Ala Lys

```
            185                 190                 195

tct ggt ggt tcc tcg ctt gag aag aag tac aac tac acc tct gtg ggt   739
Ser Gly Gly Ser Ser Leu Glu Lys Lys Tyr Asn Tyr Thr Ser Val Gly
        200                 205                 210

act gct att cac gag gac ttt agc agt tac tat ccg ctc ttg ctc acc   787
Thr Ala Ile His Glu Asp Phe Ser Ser Tyr Tyr Pro Leu Leu Leu Thr
    215                 220                 225

aat atg gct gca ttt acc aat gct gac tta ggt att gat gag aaa acc   835
Asn Met Ala Ala Phe Thr Asn Ala Asp Leu Gly Ile Asp Glu Lys Thr
230                 235                 240                 245

ggg cgc cct cgt gac cgc tac cgt gaa atc tac gaa caa aaa gag atc   883
Gly Arg Pro Arg Asp Arg Tyr Arg Glu Ile Tyr Glu Gln Lys Glu Ile
                250                 255                 260

tat ggc gca cag cgc aaa gac ccc tcc att gat gaa gaa aca aag caa   931
Tyr Gly Ala Gln Arg Lys Asp Pro Ser Ile Asp Glu Glu Thr Lys Gln
            265                 270                 275

cgt cta ggg att ttg cgc gaa ggt acc aag ttg att ctt aac tcg gcc   979
Arg Leu Gly Ile Leu Arg Glu Gly Thr Lys Leu Ile Leu Asn Ser Ala
        280                 285                 290

acc ggt gct gct gat gct ggt cac gac acc ccg atc ctc atg aac aat   1027
Thr Gly Ala Ala Asp Ala Gly His Asp Thr Pro Ile Leu Met Asn Asn
    295                 300                 305

cgc gtt att gcc atg agg att att ggg cag cta ttt tct tgg aga att   1075
Arg Val Ile Ala Met Arg Ile Ile Gly Gln Leu Phe Ser Trp Arg Ile
310                 315                 320                 325

ggg caa gct caa tca ctg gct ggt gca acg att att tcc act aac act   1123
Gly Gln Ala Gln Ser Leu Ala Gly Ala Thr Ile Ile Ser Thr Asn Thr
                330                 335                 340

gat ggc ctg tat tcc gta ctc gat atg ggg act aac cag cgc gtt ctt   1171
Asp Gly Leu Tyr Ser Val Leu Asp Met Gly Thr Asn Gln Arg Val Leu
            345                 350                 355

gat gaa cac gct aca gcc atc ggt gtg caa att gag cct gaa gaa ctg   1219
Asp Glu His Ala Thr Ala Ile Gly Val Gln Ile Glu Pro Glu Glu Leu
        360                 365                 370

gat att gtc tcc aag gat tcc aac tca cgt gcc gaa ttt ctc ggc aat   1267
Asp Ile Val Ser Lys Asp Ser Asn Ser Arg Ala Glu Phe Leu Gly Asn
    375                 380                 385

ggc tac atc aat gcg gcc ggt gac ttg gcg tgt tgg gat gga ccc aac   1315
Gly Tyr Ile Asn Ala Ala Gly Asp Leu Ala Cys Trp Asp Gly Pro Asn
390                 395                 400                 405

tct cgg aac tca cta gat cac ccg gcc ttt gtt gac cat gtg ctg gtg   1363
Ser Arg Asn Ser Leu Asp His Pro Ala Phe Val Asp His Val Leu Val
                410                 415                 420

aag tat ttc cag ctc gtc gtc aac aac act gtg cca gag att cca gaa   1411
Lys Tyr Phe Gln Leu Val Val Asn Asn Thr Val Pro Glu Ile Pro Glu
            425                 430                 435
```

```
aca cct gag ctt gag ggt gta ccg ctg gct ctt gat caa ccc atg aac   1459
Thr Pro Glu Leu Glu Gly Val Pro Leu Ala Leu Asp Gln Pro Met Asn
        440                 445                 450

cgc cac gaa gtc tcg aag att gtc gcc act atg cac aag gaa ttc gag   1507
Arg His Glu Val Ser Lys Ile Val Ala Thr Met His Lys Glu Phe Glu
    455                 460                 465

ccg aaa aag ctg ctg tcg ttt tac caa aac att ttg gcc tct tca cgc   1555
Pro Lys Lys Leu Leu Ser Phe Tyr Gln Asn Ile Leu Ala Ser Ser Arg
470                 475                 480                 485

ggt tct aat acc ttc cta ttc tct gtc ccc tat atc cct gca aca gaa   1603
Gly Ser Asn Thr Phe Leu Phe Ser Val Pro Tyr Ile Pro Ala Thr Glu
                490                 495                 500

gga gaa gaa acc cac cct gca aca gat acc agc act att gcg aca cca   1651
Gly Glu Glu Thr His Pro Ala Thr Asp Thr Ser Thr Ile Ala Thr Pro
            505                 510                 515

acc ttg agc ttt gat gct tat ggt aat aag gcc gag gtc atg ccg act   1699
Thr Leu Ser Phe Asp Ala Tyr Gly Asn Lys Ala Glu Val Met Pro Thr
        520                 525                 530

caa tcc act gtg gat aag cgc gtg ccc tct ttg ctg cag tat tac acg   1747
Gln Ser Thr Val Asp Lys Arg Val Pro Ser Leu Leu Gln Tyr Tyr Thr
    535                 540                 545

cgt aca ttc cat gtg cga caa gat acg cag cag gct gtc ttt gat gtt   1795
Arg Thr Phe His Val Arg Gln Asp Thr Gln Gln Ala Val Phe Asp Val
550                 555                 560                 565

att ggc gcc aac ccc gtg ctc atc gcc gca gca aaa gct gca tcc ata   1843
Ile Gly Ala Asn Pro Val Leu Ile Ala Ala Ala Lys Ala Ala Ser Ile
                570                 575                 580

tca ccg gct tct gct gat tca cgt aga aag aag ggc ctg gcc tcc acc   1891
Ser Pro Ala Ser Ala Asp Ser Arg Arg Lys Lys Gly Leu Ala Ser Thr
            585                 590                 595

aac gct gac cca gta gcc aag cat gta cta gaa att gca gga gct gat   1939
Asn Ala Asp Pro Val Ala Lys His Val Leu Glu Ile Ala Gly Ala Asp
        600                 605                 610

gtg gaa tcg ctg cgc cat gaa aag gat ctc aag gtc acc aag cac act   1987
Val Glu Ser Leu Arg His Glu Lys Asp Leu Lys Val Thr Lys His Thr
    615                 620                 625

ggc caa gac cca gca ctg cct gtc gtg gtc ttt aac caa acc att tgg   2035
Gly Gln Asp Pro Ala Leu Pro Val Val Val Phe Asn Gln Thr Ile Trp
630                 635                 640                 645

cat aac ccc aac gac gat gtg att aat gca tta ctg ggc gct att gac   2083
His Asn Pro Asn Asp Asp Val Ile Asn Ala Leu Leu Gly Ala Ile Asp
                650                 655                 660

cag gat gcc tac att gac atg gcg atc tcg tcc tac aac aag tcc tgg   2131
Gln Asp Ala Tyr Ile Asp Met Ala Ile Ser Ser Tyr Asn Lys Ser Trp
            665                 670                 675
```

```
cac aac att atc ccg gct taactaccgc tgggtagacc cct                2172
His Asn Ile Ile Pro Ala
        680


<210> 480
<211> 683
<212> PRT
<213> Corynebacterium glutamicum

<400> 480
Val Ile Tyr Pro Pro Leu Thr Pro Ala Ser Glu Glu Lys Phe Asn Lys
  1               5                  10                  15

Ile Thr Ser Val Ala Ala Val Ser Lys Arg Pro Thr Thr Leu Pro Tyr
             20                  25                  30

Phe Arg Ala Asp Gly Ser Pro Thr Arg Gly Phe Ala Asn Phe Ser Thr
         35                  40                  45

Gly Gly Ile His Gly Ala Glu Tyr Asn Glu Asp Arg Phe Asp His Asp
     50                  55                  60

Gln Asp Leu His Thr Val Ala Thr Arg Glu Phe Phe Ala Ile Leu Asp
 65                  70                  75                  80

Ala Thr Leu Ala Ala Leu Tyr Ala Ala His Gln Ala Glu Pro Glu Ser
                 85                  90                  95

Ala Asp Tyr Gln Ile Ala Gln Asp Ala Leu Ala Trp Ala Lys Asn Val
            100                 105                 110

Leu Ser Asp Gln Lys Leu Ile Ala Lys Ser Pro Gln Leu Tyr Asn Pro
        115                 120                 125

Glu Thr Gly Val Thr Tyr Glu Trp Glu Phe Val Ala Gln Ala Ala Trp
    130                 135                 140

Trp Ile Arg Asn Lys Pro Val Glu Val Ile Leu Pro Thr Gly Glu Ser
145                 150                 155                 160

Met Thr Val Lys His Lys Ser Val Leu Ala Ser Ala Ser Tyr Pro Leu
                165                 170                 175

Arg Asp Asn Val Ala Tyr Trp Arg Ser Glu Pro Lys Thr Pro Gln Leu
            180                 185                 190

Phe Pro Val Ala Lys Ser Gly Gly Ser Ser Leu Glu Lys Lys Tyr Asn
        195                 200                 205

Tyr Thr Ser Val Gly Thr Ala Ile His Glu Asp Phe Ser Ser Tyr Tyr
    210                 215                 220

Pro Leu Leu Leu Thr Asn Met Ala Ala Phe Thr Asn Ala Asp Leu Gly
225                 230                 235                 240

Ile Asp Glu Lys Thr Gly Arg Pro Arg Asp Arg Tyr Arg Glu Ile Tyr
                245                 250                 255

Glu Gln Lys Glu Ile Tyr Gly Ala Gln Arg Lys Asp Pro Ser Ile Asp
            260                 265                 270
```

Glu Glu Thr Lys Gln Arg Leu Gly Ile Leu Arg Glu Gly Thr Lys Leu
275 280 285

Ile Leu Asn Ser Ala Thr Gly Ala Ala Asp Ala Gly His Asp Thr Pro
290 295 300

Ile Leu Met Asn Asn Arg Val Ile Ala Met Arg Ile Ile Gly Gln Leu
305 310 315 320

Phe Ser Trp Arg Ile Gly Gln Ala Gln Ser Leu Ala Gly Ala Thr Ile
325 330 335

Ile Ser Thr Asn Thr Asp Gly Leu Tyr Ser Val Leu Asp Met Gly Thr
340 345 350

Asn Gln Arg Val Leu Asp Glu His Ala Thr Ala Ile Gly Val Gln Ile
355 360 365

Glu Pro Glu Glu Leu Asp Ile Val Ser Lys Asp Ser Asn Ser Arg Ala
370 375 380

Glu Phe Leu Gly Asn Gly Tyr Ile Asn Ala Ala Gly Asp Leu Ala Cys
385 390 395 400

Trp Asp Gly Pro Asn Ser Arg Asn Ser Leu Asp His Pro Ala Phe Val
405 410 415

Asp His Val Leu Val Lys Tyr Phe Gln Leu Val Val Asn Asn Thr Val
420 425 430

Pro Glu Ile Pro Glu Thr Pro Glu Leu Glu Gly Val Pro Leu Ala Leu
435 440 445

Asp Gln Pro Met Asn Arg His Glu Val Ser Lys Ile Val Ala Thr Met
450 455 460

His Lys Glu Phe Glu Pro Lys Lys Leu Leu Ser Phe Tyr Gln Asn Ile
465 470 475 480

Leu Ala Ser Ser Arg Gly Ser Asn Thr Phe Leu Phe Ser Val Pro Tyr
485 490 495

Ile Pro Ala Thr Glu Gly Glu Glu Thr His Pro Ala Thr Asp Thr Ser
500 505 510

Thr Ile Ala Thr Pro Thr Leu Ser Phe Asp Ala Tyr Gly Asn Lys Ala
515 520 525

Glu Val Met Pro Thr Gln Ser Thr Val Asp Lys Arg Val Pro Ser Leu
530 535 540

Leu Gln Tyr Tyr Thr Arg Thr Phe His Val Arg Gln Asp Thr Gln Gln
545 550 555 560

Ala Val Phe Asp Val Ile Gly Ala Asn Pro Val Leu Ile Ala Ala Ala
565 570 575

Lys Ala Ala Ser Ile Ser Pro Ala Ser Ala Asp Ser Arg Arg Lys Lys
580 585 590

```
Gly Leu Ala Ser Thr Asn Ala Asp Pro Val Ala Lys His Val Leu Glu
        595                 600                 605

Ile Ala Gly Ala Asp Val Glu Ser Leu Arg His Glu Lys Asp Leu Lys
    610                 615                 620

Val Thr Lys His Thr Gly Gln Asp Pro Ala Leu Pro Val Val Val Phe
625                 630                 635                 640

Asn Gln Thr Ile Trp His Asn Pro Asn Asp Asp Val Ile Asn Ala Leu
                645                 650                 655

Leu Gly Ala Ile Asp Gln Asp Ala Tyr Ile Asp Met Ala Ile Ser Ser
            660                 665                 670

Tyr Asn Lys Ser Trp His Asn Ile Ile Pro Ala
        675                 680


<210> 481
<211> 647
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(624)
<223> FRXA01028

<400> 481
ttt tac caa aac att ttg gcc tct tca cgc ggt tct aat acc ttc cta   48
Phe Tyr Gln Asn Ile Leu Ala Ser Ser Arg Gly Ser Asn Thr Phe Leu
  1               5                  10                  15

ttc tct gtc ccc tat atc cct gca aca gaa gga gaa gaa acc cac cct   96
Phe Ser Val Pro Tyr Ile Pro Ala Thr Glu Gly Glu Glu Thr His Pro
             20                  25                  30

gca aca gat acc agc act att gcg aca cca acc ttg agc ttt gat gct   144
Ala Thr Asp Thr Ser Thr Ile Ala Thr Pro Thr Leu Ser Phe Asp Ala
         35                  40                  45

tat ggt aat aag gcc gag gtc atg ccg act caa tcc act gtg gat aag   192
Tyr Gly Asn Lys Ala Glu Val Met Pro Thr Gln Ser Thr Val Asp Lys
     50                  55                  60

cgc gtg ccc tct ttg ctg cag tat tac acg cgt aca ttc cat gtg cga   240
Arg Val Pro Ser Leu Leu Gln Tyr Tyr Thr Arg Thr Phe His Val Arg
 65                  70                  75                  80

caa gat acg cag cag gct gtc ttt gat gtt att ggc gcc aac ccc gtg   288
Gln Asp Thr Gln Gln Ala Val Phe Asp Val Ile Gly Ala Asn Pro Val
                 85                  90                  95

ctc atc gcc gca gca aaa gct gca tcc ata tca ccg gct tct gct gat   336
Leu Ile Ala Ala Ala Lys Ala Ala Ser Ile Ser Pro Ala Ser Ala Asp
            100                 105                 110

tca cgt aga aag aag ggc ctg gcc tcc acc aac gct gac cca gta gcc   384
Ser Arg Arg Lys Lys Gly Leu Ala Ser Thr Asn Ala Asp Pro Val Ala
        115                 120                 125
```

```
aag cat gta cta gaa att gca gga gct gat gtg gaa tcg ctg cgc cat   432
Lys His Val Leu Glu Ile Ala Gly Ala Asp Val Glu Ser Leu Arg His
    130                 135                 140

gaa aag gat ctc aag gtc acc aag cac act ggc caa gac cca gca ctg   480
Glu Lys Asp Leu Lys Val Thr Lys His Thr Gly Gln Asp Pro Ala Leu
145                 150                 155                 160

cct gtc gtg gtc ttt aac caa acc att tgg cat aac ccc aac gac gat   528
Pro Val Val Val Phe Asn Gln Thr Ile Trp His Asn Pro Asn Asp Asp
                165                 170                 175

gtg att aat gca tta ctg ggc gct att gac cag gat gcc tac att gac   576
Val Ile Asn Ala Leu Leu Gly Ala Ile Asp Gln Asp Ala Tyr Ile Asp
            180                 185                 190

atg gcg atc tcg tcc tac aac aag tcc tgg cac aac att atc ccg gct   624
Met Ala Ile Ser Ser Tyr Asn Lys Ser Trp His Asn Ile Ile Pro Ala
        195                 200                 205

taactaccgc tgggtagacc cct                                        647
```

Application Sequence Listing

```
<210> 482
<211> 208
<212> PRT
<213> Corynebacterium glutamicum

<400> 482
Phe Tyr Gln Asn Ile Leu Ala Ser Ser Arg Gly Ser Asn Thr Phe Leu
  1               5                  10                  15

Phe Ser Val Pro Tyr Ile Pro Ala Thr Glu Gly Glu Glu Thr His Pro
             20                  25                  30

Ala Thr Asp Thr Ser Thr Ile Ala Thr Pro Thr Leu Ser Phe Asp Ala
         35                  40                  45

Tyr Gly Asn Lys Ala Glu Val Met Pro Thr Gln Ser Thr Val Asp Lys
     50                  55                  60

Arg Val Pro Ser Leu Leu Gln Tyr Tyr Thr Arg Thr Phe His Val Arg
 65                  70                  75                  80

Gln Asp Thr Gln Gln Ala Val Phe Asp Val Ile Gly Ala Asn Pro Val
                 85                  90                  95

Leu Ile Ala Ala Ala Lys Ala Ala Ser Ile Ser Pro Ala Ser Ala Asp
            100                 105                 110

Ser Arg Arg Lys Lys Gly Leu Ala Ser Thr Asn Ala Asp Pro Val Ala
        115                 120                 125

Lys His Val Leu Glu Ile Ala Gly Ala Asp Val Glu Ser Leu Arg His
    130                 135                 140

Glu Lys Asp Leu Lys Val Thr Lys His Thr Gly Gln Asp Pro Ala Leu
145                 150                 155                 160

Pro Val Val Val Phe Asn Gln Thr Ile Trp His Asn Pro Asn Asp Asp
```

```
                165                 170                 175

Val Ile Asn Ala Leu Leu Gly Ala Ile Asp Gln Asp Ala Tyr Ile Asp
            180                 185                 190

Met Ala Ile Ser Ser Tyr Asn Lys Ser Trp His Asn Ile Ile Pro Ala
        195                 200                 205
```

<210> 483
<211> 1230
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1230)
<223> FRXA01812

<400> 483

```
agc ttc aat gac gtt gac cca gcg gtg acc cat ccg cat ctc aca gtg   48
Ser Phe Asn Asp Val Asp Pro Ala Val Thr His Pro His Leu Thr Val
  1               5                  10                  15

atc tac cca ccg ctc acc cct gca tcc gaa gag aaa ttc aac aag atc   96
Ile Tyr Pro Pro Leu Thr Pro Ala Ser Glu Glu Lys Phe Asn Lys Ile
             20                  25                  30

acc tca gtc gct gct gtg agc aag cgc cca acc acc ctg ccg tat ttc   144
Thr Ser Val Ala Ala Val Ser Lys Arg Pro Thr Thr Leu Pro Tyr Phe
         35                  40                  45

cgt gca gat ggt tca cct act cgt ggc ttt gct aac ttc tcc aca gga   192
Arg Ala Asp Gly Ser Pro Thr Arg Gly Phe Ala Asn Phe Ser Thr Gly
     50                  55                  60

ggt att cac ggt gcg gaa tac aac gaa gat cgt ttt gac cat gat caa   240
Gly Ile His Gly Ala Glu Tyr Asn Glu Asp Arg Phe Asp His Asp Gln
 65                  70                  75                  80

gat cta cac aca gtg gca acc cgt gaa ttc ttc gcc att ctt gat gcg   288
Asp Leu His Thr Val Ala Thr Arg Glu Phe Phe Ala Ile Leu Asp Ala
                85                  90                  95

aca tta gcg gct ctc tac gca gcc cac caa gcc gaa cct gaa tcg gcg   336
Thr Leu Ala Ala Leu Tyr Ala Ala His Gln Ala Glu Pro Glu Ser Ala
            100                 105                 110

gac tac cag att gca caa gac gca ctc gcc tgg gca aag aat gta ctt   384
Asp Tyr Gln Ile Ala Gln Asp Ala Leu Ala Trp Ala Lys Asn Val Leu
        115                 120                 125

agc gat caa aaa ctc atc gct aag tcg cct cag tta tac aac ccc gaa   432
Ser Asp Gln Lys Leu Ile Ala Lys Ser Pro Gln Leu Tyr Asn Pro Glu
    130                 135                 140

acc ggg gtc acc tat gag tgg gag ttt gtc gct caa gca gca tgg tgg   480
Thr Gly Val Thr Tyr Glu Trp Glu Phe Val Ala Gln Ala Ala Trp Trp
```

```
145                 150                 155                 160

att cgc aac aaa ccg gtt gag gtt att tta cca aca ggt gaa tca atg   528
Ile Arg Asn Lys Pro Val Glu Val Ile Leu Pro Thr Gly Glu Ser Met
                165                 170                 175

acc gta aaa cac aaa tct gta ttg gca tct gcg tcc tac cca ctc cga   576
Thr Val Lys His Lys Ser Val Leu Ala Ser Ala Ser Tyr Pro Leu Arg
            180                 185                 190

gac aac gtg gcg tac tgg cgt agc gaa ccc aaa aca cca cag ctg ttt   624
Asp Asn Val Ala Tyr Trp Arg Ser Glu Pro Lys Thr Pro Gln Leu Phe
        195                 200                 205

ccc gta gca aaa tct ggt ggt tcc tcg ctt gag aag aag tac aac tac   672
Pro Val Ala Lys Ser Gly Gly Ser Ser Leu Glu Lys Lys Tyr Asn Tyr
    210                 215                 220

acc tct gtg ggt act gct att cac gag gac ttt agc agt tac tat ccg   720
Thr Ser Val Gly Thr Ala Ile His Glu Asp Phe Ser Ser Tyr Tyr Pro
225                 230                 235                 240

ctc ttg ctc acc aat atg gct gca ttt acc aat gct gac tta ggt att   768
Leu Leu Leu Thr Asn Met Ala Ala Phe Thr Asn Ala Asp Leu Gly Ile
                245                 250                 255

gat gag aaa acc ggg cgc cct cgt gac cgc tac cgt gaa atc tac gaa   816
Asp Glu Lys Thr Gly Arg Pro Arg Asp Arg Tyr Arg Glu Ile Tyr Glu
            260                 265                 270

caa aaa gag atc tat ggc gca cag cgc aaa gac ccc tcc att gat gaa   864
Gln Lys Glu Ile Tyr Gly Ala Gln Arg Lys Asp Pro Ser Ile Asp Glu
        275                 280                 285

gaa aca aag caa cgt cta ggg att ttg cgc gaa ggt acc aag ttg att   912
Glu Thr Lys Gln Arg Leu Gly Ile Leu Arg Glu Gly Thr Lys Leu Ile
    290                 295                 300

ctt aac tcg gcc acc ggt gct gct gat gct ggt cac gac acc ccg atc   960
Leu Asn Ser Ala Thr Gly Ala Ala Asp Ala Gly His Asp Thr Pro Ile
305                 310                 315                 320

ctc atg aac aat cgc gtt att gcc atg agg att att ggg cag cta ttt  1008
Leu Met Asn Asn Arg Val Ile Ala Met Arg Ile Ile Gly Gln Leu Phe
                325                 330                 335

tct tgg aga att ggg caa gct caa tca ctg gct ggt gca acg att att  1056
Ser Trp Arg Ile Gly Gln Ala Gln Ser Leu Ala Gly Ala Thr Ile Ile
            340                 345                 350

tcc act aac act gat ggc ctg tat tcc gta ctc gat atg ggg act aac  1104
Ser Thr Asn Thr Asp Gly Leu Tyr Ser Val Leu Asp Met Gly Thr Asn
        355                 360                 365

cag cgc gtt ctt gat gaa cac gct aca gcc atc ggt gtg caa att gag  1152
Gln Arg Val Leu Asp Glu His Ala Thr Ala Ile Gly Val Gln Ile Glu
    370                 375                 380

cct gaa gaa ctg gat att gtc tcc aag gat tcc aac tca cgt gcc gaa  1200
Pro Glu Glu Leu Asp Ile Val Ser Lys Asp Ser Asn Ser Arg Ala Glu
385                 390                 395                 400
```

```
ttt ctc ggc aat ggc tac atc aat gcg gcc                                  1230
Phe Leu Gly Asn Gly Tyr Ile Asn Ala Ala
                405                 410


<210> 484
<211> 410
<212> PRT
<213> Corynebacterium glutamicum

<400> 484
Ser Phe Asn Asp Val Asp Pro Ala Val Thr His Pro His Leu Thr Val
  1               5                  10                  15

Ile Tyr Pro Pro Leu Thr Pro Ala Ser Glu Glu Lys Phe Asn Lys Ile
             20                  25                  30

Thr Ser Val Ala Ala Val Ser Lys Arg Pro Thr Thr Leu Pro Tyr Phe
         35                  40                  45

Arg Ala Asp Gly Ser Pro Thr Arg Gly Phe Ala Asn Phe Ser Thr Gly
     50                  55                  60

Gly Ile His Gly Ala Glu Tyr Asn Glu Asp Arg Phe Asp His Asp Gln
 65                  70                  75                  80

Asp Leu His Thr Val Ala Thr Arg Glu Phe Phe Ala Ile Leu Asp Ala
                85                  90                  95

Thr Leu Ala Ala Leu Tyr Ala Ala His Gln Ala Glu Pro Glu Ser Ala
            100                 105                 110

Asp Tyr Gln Ile Ala Gln Asp Ala Leu Ala Trp Ala Lys Asn Val Leu
        115                 120                 125

Ser Asp Gln Lys Leu Ile Ala Lys Ser Pro Gln Leu Tyr Asn Pro Glu
    130                 135                 140

Thr Gly Val Thr Tyr Glu Trp Glu Phe Val Ala Gln Ala Ala Trp Trp
145                 150                 155                 160

Ile Arg Asn Lys Pro Val Glu Val Ile Leu Pro Thr Gly Glu Ser Met
                165                 170                 175

Thr Val Lys His Lys Ser Val Leu Ala Ser Ala Ser Tyr Pro Leu Arg
            180                 185                 190

Asp Asn Val Ala Tyr Trp Arg Ser Glu Pro Lys Thr Pro Gln Leu Phe
        195                 200                 205

Pro Val Ala Lys Ser Gly Gly Ser Ser Leu Glu Lys Lys Tyr Asn Tyr
    210                 215                 220

Thr Ser Val Gly Thr Ala Ile His Glu Asp Phe Ser Ser Tyr Tyr Pro
225                 230                 235                 240

Leu Leu Leu Thr Asn Met Ala Ala Phe Thr Asn Ala Asp Leu Gly Ile
                245                 250                 255

Asp Glu Lys Thr Gly Arg Pro Arg Asp Arg Tyr Arg Glu Ile Tyr Glu
```

```
            260                 265                 270

Gln Lys Glu Ile Tyr Gly Ala Gln Arg Lys Asp Pro Ser Ile Asp Glu
        275                 280                 285

Glu Thr Lys Gln Arg Leu Gly Ile Leu Arg Glu Gly Thr Lys Leu Ile
    290                 295                 300

Leu Asn Ser Ala Thr Gly Ala Ala Asp Ala Gly His Asp Thr Pro Ile
305                 310                 315                 320

Leu Met Asn Asn Arg Val Ile Ala Met Arg Ile Ile Gly Gln Leu Phe
                325                 330                 335

Ser Trp Arg Ile Gly Gln Ala Gln Ser Leu Ala Gly Ala Thr Ile Ile
            340                 345                 350

Ser Thr Asn Thr Asp Gly Leu Tyr Ser Val Leu Asp Met Gly Thr Asn
        355                 360                 365

Gln Arg Val Leu Asp Glu His Ala Thr Ala Ile Gly Val Gln Ile Glu
    370                 375                 380

Pro Glu Glu Leu Asp Ile Val Ser Lys Asp Ser Asn Ser Arg Ala Glu
385                 390                 395                 400

Phe Leu Gly Asn Gly Tyr Ile Asn Ala Ala
                405                 410


<210> 485
<211> 837
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(814)
<223> RXN01069

<400> 485
tcctaagctc tcttgagtac ctgagacctt ctcagcaaaa cacaaagtgc cttcacccaa 60

cctggggtgg aggcactttc tcattgctaa ggtgtgcatc gtg aac gat tta ccg   115
                                            Val Asn Asp Leu Pro
                                              1               5

aac cta cca aag ctg ccc ttc aac tgg aca tgg gtg ctg gca act gtt   163
Asn Leu Pro Lys Leu Pro Phe Asn Trp Thr Trp Val Leu Ala Thr Val
                 10                  15                  20

gcc acg aca gtg gtg ttg gcg ggt att ggt ttg tat gtg tat tac ccg   211
Ala Thr Thr Val Val Leu Ala Gly Ile Gly Leu Tyr Val Tyr Tyr Pro
             25                  30                  35

tcg ttg cca gat cct atg ccg gtg cat tgg aat gga tcc ggg gag gcg   259
Ser Leu Pro Asp Pro Met Pro Val His Trp Asn Gly Ser Gly Glu Ala
         40                  45                  50

gat aat tgg acg cct aaa tcg gtg ggt tcg ttt ctt tca ctg att ttg   307
Asp Asn Trp Thr Pro Lys Ser Val Gly Ser Phe Leu Ser Leu Ile Leu
```

```
     55                  60                  65

ata ggg cca ggc att att ttg ctg acc ctg tcg ggt atg cag gcg ttg   355
Ile Gly Pro Gly Ile Ile Leu Leu Thr Leu Ser Gly Met Gln Ala Leu
 70                  75                  80                  85

ctg acc atg cag tct gga gtg atc acg caa cgc ggt ggg gcg aaa tcg   403
Leu Thr Met Gln Ser Gly Val Ile Thr Gln Arg Gly Gly Ala Lys Ser
                90                  95                 100

gcg aat gaa gcg cac cgg cag tgg gaa acc tac aag gca aca agc atg   451
Ala Asn Glu Ala His Arg Gln Trp Glu Thr Tyr Lys Ala Thr Ser Met
            105                 110                 115

cac atg ggt tgg tac atg ttt gtg ctc aac gct ttg att ttg gtg atg   499
His Met Gly Trp Tyr Met Phe Val Leu Asn Ala Leu Ile Leu Val Met
        120                 125                 130

atc ctc aat gag ttc cgc cca aac cct ctg cct ggt gga ttt atc atc   547
Ile Leu Asn Glu Phe Arg Pro Asn Pro Leu Pro Gly Gly Phe Ile Ile
    135                 140                 145

ggg ctt att gga att att gct gcc acg att gtc ctg ttg gtt ctg att   595
Gly Leu Ile Gly Ile Ile Ala Ala Thr Ile Val Leu Leu Val Leu Ile
150                 155                 160                 165

gga aaa aca acc acg agt ttg gca aag aaa tac ccc atg cct gac caa   643
Gly Lys Thr Thr Thr Ser Leu Ala Lys Lys Tyr Pro Met Pro Asp Gln
                170                 175                 180

gat gga aag acg tgg ggg att ttc tac aac gat ccg gac gat aat cgg   691
Asp Gly Lys Thr Trp Gly Ile Phe Tyr Asn Asp Pro Asp Asp Asn Arg
            185                 190                 195

atc tta gtg gac acc ggg atg ggg atg aat tac acg ttt aac att gcc   739
Ile Leu Val Asp Thr Gly Met Gly Met Asn Tyr Thr Phe Asn Ile Ala
        200                 205                 210

cat acg tgg ggc aag atc ttc gcg gtt ttg atc ttc gcg gtg cca gta   787
His Thr Trp Gly Lys Ile Phe Ala Val Leu Ile Phe Ala Val Pro Val
    215                 220                 225

ctc atc gtt tta tta acc gtt ctc ctt taacctcgat ccaccgatgt         834
Leu Ile Val Leu Leu Thr Val Leu Leu
230                 235

gcc                                                               837


<210> 486
<211> 238
<212> PRT
<213> Corynebacterium glutamicum

<400> 486
Val Asn Asp Leu Pro Asn Leu Pro Lys Leu Pro Phe Asn Trp Thr Trp
  1               5                  10                  15

Val Leu Ala Thr Val Ala Thr Thr Val Val Leu Ala Gly Ile Gly Leu
             20                  25                  30
```

```
Tyr Val Tyr Tyr Pro Ser Leu Pro Asp Pro Met Pro Val His Trp Asn
         35                  40                  45

Gly Ser Gly Glu Ala Asp Asn Trp Thr Pro Lys Ser Val Gly Ser Phe
     50                  55                  60

Leu Ser Leu Ile Leu Ile Gly Pro Gly Ile Ile Leu Leu Thr Leu Ser
 65                  70                  75                  80

Gly Met Gln Ala Leu Leu Thr Met Gln Ser Gly Val Ile Thr Gln Arg
                 85                  90                  95

Gly Gly Ala Lys Ser Ala Asn Glu Ala His Arg Gln Trp Glu Thr Tyr
            100                 105                 110

Lys Ala Thr Ser Met His Met Gly Trp Tyr Met Phe Val Leu Asn Ala
        115                 120                 125

Leu Ile Leu Val Met Ile Leu Asn Glu Phe Arg Pro Asn Pro Leu Pro
    130                 135                 140

Gly Gly Phe Ile Ile Gly Leu Ile Gly Ile Ile Ala Ala Thr Ile Val
145                 150                 155                 160

Leu Leu Val Leu Ile Gly Lys Thr Thr Thr Ser Leu Ala Lys Lys Tyr
                165                 170                 175

Pro Met Pro Asp Gln Asp Gly Lys Thr Trp Gly Ile Phe Tyr Asn Asp
            180                 185                 190

Pro Asp Asp Asn Arg Ile Leu Val Asp Thr Gly Met Gly Met Asn Tyr
        195                 200                 205

Thr Phe Asn Ile Ala His Thr Trp Gly Lys Ile Phe Ala Val Leu Ile
    210                 215                 220

Phe Ala Val Pro Val Leu Ile Val Leu Leu Thr Val Leu Leu
225                 230                 235
```

<210> 487
<211> 703
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(703)
<223> FRXA01069

<400> 487
tcctaagctc tcttgagtac ctgagacctt ctcagcaaaa cacaaagtgc cttcacccaa 60

cctggggtgg aggcactttc tcattgctaa ggtgtgcatc gtg aac gat tta ccg 115
                                            Val Asn Asp Leu Pro
                                              1   5

aac cta cca aag ctg ccc ttc aac tgg aca tgg gtg ctg gca act gtt 163
Asn Leu Pro Lys Leu Pro Phe Asn Trp Thr Trp Val Leu Ala Thr Val
                10   15   20

```
gcc acg aca gtg gtg ttg gcg ggt att ggt ttg tat gtg tat tac ccg   211
Ala Thr Thr Val Val Leu Ala Gly Ile Gly Leu Tyr Val Tyr Tyr Pro
             25                  30                  35

tcg ttg cca gat cct atg ccg gtg cat tgg aat gga tcc ggg gag gcg   259
Ser Leu Pro Asp Pro Met Pro Val His Trp Asn Gly Ser Gly Glu Ala
         40                  45                  50

gat aat tgg acg cct aaa tcg gtg ggt tcg ttt ctt tca ctg att ttg   307
Asp Asn Trp Thr Pro Lys Ser Val Gly Ser Phe Leu Ser Leu Ile Leu
     55                  60                  65

ata ggg cca ggc att att ttg ctg acc ctg tcg ggt atg cag gcg ttg   355
Ile Gly Pro Gly Ile Ile Leu Leu Thr Leu Ser Gly Met Gln Ala Leu
 70                  75                  80                  85

ctg acc atg cag tct gga gtg atc acg caa cgc ggt ggg gcg aaa tcg   403
Leu Thr Met Gln Ser Gly Val Ile Thr Gln Arg Gly Gly Ala Lys Ser
                 90                  95                 100

gcg aat gaa gcg cac cgg cag tgg gaa acc tac aag gca aca agc atg   451
Ala Asn Glu Ala His Arg Gln Trp Glu Thr Tyr Lys Ala Thr Ser Met
            105                 110                 115

cac atg ggt tgg tac atg ttt gtg ctc aac gct ttg att ttg gtg atg   499
His Met Gly Trp Tyr Met Phe Val Leu Asn Ala Leu Ile Leu Val Met
        120                 125                 130

atc ctc aat gag ttc cgc cca aac cct ctg cct ggt gga ttt atc atc   547
Ile Leu Asn Glu Phe Arg Pro Asn Pro Leu Pro Gly Gly Phe Ile Ile
    135                 140                 145

ggg ctt att gga att att gct gcc acg att gtc ctg ttg gtt ctg att   595
Gly Leu Ile Gly Ile Ile Ala Ala Thr Ile Val Leu Leu Val Leu Ile
150                 155                 160                 165

gga aaa aca acc acg agt ttg gca aag aaa tac ccc atg cct gac caa   643
Gly Lys Thr Thr Thr Ser Leu Ala Lys Lys Tyr Pro Met Pro Asp Gln
                170                 175                 180

gat gga aag acg tgg ggg att ttc tac aac gat ccg gac gat aat cgg   691
Asp Gly Lys Thr Trp Gly Ile Phe Tyr Asn Asp Pro Asp Asp Asn Arg
            185                 190                 195

atc tta gtg gac                                                  703
Ile Leu Val Asp
        200
```

<210> 488
<211> 201
<212> PRT
<213> Corynebacterium glutamicum

<400> 488

```
Val Asn Asp Leu Pro Asn Leu Pro Lys Leu Pro Phe Asn Trp Thr Trp
  1               5                  10                  15

Val Leu Ala Thr Val Ala Thr Thr Val Val Leu Ala Gly Ile Gly Leu
             20                  25                  30
```

```
Tyr Val Tyr Tyr Pro Ser Leu Pro Asp Pro Met Pro Val His Trp Asn
         35                  40                  45

Gly Ser Gly Glu Ala Asp Asn Trp Thr Pro Lys Ser Val Gly Ser Phe
     50                  55                  60

Leu Ser Leu Ile Leu Ile Gly Pro Gly Ile Ile Leu Leu Thr Leu Ser
 65                  70                  75                  80

Gly Met Gln Ala Leu Leu Thr Met Gln Ser Gly Val Ile Thr Gln Arg
                 85                  90                  95

Gly Gly Ala Lys Ser Ala Asn Glu Ala His Arg Gln Trp Glu Thr Tyr
            100                 105                 110

Lys Ala Thr Ser Met His Met Gly Trp Tyr Met Phe Val Leu Asn Ala
        115                 120                 125

Leu Ile Leu Val Met Ile Leu Asn Glu Phe Arg Pro Asn Pro Leu Pro
    130                 135                 140

Gly Gly Phe Ile Ile Gly Leu Ile Gly Ile Ile Ala Ala Thr Ile Val
145                 150                 155                 160

Leu Leu Val Leu Ile Gly Lys Thr Thr Thr Ser Leu Ala Lys Lys Tyr
                165                 170                 175

Pro Met Pro Asp Gln Asp Gly Lys Thr Trp Gly Ile Phe Tyr Asn Asp
            180                 185                 190

Pro Asp Asp Asn Arg Ile Leu Val Asp
        195                 200


<210> 489
<211> 2187
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2164)
<223> RXN01071

<400> 489
cacctgaatt ggctgaggga gaggcaccga ctggcaccga agaggtgctt gcctcgaagg 60

cgggcgctga ggcgaatggc ctggagtagg ggaccagatc ttg gtc gtg gac tcc   115
                                              Leu Val Val Asp Ser
                                                1               5

agt ggc cgc tac aac gtc acc atc aca ggc ctg acc acc act gag acg   163
Ser Gly Arg Tyr Asn Val Thr Ile Thr Gly Leu Thr Thr Thr Glu Thr
                10                  15                  20

gat tcg gcc acc gcg ctg aac ctg cag atg tcg gaa gct ggc tac ctg   211
Asp Ser Ala Thr Ala Leu Asn Leu Gln Met Ser Glu Ala Gly Tyr Leu
            25                  30                  35

gag cgt tac acc gac ggg gct acc gtc ccc agc gtc atg ctg tcg gct   259
Glu Arg Tyr Thr Asp Gly Ala Thr Val Pro Ser Val Met Leu Ser Ala
```

```
         40                  45                  50

gca gat ggc acc acg cct caa gag ctt gtc gac gcc ctc gct gcc gaa   307
Ala Asp Gly Thr Thr Pro Gln Glu Leu Val Asp Ala Leu Ala Ala Glu
     55                  60                  65

ctt gga tcg aac ttt gat gta gaa acc ggc gaa gcg cta gtc gag cag   355
Leu Gly Ser Asn Phe Asp Val Glu Thr Gly Glu Ala Leu Val Glu Gln
 70                  75                  80                  85

gct aca gga atg atc acg cag gcc ttg agc ttc gtg cag tac ttc ctc   403
Ala Thr Gly Met Ile Thr Gln Ala Leu Ser Phe Val Gln Tyr Phe Leu
                 90                  95                 100

gtt gcc ttc ggt ctc att gca ctg ctg gtt ggt acc ttc atc atc gcg   451
Val Ala Phe Gly Leu Ile Ala Leu Leu Val Gly Thr Phe Ile Ile Ala
            105                 110                 115

aat acc ttc tcc atg att gtg gct cag cgc atg cgt gag ttc gct ctc   499
Asn Thr Phe Ser Met Ile Val Ala Gln Arg Met Arg Glu Phe Ala Leu
        120                 125                 130

ctg cga gcc ctg ggt gcg gcg cca gga cag atc act cgc tct gtg gtg   547
Leu Arg Ala Leu Gly Ala Ala Pro Gly Gln Ile Thr Arg Ser Val Val
    135                 140                 145

ctg gaa gca acc atc gtt ggc ctc ttc ggc tct gct ctt ggt gtg ctg   595
Leu Glu Ala Thr Ile Val Gly Leu Phe Gly Ser Ala Leu Gly Val Leu
150                 155                 160                 165

ggt ggt atg ggc ctc gta gcg atc att tca gct gtc ctc aat aac ctg   643
Gly Gly Met Gly Leu Val Ala Ile Ile Ser Ala Val Leu Asn Asn Leu
                170                 175                 180

ggc atg ccg atg gga tcc agc gtt ggc ttg act cct tct gca gtg gtt   691
Gly Met Pro Met Gly Ser Ser Val Gly Leu Thr Pro Ser Ala Val Val
            185                 190                 195

acc gcg ctc gta ttg ggc acc gtt gtc acc att gtg agc gcg tgg gct   739
Thr Ala Leu Val Leu Gly Thr Val Val Thr Ile Val Ser Ala Trp Ala
        200                 205                 210

ccg gct cgt cgt gca ggt gag gtt aag cct gtt gaa gcg atg cgc aac   787
Pro Ala Arg Arg Ala Gly Glu Val Lys Pro Val Glu Ala Met Arg Asn
    215                 220                 225

atg gaa acc acc act atg cgt tcc atg atg ggg cgc acg atc acc ggt   835
Met Glu Thr Thr Thr Met Arg Ser Met Met Gly Arg Thr Ile Thr Gly
230                 235                 240                 245

ggc atc gtt cta gca ctc ggc atc atc ttt gcg att gcc ggt gcg atg   883
Gly Ile Val Leu Ala Leu Gly Ile Ile Phe Ala Ile Ala Gly Ala Met
                250                 255                 260

atg act gat tct tcc acc gct act cgt tcc atc ctg gtg ggc att ggt   931
Met Thr Asp Ser Ser Thr Ala Thr Arg Ser Ile Leu Val Gly Ile Gly
            265                 270                 275

gca ctg ttt gtc atc gtg ggt acg ttc ctc ttc tca cca gcg ctc tcc   979
Ala Leu Phe Val Ile Val Gly Thr Phe Leu Phe Ser Pro Ala Leu Ser
        280                 285                 290
```

```
atg cct gtg gtg ggt ggc ctg ggc aag gtt atc ggt gca ccg ttt ggc   1027
Met Pro Val Val Gly Gly Leu Gly Lys Val Ile Gly Ala Pro Phe Gly
    295                 300                 305

agc gtt gga agc ctt gct gcg acc aac tcc aag cga aac cct cgc cgt   1075
Ser Val Gly Ser Leu Ala Ala Thr Asn Ser Lys Arg Asn Pro Arg Arg
310                 315                 320                 325

acc gca act aca gcg ttc gca ctg acg ttg ggc att gcc tta gtg act   1123
Thr Ala Thr Thr Ala Phe Ala Leu Thr Leu Gly Ile Ala Leu Val Thr
                330                 335                 340

gca att ggc atg ctt tct gca acc atg aag gac gca gtc tcc gac atg   1171
Ala Ile Gly Met Leu Ser Ala Thr Met Lys Asp Ala Val Ser Asp Met
            345                 350                 355

atg gcg gag cag tac acc gca gat tac atc ctg cag gga cca acc aac   1219
Met Ala Glu Gln Tyr Thr Ala Asp Tyr Ile Leu Gln Gly Pro Thr Asn
        360                 365                 370

ggt tcc atc acc atg ccg aag gaa tct gtc aat gat gtt cgc gat gct   1267
Gly Ser Ile Thr Met Pro Lys Glu Ser Val Asn Asp Val Arg Asp Ala
    375                 380                 385

gag ggc gtt gcc gat gtc gtg ctc gtt tcc atg aac tct gcc tcg gtg   1315
Glu Gly Val Ala Asp Val Val Leu Val Ser Met Asn Ser Ala Ser Val
390                 395                 400                 405

aac ggt cag gct tca tac agc cag ctg ggc cag tct gta acc ttt gtc   1363
Asn Gly Gln Ala Ser Tyr Ser Gln Leu Gly Gln Ser Val Thr Phe Val
                410                 415                 420

gct gac ggc gac ctg agc aag gtc atc agc aca gaa agc att gat ggc   1411
Ala Asp Gly Asp Leu Ser Lys Val Ile Ser Thr Glu Ser Ile Asp Gly
            425                 430                 435

tcc ctc gac ttg agc aac cca ggt gtt gtg act aac cag acg ttt gct   1459
Ser Leu Asp Leu Ser Asn Pro Gly Val Val Thr Asn Gln Thr Phe Ala
        440                 445                 450

gat gaa aac ggc tgg gca gta ggc gat act ctg cag ctt gaa tca atg   1507
Asp Glu Asn Gly Trp Ala Val Gly Asp Thr Leu Gln Leu Glu Ser Met
    455                 460                 465

ggg cag acc atc ggc gat atc gag ttg atc ggt acc ttc acc gga aac   1555
Gly Gln Thr Ile Gly Asp Ile Glu Leu Ile Gly Thr Phe Thr Gly Asn
470                 475                 480                 485

gac gcc atc gga aat atg atc atc tcc gaa agt tcc ttg gct gat aca   1603
Asp Ala Ile Gly Asn Met Ile Ile Ser Glu Ser Ser Leu Ala Asp Thr
                490                 495                 500

cca gcg gca gac act gct gtt cct cag atg atg ctg gtg gta ggc gaa   1651
Pro Ala Ala Asp Thr Ala Val Pro Gln Met Met Leu Val Val Gly Glu
            505                 510                 515

gaa ggc ttt gat aag gaa caa ctg cgc acc aac ttg gaa gac gca gtc   1699
Glu Gly Phe Asp Lys Glu Gln Leu Arg Thr Asn Leu Glu Asp Ala Val
        520                 525                 530
```

```
gct gat tac att gtc atc tct gtg aaa tca gca acc gag ttc gct ggt   1747
Ala Asp Tyr Ile Val Ile Ser Val Lys Ser Ala Thr Glu Phe Ala Gly
    535                 540                 545

gaa acg gtt gcg atg atc gac acc atg atg aac att ctg tac gcg ctg   1795
Glu Thr Val Ala Met Ile Asp Thr Met Met Asn Ile Leu Tyr Ala Leu
550                 555                 560                 565

ctt gct ctg tct gtc att gtt gcc atc atc ggc atc atc aac acc ctg   1843
Leu Ala Leu Ser Val Ile Val Ala Ile Ile Gly Ile Ile Asn Thr Leu
                570                 575                 580

gca ctg aat gtg atc gag cgt cgc cag gag atc ggt atg ctc cgc gca   1891
Ala Leu Asn Val Ile Glu Arg Arg Gln Glu Ile Gly Met Leu Arg Ala
            585                 590                 595

gtt ggc gtg aag cgc gga cag gtc cgc acc atg atc acc tta gaa tct   1939
Val Gly Val Lys Arg Gly Gln Val Arg Thr Met Ile Thr Leu Glu Ser
        600                 605                 610

gtt cag atc gcc atc tac ggt gct gtg att ggt atc gcg att ggt ctt   1987
Val Gln Ile Ala Ile Tyr Gly Ala Val Ile Gly Ile Ala Ile Gly Leu
    615                 620                 625

ggt ctg ggc tgg gcc ttt gtg aca gtg atg tca ggc gaa gga cta gac   2035
Gly Leu Gly Trp Ala Phe Val Thr Val Met Ser Gly Glu Gly Leu Asp
630                 635                 640                 645

gct gcg gtt agt atc ccg tgg ggt cag gtc gga ctg atg ctt gtt ggt   2083
Ala Ala Val Ser Ile Pro Trp Gly Gln Val Gly Leu Met Leu Val Gly
                650                 655                 660

tcc gct gta gtc ggt gtt atc gcc gcg ctg tgg ccg gca gtc aag gca   2131
Ser Ala Val Val Gly Val Ile Ala Ala Leu Trp Pro Ala Val Lys Ala
            665                 670                 675

tct agg aca cca cct ttg gat gcg att acc gac tagttttagc ggcagttgaa 2184
Ser Arg Thr Pro Pro Leu Asp Ala Ile Thr Asp
        680                 685

tca                                                               2187


<210> 490
<211> 688
<212> PRT
<213> Corynebacterium glutamicum

<400> 490
Leu Val Val Asp Ser Ser Gly Arg Tyr Asn Val Thr Ile Thr Gly Leu
  1               5                  10                  15

Thr Thr Thr Glu Thr Asp Ser Ala Thr Ala Leu Asn Leu Gln Met Ser
             20                  25                  30

Glu Ala Gly Tyr Leu Glu Arg Tyr Thr Asp Gly Ala Thr Val Pro Ser
         35                  40                  45

Val Met Leu Ser Ala Ala Asp Gly Thr Thr Pro Gln Glu Leu Val Asp
     50                  55                  60
```

```
Ala Leu Ala Ala Glu Leu Gly Ser Asn Phe Asp Val Glu Thr Gly Glu
 65                  70                  75                  80

Ala Leu Val Glu Gln Ala Thr Gly Met Ile Thr Gln Ala Leu Ser Phe
                85                  90                  95

Val Gln Tyr Phe Leu Val Ala Phe Gly Leu Ile Ala Leu Leu Val Gly
            100                 105                 110

Thr Phe Ile Ile Ala Asn Thr Phe Ser Met Ile Val Ala Gln Arg Met
        115                 120                 125

Arg Glu Phe Ala Leu Leu Arg Ala Leu Gly Ala Ala Pro Gly Gln Ile
    130                 135                 140

Thr Arg Ser Val Val Leu Glu Ala Thr Ile Val Gly Leu Phe Gly Ser
145                 150                 155                 160

Ala Leu Gly Val Leu Gly Gly Met Gly Leu Val Ala Ile Ile Ser Ala
                165                 170                 175

Val Leu Asn Asn Leu Gly Met Pro Met Gly Ser Ser Val Gly Leu Thr
            180                 185                 190

Pro Ser Ala Val Val Thr Ala Leu Val Leu Gly Thr Val Val Thr Ile
        195                 200                 205

Val Ser Ala Trp Ala Pro Ala Arg Arg Ala Gly Glu Val Lys Pro Val
    210                 215                 220

Glu Ala Met Arg Asn Met Glu Thr Thr Thr Met Arg Ser Met Met Gly
225                 230                 235                 240

Arg Thr Ile Thr Gly Gly Ile Val Leu Ala Leu Gly Ile Ile Phe Ala
                245                 250                 255

Ile Ala Gly Ala Met Met Thr Asp Ser Ser Thr Ala Thr Arg Ser Ile
            260                 265                 270

Leu Val Gly Ile Gly Ala Leu Phe Val Ile Val Gly Thr Phe Leu Phe
        275                 280                 285

Ser Pro Ala Leu Ser Met Pro Val Val Gly Gly Leu Gly Lys Val Ile
    290                 295                 300

Gly Ala Pro Phe Gly Ser Val Gly Ser Leu Ala Ala Thr Asn Ser Lys
305                 310                 315                 320

Arg Asn Pro Arg Arg Thr Ala Thr Thr Ala Phe Ala Leu Thr Leu Gly
                325                 330                 335

Ile Ala Leu Val Thr Ala Ile Gly Met Leu Ser Ala Thr Met Lys Asp
            340                 345                 350

Ala Val Ser Asp Met Met Ala Glu Gln Tyr Thr Ala Asp Tyr Ile Leu
        355                 360                 365

Gln Gly Pro Thr Asn Gly Ser Ile Thr Met Pro Lys Glu Ser Val Asn
    370                 375                 380

Asp Val Arg Asp Ala Glu Gly Val Ala Asp Val Val Leu Val Ser Met
```

385 390 395 400

Asn Ser Ala Ser Val Asn Gly Gln Ala Ser Tyr Ser Gln Leu Gly Gln
405 410 415

Ser Val Thr Phe Val Ala Asp Gly Asp Leu Ser Lys Val Ile Ser Thr
420 425 430

Glu Ser Ile Asp Gly Ser Leu Asp Leu Ser Asn Pro Gly Val Val Thr
435 440 445

Asn Gln Thr Phe Ala Asp Glu Asn Gly Trp Ala Val Gly Asp Thr Leu
450 455 460

Gln Leu Glu Ser Met Gly Gln Thr Ile Gly Asp Ile Glu Leu Ile Gly
465 470 475 480

Thr Phe Thr Gly Asn Asp Ala Ile Gly Asn Met Ile Ile Ser Glu Ser
485 490 495

Ser Leu Ala Asp Thr Pro Ala Ala Asp Thr Ala Val Pro Gln Met Met
500 505 510

Leu Val Val Gly Glu Glu Gly Phe Asp Lys Glu Gln Leu Arg Thr Asn
515 520 525

Leu Glu Asp Ala Val Ala Asp Tyr Ile Val Ile Ser Val Lys Ser Ala
530 535 540

Thr Glu Phe Ala Gly Glu Thr Val Ala Met Ile Asp Thr Met Met Asn
545 550 555 560

Ile Leu Tyr Ala Leu Leu Ala Leu Ser Val Ile Val Ala Ile Ile Gly
565 570 575

Ile Ile Asn Thr Leu Ala Leu Asn Val Ile Glu Arg Arg Gln Glu Ile
580 585 590

Gly Met Leu Arg Ala Val Gly Val Lys Arg Gly Gln Val Arg Thr Met
595 600 605

Ile Thr Leu Glu Ser Val Gln Ile Ala Ile Tyr Gly Ala Val Ile Gly
610 615 620

Ile Ala Ile Gly Leu Gly Leu Gly Trp Ala Phe Val Thr Val Met Ser
625 630 635 640

Gly Glu Gly Leu Asp Ala Ala Val Ser Ile Pro Trp Gly Gln Val Gly
645 650 655

Leu Met Leu Val Gly Ser Ala Val Val Gly Val Ile Ala Ala Leu Trp
660 665 670

Pro Ala Val Lys Ala Ser Arg Thr Pro Pro Leu Asp Ala Ile Thr Asp
675 680 685

<210> 491

<211> 1726
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1726)
<223> FRXA02898

<400> 491
cacctgaatt ggctgaggga gaggcaccga ctggcaccga agaggtgctt gcctcgaagg 60

cgggcgctga ggcgaatggc ctggagtagg ggaccagatc ttg gtc gtg gac tcc 115
Leu Val Val Asp Ser
1 5

agt ggc cgc tac aac gtc acc atc aca ggc ctg acc acc act gag acg 163
Ser Gly Arg Tyr Asn Val Thr Ile Thr Gly Leu Thr Thr Thr Glu Thr
10 15 20

gat tcg gcc acc gcg ctg aac ctg cag atg tcg gaa gct ggc tac ctg 211
Asp Ser Ala Thr Ala Leu Asn Leu Gln Met Ser Glu Ala Gly Tyr Leu
25 30 35

gag cgt tac acc gac ggg gct acc gtc ccc agc gtc atg ctg tcg gct 259
Glu Arg Tyr Thr Asp Gly Ala Thr Val Pro Ser Val Met Leu Ser Ala
40 45 50

gca gat ggc acc acg cct caa gag ctt gtc gac gcc ctc gct gcc gaa 307
Ala Asp Gly Thr Thr Pro Gln Glu Leu Val Asp Ala Leu Ala Ala Glu
55 60 65

ctt gga tcg aac ttt gat gta gaa acc ggc gaa gcg cta gtc gag cag 355
Leu Gly Ser Asn Phe Asp Val Glu Thr Gly Glu Ala Leu Val Glu Gln
70 75 80 85

gct aca gga atg atc acg cag gcc ttg agc ttc gtg cag tac ttc ctc 403
Ala Thr Gly Met Ile Thr Gln Ala Leu Ser Phe Val Gln Tyr Phe Leu
90 95 100

gtt gcc ttc ggt ctc att gca ctg ctg gtt ggt acc ttc atc atc gcg 451
Val Ala Phe Gly Leu Ile Ala Leu Leu Val Gly Thr Phe Ile Ile Ala
105 110 115

aat acc ttc tcc atg att gtg gct cag cgc atg cgt gag ttc gct ctc 499
Asn Thr Phe Ser Met Ile Val Ala Gln Arg Met Arg Glu Phe Ala Leu
120 125 130

ctg cga gcc ctg ggt gcg gcg cca gga cag atc act cgc tct gtg gtg 547
Leu Arg Ala Leu Gly Ala Ala Pro Gly Gln Ile Thr Arg Ser Val Val
135 140 145

ctg gaa gca acc atc gtt ggc ctc ttc ggc tct gct ctt ggt gtg ctg 595
Leu Glu Ala Thr Ile Val Gly Leu Phe Gly Ser Ala Leu Gly Val Leu
150 155 160 165

ggt ggt atg ggc ctc gta gcg atc att tca gct gtc ctc aat aac ctg 643
Gly Gly Met Gly Leu Val Ala Ile Ile Ser Ala Val Leu Asn Asn Leu
170 175 180

ggc atg ccg atg gga tcc agc gtt ggc ttg act cct tct gca gtg gtt 691

```
Gly Met Pro Met Gly Ser Ser Val Gly Leu Thr Pro Ser Ala Val Val
          185                 190                 195

acc gcg ctc gta ttg ggc acc gtt gtc acc att gtg agc gcg tgg gct   739
Thr Ala Leu Val Leu Gly Thr Val Val Thr Ile Val Ser Ala Trp Ala
        200                 205                 210

ccg gct cgt cgt gca ggt gag gtt aag cct gtt gaa gcg atg cgc aac   787
Pro Ala Arg Arg Ala Gly Glu Val Lys Pro Val Glu Ala Met Arg Asn
    215                 220                 225

atg gaa acc acc act atg cgt tcc atg atg ggg cgc acg atc acc ggt   835
Met Glu Thr Thr Thr Met Arg Ser Met Met Gly Arg Thr Ile Thr Gly
230                 235                 240                 245

ggc atc gtt cta gca ctc ggc atc atc ttt gcg att gcc ggt gcg atg   883
Gly Ile Val Leu Ala Leu Gly Ile Ile Phe Ala Ile Ala Gly Ala Met
                250                 255                 260

atg act gat tct tcc acc gct act cgt tcc atc ctg gtg ggc att ggt   931
Met Thr Asp Ser Ser Thr Ala Thr Arg Ser Ile Leu Val Gly Ile Gly
            265                 270                 275

gca ctg ttt gtc atc gtg ggt acg ttc ctc ttc tca cca gcg ctc tcc   979
Ala Leu Phe Val Ile Val Gly Thr Phe Leu Phe Ser Pro Ala Leu Ser
        280                 285                 290

atg cct gtg gtg ggt ggc ctg ggc aag gtt atc ggt gca ccg ttt ggc  1027
Met Pro Val Val Gly Gly Leu Gly Lys Val Ile Gly Ala Pro Phe Gly
    295                 300                 305

agc gtt gga agc ctt gct gcg acc aac tcc aag cga aac cct cgc cgt  1075
Ser Val Gly Ser Leu Ala Ala Thr Asn Ser Lys Arg Asn Pro Arg Arg
310                 315                 320                 325

acc gca act aca gcg ttc gca ctg acg ttg ggc att gcc tta gtg act  1123
Thr Ala Thr Thr Ala Phe Ala Leu Thr Leu Gly Ile Ala Leu Val Thr
                330                 335                 340

gca att ggc atg ctt tct gca acc atg aag gac gca gtc tcc gac atg  1171
Ala Ile Gly Met Leu Ser Ala Thr Met Lys Asp Ala Val Ser Asp Met
            345                 350                 355

atg gcg gag cag tac acc gca gat tac atc ctg cag gga cca acc aac  1219
Met Ala Glu Gln Tyr Thr Ala Asp Tyr Ile Leu Gln Gly Pro Thr Asn
        360                 365                 370

ggt tcc atc acc atg ccg aag gaa tct gtc aat gat gtt cgc gat gct  1267
Gly Ser Ile Thr Met Pro Lys Glu Ser Val Asn Asp Val Arg Asp Ala
    375                 380                 385

gag ggc gtt gcc gat gtc gtg ctc gtt tcc atg aac tct gcc tcg gtg  1315
Glu Gly Val Ala Asp Val Val Leu Val Ser Met Asn Ser Ala Ser Val
390                 395                 400                 405

aac ggt cag gct tca tac agc cag ctg ggc cag tct gta acc ttt gtc  1363
Asn Gly Gln Ala Ser Tyr Ser Gln Leu Gly Gln Ser Val Thr Phe Val
                410                 415                 420

gct gac ggc gac ctg agc aag gtc atc agc aca gaa agc att gat ggc  1411
Ala Asp Gly Asp Leu Ser Lys Val Ile Ser Thr Glu Ser Ile Asp Gly
```

```
            425                 430                 435

tcc ctc gac ttg agc aac cca ggt gtt gtg act aac cag acg ttt gct   1459
Ser Leu Asp Leu Ser Asn Pro Gly Val Val Thr Asn Gln Thr Phe Ala
        440                 445                 450

gat gaa aac ggc tgg gca gta ggc gat act ctg cag ctt gaa tca atg   1507
Asp Glu Asn Gly Trp Ala Val Gly Asp Thr Leu Gln Leu Glu Ser Met
    455                 460                 465

ggg cag acc atc ggc gat atc gag ttg atc ggt acc ttc acc gga aac   1555
Gly Gln Thr Ile Gly Asp Ile Glu Leu Ile Gly Thr Phe Thr Gly Asn
470                 475                 480                 485

gac gcc atc gga aat atg atc atc tcc gaa agt tcc ttg gct gat aca   1603
Asp Ala Ile Gly Asn Met Ile Ile Ser Glu Ser Ser Leu Ala Asp Thr
                490                 495                 500

cca gcg gca gac act gct gtt cct cag atg atg ctg gtg gta ggc gaa   1651
Pro Ala Ala Asp Thr Ala Val Pro Gln Met Met Leu Val Val Gly Glu
            505                 510                 515

gaa ggc ttt gat aag gaa caa ctg cgc acc aac ttg gaa gac gca gtc   1699
Glu Gly Phe Asp Lys Glu Gln Leu Arg Thr Asn Leu Glu Asp Ala Val
        520                 525                 530

gct gat tac att gtc atc tct gtg aaa                              1726
Ala Asp Tyr Ile Val Ile Ser Val Lys
    535                 540
```

<210> 492
<211> 542
<212> PRT
<213> Corynebacterium glutamicum

<400> 492

```
Leu Val Val Asp Ser Ser Gly Arg Tyr Asn Val Thr Ile Thr Gly Leu
  1               5                  10                  15

Thr Thr Thr Glu Thr Asp Ser Ala Thr Ala Leu Asn Leu Gln Met Ser
             20                  25                  30

Glu Ala Gly Tyr Leu Glu Arg Tyr Thr Asp Gly Ala Thr Val Pro Ser
         35                  40                  45

Val Met Leu Ser Ala Ala Asp Gly Thr Thr Pro Gln Glu Leu Val Asp
     50                  55                  60

Ala Leu Ala Ala Glu Leu Gly Ser Asn Phe Asp Val Glu Thr Gly Glu
 65                  70                  75                  80

Ala Leu Val Glu Gln Ala Thr Gly Met Ile Thr Gln Ala Leu Ser Phe
                 85                  90                  95

Val Gln Tyr Phe Leu Val Ala Phe Gly Leu Ile Ala Leu Leu Val Gly
            100                 105                 110

Thr Phe Ile Ile Ala Asn Thr Phe Ser Met Ile Val Ala Gln Arg Met
        115                 120                 125
```

```
Arg Glu Phe Ala Leu Leu Arg Ala Leu Gly Ala Ala Pro Gly Gln Ile
    130                 135                 140

Thr Arg Ser Val Val Leu Glu Ala Thr Ile Val Gly Leu Phe Gly Ser
145                 150                 155                 160

Ala Leu Gly Val Leu Gly Gly Met Gly Leu Val Ala Ile Ile Ser Ala
                165                 170                 175

Val Leu Asn Asn Leu Gly Met Pro Met Gly Ser Ser Val Gly Leu Thr
            180                 185                 190

Pro Ser Ala Val Val Thr Ala Leu Val Leu Gly Thr Val Val Thr Ile
        195                 200                 205

Val Ser Ala Trp Ala Pro Ala Arg Arg Ala Gly Glu Val Lys Pro Val
    210                 215                 220

Glu Ala Met Arg Asn Met Glu Thr Thr Thr Met Arg Ser Met Met Gly
225                 230                 235                 240

Arg Thr Ile Thr Gly Gly Ile Val Leu Ala Leu Gly Ile Ile Phe Ala
                245                 250                 255

Ile Ala Gly Ala Met Met Thr Asp Ser Ser Thr Ala Thr Arg Ser Ile
            260                 265                 270

Leu Val Gly Ile Gly Ala Leu Phe Val Ile Val Gly Thr Phe Leu Phe
        275                 280                 285

Ser Pro Ala Leu Ser Met Pro Val Val Gly Gly Leu Gly Lys Val Ile
    290                 295                 300

Gly Ala Pro Phe Gly Ser Val Gly Ser Leu Ala Ala Thr Asn Ser Lys
305                 310                 315                 320

Arg Asn Pro Arg Arg Thr Ala Thr Thr Ala Phe Ala Leu Thr Leu Gly
                325                 330                 335

Ile Ala Leu Val Thr Ala Ile Gly Met Leu Ser Ala Thr Met Lys Asp
            340                 345                 350

Ala Val Ser Asp Met Met Ala Glu Gln Tyr Thr Ala Asp Tyr Ile Leu
        355                 360                 365

Gln Gly Pro Thr Asn Gly Ser Ile Thr Met Pro Lys Glu Ser Val Asn
    370                 375                 380

Asp Val Arg Asp Ala Glu Gly Val Ala Asp Val Val Leu Val Ser Met
385                 390                 395                 400

Asn Ser Ala Ser Val Asn Gly Gln Ala Ser Tyr Ser Gln Leu Gly Gln
                405                 410                 415

Ser Val Thr Phe Val Ala Asp Gly Asp Leu Ser Lys Val Ile Ser Thr
            420                 425                 430

Glu Ser Ile Asp Gly Ser Leu Asp Leu Ser Asn Pro Gly Val Val Thr
        435                 440                 445

Asn Gln Thr Phe Ala Asp Glu Asn Gly Trp Ala Val Gly Asp Thr Leu
```

```
    450                 455                 460

Gln Leu Glu Ser Met Gly Gln Thr Ile Gly Asp Ile Glu Leu Ile Gly
465                 470                 475                 480

Thr Phe Thr Gly Asn Asp Ala Ile Gly Asn Met Ile Ile Ser Glu Ser
                485                 490                 495

Ser Leu Ala Asp Thr Pro Ala Ala Asp Thr Ala Val Pro Gln Met Met
            500                 505                 510

Leu Val Val Gly Glu Glu Gly Phe Asp Lys Glu Gln Leu Arg Thr Asn
        515                 520                 525

Leu Glu Asp Ala Val Ala Asp Tyr Ile Val Ile Ser Val Lys
    530                 535                 540


<210> 493
<211> 410
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(387)
<223> FRXA01071

<400> 493
aac att ctg tac gcg ctg ctt gct ctg tct gtc att gtt gcc atc atc   48
Asn Ile Leu Tyr Ala Leu Leu Ala Leu Ser Val Ile Val Ala Ile Ile
  1               5                  10                  15

ggc atc atc aac acc ctg gca ctg aat gtg atc gag cgt cgc cag gag   96
Gly Ile Ile Asn Thr Leu Ala Leu Asn Val Ile Glu Arg Arg Gln Glu
             20                  25                  30

atc ggt atg ctc cgc gca gtt ggc gtg aag cgc gga cag gtc cgc acc   144
Ile Gly Met Leu Arg Ala Val Gly Val Lys Arg Gly Gln Val Arg Thr
         35                  40                  45

atg atc acc tta gaa tct gtt cag atc gcc atc tac ggt gct gtg att   192
Met Ile Thr Leu Glu Ser Val Gln Ile Ala Ile Tyr Gly Ala Val Ile
     50                  55                  60

ggt atc gcg att ggt ctt ggt ctg ggc tgg gcc ttt gtg aca gtg atg   240
Gly Ile Ala Ile Gly Leu Gly Leu Gly Trp Ala Phe Val Thr Val Met
 65                  70                  75                  80

tca ggc gaa gga cta gac gct gcg gtt agt atc ccg tgg ggt cag gtc   288
Ser Gly Glu Gly Leu Asp Ala Ala Val Ser Ile Pro Trp Gly Gln Val
                 85                  90                  95

gga ctg atg ctt gtt ggt tcc gct gta gtc ggt gtt atc gcc gcg ctg   336
Gly Leu Met Leu Val Gly Ser Ala Val Val Gly Val Ile Ala Ala Leu
            100                 105                 110

tgg ccg gca gtc aag gca tct agg aca cca cct ttg gat gcg att acc   384
Trp Pro Ala Val Lys Ala Ser Arg Thr Pro Pro Leu Asp Ala Ile Thr
        115                 120                 125
```

gac tagttttagc ggcagttgaa tca 410
Asp

<210> 494
<211> 129
<212> PRT
<213> Corynebacterium glutamicum

<400> 494
Asn Ile Leu Tyr Ala Leu Leu Ala Leu Ser Val Ile Val Ala Ile Ile
1 5 10 15

Gly Ile Ile Asn Thr Leu Ala Leu Asn Val Ile Glu Arg Arg Gln Glu
20 25 30

Ile Gly Met Leu Arg Ala Val Gly Val Lys Arg Gly Gln Val Arg Thr
35 40 45

Met Ile Thr Leu Glu Ser Val Gln Ile Ala Ile Tyr Gly Ala Val Ile
50 55 60

Gly Ile Ala Ile Gly Leu Gly Leu Gly Trp Ala Phe Val Thr Val Met
65 70 75 80

Ser Gly Glu Gly Leu Asp Ala Ala Val Ser Ile Pro Trp Gly Gln Val
85 90 95

Gly Leu Met Leu Val Gly Ser Ala Val Val Gly Val Ile Ala Ala Leu
100 105 110

Trp Pro Ala Val Lys Ala Ser Arg Thr Pro Pro Leu Asp Ala Ile Thr
115 120 125

Asp

<210> 495
<211> 534
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(511)
<223> RXN01075

<400> 495
gcggtgcgtg ttcattagca ggtcaagcgc gtaattgagg gctagactgg ttagtaccgg 60

atattctttt tttctttagt ttgtgggagt ggagataact atg gac aat cca gtc 115
Met Asp Asn Pro Val
1 5

aac atc ctc aat gag cag gaa gct ttg gag cgc ctg cag tcg gtg tct 163
Asn Ile Leu Asn Glu Gln Glu Ala Leu Glu Arg Leu Gln Ser Val Ser
10 15 20

ctt ggt cgc gtg gtg gtt cgt cgc agc gat gag atg gac att ttc ccg 211

```
Leu Gly Arg Val Val Val Arg Arg Ser Asp Glu Met Asp Ile Phe Pro
            25                  30                  35

gtg aac ttc att gtg gat aag ggc gca att tac att cgt aca gct gag   259
Val Asn Phe Ile Val Asp Lys Gly Ala Ile Tyr Ile Arg Thr Ala Glu
        40                  45                  50

ggc aac aag ttg ttc agc atg aat ctc aac cac gat gtg ctc ttt gaa   307
Gly Asn Lys Leu Phe Ser Met Asn Leu Asn His Asp Val Leu Phe Glu
    55                  60                  65

gcc gat gag gtc aag gac gga aag gcc tgg tcc gtg gtg gtt cgt gcg   355
Ala Asp Glu Val Lys Asp Gly Lys Ala Trp Ser Val Val Val Arg Ala
70                  75                  80                  85

acc gca gag att gtg cgc aag ctg gat gag atc gct act gcc gac act   403
Thr Ala Glu Ile Val Arg Lys Leu Asp Glu Ile Ala Thr Ala Asp Thr
                90                  95                  100

ttg gag ttg aag cct tgg att cca acc ctg aag tcc aac ttt gcc cgt   451
Leu Glu Leu Lys Pro Trp Ile Pro Thr Leu Lys Ser Asn Phe Ala Arg
            105                 110                 115

att gtt ccg aat gaa atc act ggg cgg gag ttc acc ctc ggc gag gag   499
Ile Val Pro Asn Glu Ile Thr Gly Arg Glu Phe Thr Leu Gly Glu Glu
        120                 125                 130

cct gag cgc tac tagctttgcc acatttcact aaa                        534
Pro Glu Arg Tyr
    135
```

Sequence Listing Page 594 of 1144

<210> 496
<211> 137
<212> PRT
<213> Corynebacterium glutamicum

<400> 496

```
Met Asp Asn Pro Val Asn Ile Leu Asn Glu Gln Glu Ala Leu Glu Arg
  1               5                  10                  15

Leu Gln Ser Val Ser Leu Gly Arg Val Val Val Arg Arg Ser Asp Glu
            20                  25                  30

Met Asp Ile Phe Pro Val Asn Phe Ile Val Asp Lys Gly Ala Ile Tyr
        35                  40                  45

Ile Arg Thr Ala Glu Gly Asn Lys Leu Phe Ser Met Asn Leu Asn His
    50                  55                  60

Asp Val Leu Phe Glu Ala Asp Glu Val Lys Asp Gly Lys Ala Trp Ser
65                  70                  75                  80

Val Val Val Arg Ala Thr Ala Glu Ile Val Arg Lys Leu Asp Glu Ile
                85                  90                  95

Ala Thr Ala Asp Thr Leu Glu Leu Lys Pro Trp Ile Pro Thr Leu Lys
            100                 105                 110

Ser Asn Phe Ala Arg Ile Val Pro Asn Glu Ile Thr Gly Arg Glu Phe
        115                 120                 125
```

```
Thr Leu Gly Glu Glu Pro Glu Arg Tyr
    130                 135


<210> 497
<211> 534
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(511)
<223> FRXA01075

<400> 497
gcggtgcgtg ttcattagca ggtcaagcgc gtaattgagg gctagactgg ttagtaccgg 60

atattctttt tttctttagt ttgtgggagt ggagataact atg gac aat cca gtc   115
                                              Met Asp Asn Pro Val
                                                1               5

aac atc ctc aat gag cag gaa gct ttg gag cgc ctg cag tcg gtg tct   163
Asn Ile Leu Asn Glu Gln Glu Ala Leu Glu Arg Leu Gln Ser Val Ser
                10                  15                  20

ctt ggt cgc gtg gtg gtt cgt cgc agc gat gag atg gac att ttc ccg   211
Leu Gly Arg Val Val Val Arg Arg Ser Asp Glu Met Asp Ile Phe Pro
            25                  30                  35

gtg aac ttc att gtg gat aag ggc gca att tac att cgt aca gct gag   259
Val Asn Phe Ile Val Asp Lys Gly Ala Ile Tyr Ile Arg Thr Ala Glu
        40                  45                  50

ggc aac aag ttg ttc agc atg aat ctc aac cac gat gtg ctc ttt gaa   307
Gly Asn Lys Leu Phe Ser Met Asn Leu Asn His Asp Val Leu Phe Glu
    55                  60                  65

gcc gat gag gtc aag gac gga aag gcc tgg tcc gtg gtg gtt cgt gcg   355
Ala Asp Glu Val Lys Asp Gly Lys Ala Trp Ser Val Val Val Arg Ala
70                  75                  80                  85

acc gca gag att gtg cgc aag ctg gat gag atc gct act gcc gac act   403
Thr Ala Glu Ile Val Arg Lys Leu Asp Glu Ile Ala Thr Ala Asp Thr
                90                  95                 100

ttg gag ttg aag cct tgg att cca acc ctg aag tcc aac ttt gcc cgt   451
Leu Glu Leu Lys Pro Trp Ile Pro Thr Leu Lys Ser Asn Phe Ala Arg
            105                 110                 115

att gtt ccg aat gaa atc act ggg cgg gag ttc acc ctc ggc gag gag   499
Ile Val Pro Asn Glu Ile Thr Gly Arg Glu Phe Thr Leu Gly Glu Glu
        120                 125                 130

cct gag cgc tac tagctttgcc acatttcact aaa                        534
Pro Glu Arg Tyr
    135


<210> 498
<211> 137
```

<212> PRT
<213> Corynebacterium glutamicum

<400> 498
Met Asp Asn Pro Val Asn Ile Leu Asn Glu Gln Glu Ala Leu Glu Arg
1 5 10 15

Leu Gln Ser Val Ser Leu Gly Arg Val Val Val Arg Arg Ser Asp Glu
20 25 30

Met Asp Ile Phe Pro Val Asn Phe Ile Val Asp Lys Gly Ala Ile Tyr
35 40 45

Ile Arg Thr Ala Glu Gly Asn Lys Leu Phe Ser Met Asn Leu Asn His
50 55 60

Asp Val Leu Phe Glu Ala Asp Glu Val Lys Asp Gly Lys Ala Trp Ser
65 70 75 80

Val Val Val Arg Ala Thr Ala Glu Ile Val Arg Lys Leu Asp Glu Ile
85 90 95

Ala Thr Ala Asp Thr Leu Glu Leu Lys Pro Trp Ile Pro Thr Leu Lys
100 105 110

Ser Asn Phe Ala Arg Ile Val Pro Asn Glu Ile Thr Gly Arg Glu Phe
115 120 125

Thr Leu Gly Glu Glu Pro Glu Arg Tyr
130 135

<210> 499
<211> 1137
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1114)
<223> RXN01128

<400> 499
attcgagtac aaataaattt gagaacaaaa agatgggggg aaatatgtta aagtgcgtta 60

tattgcttta gcgaaagtaa cttccatgca tcaacgttcg atg agc ttc act ttc 115
Met Ser Phe Thr Phe
1 5

att cgt act ttt ttc gta ctt ttt ggc atc acg ttg tta gtg tca tgc 163
Ile Arg Thr Phe Phe Val Leu Phe Gly Ile Thr Leu Leu Val Ser Cys
10 15 20

gtt cca gag cct cct gac tcc tac act aaa gaa tcc act gtg ctg cgg 211
Val Pro Glu Pro Pro Asp Ser Tyr Thr Lys Glu Ser Thr Val Leu Arg
25 30 35

tat cag gtc tct gat ttc aat cta aac ttc gtg gaa tta gca gtt gcg 259
Tyr Gln Val Ser Asp Phe Asn Leu Asn Phe Val Glu Leu Ala Val Ala
40 45 50

```
ctt ggg tat ttg aac aac att gag ctc caa gta gtc gga tct gta caa   307
Leu Gly Tyr Leu Asn Asn Ile Glu Leu Gln Val Val Gly Ser Val Gln
     55                  60                  65

ggc ggc gtt gag tcc att gaa tcg ctc aaa aag gat gac att gac ttc   355
Gly Gly Val Glu Ser Ile Glu Ser Leu Lys Lys Asp Asp Ile Asp Phe
 70                  75                  80                  85

gcg gca gtc ccc ttc att ggc ctt gtt gca gga gag ata gcc acc ggt   403
Ala Ala Val Pro Phe Ile Gly Leu Val Ala Gly Glu Ile Ala Thr Gly
                90                  95                 100

gcg ccc atc aaa gca gtg gcc gca agt tac gga att tcc cac gat tct   451
Ala Pro Ile Lys Ala Val Ala Ala Ser Tyr Gly Ile Ser His Asp Ser
            105                 110                 115

tct tct gca ctt cta gtc ctt aaa gac agt gag ata cac gaa gtg cac   499
Ser Ser Ala Leu Leu Val Leu Lys Asp Ser Glu Ile His Glu Val His
        120                 125                 130

gat ctc att ggc aaa aca gtt ggc ata aac acc ctc ggt gct ctg gga   547
Asp Leu Ile Gly Lys Thr Val Gly Ile Asn Thr Leu Gly Ala Leu Gly
    135                 140                 145

tct gcg atg gtt gag cgt cat cta ttc gac gcc ggt ctc acc gaa cct   595
Ser Ala Met Val Glu Arg His Leu Phe Asp Ala Gly Leu Thr Glu Pro
150                 155                 160                 165

gag atc gtg agc gtc act caa cgt gca tta ccc ggt gag tac tta gaa   643
Glu Ile Val Ser Val Thr Gln Arg Ala Leu Pro Gly Glu Tyr Leu Glu
                170                 175                 180

caa cgc ctc tac cag ggg caa gtt gat gca att tgg gtc acc gat agc   691
Gln Arg Leu Tyr Gln Gly Gln Val Asp Ala Ile Trp Val Thr Asp Ser
            185                 190                 195

gct aaa cac caa gcg ctt gaa act gga gat ttt cgg atc ttg gca gag   739
Ala Lys His Gln Ala Leu Glu Thr Gly Asp Phe Arg Ile Leu Ala Glu
        200                 205                 210

gat tca gac ctt gtg cag gaa ctc aac act ggc tgc atg gtg gtg tcg   787
Asp Ser Asp Leu Val Gln Glu Leu Asn Thr Gly Cys Met Val Val Ser
    215                 220                 225

caa aaa ctc atc gac gag cac ccc gca gtg gtt gga gaa tta gtg gat   835
Gln Lys Leu Ile Asp Glu His Pro Ala Val Val Gly Glu Leu Val Asp
230                 235                 240                 245

gga gta gct cag gca atc gag ttt gaa cga tcc cac tcc cct gaa gaa   883
Gly Val Ala Gln Ala Ile Glu Phe Glu Arg Ser His Ser Pro Glu Glu
                250                 255                 260

gtg cgc gaa gtt tat ttc aac tac ctc gaa gcc cat ggt cag agt gat   931
Val Arg Glu Val Tyr Phe Asn Tyr Leu Glu Ala His Gly Gln Ser Asp
            265                 270                 275

aga ata tcc agc ttt aga tat tgg gag cat tcg ggc atc gca acc cga   979
Arg Ile Ser Ser Phe Arg Tyr Trp Glu His Ser Gly Ile Ala Thr Arg
        280                 285                 290

ggt gga gtg ctc agt gat agg gag ttc agc atg tgg tcc cac tgg att  1027
```

```
Gly Gly Val Leu Ser Asp Arg Glu Phe Ser Met Trp Ser His Trp Ile
    295                 300                 305

gac cgc caa tac gac gtc ccc gat atc aat cca gca agt att tac acc   1075
Asp Arg Gln Tyr Asp Val Pro Asp Ile Asn Pro Ala Ser Ile Tyr Thr
310                 315                 320                 325

aac caa ttc aac cca tac cga aaa gta aac ccc tcg cca taaaaggcaa    1124
Asn Gln Phe Asn Pro Tyr Arg Lys Val Asn Pro Ser Pro
                330                 335

gggggtcggc gtt                                                   1137


<210> 500
<211> 338
<212> PRT
<213> Corynebacterium glutamicum

<400> 500
Met Ser Phe Thr Phe Ile Arg Thr Phe Phe Val Leu Phe Gly Ile Thr
  1               5                  10                  15

Leu Leu Val Ser Cys Val Pro Glu Pro Pro Asp Ser Tyr Thr Lys Glu
             20                  25                  30

Ser Thr Val Leu Arg Tyr Gln Val Ser Asp Phe Asn Leu Asn Phe Val
         35                  40                  45

Glu Leu Ala Val Ala Leu Gly Tyr Leu Asn Asn Ile Glu Leu Gln Val
     50                  55                  60

Val Gly Ser Val Gln Gly Gly Val Glu Ser Ile Glu Ser Leu Lys Lys
 65                  70                  75                  80

Asp Asp Ile Asp Phe Ala Ala Val Pro Phe Ile Gly Leu Val Ala Gly
                 85                  90                  95

Glu Ile Ala Thr Gly Ala Pro Ile Lys Ala Val Ala Ala Ser Tyr Gly
            100                 105                 110

Ile Ser His Asp Ser Ser Ser Ala Leu Leu Val Leu Lys Asp Ser Glu
        115                 120                 125

Ile His Glu Val His Asp Leu Ile Gly Lys Thr Val Gly Ile Asn Thr
    130                 135                 140

Leu Gly Ala Leu Gly Ser Ala Met Val Glu Arg His Leu Phe Asp Ala
145                 150                 155                 160

Gly Leu Thr Glu Pro Glu Ile Val Ser Val Thr Gln Arg Ala Leu Pro
                165                 170                 175

Gly Glu Tyr Leu Glu Gln Arg Leu Tyr Gln Gly Gln Val Asp Ala Ile
            180                 185                 190

Trp Val Thr Asp Ser Ala Lys His Gln Ala Leu Glu Thr Gly Asp Phe
        195                 200                 205

Arg Ile Leu Ala Glu Asp Ser Asp Leu Val Gln Glu Leu Asn Thr Gly
    210                 215                 220
```

```
Cys Met Val Val Ser Gln Lys Leu Ile Asp Glu His Pro Ala Val Val
225                 230                 235                 240

Gly Glu Leu Val Asp Gly Val Ala Gln Ala Ile Glu Phe Glu Arg Ser
                245                 250                 255

His Ser Pro Glu Glu Val Arg Glu Val Tyr Phe Asn Tyr Leu Glu Ala
            260                 265                 270

His Gly Gln Ser Asp Arg Ile Ser Ser Phe Arg Tyr Trp Glu His Ser
        275                 280                 285

Gly Ile Ala Thr Arg Gly Gly Val Leu Ser Asp Arg Glu Phe Ser Met
    290                 295                 300

Trp Ser His Trp Ile Asp Arg Gln Tyr Asp Val Pro Asp Ile Asn Pro
305                 310                 315                 320

Ala Ser Ile Tyr Thr Asn Gln Phe Asn Pro Tyr Arg Lys Val Asn Pro
                325                 330                 335

Ser Pro
```

US 2004/0253679 A1 Dec. 16, 2004

<210> 501
<211> 1137
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1114)
<223> FRXA01128

<400> 501

```
attcgagtac aaataaattt gagaacaaaa agatgggggg aaatatgtta aagtgcgtta 60

tattgcttta gcgaaagtaa cttccatgca tcaacgttcg atg agc ttc act ttc   115
                                              Met Ser Phe Thr Phe
                                                1               5

att cgt act ttt ttc gta ctt ttt ggc atc acg ttg tta gtg tca tgc   163
Ile Arg Thr Phe Phe Val Leu Phe Gly Ile Thr Leu Leu Val Ser Cys
                10                  15                  20

gtt cca gag cct cct gac tcc tac act aaa gaa tcc act gtg ctg cgg   211
Val Pro Glu Pro Pro Asp Ser Tyr Thr Lys Glu Ser Thr Val Leu Arg
            25                  30                  35

tat cag gtc tct gat ttc aat cta aac ttc gtg gaa tta gca gtt gcg   259
Tyr Gln Val Ser Asp Phe Asn Leu Asn Phe Val Glu Leu Ala Val Ala
        40                  45                  50

ctt ggg tat ttg aac aac att gag ctc caa gta gtc gga tct gta caa   307
Leu Gly Tyr Leu Asn Asn Ile Glu Leu Gln Val Val Gly Ser Val Gln
    55                  60                  65

ggc ggc gtt gag tcc att gaa tcg ctc aaa aag gat gac att gac ttc   355
Gly Gly Val Glu Ser Ile Glu Ser Leu Lys Lys Asp Asp Ile Asp Phe
```

```
 70                  75                  80                  85

gcg gca gtc ccc ttc att ggc ctt gtt gca gga gag ata gcc acc ggt   403
Ala Ala Val Pro Phe Ile Gly Leu Val Ala Gly Glu Ile Ala Thr Gly
                90                  95                 100

gcg ccc atc aaa gca gtg gcc gca agt tac gga att tcc cac gat tct   451
Ala Pro Ile Lys Ala Val Ala Ala Ser Tyr Gly Ile Ser His Asp Ser
            105                 110                 115

tct tct gca ctt cta gtc ctt aaa gac agt gag ata cac gaa gtg cac   499
Ser Ser Ala Leu Leu Val Leu Lys Asp Ser Glu Ile His Glu Val His
        120                 125                 130

gat ctc att ggc aaa aca gtt ggc ata aac acc ctc ggt gct ctg gga   547
Asp Leu Ile Gly Lys Thr Val Gly Ile Asn Thr Leu Gly Ala Leu Gly
    135                 140                 145

tct gcg atg gtt gag cgt cat cta ttc gac gcc ggt ctc acc gaa cct   595
Ser Ala Met Val Glu Arg His Leu Phe Asp Ala Gly Leu Thr Glu Pro
150                 155                 160                 165

gag atc gtg agc gtc act caa cgt gca tta ccc ggt gag tac tta gaa   643
Glu Ile Val Ser Val Thr Gln Arg Ala Leu Pro Gly Glu Tyr Leu Glu
                170                 175                 180

caa cgc ctc tac cag ggg caa gtt gat gca att tgg gtc acc gat agc   691
Gln Arg Leu Tyr Gln Gly Gln Val Asp Ala Ile Trp Val Thr Asp Ser
            185                 190                 195

gct aaa cac caa gcg ctt gaa act gga gat ttt cgg atc ttg gca gag   739
Ala Lys His Gln Ala Leu Glu Thr Gly Asp Phe Arg Ile Leu Ala Glu
        200                 205                 210

gat tca gac ctt gtg cag gaa ctc aac act ggc tgc atg gtg gtg tcg   787
Asp Ser Asp Leu Val Gln Glu Leu Asn Thr Gly Cys Met Val Val Ser
    215                 220                 225

caa aaa ctc atc gac gag cac ccc gca gtg gtt gga gaa tta gtg gat   835
Gln Lys Leu Ile Asp Glu His Pro Ala Val Val Gly Glu Leu Val Asp
230                 235                 240                 245

gga gta gct cag gca atc gag ttt gaa cga tcc cac tcc cct gaa gaa   883
Gly Val Ala Gln Ala Ile Glu Phe Glu Arg Ser His Ser Pro Glu Glu
                250                 255                 260

gtg cgc gaa gtt tat ttc aac tac ctc gaa gcc cat ggt cag agt gat   931
Val Arg Glu Val Tyr Phe Asn Tyr Leu Glu Ala His Gly Gln Ser Asp
            265                 270                 275

aga ata tcc agc ttt aga tat tgg gag cat tcg ggc atc gca acc cga   979
Arg Ile Ser Ser Phe Arg Tyr Trp Glu His Ser Gly Ile Ala Thr Arg
        280                 285                 290

ggt gga gtg ctc agt gat agg gag ttc agc atg tgg tcc cac tgg att  1027
Gly Gly Val Leu Ser Asp Arg Glu Phe Ser Met Trp Ser His Trp Ile
    295                 300                 305

gac cgc caa tac gac gtc ccc gat atc aat cca gca agt att tac acc  1075
Asp Arg Gln Tyr Asp Val Pro Asp Ile Asn Pro Ala Ser Ile Tyr Thr
310                 315                 320                 325
```

```
aac caa ttc aac cca tac cga aaa gta aac ccc tcg cca taaaaggcaa    1124
Asn Gln Phe Asn Pro Tyr Arg Lys Val Asn Pro Ser Pro
                330                 335

gggggtcggc gtt                                                  1137
```

<210> 502
<211> 338
<212> PRT
<213> Corynebacterium glutamicum

<400> 502

```
Met Ser Phe Thr Phe Ile Arg Thr Phe Phe Val Leu Phe Gly Ile Thr
  1               5                  10                  15

Leu Leu Val Ser Cys Val Pro Glu Pro Pro Asp Ser Tyr Thr Lys Glu
            20                  25                  30

Ser Thr Val Leu Arg Tyr Gln Val Ser Asp Phe Asn Leu Asn Phe Val
         35                  40                  45

Glu Leu Ala Val Ala Leu Gly Tyr Leu Asn Asn Ile Glu Leu Gln Val
     50                  55                  60

Val Gly Ser Val Gln Gly Gly Val Glu Ser Ile Glu Ser Leu Lys Lys
 65                  70                  75                  80

Asp Asp Ile Asp Phe Ala Ala Val Pro Phe Ile Gly Leu Val Ala Gly
                85                  90                  95

Glu Ile Ala Thr Gly Ala Pro Ile Lys Ala Val Ala Ala Ser Tyr Gly
            100                 105                 110

Ile Ser His Asp Ser Ser Ser Ala Leu Leu Val Leu Lys Asp Ser Glu
        115                 120                 125

Ile His Glu Val His Asp Leu Ile Gly Lys Thr Val Gly Ile Asn Thr
    130                 135                 140

Leu Gly Ala Leu Gly Ser Ala Met Val Glu Arg His Leu Phe Asp Ala
145                 150                 155                 160

Gly Leu Thr Glu Pro Glu Ile Val Ser Val Thr Gln Arg Ala Leu Pro
                165                 170                 175

Gly Glu Tyr Leu Glu Gln Arg Leu Tyr Gln Gly Gln Val Asp Ala Ile
            180                 185                 190

Trp Val Thr Asp Ser Ala Lys His Gln Ala Leu Glu Thr Gly Asp Phe
        195                 200                 205

Arg Ile Leu Ala Glu Asp Ser Asp Leu Val Gln Glu Leu Asn Thr Gly
    210                 215                 220

Cys Met Val Val Ser Gln Lys Leu Ile Asp Glu His Pro Ala Val Val
225                 230                 235                 240

Gly Glu Leu Val Asp Gly Val Ala Gln Ala Ile Glu Phe Glu Arg Ser
                245                 250                 255
```

```
His Ser Pro Glu Glu Val Arg Glu Val Tyr Phe Asn Tyr Leu Glu Ala
            260                 265                 270

His Gly Gln Ser Asp Arg Ile Ser Ser Phe Arg Tyr Trp Glu His Ser
        275                 280                 285

Gly Ile Ala Thr Arg Gly Gly Val Leu Ser Asp Arg Glu Phe Ser Met
    290                 295                 300

Trp Ser His Trp Ile Asp Arg Gln Tyr Asp Val Pro Asp Ile Asn Pro
305                 310                 315                 320

Ala Ser Ile Tyr Thr Asn Gln Phe Asn Pro Tyr Arg Lys Val Asn Pro
                325                 330                 335

Ser Pro
```

<210> 503
<211> 871
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(871)
<223> RXN01134

<400> 503

```
gatatcttga acttgacgct ggctgaatac attcctgctg ccgatgaaat gatcaagggc 60

ttcgacgagg cggctgaatt cctgcgtcag cgatgcattt ttg agt ctc gac cag   115
                                              Leu Ser Leu Asp Gln
                                                1               5

gtt cca tac acc gcg cag att gtt cca ctg gcc gtg atc ctc acc ctg   163
Val Pro Tyr Thr Ala Gln Ile Val Pro Leu Ala Val Ile Leu Thr Leu
                10                  15                  20

ctt gat gca gaa gaa atg gcc acc gca cgt tca tgg gat cgt ttg aat   211
Leu Asp Ala Glu Glu Met Ala Thr Ala Arg Ser Trp Asp Arg Leu Asn
            25                  30                  35

cag tgg ttc tgg agc ggt gtc ttg ggt gag ctt tat ggc tcg cct gct   259
Gln Trp Phe Trp Ser Gly Val Leu Gly Glu Leu Tyr Gly Ser Pro Ala
        40                  45                  50

gtg atc gca cgt tcc ggt cgc gat acc gat caa gtt gct gcg tgg att   307
Val Ile Ala Arg Ser Gly Arg Asp Thr Asp Gln Val Ala Ala Trp Ile
    55                  60                  65

cgt gaa ggt gcc ggc gaa act gcg gtt gtg cca aag act att cgc gat   355
Arg Glu Gly Ala Gly Glu Thr Ala Val Val Pro Lys Thr Ile Arg Asp
70                  75                  80                  85

acc gtt ttc cac gaa tca cgt ctt ctc agt gca acc caa gac acc gga   403
Thr Val Phe His Glu Ser Arg Leu Leu Ser Ala Thr Gln Asp Thr Gly
                90                  95                  100
```

```
gtg tgg aag ggt atc ttc gca ctg ctc atg ggc agg gga gca cgc gac   451
Val Trp Lys Gly Ile Phe Ala Leu Leu Met Gly Arg Gly Ala Arg Asp
            105                 110                 115

tgg cgc acc gga cag cag ttt gat cgc tgg act ttt gat gag ctg ggt   499
Trp Arg Thr Gly Gln Gln Phe Asp Arg Trp Thr Phe Asp Glu Leu Gly
        120                 125                 130

tgc aat ttc cac cag att ttc ccc acc aaa tgg tgc aag gaa cgc ggc   547
Cys Asn Phe His Gln Ile Phe Pro Thr Lys Trp Cys Lys Glu Arg Gly
    135                 140                 145

atc gat cct gtc ctt acg gaa tca gta ctg aac cgc acc ccg atg ggt   595
Ile Asp Pro Val Leu Thr Glu Ser Val Leu Asn Arg Thr Pro Met Gly
150                 155                 160                 165

cgc cgt acc gaa gta gtc atc ggc gat acc cct cca tcc cgc tac ctg   643
Arg Arg Thr Glu Val Val Ile Gly Asp Thr Pro Pro Ser Arg Tyr Leu
                170                 175                 180

tct cgt gtt caa tcc aag tcg ctc atg ggt gat gag gaa ttc gat cag   691
Ser Arg Val Gln Ser Lys Ser Leu Met Gly Asp Glu Glu Phe Asp Gln
            185                 190                 195

atg ctg gat acc cac ctg ctc agc gcg gaa gac ctg cac agt tcc aac   739
Met Leu Asp Thr His Leu Leu Ser Ala Glu Asp Leu His Ser Ser Asn
        200                 205                 210

acc acg cac ttc ttt gct tct cga cgc acc aac ttc atc gac atg gtc   787
Thr Thr His Phe Phe Ala Ser Arg Arg Thr Asn Phe Ile Asp Met Val
    215                 220                 225

gag gat gcc atc ggt aaa gcg gtg atc agg gac gtc aac gag tca gat   835
Glu Asp Ala Ile Gly Lys Ala Val Ile Arg Asp Val Asn Glu Ser Asp
230                 235                 240                 245

ctc acc ggt gga cac gat ggt ccc tcg gta cac ggg                   871
Leu Thr Gly Gly His Asp Gly Pro Ser Val His Gly
                250                 255
```

Sequence Listing Page 603 of 2744

<210> 504
<211> 257
<212> PRT
<213> Corynebacterium glutamicum

<400> 504

```
Leu Ser Leu Asp Gln Val Pro Tyr Thr Ala Gln Ile Val Pro Leu Ala
  1               5                  10                  15

Val Ile Leu Thr Leu Leu Asp Ala Glu Glu Met Ala Thr Ala Arg Ser
             20                  25                  30

Trp Asp Arg Leu Asn Gln Trp Phe Trp Ser Gly Val Leu Gly Glu Leu
         35                  40                  45

Tyr Gly Ser Pro Ala Val Ile Ala Arg Ser Gly Arg Asp Thr Asp Gln
     50                  55                  60

Val Ala Ala Trp Ile Arg Glu Gly Ala Gly Glu Thr Ala Val Val Pro
 65                  70                  75                  80
```

```
Lys Thr Ile Arg Asp Thr Val Phe His Glu Ser Arg Leu Leu Ser Ala
                85                  90                  95

Thr Gln Asp Thr Gly Val Trp Lys Gly Ile Phe Ala Leu Leu Met Gly
            100                 105                 110

Arg Gly Ala Arg Asp Trp Arg Thr Gly Gln Gln Phe Asp Arg Trp Thr
        115                 120                 125

Phe Asp Glu Leu Gly Cys Asn Phe His Gln Ile Phe Pro Thr Lys Trp
    130                 135                 140

Cys Lys Glu Arg Gly Ile Asp Pro Val Leu Thr Glu Ser Val Leu Asn
145                 150                 155                 160

Arg Thr Pro Met Gly Arg Arg Thr Glu Val Val Ile Gly Asp Thr Pro
                165                 170                 175

Pro Ser Arg Tyr Leu Ser Arg Val Gln Ser Lys Ser Leu Met Gly Asp
            180                 185                 190

Glu Glu Phe Asp Gln Met Leu Asp Thr His Leu Leu Ser Ala Glu Asp
        195                 200                 205

Leu His Ser Ser Asn Thr Thr His Phe Phe Ala Ser Arg Arg Thr Asn
    210                 215                 220

Phe Ile Asp Met Val Glu Asp Ala Ile Gly Lys Ala Val Ile Arg Asp
225                 230                 235                 240

Val Asn Glu Ser Asp Leu Thr Gly Gly His Asp Gly Pro Ser Val His
                245                 250                 255

Gly
```

Document ID: US 20030175845 A1

<210> 505
<211> 459
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(459)
<223> FRXA01134

<400> 505

```
agt gca acc caa gac acc gga gtg tgg aag ggt atc ttc gca ctg ctc   48
Ser Ala Thr Gln Asp Thr Gly Val Trp Lys Gly Ile Phe Ala Leu Leu
  1               5                  10                  15

atg ggc agg gga gca cgc gac tgg cgc acc gga cag cag ttt gat cgc   96
Met Gly Arg Gly Ala Arg Asp Trp Arg Thr Gly Gln Gln Phe Asp Arg
             20                  25                  30

tgg act ttt gat gag ctg ggt tgc aat ttc cac cag att ttc ccc acc   144
Trp Thr Phe Asp Glu Leu Gly Cys Asn Phe His Gln Ile Phe Pro Thr
         35                  40                  45
```

```
aaa tgg tgc aag gaa cgc ggc atc gat cct gtc ctt acg gaa tca gta   192
Lys Trp Cys Lys Glu Arg Gly Ile Asp Pro Val Leu Thr Glu Ser Val
     50                  55                  60

ctg aac cgc acc ccg atg ggt cgc cgt acc gaa gta gtc atc ggc gat   240
Leu Asn Arg Thr Pro Met Gly Arg Arg Thr Glu Val Val Ile Gly Asp
 65                  70                  75                  80

acc cct cca tcc cgc tac ctg tct cgt gtt caa tcc aag tcg ctc atg   288
Thr Pro Pro Ser Arg Tyr Leu Ser Arg Val Gln Ser Lys Ser Leu Met
                85                  90                  95

ggt gat gag gaa ttc gat cag atg ctg gat acc cac ctg ctc agc gcg   336
Gly Asp Glu Glu Phe Asp Gln Met Leu Asp Thr His Leu Leu Ser Ala
            100                 105                 110

gaa gac ctg cac agt tcc aac acc acg cac ttc ttt gct tct cga cgc   384
Glu Asp Leu His Ser Ser Asn Thr Thr His Phe Phe Ala Ser Arg Arg
        115                 120                 125

acc aac ttc atc gac atg gtc gag gat gcc atc ggt aaa gcg gtg atc   432
Thr Asn Phe Ile Asp Met Val Glu Asp Ala Ile Gly Lys Ala Val Ile
    130                 135                 140

agg gac gtc aac gag tca gat ctc acc                              459
Arg Asp Val Asn Glu Ser Asp Leu Thr
145                 150
```

Sequence Listing - Page 605 of 1000

<210> 506
<211> 153
<212> PRT
<213> Corynebacterium glutamicum

<400> 506

```
Ser Ala Thr Gln Asp Thr Gly Val Trp Lys Gly Ile Phe Ala Leu Leu
  1               5                  10                  15

Met Gly Arg Gly Ala Arg Asp Trp Arg Thr Gly Gln Gln Phe Asp Arg
             20                  25                  30

Trp Thr Phe Asp Glu Leu Gly Cys Asn Phe His Gln Ile Phe Pro Thr
         35                  40                  45

Lys Trp Cys Lys Glu Arg Gly Ile Asp Pro Val Leu Thr Glu Ser Val
     50                  55                  60

Leu Asn Arg Thr Pro Met Gly Arg Arg Thr Glu Val Val Ile Gly Asp
 65                  70                  75                  80

Thr Pro Pro Ser Arg Tyr Leu Ser Arg Val Gln Ser Lys Ser Leu Met
                85                  90                  95

Gly Asp Glu Glu Phe Asp Gln Met Leu Asp Thr His Leu Leu Ser Ala
            100                 105                 110

Glu Asp Leu His Ser Ser Asn Thr Thr His Phe Phe Ala Ser Arg Arg
        115                 120                 125

Thr Asn Phe Ile Asp Met Val Glu Asp Ala Ile Gly Lys Ala Val Ile
    130                 135                 140
```

```
Arg Asp Val Asn Glu Ser Asp Leu Thr
145                 150


<210> 507
<211> 1056
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1033)
<223> RXN01140

<400> 507
tatccaactt cccgattttc aacgggatta cgcttgggat gttgatcgca tccgaagcct 60

tataaccact gttcttcgtg gttttccagt aggtgtgctg atg gca cta gac acc   115
                                            Met Ala Leu Asp Thr
                                              1               5

cgc ggc gag gaa atg cgt ttc cgg cca cgc gcg ctg tcc ggc gcc cca   163
Arg Gly Glu Glu Met Arg Phe Arg Pro Arg Ala Leu Ser Gly Ala Pro
                10                  15                  20

gat acg ggc aag gat cca ggt ctt ttg ctt ctc gac gga caa cag cgc   211
Asp Thr Gly Lys Asp Pro Gly Leu Leu Leu Leu Asp Gly Gln Gln Arg
            25                  30                  35

ctc acc acc ctt tat cat tgc ttc agt ggc gat ggc tat gta aat acg   259
Leu Thr Thr Leu Tyr His Cys Phe Ser Gly Asp Gly Tyr Val Asn Thr
        40                  45                  50

gtg gac ttc cga tca aag aaa gtg acc cgg aag ttt tat att gat gtt   307
Val Asp Phe Arg Ser Lys Lys Val Thr Arg Lys Phe Tyr Ile Asp Val
    55                  60                  65

gct aag gct gtt gaa tct ccg gtc atg tcc gat gag gct att ttt tca   355
Ala Lys Ala Val Glu Ser Pro Val Met Ser Asp Glu Ala Ile Phe Ser
70                  75                  80                  85

gtc gac gaa acc ggc aaa atc atc tcc cac ttc ggt cca gtg atc gac   403
Val Asp Glu Thr Gly Lys Ile Ile Ser His Phe Gly Pro Val Ile Asp
                90                  95                  100

ggc ggc atc acc gat tta gaa aca gca ctt gct cat ggt tgc ctt cca   451
Gly Gly Ile Thr Asp Leu Glu Thr Ala Leu Ala His Gly Cys Leu Pro
            105                 110                 115

gtt tct gtg ctg ctg gat gat aac ggc act gat ttc ctc ttt gac ctc   499
Val Ser Val Leu Leu Asp Asp Asn Gly Thr Asp Phe Leu Phe Asp Leu
        120                 125                 130

gcc gat atg gca gga gaa ggc gct cgc gaa cac gcg aag cgc ttc caa   547
Ala Asp Met Ala Gly Glu Gly Ala Arg Glu His Ala Lys Arg Phe Gln
    135                 140                 145

tca caa atc gtt aag acc tta gtt agt tac gac atc cca atg atc cga   595
Ser Gln Ile Val Lys Thr Leu Val Ser Tyr Asp Ile Pro Met Ile Arg
150                 155                 160                 165
```

```
ctg gat cgt gaa acc gcc aag ggt gga att ggt tcc atc ttt gct cag   643
Leu Asp Arg Glu Thr Ala Lys Gly Gly Ile Gly Ser Ile Phe Ala Gln
                170                 175                 180

gcc aat agc tct ggc ttg cag atg gat gtc ttt gat ttg ctc acc gcg   691
Ala Asn Ser Ser Gly Leu Gln Met Asp Val Phe Asp Leu Leu Thr Ala
            185                 190                 195

gtg ttc gca gcc gat gaa tcg gtg gag acc gaa ttc tca ctg cgt gat   739
Val Phe Ala Ala Asp Glu Ser Val Glu Thr Glu Phe Ser Leu Arg Asp
        200                 205                 210

gac tgg gtg cgg gtt gaa cga aac ctt cgc caa cac tcc gca ctt gat   787
Asp Trp Val Arg Val Glu Arg Asn Leu Arg Gln His Ser Ala Leu Asp
    215                 220                 225

ggc atc ggc agc acg gag ttc ctc acc gca gta gcc ctg ttg gtc agt   835
Gly Ile Gly Ser Thr Glu Phe Leu Thr Ala Val Ala Leu Leu Val Ser
230                 235                 240                 245

gcc cgc aag gga cat gcg tct ggt tac cgt gaa gat atc ttg aac ttg   883
Ala Arg Lys Gly His Ala Ser Gly Tyr Arg Glu Asp Ile Leu Asn Leu
                250                 255                 260

acg ctg gct gaa tac att cct gct gcc gat gaa atg atc aag ggc ttc   931
Thr Leu Ala Glu Tyr Ile Pro Ala Ala Asp Glu Met Ile Lys Gly Phe
            265                 270                 275

gac gag gcg gct gaa ttc ctg cgt cag cga tgc att ttt gag tct cga   979
Asp Glu Ala Ala Glu Phe Leu Arg Gln Arg Cys Ile Phe Glu Ser Arg
        280                 285                 290

cca ggt tcc ata cac cgc gca gat tgt tcc act ggc cgt gat cct cac   1027
Pro Gly Ser Ile His Arg Ala Asp Cys Ser Thr Gly Arg Asp Pro His
    295                 300                 305

cct gct tgatgcagaa gaaatggcca ccg                                1056
Pro Ala
310
```

<210> 508
<211> 311
<212> PRT
<213> Corynebacterium glutamicum

<400> 508

```
Met Ala Leu Asp Thr Arg Gly Glu Glu Met Arg Phe Arg Pro Arg Ala
  1               5                  10                  15

Leu Ser Gly Ala Pro Asp Thr Gly Lys Asp Pro Gly Leu Leu Leu Leu
             20                  25                  30

Asp Gly Gln Gln Arg Leu Thr Thr Leu Tyr His Cys Phe Ser Gly Asp
         35                  40                  45

Gly Tyr Val Asn Thr Val Asp Phe Arg Ser Lys Lys Val Thr Arg Lys
     50                  55                  60

Phe Tyr Ile Asp Val Ala Lys Ala Val Glu Ser Pro Val Met Ser Asp
```

```
 65                  70                  75                  80

Glu Ala Ile Phe Ser Val Asp Glu Thr Gly Lys Ile Ile Ser His Phe
                 85                  90                  95

Gly Pro Val Ile Asp Gly Gly Ile Thr Asp Leu Glu Thr Ala Leu Ala
            100                 105                 110

His Gly Cys Leu Pro Val Ser Val Leu Leu Asp Asp Asn Gly Thr Asp
        115                 120                 125

Phe Leu Phe Asp Leu Ala Asp Met Ala Gly Glu Gly Ala Arg Glu His
    130                 135                 140

Ala Lys Arg Phe Gln Ser Gln Ile Val Lys Thr Leu Val Ser Tyr Asp
145                 150                 155                 160

Ile Pro Met Ile Arg Leu Asp Arg Glu Thr Ala Lys Gly Gly Ile Gly
                165                 170                 175

Ser Ile Phe Ala Gln Ala Asn Ser Ser Gly Leu Gln Met Asp Val Phe
            180                 185                 190

Asp Leu Leu Thr Ala Val Phe Ala Ala Asp Glu Ser Val Glu Thr Glu
        195                 200                 205

Phe Ser Leu Arg Asp Asp Trp Val Arg Val Glu Arg Asn Leu Arg Gln
    210                 215                 220

His Ser Ala Leu Asp Gly Ile Gly Ser Thr Glu Phe Leu Thr Ala Val
225                 230                 235                 240

Ala Leu Leu Val Ser Ala Arg Lys Gly His Ala Ser Gly Tyr Arg Glu
                245                 250                 255

Asp Ile Leu Asn Leu Thr Leu Ala Glu Tyr Ile Pro Ala Ala Asp Glu
            260                 265                 270

Met Ile Lys Gly Phe Asp Glu Ala Ala Glu Phe Leu Arg Gln Arg Cys
        275                 280                 285

Ile Phe Glu Ser Arg Pro Gly Ser Ile His Arg Ala Asp Cys Ser Thr
    290                 295                 300

Gly Arg Asp Pro His Pro Ala
305                 310


<210> 509
<211> 886
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(886)
<223> FRXA01140

<400> 509
tatccaactt cccgattttc aacgggatta cgcttgggat gttgatcgca tccgaagcct 60
```

```
tataaccact gttcttcgtg gttttccagt aggtgtgctg atg gca cta gac acc   115
                                              Met Ala Leu Asp Thr
                                                1               5

cgc ggc gag gaa atg cgt ttc cgg cca cgc gcg ctg tcc ggc gcc cca   163
Arg Gly Glu Glu Met Arg Phe Arg Pro Arg Ala Leu Ser Gly Ala Pro
                10                  15                  20

gat acg ggc aag gat cca ggt ctt ttg ctt ctc gac gga caa cag cgc   211
Asp Thr Gly Lys Asp Pro Gly Leu Leu Leu Leu Asp Gly Gln Gln Arg
            25                  30                  35

ctc acc acc ctt tat cat tgc ttc agt ggc gat ggc tat gta aat acg   259
Leu Thr Thr Leu Tyr His Cys Phe Ser Gly Asp Gly Tyr Val Asn Thr
        40                  45                  50

gtg gac ttc cga tca aag aaa gtg acc cgg aag ttt tat att gat gtt   307
Val Asp Phe Arg Ser Lys Lys Val Thr Arg Lys Phe Tyr Ile Asp Val
    55                  60                  65

gct aag gct gtt gaa tct ccg gtc atg tcc gat gag gct att ttt tca   355
Ala Lys Ala Val Glu Ser Pro Val Met Ser Asp Glu Ala Ile Phe Ser
70                  75                  80                  85

gtc gac gaa acc ggc aaa atc atc tcc cac ttc ggt cca gtg atc gac   403
Val Asp Glu Thr Gly Lys Ile Ile Ser His Phe Gly Pro Val Ile Asp
                90                  95                  100

ggc ggc atc acc gat tta gaa aca gca ctt gct cat ggt tgc ctt cca   451
Gly Gly Ile Thr Asp Leu Glu Thr Ala Leu Ala His Gly Cys Leu Pro
            105                 110                 115

gtt tct gtg ctg ctg gat gat aac ggc act gat ttc ctc ttt gac ctc   499
Val Ser Val Leu Leu Asp Asp Asn Gly Thr Asp Phe Leu Phe Asp Leu
        120                 125                 130

gcc gat atg gca gga gaa ggc gct cgc gaa cac gcg aag cgc ttc caa   547
Ala Asp Met Ala Gly Glu Gly Ala Arg Glu His Ala Lys Arg Phe Gln
    135                 140                 145

tca caa atc gtt aag acc tta gtt agt tac gac atc cca atg atc cga   595
Ser Gln Ile Val Lys Thr Leu Val Ser Tyr Asp Ile Pro Met Ile Arg
150                 155                 160                 165

ctg gat cgt gaa acc gcc aag ggt gga att ggt tcc atc ttt gct cag   643
Leu Asp Arg Glu Thr Ala Lys Gly Gly Ile Gly Ser Ile Phe Ala Gln
                170                 175                 180

gcc aat agc tct ggc ttg cag atg gat gtc ttt gat ttg ctc acc gcg   691
Ala Asn Ser Ser Gly Leu Gln Met Asp Val Phe Asp Leu Leu Thr Ala
            185                 190                 195

gtg ttc gca gcc gat gaa tcg gtg gag acc gaa ttc tca ctg cgt gat   739
Val Phe Ala Ala Asp Glu Ser Val Glu Thr Glu Phe Ser Leu Arg Asp
        200                 205                 210

gac tgg gtg cgg gtt gaa cga aac ctt cgc caa cac tcc gca ctt gat   787
Asp Trp Val Arg Val Glu Arg Asn Leu Arg Gln His Ser Ala Leu Asp
    215                 220                 225

ggc atc ggc agc acg gag ttc ctc acc gca gta gcc ctg ttg gtc agt   835
```

```
Gly Ile Gly Ser Thr Glu Phe Leu Thr Ala Val Ala Leu Leu Val Ser
230                 235                 240                 245

gcc cgc aag gga cat gcg tct ggt tac cgt gaa gat atc ttg aac ttg   883
Ala Arg Lys Gly His Ala Ser Gly Tyr Arg Glu Asp Ile Leu Asn Leu
                250                 255                 260

acg                                                               886
Thr
```

<210> 510
<211> 262
<212> PRT
<213> Corynebacterium glutamicum

<400> 510

```
Met Ala Leu Asp Thr Arg Gly Glu Glu Met Arg Phe Arg Pro Arg Ala
  1               5                  10                  15

Leu Ser Gly Ala Pro Asp Thr Gly Lys Asp Pro Gly Leu Leu Leu Leu
             20                  25                  30

Asp Gly Gln Gln Arg Leu Thr Thr Leu Tyr His Cys Phe Ser Gly Asp
         35                  40                  45

Gly Tyr Val Asn Thr Val Asp Phe Arg Ser Lys Lys Val Thr Arg Lys
     50                  55                  60

Phe Tyr Ile Asp Val Ala Lys Ala Val Glu Ser Pro Val Met Ser Asp
 65                  70                  75                  80

Glu Ala Ile Phe Ser Val Asp Glu Thr Gly Lys Ile Ile Ser His Phe
                 85                  90                  95

Gly Pro Val Ile Asp Gly Gly Ile Thr Asp Leu Glu Thr Ala Leu Ala
            100                 105                 110

His Gly Cys Leu Pro Val Ser Val Leu Leu Asp Asp Asn Gly Thr Asp
        115                 120                 125

Phe Leu Phe Asp Leu Ala Asp Met Ala Gly Glu Gly Ala Arg Glu His
    130                 135                 140

Ala Lys Arg Phe Gln Ser Gln Ile Val Lys Thr Leu Val Ser Tyr Asp
145                 150                 155                 160

Ile Pro Met Ile Arg Leu Asp Arg Glu Thr Ala Lys Gly Gly Ile Gly
                165                 170                 175

Ser Ile Phe Ala Gln Ala Asn Ser Ser Gly Leu Gln Met Asp Val Phe
            180                 185                 190

Asp Leu Leu Thr Ala Val Phe Ala Ala Asp Glu Ser Val Glu Thr Glu
        195                 200                 205

Phe Ser Leu Arg Asp Asp Trp Val Arg Val Glu Arg Asn Leu Arg Gln
    210                 215                 220

His Ser Ala Leu Asp Gly Ile Gly Ser Thr Glu Phe Leu Thr Ala Val
```

```
225                 230                 235                 240

Ala Leu Leu Val Ser Ala Arg Lys Gly His Ala Ser Gly Tyr Arg Glu
                245                 250                 255

Asp Ile Leu Asn Leu Thr
            260


<210> 511
<211> 723
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(700)
<223> RXN01148

<400> 511
atagaacaag ggtagccaaa ttcttggaaa cagcgcgggc ccccgaatcc acaatgcgaa 60

tccacaatgt cacctgaagc cgttaaagta ggtgatcatt atg acc agc cca gtt   115
                                            Met Thr Ser Pro Val
                                              1               5

gaa aac gtt aag aaa aag cca cgc cca ttg gcg ctg tca ccg tcg cgc   163
Glu Asn Val Lys Lys Lys Pro Arg Pro Leu Ala Leu Ser Pro Ser Arg
                10                  15                  20

gcc ggg gat tac cag cag tgt ccc ctg ttg tat cgc ttc cgc gcg att   211
Ala Gly Asp Tyr Gln Gln Cys Pro Leu Leu Tyr Arg Phe Arg Ala Ile
            25                  30                  35

gat cgc ctg cca gag cct aag acc gtc gcc cag gtc aaa ggc acg ttg   259
Asp Arg Leu Pro Glu Pro Lys Thr Val Ala Gln Val Lys Gly Thr Leu
        40                  45                  50

gtg cac gct gtg ttg gaa tat atg cac aag ttg ccg cgt gaa gaa cgc   307
Val His Ala Val Leu Glu Tyr Met His Lys Leu Pro Arg Glu Glu Arg
    55                  60                  65

gaa tat cca gcc atg gtg aag caa ctc aag ccc acc tgg gcg cag atg   355
Glu Tyr Pro Ala Met Val Lys Gln Leu Lys Pro Thr Trp Ala Gln Met
70                  75                  80                  85

tgt gaa gaa gac gca gag ctc aaa gag ctt gtt cca gaa gat gag ctt   403
Cys Glu Glu Asp Ala Glu Leu Lys Glu Leu Val Pro Glu Asp Glu Leu
                90                  95                  100

tat gat ttc ctc gtg gat tcc cgc acc ctg ctg cgt ggc tac ttt gaa   451
Tyr Asp Phe Leu Val Asp Ser Arg Thr Leu Leu Arg Gly Tyr Phe Glu
            105                 110                 115

atg gaa aat cct caa ggt ttc gac gcc acc gaa tgc gaa atg tac gtg   499
Met Glu Asn Pro Gln Gly Phe Asp Ala Thr Glu Cys Glu Met Tyr Val
        120                 125                 130

gac act gtg ctg ccc aac ggc gtt cct gtt cgt ggt ttt atc gac cgt   547
Asp Thr Val Leu Pro Asn Gly Val Pro Val Arg Gly Phe Ile Asp Arg
    135                 140                 145
```

```
gtg gat acc gcc cca ccg gcc aag tcc gag tta tcg act aca aga ctg   595
Val Asp Thr Ala Pro Pro Ala Lys Ser Glu Leu Ser Thr Thr Arg Leu
150                 155                 160                 165

gca aga aac caa agc cgc agt gga gcc agc aag cgc agt tcc aga tgc   643
Ala Arg Asn Gln Ser Arg Ser Gly Ala Ser Lys Arg Ser Ser Arg Cys
                170                 175                 180

tgt tct atg cac tgg tct act ggc gca tgt tca atg aaa tcc cag ctc   691
Cys Ser Met His Trp Ser Thr Gly Ala Cys Ser Met Lys Ser Gln Leu
            185                 190                 195

agc ttc gtt taatgtacct caaagtcaac gat                            723
Ser Phe Val
        200
```

<210> 512
<211> 200
<212> PRT
<213> Corynebacterium glutamicum

<400> 512

```
Met Thr Ser Pro Val Glu Asn Val Lys Lys Lys Pro Arg Pro Leu Ala
  1               5                  10                  15

Leu Ser Pro Ser Arg Ala Gly Asp Tyr Gln Gln Cys Pro Leu Leu Tyr
             20                  25                  30

Arg Phe Arg Ala Ile Asp Arg Leu Pro Glu Pro Lys Thr Val Ala Gln
         35                  40                  45

Val Lys Gly Thr Leu Val His Ala Val Leu Glu Tyr Met His Lys Leu
     50                  55                  60

Pro Arg Glu Glu Arg Glu Tyr Pro Ala Met Val Lys Gln Leu Lys Pro
 65                  70                  75                  80

Thr Trp Ala Gln Met Cys Glu Glu Asp Ala Glu Leu Lys Glu Leu Val
                 85                  90                  95

Pro Glu Asp Glu Leu Tyr Asp Phe Leu Val Asp Ser Arg Thr Leu Leu
            100                 105                 110

Arg Gly Tyr Phe Glu Met Glu Asn Pro Gln Gly Phe Asp Ala Thr Glu
        115                 120                 125

Cys Glu Met Tyr Val Asp Thr Val Leu Pro Asn Gly Val Pro Val Arg
    130                 135                 140

Gly Phe Ile Asp Arg Val Asp Thr Ala Pro Pro Ala Lys Ser Glu Leu
145                 150                 155                 160

Ser Thr Thr Arg Leu Ala Arg Asn Gln Ser Arg Ser Gly Ala Ser Lys
                165                 170                 175

Arg Ser Ser Arg Cys Cys Ser Met His Trp Ser Thr Gly Ala Cys Ser
            180                 185                 190

Met Lys Ser Gln Leu Ser Phe Val
```

195 200

<210> 513
<211> 723
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(700)
<223> FRXA01148

<400> 513
atagaacaag ggtagccaaa ttcttggaaa cagcgcgggc ccccgaatcc acaatgcgaa 60

tccacaatgt cacctgaagc cgttaaagta ggtgatcatt atg acc agc cca gtt 115
Met Thr Ser Pro Val
1 5

gaa aac gtt aag aaa aag cca cgc cca ttg gcg ctg tca ccg tcg cgc 163
Glu Asn Val Lys Lys Lys Pro Arg Pro Leu Ala Leu Ser Pro Ser Arg
10 15 20

gcc ggg gat tac cag cag tgt ccc ctg ttg tat cgc ttc cgc gcg att 211
Ala Gly Asp Tyr Gln Gln Cys Pro Leu Leu Tyr Arg Phe Arg Ala Ile
25 30 35

gat cgc ctg cca gag cct aag acc gtc gcc cag gtc aaa ggc acg ttg 259
Asp Arg Leu Pro Glu Pro Lys Thr Val Ala Gln Val Lys Gly Thr Leu
40 45 50

gtg cac gct gtg ttg gaa tat atg cac aag ttg ccg cgt gaa gaa cgc 307
Val His Ala Val Leu Glu Tyr Met His Lys Leu Pro Arg Glu Glu Arg
55 60 65

gaa tat cca gcc atg gtg aag caa ctc aag ccc acc tgg gcg cag atg 355
Glu Tyr Pro Ala Met Val Lys Gln Leu Lys Pro Thr Trp Ala Gln Met
70 75 80 85

tgt gaa gaa gac gca gag ctc aaa gag ctt gtt cca gaa gat gag ctt 403
Cys Glu Glu Asp Ala Glu Leu Lys Glu Leu Val Pro Glu Asp Glu Leu
90 95 100

tat gat ttc ctc gtg gat tcc cgc acc ctg ctg cgt ggc tac ttt gaa 451
Tyr Asp Phe Leu Val Asp Ser Arg Thr Leu Leu Arg Gly Tyr Phe Glu
105 110 115

atg gaa aat cct caa ggt ttc gac gcc acc gaa tgc gaa atg tac gtg 499
Met Glu Asn Pro Gln Gly Phe Asp Ala Thr Glu Cys Glu Met Tyr Val
120 125 130

gac act gtg ctg ccc aac ggc gtt cct gtt cgt ggt ttt atc gac cgt 547
Asp Thr Val Leu Pro Asn Gly Val Pro Val Arg Gly Phe Ile Asp Arg
135 140 145

gtg gat acc gcc cca ccg gcc aag tcc gag tta tcg act aca aga ctg 595
Val Asp Thr Ala Pro Pro Ala Lys Ser Glu Leu Ser Thr Thr Arg Leu
150 155 160 165

gca aga aac caa agc cgc agt gga gcc agc aag cgc agt tcc aga tgc 643

```
Ala Arg Asn Gln Ser Arg Ser Gly Ala Ser Lys Arg Ser Ser Arg Cys
               170                 175                 180

tgt tct atg cac tgg tct act ggc gca tgt tca atg aaa tcc cag ctc   691
Cys Ser Met His Trp Ser Thr Gly Ala Cys Ser Met Lys Ser Gln Leu
            185                 190                 195

agc ttc gtt taatgtacct caaagtcaac gat                             723
Ser Phe Val
        200


<210> 514
<211> 200
<212> PRT
<213> Corynebacterium glutamicum

<400> 514
Met Thr Ser Pro Val Glu Asn Val Lys Lys Lys Pro Arg Pro Leu Ala
  1               5                  10                  15

Leu Ser Pro Ser Arg Ala Gly Asp Tyr Gln Gln Cys Pro Leu Leu Tyr
             20                  25                  30

Arg Phe Arg Ala Ile Asp Arg Leu Pro Glu Pro Lys Thr Val Ala Gln
         35                  40                  45

Val Lys Gly Thr Leu Val His Ala Val Leu Glu Tyr Met His Lys Leu
     50                  55                  60

Pro Arg Glu Glu Arg Glu Tyr Pro Ala Met Val Lys Gln Leu Lys Pro
 65                  70                  75                  80

Thr Trp Ala Gln Met Cys Glu Glu Asp Ala Glu Leu Lys Glu Leu Val
                 85                  90                  95

Pro Glu Asp Glu Leu Tyr Asp Phe Leu Val Asp Ser Arg Thr Leu Leu
            100                 105                 110

Arg Gly Tyr Phe Glu Met Glu Asn Pro Gln Gly Phe Asp Ala Thr Glu
        115                 120                 125

Cys Glu Met Tyr Val Asp Thr Val Leu Pro Asn Gly Val Pro Val Arg
    130                 135                 140

Gly Phe Ile Asp Arg Val Asp Thr Ala Pro Pro Ala Lys Ser Glu Leu
145                 150                 155                 160

Ser Thr Thr Arg Leu Ala Arg Asn Gln Ser Arg Ser Gly Ala Ser Lys
                165                 170                 175

Arg Ser Ser Arg Cys Cys Ser Met His Trp Ser Thr Gly Ala Cys Ser
            180                 185                 190

Met Lys Ser Gln Leu Ser Phe Val
        195                 200


<210> 515
<211> 543
<212> DNA
```

<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(543)
<223> RXN01153

<400> 515

```
ccg ttt tta agc ccg atc gtt act tcc acg cac gcg gtg gtg gcg tat   48
Pro Phe Leu Ser Pro Ile Val Thr Ser Thr His Ala Val Val Ala Tyr
  1               5                  10                  15

tcc acc gcg cgt gga ttt ggt gag cac cgg gtg cgt tgg gac tat gcg   96
Ser Thr Ala Arg Gly Phe Gly Glu His Arg Val Arg Trp Asp Tyr Ala
             20                  25                  30

caa gag tcc cca ctg cgc gat act cgt ggc ttt gat ctg cgc cga tac   144
Gln Glu Ser Pro Leu Arg Asp Thr Arg Gly Phe Asp Leu Arg Arg Tyr
         35                  40                  45

cac cag gcc cct gtg gtg gat ccg cac gcc att ggt gtg gcc aac gtg   192
His Gln Ala Pro Val Val Asp Pro His Ala Ile Gly Val Ala Asn Val
     50                  55                  60

ttt gtg ccc aat ggt gcc agg ttt tat gtc gat cac gcg cac ccg gaa   240
Phe Val Pro Asn Gly Ala Arg Phe Tyr Val Asp His Ala His Pro Glu
 65                  70                  75                  80

tac tcc tcc cca gag gtc acc aat gcg tgg gat gcc atg gtt tac gac   288
Tyr Ser Ser Pro Glu Val Thr Asn Ala Trp Asp Ala Met Val Tyr Asp
                 85                  90                  95

gcc gct ggt gac cac atc ctt atg cag gcc gtc tct gat gtt gcg agt   336
Ala Ala Gly Asp His Ile Leu Met Gln Ala Val Ser Asp Val Ala Ser
            100                 105                 110

ttc acc agc cag aat agg tct gtg ttg gac ggc cat gat ccg tgt cca   384
Phe Thr Ser Gln Asn Arg Ser Val Leu Asp Gly His Asp Pro Cys Pro
        115                 120                 125

gct ttg aaa atc tac aaa aac aat gtc gac ggt aag ggt gct agc tac   432
Ala Leu Lys Ile Tyr Lys Asn Asn Val Asp Gly Lys Gly Ala Ser Tyr
    130                 135                 140

ggg ttc cac gag aat tac ctc tac tca cgt gag acg gat ttt gat gtg   480
Gly Phe His Glu Asn Tyr Leu Tyr Ser Arg Glu Thr Asp Phe Asp Val
145                 150                 155                 160

ctg gct cag gca ttg atc cca ttt ttt gtg tgc cgg cag gtc atc atc   528
Leu Ala Gln Ala Leu Ile Pro Phe Phe Val Cys Arg Gln Val Ile Ile
                165                 170                 175

ggt gcc gga cgt gtg                                              543
Gly Ala Gly Arg Val
            180
```

<210> 516
<211> 181
<212> PRT
<213> Corynebacterium glutamicum

<400> 516
Pro Phe Leu Ser Pro Ile Val Thr Ser Thr His Ala Val Val Ala Tyr
1 5 10 15

Ser Thr Ala Arg Gly Phe Gly Glu His Arg Val Arg Trp Asp Tyr Ala
20 25 30

Gln Glu Ser Pro Leu Arg Asp Thr Arg Gly Phe Asp Leu Arg Arg Tyr
35 40 45

His Gln Ala Pro Val Val Asp Pro His Ala Ile Gly Val Ala Asn Val
50 55 60

Phe Val Pro Asn Gly Ala Arg Phe Tyr Val Asp His Ala His Pro Glu
65 70 75 80

Tyr Ser Ser Pro Glu Val Thr Asn Ala Trp Asp Ala Met Val Tyr Asp
85 90 95

Ala Ala Gly Asp His Ile Leu Met Gln Ala Val Ser Asp Val Ala Ser
100 105 110

Phe Thr Ser Gln Asn Arg Ser Val Leu Asp Gly His Asp Pro Cys Pro
115 120 125

Ala Leu Lys Ile Tyr Lys Asn Asn Val Asp Gly Lys Gly Ala Ser Tyr
130 135 140

Gly Phe His Glu Asn Tyr Leu Tyr Ser Arg Glu Thr Asp Phe Asp Val
145 150 155 160

Leu Ala Gln Ala Leu Ile Pro Phe Phe Val Cys Arg Gln Val Ile Ile
165 170 175

Gly Ala Gly Arg Val
180

<210> 517
<211> 543
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(543)
<223> FRXA01153

<400> 517
ccg ttt tta agc ccg atc gtt act tcc acg cac gcg gtg gtg gcg tat 48
Pro Phe Leu Ser Pro Ile Val Thr Ser Thr His Ala Val Val Ala Tyr
1 5 10 15

tcc acc gcg cgt gga ttt ggt gag cac cgg gtg cgt tgg gac tat gcg 96
Ser Thr Ala Arg Gly Phe Gly Glu His Arg Val Arg Trp Asp Tyr Ala
20 25 30

caa gag tcc cca ctg cgc gat act cgt ggc ttt gat ctg cgc cga tac 144
Gln Glu Ser Pro Leu Arg Asp Thr Arg Gly Phe Asp Leu Arg Arg Tyr
35 40 45

```
cac cag gcc cct gtg gtg gat ccg cac gcc att ggt gtg gcc aac gtg   192
His Gln Ala Pro Val Val Asp Pro His Ala Ile Gly Val Ala Asn Val
     50                  55                  60

ttt gtg ccc aat ggt gcc agg ttt tat gtc gat cac gcg cac ccg gaa   240
Phe Val Pro Asn Gly Ala Arg Phe Tyr Val Asp His Ala His Pro Glu
 65                  70                  75                  80

tac tcc tcc cca gag gtc acc aat gcg tgg gat gcc atg gtt tac gac   288
Tyr Ser Ser Pro Glu Val Thr Asn Ala Trp Asp Ala Met Val Tyr Asp
                85                  90                  95

gcc gct ggt gac cac atc ctt atg cag gcc gtc tct gat gtt gcg agt   336
Ala Ala Gly Asp His Ile Leu Met Gln Ala Val Ser Asp Val Ala Ser
            100                 105                 110

ttc acc agc cag aat agg tct gtg ttg gac ggc cat gat ccg tgt cca   384
Phe Thr Ser Gln Asn Arg Ser Val Leu Asp Gly His Asp Pro Cys Pro
        115                 120                 125

gct ttg aaa atc tac aaa aac aat gtc gac ggt aag ggt gct agc tac   432
Ala Leu Lys Ile Tyr Lys Asn Asn Val Asp Gly Lys Gly Ala Ser Tyr
    130                 135                 140

ggg ttc cac gag aat tac ctc tac tca cgt gag acg gat ttt gat gtg   480
Gly Phe His Glu Asn Tyr Leu Tyr Ser Arg Glu Thr Asp Phe Asp Val
145                 150                 155                 160

ctg gct cag gca ttg atc cca ttt ttt gtg tgc cgg cag gtc atc atc   528
Leu Ala Gln Ala Leu Ile Pro Phe Phe Val Cys Arg Gln Val Ile Ile
                165                 170                 175

ggt gcc gga cgt gtg                                              543
Gly Ala Gly Arg Val
            180
```

Sequence Listing - Copy

<210> 518
<211> 181
<212> PRT
<213> Corynebacterium glutamicum

<400> 518

```
Pro Phe Leu Ser Pro Ile Val Thr Ser Thr His Ala Val Val Ala Tyr
  1               5                  10                  15

Ser Thr Ala Arg Gly Phe Gly Glu His Arg Val Arg Trp Asp Tyr Ala
             20                  25                  30

Gln Glu Ser Pro Leu Arg Asp Thr Arg Gly Phe Asp Leu Arg Arg Tyr
         35                  40                  45

His Gln Ala Pro Val Val Asp Pro His Ala Ile Gly Val Ala Asn Val
     50                  55                  60

Phe Val Pro Asn Gly Ala Arg Phe Tyr Val Asp His Ala His Pro Glu
 65                  70                  75                  80

Tyr Ser Ser Pro Glu Val Thr Asn Ala Trp Asp Ala Met Val Tyr Asp
                85                  90                  95
```

```
Ala Ala Gly Asp His Ile Leu Met Gln Ala Val Ser Asp Val Ala Ser
            100                 105                 110

Phe Thr Ser Gln Asn Arg Ser Val Leu Asp Gly His Asp Pro Cys Pro
        115                 120                 125

Ala Leu Lys Ile Tyr Lys Asn Asn Val Asp Gly Lys Gly Ala Ser Tyr
    130                 135                 140

Gly Phe His Glu Asn Tyr Leu Tyr Ser Arg Glu Thr Asp Phe Asp Val
145                 150                 155                 160

Leu Ala Gln Ala Leu Ile Pro Phe Phe Val Cys Arg Gln Val Ile Ile
                165                 170                 175

Gly Ala Gly Arg Val
            180
```

<210> 519
<211> 677
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (39)..(677)
<223> RXN01154

<400> 519

```
ccggggaatt ccaggtcagt cagcgagcct gactaccattg agc aag aaa att tca  56
                                          Leu Ser Lys Lys Ile Ser
                                            1               5

ctg gaa acc aca ctc aac cgc ggc att atc aac acc cgc gat gaa cca   104
Leu Glu Thr Thr Leu Asn Arg Gly Ile Ile Asn Thr Arg Asp Glu Pro
             10                  15                  20

cac acc gac gct gat cac tgg ggt cgc ctg cac gtg atc atc ggc gat   152
His Thr Asp Ala Asp His Trp Gly Arg Leu His Val Ile Ile Gly Asp
         25                  30                  35

gcc aac atg tcg cag act gcg aat ttc ctc aaa ttc ggc atg acc tcc   200
Ala Asn Met Ser Gln Thr Ala Asn Phe Leu Lys Phe Gly Met Thr Ser
     40                  45                  50

cta gtg ctg gat gcc att gag gct ggg gtg gat ttc tct gaa ctc aag   248
Leu Val Leu Asp Ala Ile Glu Ala Gly Val Asp Phe Ser Glu Leu Lys
 55                  60                  65                  70

ctg aag aac gca gtg agt gaa gta gca aag gtc tcc cat gat ctt tcc   296
Leu Lys Asn Ala Val Ser Glu Val Ala Lys Val Ser His Asp Leu Ser
                 75                  80                  85

ctt acc cac cag ctg cga ttg gcg gat ggt tca gag ctc acc gct att   344
Leu Thr His Gln Leu Arg Leu Ala Asp Gly Ser Glu Leu Thr Ala Ile
             90                  95                  100

gat att ctg cgc cgc tat ttg gac aag gtg cag ccg ttt gca gaa acc   392
Asp Ile Leu Arg Arg Tyr Leu Asp Lys Val Gln Pro Phe Ala Glu Thr
```

```
        105                 110                 115

cca gtg gaa cag cgt gtc act gcg ctg tgg ggt gaa gtg ctg ggg ctc   440
Pro Val Glu Gln Arg Val Thr Ala Leu Trp Gly Glu Val Leu Gly Leu
    120                 125                 130

ctg gag aat gat ctg ctc tcc acc agc cat ctc ctt gat tgg act gca   488
Leu Glu Asn Asp Leu Leu Ser Thr Ser His Leu Leu Asp Trp Thr Ala
135                 140                 145                 150

aaa ctt gcc ctg atc aag tct ttt gag gcg cgt ggg ctg tcc att aac   536
Lys Leu Ala Leu Ile Lys Ser Phe Glu Ala Arg Gly Leu Ser Ile Asn
                155                 160                 165

gat ccc aag atg tac ctc att gac ctg cag tac agc gat att gat cca   584
Asp Pro Lys Met Tyr Leu Ile Asp Leu Gln Tyr Ser Asp Ile Asp Pro
            170                 175                 180

cag aag agt ctg tat cac gca ctg gta tcc aag ggg cgg atg aaa aca   632
Gln Lys Ser Leu Tyr His Ala Leu Val Ser Lys Gly Arg Met Lys Thr
        185                 190                 195

ctg tgc agt gcg cag gac att gca gat gca gcg gcc act tca ccg       677
Leu Cys Ser Ala Gln Asp Ile Ala Asp Ala Ala Ala Thr Ser Pro
    200                 205                 210


<210> 520
<211> 213
<212> PRT
<213> Corynebacterium glutamicum

<400> 520
Leu Ser Lys Lys Ile Ser Leu Glu Thr Thr Leu Asn Arg Gly Ile Ile
  1               5                  10                  15

Asn Thr Arg Asp Glu Pro His Thr Asp Ala Asp His Trp Gly Arg Leu
             20                  25                  30

His Val Ile Ile Gly Asp Ala Asn Met Ser Gln Thr Ala Asn Phe Leu
         35                  40                  45

Lys Phe Gly Met Thr Ser Leu Val Leu Asp Ala Ile Glu Ala Gly Val
     50                  55                  60

Asp Phe Ser Glu Leu Lys Leu Lys Asn Ala Val Ser Glu Val Ala Lys
 65                  70                  75                  80

Val Ser His Asp Leu Ser Leu Thr His Gln Leu Arg Leu Ala Asp Gly
                 85                  90                  95

Ser Glu Leu Thr Ala Ile Asp Ile Leu Arg Arg Tyr Leu Asp Lys Val
            100                 105                 110

Gln Pro Phe Ala Glu Thr Pro Val Glu Gln Arg Val Thr Ala Leu Trp
        115                 120                 125

Gly Glu Val Leu Gly Leu Leu Glu Asn Asp Leu Leu Ser Thr Ser His
    130                 135                 140

Leu Leu Asp Trp Thr Ala Lys Leu Ala Leu Ile Lys Ser Phe Glu Ala
```

```
145                 150                 155                 160

Arg Gly Leu Ser Ile Asn Asp Pro Lys Met Tyr Leu Ile Asp Leu Gln
                165                 170                 175

Tyr Ser Asp Ile Asp Pro Gln Lys Ser Leu Tyr His Ala Leu Val Ser
            180                 185                 190

Lys Gly Arg Met Lys Thr Leu Cys Ser Ala Gln Asp Ile Ala Asp Ala
        195                 200                 205

Ala Ala Thr Ser Pro
    210
```

<210> 521
<211> 603
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(603)
<223> FRXA01154

<400> 521

```
gag ggc att atc aac acc cgc gat gaa cca cac acc gac gct gat cac   48
Glu Gly Ile Ile Asn Thr Arg Asp Glu Pro His Thr Asp Ala Asp His
  1               5                  10                  15

tgg ggt cgc ctg cac gtg atc atc ggc gat gcc aac atg tcg cag act   96
Trp Gly Arg Leu His Val Ile Ile Gly Asp Ala Asn Met Ser Gln Thr
             20                  25                  30

gcg aat ttc ctc aaa ttc ggc atg acc tcc cta gtg ctg gat gcc att  144
Ala Asn Phe Leu Lys Phe Gly Met Thr Ser Leu Val Leu Asp Ala Ile
         35                  40                  45

gag gct ggg gtg gat ttc tct gaa ctc aag ctg aag aac gca gtg agt  192
Glu Ala Gly Val Asp Phe Ser Glu Leu Lys Leu Lys Asn Ala Val Ser
     50                  55                  60

gaa gta gca aag gtc tcc cat gat ctt tcc ctt acc cac cag ctg cga  240
Glu Val Ala Lys Val Ser His Asp Leu Ser Leu Thr His Gln Leu Arg
 65                  70                  75                  80

ttg gcg gat ggt tca gag ctc acc gct att gat att ctg cgc cgc tat  288
Leu Ala Asp Gly Ser Glu Leu Thr Ala Ile Asp Ile Leu Arg Arg Tyr
                 85                  90                  95

ttg gac aag gtg cag ccg ttt gca gaa acc cca gtg gaa cag cgt gtc  336
Leu Asp Lys Val Gln Pro Phe Ala Glu Thr Pro Val Glu Gln Arg Val
            100                 105                 110

act gcg ctg tgg ggt gaa gtg ctg ggg ctc ctg gag aat gat ctg ctc  384
Thr Ala Leu Trp Gly Glu Val Leu Gly Leu Leu Glu Asn Asp Leu Leu
        115                 120                 125

tcc acc agc cat ctc ctt gat tgg act gca aaa ctt gcc ctg atc aag  432
Ser Thr Ser His Leu Leu Asp Trp Thr Ala Lys Leu Ala Leu Ile Lys
    130                 135                 140
```

```
tct ttt gag gcg cgt ggg ctg tcc att aac gat ccc aag atg tac ctc   480
Ser Phe Glu Ala Arg Gly Leu Ser Ile Asn Asp Pro Lys Met Tyr Leu
145                 150                 155                 160

att gac ctg cag tac agc gat att gat cca cag aag agt ctg tat cac   528
Ile Asp Leu Gln Tyr Ser Asp Ile Asp Pro Gln Lys Ser Leu Tyr His
                165                 170                 175

gca ctg gta tcc aag ggg cgg atg aaa aca ctg tgc agt gcg cag gac   576
Ala Leu Val Ser Lys Gly Arg Met Lys Thr Leu Cys Ser Ala Gln Asp
            180                 185                 190

att gca gat gca gcg gcc act tca ccg                               603
Ile Ala Asp Ala Ala Ala Thr Ser Pro
        195                 200
```

<210> 522
<211> 201
<212> PRT
<213> Corynebacterium glutamicum

<400> 522

```
Glu Gly Ile Ile Asn Thr Arg Asp Glu Pro His Thr Asp Ala Asp His
  1               5                  10                  15

Trp Gly Arg Leu His Val Ile Ile Gly Asp Ala Asn Met Ser Gln Thr
             20                  25                  30

Ala Asn Phe Leu Lys Phe Gly Met Thr Ser Leu Val Leu Asp Ala Ile
         35                  40                  45

Glu Ala Gly Val Asp Phe Ser Glu Leu Lys Leu Lys Asn Ala Val Ser
     50                  55                  60

Glu Val Ala Lys Val Ser His Asp Leu Ser Leu Thr His Gln Leu Arg
 65                  70                  75                  80

Leu Ala Asp Gly Ser Glu Leu Thr Ala Ile Asp Ile Leu Arg Arg Tyr
                 85                  90                  95

Leu Asp Lys Val Gln Pro Phe Ala Glu Thr Pro Val Glu Gln Arg Val
            100                 105                 110

Thr Ala Leu Trp Gly Glu Val Leu Gly Leu Leu Glu Asn Asp Leu Leu
        115                 120                 125

Ser Thr Ser His Leu Leu Asp Trp Thr Ala Lys Leu Ala Leu Ile Lys
    130                 135                 140

Ser Phe Glu Ala Arg Gly Leu Ser Ile Asn Asp Pro Lys Met Tyr Leu
145                 150                 155                 160

Ile Asp Leu Gln Tyr Ser Asp Ile Asp Pro Gln Lys Ser Leu Tyr His
                165                 170                 175

Ala Leu Val Ser Lys Gly Arg Met Lys Thr Leu Cys Ser Ala Gln Asp
            180                 185                 190

Ile Ala Asp Ala Ala Ala Thr Ser Pro
```

195 200

<210> 523
<211> 1570
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1570)
<223> RXN01155

<400> 523
acagcttgct ggatgaaatc gacggactgt tggaaaacaa cgccgaggaa ttcgttcgtt 60

cctatgtaca aaagggtggc gaatagtcac tgtgagtacc gtg gaa tcc gca ttg 115
Val Glu Ser Ala Leu
1 5

acc cgc agg atc atg ggc att gaa acg gag tat ggc ctc acc ttt gtt 163
Thr Arg Arg Ile Met Gly Ile Glu Thr Glu Tyr Gly Leu Thr Phe Val
10 15 20

gat ggt gat tcc aaa aag ctt cgc cca gat gag ata gct cga agg atg 211
Asp Gly Asp Ser Lys Lys Leu Arg Pro Asp Glu Ile Ala Arg Arg Met
25 30 35

ttt cgt ccc atc gtg gag aaa tat tcc agc tct aat atc ttc ata ccc 259
Phe Arg Pro Ile Val Glu Lys Tyr Ser Ser Ser Asn Ile Phe Ile Pro
40 45 50

aat ggt tcc cgg ttg tat ctt gat gtg ggt tcc cac ccg gag tac gcc 307
Asn Gly Ser Arg Leu Tyr Leu Asp Val Gly Ser His Pro Glu Tyr Ala
55 60 65

acc gcc gag tgt gat aat ttg acc cag ctg atc aat ttt gaa aaa gct 355
Thr Ala Glu Cys Asp Asn Leu Thr Gln Leu Ile Asn Phe Glu Lys Ala
70 75 80 85

ggc gat gtt att gca gat cgc atg gct gta gat gcc gaa gag tcg ctg 403
Gly Asp Val Ile Ala Asp Arg Met Ala Val Asp Ala Glu Glu Ser Leu
90 95 100

gcg aaa gaa gac att gct ggg cag gtg tac ctg ttt aaa aac aat gtc 451
Ala Lys Glu Asp Ile Ala Gly Gln Val Tyr Leu Phe Lys Asn Asn Val
105 110 115

gat tcc gtg ggc aat tct tat ggc tgc cac gaa aac tac ctt gtg ggt 499
Asp Ser Val Gly Asn Ser Tyr Gly Cys His Glu Asn Tyr Leu Val Gly
120 125 130

cgc tcc atg ccg ttg aag gcg ttg ggt aaa agg ctg atg ccg ttt ctg 547
Arg Ser Met Pro Leu Lys Ala Leu Gly Lys Arg Leu Met Pro Phe Leu
135 140 145

att acc cgc cag ctc atc tgc ggc gcc ggc agg atc cat cac ccc aat 595
Ile Thr Arg Gln Leu Ile Cys Gly Ala Gly Arg Ile His His Pro Asn
150 155 160 165

cct ttg gat aaa ggc gaa tcc ttc ccc ttg ggc tac tgc ata tcc cag 643

```
Pro Leu Asp Lys Gly Glu Ser Phe Pro Leu Gly Tyr Cys Ile Ser Gln
                170                 175                 180

cgc tct gac cac gtg tgg gag ggc gta tca agt gcc acc act aga tca   691
Arg Ser Asp His Val Trp Glu Gly Val Ser Ser Ala Thr Thr Arg Ser
            185                 190                 195

cgc ccc att atc aac acc cgt gat gag cca cat gcg gat tcc cat tct   739
Arg Pro Ile Ile Asn Thr Arg Asp Glu Pro His Ala Asp Ser His Ser
        200                 205                 210

tac cgc agg ctg cac gtg att gtg ggt gat gcc aac atg gca gag ccc   787
Tyr Arg Arg Leu His Val Ile Val Gly Asp Ala Asn Met Ala Glu Pro
    215                 220                 225

agc atc gcg ttg aag gtc ggc tcc acg ttg ctg gtt ctg gaa atg att   835
Ser Ile Ala Leu Lys Val Gly Ser Thr Leu Leu Val Leu Glu Met Ile
230                 235                 240                 245

gag gca gat ttc ggt ttg ccc agc tta gag ctt gcc aat gat att gcc   883
Glu Ala Asp Phe Gly Leu Pro Ser Leu Glu Leu Ala Asn Asp Ile Ala
                250                 255                 260

tca att agg gaa atc tcc cgc gat gca aca gga tcc aca ctg ttg tcc   931
Ser Ile Arg Glu Ile Ser Arg Asp Ala Thr Gly Ser Thr Leu Leu Ser
            265                 270                 275

ctg aaa gat ggc acc acc atg act gcc ttg cag atc cag cag gtg gtc   979
Leu Lys Asp Gly Thr Thr Met Thr Ala Leu Gln Ile Gln Gln Val Val
        280                 285                 290

ttt gag cat gcc tcg aag tgg ttg gag cag cgc ccc gaa cca gaa ttt   1027
Phe Glu His Ala Ser Lys Trp Leu Glu Gln Arg Pro Glu Pro Glu Phe
    295                 300                 305

tct ggc acc tcc aac aca gag atg gcc cgc gtg ctg gat ctg tgg ggt   1075
Ser Gly Thr Ser Asn Thr Glu Met Ala Arg Val Leu Asp Leu Trp Gly
310                 315                 320                 325

cgc atg ttg aaa gcg att gag tcc ggt gat ttc agc gaa gtg gat aca   1123
Arg Met Leu Lys Ala Ile Glu Ser Gly Asp Phe Ser Glu Val Asp Thr
                330                 335                 340

gaa att gac tgg gtg atc aaa aag aag ctc att gat cgt ttc att cag   1171
Glu Ile Asp Trp Val Ile Lys Lys Lys Leu Ile Asp Arg Phe Ile Gln
            345                 350                 355

cgc ggc aac ctt ggg ttg gat gat cca aaa ctt gcc caa gtg gac ttg   1219
Arg Gly Asn Leu Gly Leu Asp Asp Pro Lys Leu Ala Gln Val Asp Leu
        360                 365                 370

act tat cac gat att agg cca ggt aga ggc cta ttt agc gtg ctg caa   1267
Thr Tyr His Asp Ile Arg Pro Gly Arg Gly Leu Phe Ser Val Leu Gln
    375                 380                 385

agc cgc ggc atg atc aaa cgg tgg act act gat gag gcg att tta gct   1315
Ser Arg Gly Met Ile Lys Arg Trp Thr Thr Asp Glu Ala Ile Leu Ala
390                 395                 400                 405

gcg gtg gat acc gct cct gat aca aca cgt gct cat ttg cgc ggg cga   1363
Ala Val Asp Thr Ala Pro Asp Thr Thr Arg Ala His Leu Arg Gly Arg
```

```
                410                 415                 420

atc ctt aaa gcg gcg gat act ctg gga gta cct gtg act gtc gat tgg   1411
Ile Leu Lys Ala Ala Asp Thr Leu Gly Val Pro Val Thr Val Asp Trp
            425                 430                 435

atg cgt cac aag gtc aac cga ccg gag cca caa tcg gtg gaa ttg ggg   1459
Met Arg His Lys Val Asn Arg Pro Glu Pro Gln Ser Val Glu Leu Gly
        440                 445                 450

gat cct ttt tcc ctt tta aat cct caa caa cca gcc caa gaa act gct   1507
Asp Pro Phe Ser Leu Leu Asn Pro Gln Gln Pro Ala Gln Glu Thr Ala
    455                 460                 465

ttg agc att ctt ctc cta ggc gga acc tct tac att gcc ggt gag att   1555
Leu Ser Ile Leu Leu Leu Gly Gly Thr Ser Tyr Ile Ala Gly Glu Ile
470                 475                 480                 485

gcc acg ttg acg ttt                                               1570
Ala Thr Leu Thr Phe
                490
```

<210> 524
<211> 490
<212> PRT
<213> Corynebacterium glutamicum

<400> 524

```
Val Glu Ser Ala Leu Thr Arg Arg Ile Met Gly Ile Glu Thr Glu Tyr
  1               5                  10                  15

Gly Leu Thr Phe Val Asp Gly Asp Ser Lys Lys Leu Arg Pro Asp Glu
             20                  25                  30

Ile Ala Arg Arg Met Phe Arg Pro Ile Val Glu Lys Tyr Ser Ser Ser
         35                  40                  45

Asn Ile Phe Ile Pro Asn Gly Ser Arg Leu Tyr Leu Asp Val Gly Ser
     50                  55                  60

His Pro Glu Tyr Ala Thr Ala Glu Cys Asp Asn Leu Thr Gln Leu Ile
 65                  70                  75                  80

Asn Phe Glu Lys Ala Gly Asp Val Ile Ala Asp Arg Met Ala Val Asp
                 85                  90                  95

Ala Glu Glu Ser Leu Ala Lys Glu Asp Ile Ala Gly Gln Val Tyr Leu
            100                 105                 110

Phe Lys Asn Asn Val Asp Ser Val Gly Asn Ser Tyr Gly Cys His Glu
        115                 120                 125

Asn Tyr Leu Val Gly Arg Ser Met Pro Leu Lys Ala Leu Gly Lys Arg
    130                 135                 140

Leu Met Pro Phe Leu Ile Thr Arg Gln Leu Ile Cys Gly Ala Gly Arg
145                 150                 155                 160

Ile His His Pro Asn Pro Leu Asp Lys Gly Glu Ser Phe Pro Leu Gly
                165                 170                 175
```

```
Tyr Cys Ile Ser Gln Arg Ser Asp His Val Trp Glu Gly Val Ser Ser
            180                 185                 190

Ala Thr Thr Arg Ser Arg Pro Ile Ile Asn Thr Arg Asp Glu Pro His
        195                 200                 205

Ala Asp Ser His Ser Tyr Arg Arg Leu His Val Ile Val Gly Asp Ala
    210                 215                 220

Asn Met Ala Glu Pro Ser Ile Ala Leu Lys Val Gly Ser Thr Leu Leu
225                 230                 235                 240

Val Leu Glu Met Ile Glu Ala Asp Phe Gly Leu Pro Ser Leu Glu Leu
                245                 250                 255

Ala Asn Asp Ile Ala Ser Ile Arg Glu Ile Ser Arg Asp Ala Thr Gly
            260                 265                 270

Ser Thr Leu Leu Ser Leu Lys Asp Gly Thr Thr Met Thr Ala Leu Gln
        275                 280                 285

Ile Gln Gln Val Val Phe Glu His Ala Ser Lys Trp Leu Glu Gln Arg
    290                 295                 300

Pro Glu Pro Glu Phe Ser Gly Thr Ser Asn Thr Glu Met Ala Arg Val
305                 310                 315                 320

Leu Asp Leu Trp Gly Arg Met Leu Lys Ala Ile Glu Ser Gly Asp Phe
                325                 330                 335

Ser Glu Val Asp Thr Glu Ile Asp Trp Val Ile Lys Lys Lys Leu Ile
            340                 345                 350

Asp Arg Phe Ile Gln Arg Gly Asn Leu Gly Leu Asp Asp Pro Lys Leu
        355                 360                 365

Ala Gln Val Asp Leu Thr Tyr His Asp Ile Arg Pro Gly Arg Gly Leu
    370                 375                 380

Phe Ser Val Leu Gln Ser Arg Gly Met Ile Lys Arg Trp Thr Thr Asp
385                 390                 395                 400

Glu Ala Ile Leu Ala Ala Val Asp Thr Ala Pro Asp Thr Thr Arg Ala
                405                 410                 415

His Leu Arg Gly Arg Ile Leu Lys Ala Ala Asp Thr Leu Gly Val Pro
            420                 425                 430

Val Thr Val Asp Trp Met Arg His Lys Val Asn Arg Pro Glu Pro Gln
        435                 440                 445

Ser Val Glu Leu Gly Asp Pro Phe Ser Leu Leu Asn Pro Gln Gln Pro
    450                 455                 460

Ala Gln Glu Thr Ala Leu Ser Ile Leu Leu Leu Gly Gly Thr Ser Tyr
465                 470                 475                 480

Ile Ala Gly Glu Ile Ala Thr Leu Thr Phe
                485                 490
```

<210> 525
<211> 1465
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1465)
<223> FRXA01155

<400> 525
acagcttgct ggatgaaatc gacggactgt tggaaaacaa cgccgaggaa ttcgttcgtt 60

cctatgtaca aaagggtggc gaatagtcac tgtgagtacc gtg gaa tcc gca ttg 115
Val Glu Ser Ala Leu
1 5

acc cgc agg atc atg ggc att gaa acg gag tat ggc ctc acc ttt gtt 163
Thr Arg Arg Ile Met Gly Ile Glu Thr Glu Tyr Gly Leu Thr Phe Val
10 15 20

gat ggt gat tcc aaa aag ctt cgc cca gat gag ata gct cga agg atg 211
Asp Gly Asp Ser Lys Lys Leu Arg Pro Asp Glu Ile Ala Arg Arg Met
25 30 35

ttt cgt ccc atc gtg gag aaa tat tcc agc tct aat atc ttc ata ccc 259
Phe Arg Pro Ile Val Glu Lys Tyr Ser Ser Ser Asn Ile Phe Ile Pro
40 45 50

aat ggt tcc cgg ttg tat ctt gat gtg ggt tcc cac ccg gag tac gcc 307
Asn Gly Ser Arg Leu Tyr Leu Asp Val Gly Ser His Pro Glu Tyr Ala
55 60 65

acc gcc gag tgt gat aat ttg acc cag ctg atc aat ttt gaa aaa gct 355
Thr Ala Glu Cys Asp Asn Leu Thr Gln Leu Ile Asn Phe Glu Lys Ala
70 75 80 85

ggc gat gtt att gca gat cgc atg gct gta gat gcc gaa gag tcg ctg 403
Gly Asp Val Ile Ala Asp Arg Met Ala Val Asp Ala Glu Glu Ser Leu
90 95 100

gcg aaa gaa gac att gct ggg cag gtg tac ctg ttt aaa aac aat gtc 451
Ala Lys Glu Asp Ile Ala Gly Gln Val Tyr Leu Phe Lys Asn Asn Val
105 110 115

gat tcc gtg ggc aat tct tat ggc tgc cac gaa aac tac ctt gtg ggt 499
Asp Ser Val Gly Asn Ser Tyr Gly Cys His Glu Asn Tyr Leu Val Gly
120 125 130

cgc tcc atg ccg ttg aag gcg ttg ggt aaa agg ctg atg ccg ttt ctg 547
Arg Ser Met Pro Leu Lys Ala Leu Gly Lys Arg Leu Met Pro Phe Leu
135 140 145

att acc cgc cag ctc atc tgc ggc gcc ggc agg atc cat cac ccc aat 595
Ile Thr Arg Gln Leu Ile Cys Gly Ala Gly Arg Ile His His Pro Asn
150 155 160 165

cct ttg gat aaa ggc gaa tcc ttc ccc ttg ggc tac tgc ata tcc cag 643
Pro Leu Asp Lys Gly Glu Ser Phe Pro Leu Gly Tyr Cys Ile Ser Gln
170 175 180

```
cgc tct gac cac gtg tgg gag ggc gta tca agt gcc acc act aga tca   691
Arg Ser Asp His Val Trp Glu Gly Val Ser Ser Ala Thr Thr Arg Ser
            185                 190                 195

cgc ccc att atc aac acc cgt gat gag cca cat gcg gat tcc cat tct   739
Arg Pro Ile Ile Asn Thr Arg Asp Glu Pro His Ala Asp Ser His Ser
        200                 205                 210

tac cgc agg ctg cac gtg att gtg ggt gat gcc aac atg gca gag ccc   787
Tyr Arg Arg Leu His Val Ile Val Gly Asp Ala Asn Met Ala Glu Pro
    215                 220                 225

agc atc gcg ttg aag gtc ggc tcc acg ttg ctg gtt ctg gaa atg att   835
Ser Ile Ala Leu Lys Val Gly Ser Thr Leu Leu Val Leu Glu Met Ile
230                 235                 240                 245

gag gca gat ttc ggt ttg ccc agc tta gag ctt gcc aat gat att gcc   883
Glu Ala Asp Phe Gly Leu Pro Ser Leu Glu Leu Ala Asn Asp Ile Ala
                250                 255                 260

tca att agg gaa atc tcc cgc gat gca aca gga tcc aca ctg ttg tcc   931
Ser Ile Arg Glu Ile Ser Arg Asp Ala Thr Gly Ser Thr Leu Leu Ser
            265                 270                 275

ctg aaa gat ggc acc acc atg act gcc ttg cag atc cag cag gtg gtc   979
Leu Lys Asp Gly Thr Thr Met Thr Ala Leu Gln Ile Gln Gln Val Val
        280                 285                 290

ttt gag cat gcc tcg aag tgg ttg gag cag cgc ccc gaa cca gaa ttt   1027
Phe Glu His Ala Ser Lys Trp Leu Glu Gln Arg Pro Glu Pro Glu Phe
    295                 300                 305

tct ggc acc tcc aac aca gag atg gcc cgc gtg ctg gat ctg tgg ggt   1075
Ser Gly Thr Ser Asn Thr Glu Met Ala Arg Val Leu Asp Leu Trp Gly
310                 315                 320                 325

cgc atg ttg aaa gcg att gag tcc ggt gat ttc agc gaa gtg gat aca   1123
Arg Met Leu Lys Ala Ile Glu Ser Gly Asp Phe Ser Glu Val Asp Thr
                330                 335                 340

gaa att gac tgg gtg atc aaa aag aag ctc att gat cgt ttc att cag   1171
Glu Ile Asp Trp Val Ile Lys Lys Lys Leu Ile Asp Arg Phe Ile Gln
            345                 350                 355

cgc ggc aac ctt ggg ttg gat gat cca aaa ctt gcc caa gtg gac ttg   1219
Arg Gly Asn Leu Gly Leu Asp Asp Pro Lys Leu Ala Gln Val Asp Leu
        360                 365                 370

act tat cac gat att agg cca ggt aga ggc cta ttt agc gtg ctg caa   1267
Thr Tyr His Asp Ile Arg Pro Gly Arg Gly Leu Phe Ser Val Leu Gln
    375                 380                 385

agc cgc ggc atg atc aaa cgg tgg act act gat gag gcg att tta gct   1315
Ser Arg Gly Met Ile Lys Arg Trp Thr Thr Asp Glu Ala Ile Leu Ala
390                 395                 400                 405

gcg gtg gat acc gct cct gat aca aca cgt gct cat ttg cgc ggg cga   1363
Ala Val Asp Thr Ala Pro Asp Thr Thr Arg Ala His Leu Arg Gly Arg
                410                 415                 420
```

```
atc ctt aaa gcg gcg gat act ctg gga gta cct gtg act gtc gat tgg   1411
Ile Leu Lys Ala Ala Asp Thr Leu Gly Val Pro Val Thr Val Asp Trp
            425                 430                 435

atg cgt cac aag gtc aac cga ccg gag cca caa tcg gtg gaa ttg ggg   1459
Met Arg His Lys Val Asn Arg Pro Glu Pro Gln Ser Val Glu Leu Gly
        440                 445                 450

gat cct                                                          1465
Asp Pro
    455
```

<210> 526
<211> 455
<212> PRT
<213> Corynebacterium glutamicum

<400> 526

```
Val Glu Ser Ala Leu Thr Arg Arg Ile Met Gly Ile Glu Thr Glu Tyr
  1               5                  10                  15

Gly Leu Thr Phe Val Asp Gly Asp Ser Lys Lys Leu Arg Pro Asp Glu
             20                  25                  30

Ile Ala Arg Arg Met Phe Arg Pro Ile Val Glu Lys Tyr Ser Ser Ser
         35                  40                  45

Asn Ile Phe Ile Pro Asn Gly Ser Arg Leu Tyr Leu Asp Val Gly Ser
     50                  55                  60

His Pro Glu Tyr Ala Thr Ala Glu Cys Asp Asn Leu Thr Gln Leu Ile
 65                  70                  75                  80

Asn Phe Glu Lys Ala Gly Asp Val Ile Ala Asp Arg Met Ala Val Asp
                 85                  90                  95

Ala Glu Glu Ser Leu Ala Lys Glu Asp Ile Ala Gly Gln Val Tyr Leu
            100                 105                 110

Phe Lys Asn Asn Val Asp Ser Val Gly Asn Ser Tyr Gly Cys His Glu
        115                 120                 125

Asn Tyr Leu Val Gly Arg Ser Met Pro Leu Lys Ala Leu Gly Lys Arg
    130                 135                 140

Leu Met Pro Phe Leu Ile Thr Arg Gln Leu Ile Cys Gly Ala Gly Arg
145                 150                 155                 160

Ile His His Pro Asn Pro Leu Asp Lys Gly Glu Ser Phe Pro Leu Gly
                165                 170                 175

Tyr Cys Ile Ser Gln Arg Ser Asp His Val Trp Glu Gly Val Ser Ser
            180                 185                 190

Ala Thr Thr Arg Ser Arg Pro Ile Ile Asn Thr Arg Asp Glu Pro His
        195                 200                 205

Ala Asp Ser His Ser Tyr Arg Arg Leu His Val Ile Val Gly Asp Ala
    210                 215                 220
```

```
Asn Met Ala Glu Pro Ser Ile Ala Leu Lys Val Gly Ser Thr Leu Leu
225                 230                 235                 240

Val Leu Glu Met Ile Glu Ala Asp Phe Gly Leu Pro Ser Leu Glu Leu
                245                 250                 255

Ala Asn Asp Ile Ala Ser Ile Arg Glu Ile Ser Arg Asp Ala Thr Gly
            260                 265                 270

Ser Thr Leu Leu Ser Leu Lys Asp Gly Thr Thr Met Thr Ala Leu Gln
        275                 280                 285

Ile Gln Gln Val Val Phe Glu His Ala Ser Lys Trp Leu Glu Gln Arg
    290                 295                 300

Pro Glu Pro Glu Phe Ser Gly Thr Ser Asn Thr Glu Met Ala Arg Val
305                 310                 315                 320

Leu Asp Leu Trp Gly Arg Met Leu Lys Ala Ile Glu Ser Gly Asp Phe
                325                 330                 335

Ser Glu Val Asp Thr Glu Ile Asp Trp Val Ile Lys Lys Lys Leu Ile
            340                 345                 350

Asp Arg Phe Ile Gln Arg Gly Asn Leu Gly Leu Asp Asp Pro Lys Leu
        355                 360                 365

Ala Gln Val Asp Leu Thr Tyr His Asp Ile Arg Pro Gly Arg Gly Leu
    370                 375                 380

Phe Ser Val Leu Gln Ser Arg Gly Met Ile Lys Arg Trp Thr Thr Asp
385                 390                 395                 400

Glu Ala Ile Leu Ala Ala Val Asp Thr Ala Pro Asp Thr Thr Arg Ala
                405                 410                 415

His Leu Arg Gly Arg Ile Leu Lys Ala Ala Asp Thr Leu Gly Val Pro
            420                 425                 430

Val Thr Val Asp Trp Met Arg His Lys Val Asn Arg Pro Glu Pro Gln
        435                 440                 445

Ser Val Glu Leu Gly Asp Pro
    450                 455
```

<210> 527
<211> 519
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(496)
<223> RXN01167

<400> 527
gtgtcgtttt atttgcacac tagcaggtaa actgtgtgag acgaattctt ttgcggcaac 60

ttggaggccg cattctagta ggcaaaggac tgatacctag atg gca gat cgc gtt 115
Met Ala Asp Arg Val

```
                                                    1               5

ctt cgt ggc agc cgc atg ggc gcc gtg agc tat gag acg gat agg gac   163
Leu Arg Gly Ser Arg Met Gly Ala Val Ser Tyr Glu Thr Asp Arg Asp
                10                  15                  20

cac gat ctg gct cct cgc cag ctc gtg aag tac aag acc gca gac ggg   211
His Asp Leu Ala Pro Arg Gln Leu Val Lys Tyr Lys Thr Ala Asp Gly
            25                  30                  35

gaa atc tat gag gtt ccc ttc gct gat gat gcg gaa atc ccc gag gag   259
Glu Ile Tyr Glu Val Pro Phe Ala Asp Asp Ala Glu Ile Pro Glu Glu
        40                  45                  50

tgg atg tgc aag aac ggt aag cta ggc atc ctc atg gaa ggt gag gga   307
Trp Met Cys Lys Asn Gly Lys Leu Gly Ile Leu Met Glu Gly Glu Gly
    55                  60                  65

gtc gag tcc aag ccg gtc aag cct cca cgt act cac tgg gat atg ttg   355
Val Glu Ser Lys Pro Val Lys Pro Pro Arg Thr His Trp Asp Met Leu
70                  75                  80                  85

cgt gag cgt cgc tca att gaa gag ctg gat gtg ctg ctg gaa gag cgc   403
Arg Glu Arg Arg Ser Ile Glu Glu Leu Asp Val Leu Leu Glu Glu Arg
                90                  95                  100

atc gag gca ctt cgt aag cgt cgt cgc aat gca gcg aaa ctg ctg aag   451
Ile Glu Ala Leu Arg Lys Arg Arg Arg Asn Ala Ala Lys Leu Leu Lys
            105                 110                 115

gct cag caa gag gct gaa gaa gca gaa aag gca gct gaa gag gtt       496
Ala Gln Gln Glu Ala Glu Glu Ala Glu Lys Ala Ala Glu Glu Val
        120                 125                 130

taatcttcct gcctaagtta gaa                                       519


<210> 528
<211> 132
<212> PRT
<213> Corynebacterium glutamicum

<400> 528
Met Ala Asp Arg Val Leu Arg Gly Ser Arg Met Gly Ala Val Ser Tyr
  1               5                  10                  15

Glu Thr Asp Arg Asp His Asp Leu Ala Pro Arg Gln Leu Val Lys Tyr
            20                  25                  30

Lys Thr Ala Asp Gly Glu Ile Tyr Glu Val Pro Phe Ala Asp Asp Ala
        35                  40                  45

Glu Ile Pro Glu Glu Trp Met Cys Lys Asn Gly Lys Leu Gly Ile Leu
    50                  55                  60

Met Glu Gly Glu Gly Val Glu Ser Lys Pro Val Lys Pro Pro Arg Thr
65                  70                  75                  80

His Trp Asp Met Leu Arg Glu Arg Arg Ser Ile Glu Glu Leu Asp Val
                85                  90                  95
```

```
Leu Leu Glu Glu Arg Ile Glu Ala Leu Arg Lys Arg Arg Arg Asn Ala
            100                 105                 110

Ala Lys Leu Leu Lys Ala Gln Gln Glu Ala Glu Glu Ala Glu Lys Ala
        115                 120                 125

Ala Glu Glu Val
    130
```

<210> 529
<211> 344
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(321)
<223> FRXA01167

<400> 529

```
cct cgc cag ctc gtg aag tac aag acc gca gac ggg gaa atc tat gag   48
Pro Arg Gln Leu Val Lys Tyr Lys Thr Ala Asp Gly Glu Ile Tyr Glu
  1               5                  10                  15

gtt ccc ttc gct gat gat gcg gaa atc ccc gag gag tgg atg tgc aag   96
Val Pro Phe Ala Asp Asp Ala Glu Ile Pro Glu Glu Trp Met Cys Lys
             20                  25                  30

aac ggt aag cta ggc atc ctc atg gaa ggt gag gga gtc gag tcc aag   144
Asn Gly Lys Leu Gly Ile Leu Met Glu Gly Glu Gly Val Glu Ser Lys
         35                  40                  45

ccg gtc aag cct cca cgt act cac tgg gat atg ttg cgt gag cgt cgc   192
Pro Val Lys Pro Pro Arg Thr His Trp Asp Met Leu Arg Glu Arg Arg
     50                  55                  60

tca att gaa gag ctg gat gtg ctg ctg gaa gag cgc atc gag gca ctt   240
Ser Ile Glu Glu Leu Asp Val Leu Leu Glu Glu Arg Ile Glu Ala Leu
 65                  70                  75                  80

cgt aag cgt cgt cgc aat gca gcg aaa ctg ctg aag gct cag caa gag   288
Arg Lys Arg Arg Arg Asn Ala Ala Lys Leu Leu Lys Ala Gln Gln Glu
                 85                  90                  95

gct gaa gaa gca gaa aag gca gct gaa gag gtt taatcttcct gcctaagtta 341
Ala Glu Glu Ala Glu Lys Ala Ala Glu Glu Val
            100                 105

gaa                                                               344
```

<210> 530
<211> 107
<212> PRT
<213> Corynebacterium glutamicum

<400> 530

```
Pro Arg Gln Leu Val Lys Tyr Lys Thr Ala Asp Gly Glu Ile Tyr Glu
  1               5                  10                  15
```

```
Val Pro Phe Ala Asp Asp Ala Glu Ile Pro Glu Glu Trp Met Cys Lys
            20                  25                  30

Asn Gly Lys Leu Gly Ile Leu Met Glu Gly Glu Gly Val Glu Ser Lys
        35                  40                  45

Pro Val Lys Pro Pro Arg Thr His Trp Asp Met Leu Arg Glu Arg Arg
    50                  55                  60

Ser Ile Glu Glu Leu Asp Val Leu Leu Glu Glu Arg Ile Glu Ala Leu
65                  70                  75                  80

Arg Lys Arg Arg Arg Asn Ala Ala Lys Leu Leu Lys Ala Gln Gln Glu
                85                  90                  95

Ala Glu Glu Ala Glu Lys Ala Ala Glu Glu Val
            100                 105


<210> 531
<211> 1119
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1096)
<223> RXN01169

<400> 531
tcttgatcgg aatcggcgca aacatcgtct acgaacacct cagcgcgtaa ccctcggcgc 60

attatcctca gacagctttt agcgcaaaca aggagcatca ttg aaa cgg gtc gtt   115
                                            Leu Lys Arg Val Val
                                              1               5

gaa gcg tgg gat aga ttt caa atc cca ctg tat atc acg gct ctt atc   163
Glu Ala Trp Asp Arg Phe Gln Ile Pro Leu Tyr Ile Thr Ala Leu Ile
                10                  15                  20

gcc gga gca ctg gtg ggt ttg cag tgg cca ggc tct aca ggg ggt ttc   211
Ala Gly Ala Leu Val Gly Leu Gln Trp Pro Gly Ser Thr Gly Gly Phe
            25                  30                  35

gaa agc gcc att aac cca gcg tta atg gcg ctg ctt tat gcc act ttt   259
Glu Ser Ala Ile Asn Pro Ala Leu Met Ala Leu Leu Tyr Ala Thr Phe
        40                  45                  50

ctc ggt att ccg atc act cgg att ggt gca gcg ctg aaa gat ctg aga   307
Leu Gly Ile Pro Ile Thr Arg Ile Gly Ala Ala Leu Lys Asp Leu Arg
    55                  60                  65

ttt ctc ata gtg ctc atg tcc gtc aat ttt gtt gca gtg cct ctg gtg   355
Phe Leu Ile Val Leu Met Ser Val Asn Phe Val Ala Val Pro Leu Val
70                  75                  80                  85

gct ttt gcg ttg agc aga ttc att gcg ggt gat gag gcg ctt cta atc   403
Ala Phe Ala Leu Ser Arg Phe Ile Ala Gly Asp Glu Ala Leu Leu Ile
                90                  95                  100

gga ttt tta ctg gtg att ctc gcg ccg tgc att gat tac gtc att gtc   451
```

```
Gly Phe Leu Leu Val Ile Leu Ala Pro Cys Ile Asp Tyr Val Ile Val
            105                 110                 115

ttt gct ggt ttg gcc agg gcc gcc caa gac aag ctc ctt gcc gcc acg   499
Phe Ala Gly Leu Ala Arg Ala Ala Gln Asp Lys Leu Leu Ala Ala Thr
        120                 125                 130

cca ata tta atg ctt gtc caa atc ctg ctg atc ccc gtc ttc ctg gct   547
Pro Ile Leu Met Leu Val Gln Ile Leu Leu Ile Pro Val Phe Leu Ala
    135                 140                 145

gtt ttt gtg ggt tca gat gcc ctt ggc tca atc tct ttc ggc cca ttt   595
Val Phe Val Gly Ser Asp Ala Leu Gly Ser Ile Ser Phe Gly Pro Phe
150                 155                 160                 165

gta gaa gca ttt ttc ctc ctg att ctc att cca ctt gtt gct gct gcg   643
Val Glu Ala Phe Phe Leu Leu Ile Leu Ile Pro Leu Val Ala Ala Ala
                170                 175                 180

gga act cag caa gtg gca aga aag tgg cag gta gga cgt aca att atg   691
Gly Thr Gln Gln Val Ala Arg Lys Trp Gln Val Gly Arg Thr Ile Met
            185                 190                 195

gct gct gca gaa gca atc atg gtg cct tta atg atg ctg acg ttg ttc   739
Ala Ala Ala Glu Ala Ile Met Val Pro Leu Met Met Leu Thr Leu Phe
        200                 205                 210

gct gtc atc gca tcg caa gtg gaa gct gtg agt ggt caa ttc acc gat   787
Ala Val Ile Ala Ser Gln Val Glu Ala Val Ser Gly Gln Phe Thr Asp
    215                 220                 225

atc gcc aca gta gtg cca cta tat gtc gcc ttt ttg atg gtg atg att   835
Ile Ala Thr Val Val Pro Leu Tyr Val Ala Phe Leu Met Val Met Ile
230                 235                 240                 245

cca att ggt ggc ggg ata tcc aaa ctc ggt ggc tta ggt ttc aaa gag   883
Pro Ile Gly Gly Gly Ile Ser Lys Leu Gly Gly Leu Gly Phe Lys Glu
                250                 255                 260

caa cga gcc atc gtt ttt agc gga gca acc cgt aac tct ttg gtc gtt   931
Gln Arg Ala Ile Val Phe Ser Gly Ala Thr Arg Asn Ser Leu Val Val
            265                 270                 275

tta cct tta gcg tta gca ctt ccc gca ggc ctg gaa ata gcg gcc gtc   979
Leu Pro Leu Ala Leu Ala Leu Pro Ala Gly Leu Glu Ile Ala Ala Val
        280                 285                 290

gta gtt gtc act caa acc ctc gtg gaa ctg att ggc atg gtt gtc tac  1027
Val Val Val Thr Gln Thr Leu Val Glu Leu Ile Gly Met Val Val Tyr
    295                 300                 305

gtg cgc atc atc cct tta att ttc cat gaa aag cag aca tac agg aaa  1075
Val Arg Ile Ile Pro Leu Ile Phe His Glu Lys Gln Thr Tyr Arg Lys
310                 315                 320                 325

ctt tca ggc ata ggg gag tca tgaaacagaa cggcaagcta agg            1119
Leu Ser Gly Ile Gly Glu Ser
                330
```

<210> 532

<211> 332
<212> PRT
<213> Corynebacterium glutamicum

<400> 532

```
Leu Lys Arg Val Val Glu Ala Trp Asp Arg Phe Gln Ile Pro Leu Tyr
  1               5                  10                  15

Ile Thr Ala Leu Ile Ala Gly Ala Leu Val Gly Leu Gln Trp Pro Gly
             20                  25                  30

Ser Thr Gly Gly Phe Glu Ser Ala Ile Asn Pro Ala Leu Met Ala Leu
         35                  40                  45

Leu Tyr Ala Thr Phe Leu Gly Ile Pro Ile Thr Arg Ile Gly Ala Ala
     50                  55                  60

Leu Lys Asp Leu Arg Phe Leu Ile Val Leu Met Ser Val Asn Phe Val
 65                  70                  75                  80

Ala Val Pro Leu Val Ala Phe Ala Leu Ser Arg Phe Ile Ala Gly Asp
                 85                  90                  95

Glu Ala Leu Leu Ile Gly Phe Leu Leu Val Ile Leu Ala Pro Cys Ile
            100                 105                 110

Asp Tyr Val Ile Val Phe Ala Gly Leu Ala Arg Ala Ala Gln Asp Lys
        115                 120                 125

Leu Leu Ala Ala Thr Pro Ile Leu Met Leu Val Gln Ile Leu Leu Ile
    130                 135                 140

Pro Val Phe Leu Ala Val Phe Val Gly Ser Asp Ala Leu Gly Ser Ile
145                 150                 155                 160

Ser Phe Gly Pro Phe Val Glu Ala Phe Phe Leu Leu Ile Leu Ile Pro
                165                 170                 175

Leu Val Ala Ala Ala Gly Thr Gln Gln Val Ala Arg Lys Trp Gln Val
            180                 185                 190

Gly Arg Thr Ile Met Ala Ala Ala Glu Ala Ile Met Val Pro Leu Met
        195                 200                 205

Met Leu Thr Leu Phe Ala Val Ile Ala Ser Gln Val Glu Ala Val Ser
    210                 215                 220

Gly Gln Phe Thr Asp Ile Ala Thr Val Val Pro Leu Tyr Val Ala Phe
225                 230                 235                 240

Leu Met Val Met Ile Pro Ile Gly Gly Gly Ile Ser Lys Leu Gly Gly
                245                 250                 255

Leu Gly Phe Lys Glu Gln Arg Ala Ile Val Phe Ser Gly Ala Thr Arg
            260                 265                 270

Asn Ser Leu Val Val Leu Pro Leu Ala Leu Ala Leu Pro Ala Gly Leu
        275                 280                 285

Glu Ile Ala Ala Val Val Val Val Thr Gln Thr Leu Val Glu Leu Ile
    290                 295                 300
```

```
Gly Met Val Val Tyr Val Arg Ile Ile Pro Leu Ile Phe His Glu Lys
305                 310                 315                 320

Gln Thr Tyr Arg Lys Leu Ser Gly Ile Gly Glu Ser
                325                 330


<210> 533
<211> 590
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(567)
<223> FRXA01169

<400> 533
atc ccc gtc ttc ctg gct gtt ttt gtg ggt tca gat gcc ctt ggc tca   48
Ile Pro Val Phe Leu Ala Val Phe Val Gly Ser Asp Ala Leu Gly Ser
  1               5                  10                  15

atc tct ttc ggc cca ttt gta gaa gca ttt ttc ctc ctg att ctc att   96
Ile Ser Phe Gly Pro Phe Val Glu Ala Phe Phe Leu Leu Ile Leu Ile
             20                  25                  30

cca ctt gtt gct gct gcg gga act cag caa gtg gca aga aag tgg cag   144
Pro Leu Val Ala Ala Ala Gly Thr Gln Gln Val Ala Arg Lys Trp Gln
         35                  40                  45

gta gga cgt aca att atg gct gct gca gaa gca atc atg gtg cct tta   192
Val Gly Arg Thr Ile Met Ala Ala Ala Glu Ala Ile Met Val Pro Leu
     50                  55                  60

atg atg ctg acg ttg ttc gct gtc atc gca tcg caa gtg gaa gct gtg   240
Met Met Leu Thr Leu Phe Ala Val Ile Ala Ser Gln Val Glu Ala Val
 65                  70                  75                  80

agt ggt caa ttc acc gat atc gcc aca gta gtg cca cta tat gtc gcc   288
Ser Gly Gln Phe Thr Asp Ile Ala Thr Val Val Pro Leu Tyr Val Ala
                 85                  90                  95

ttt ttg atg gtg atg att cca att ggt ggc ggg ata tcc aaa ctc ggt   336
Phe Leu Met Val Met Ile Pro Ile Gly Gly Gly Ile Ser Lys Leu Gly
            100                 105                 110

ggc tta ggt ttc aaa gag caa cga gcc atc gtt ttt agc gga gca acc   384
Gly Leu Gly Phe Lys Glu Gln Arg Ala Ile Val Phe Ser Gly Ala Thr
        115                 120                 125

cgt aac tct ttg gtc gtt tta cct tta gcg tta gca ctt ccc gca ggc   432
Arg Asn Ser Leu Val Val Leu Pro Leu Ala Leu Ala Leu Pro Ala Gly
    130                 135                 140

ctg gaa ata gcg gcc gtc gta gtt gtc act caa acc ctc gtg gaa ctg   480
Leu Glu Ile Ala Ala Val Val Val Val Thr Gln Thr Leu Val Glu Leu
145                 150                 155                 160

att ggc atg gtt gtc tac gtg cgc atc atc cct tta att ttc cat gaa   528
Ile Gly Met Val Val Tyr Val Arg Ile Ile Pro Leu Ile Phe His Glu
```

```
                165                 170                 175

aag cag aca tac agg aaa ctt tca ggc ata ggg gag tca tgaaacagaa    577
Lys Gln Thr Tyr Arg Lys Leu Ser Gly Ile Gly Glu Ser
            180                 185

cggcaagcta agg                                                    590


<210> 534
<211> 189
<212> PRT
<213> Corynebacterium glutamicum

<400> 534
Ile Pro Val Phe Leu Ala Val Phe Val Gly Ser Asp Ala Leu Gly Ser
  1               5                  10                  15

Ile Ser Phe Gly Pro Phe Val Glu Ala Phe Phe Leu Leu Ile Leu Ile
             20                  25                  30

Pro Leu Val Ala Ala Ala Gly Thr Gln Gln Val Ala Arg Lys Trp Gln
         35                  40                  45

Val Gly Arg Thr Ile Met Ala Ala Ala Glu Ala Ile Met Val Pro Leu
     50                  55                  60

Met Met Leu Thr Leu Phe Ala Val Ile Ala Ser Gln Val Glu Ala Val
 65                  70                  75                  80

Ser Gly Gln Phe Thr Asp Ile Ala Thr Val Val Pro Leu Tyr Val Ala
                 85                  90                  95

Phe Leu Met Val Met Ile Pro Ile Gly Gly Gly Ile Ser Lys Leu Gly
            100                 105                 110

Gly Leu Gly Phe Lys Glu Gln Arg Ala Ile Val Phe Ser Gly Ala Thr
        115                 120                 125

Arg Asn Ser Leu Val Val Leu Pro Leu Ala Leu Ala Leu Pro Ala Gly
    130                 135                 140

Leu Glu Ile Ala Ala Val Val Val Val Thr Gln Thr Leu Val Glu Leu
145                 150                 155                 160

Ile Gly Met Val Val Tyr Val Arg Ile Ile Pro Leu Ile Phe His Glu
                165                 170                 175

Lys Gln Thr Tyr Arg Lys Leu Ser Gly Ile Gly Glu Ser
            180                 185


<210> 535
<211> 738
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(715)
<223> RXN01173
```

<400> 535
agatctgttt ctatgtatta aagatcacac cgagtggtgg aatttcctca agtgatttac 60

ccacaatgga ctttgttgat acccaattcg agaaaggcca atg cac gtg agc act 115
Met His Val Ser Thr
1 5

ctt cca aac aag aaa ctg cgt act cgc att ttc gca ggc acc gct gcc 163
Leu Pro Asn Lys Lys Leu Arg Thr Arg Ile Phe Ala Gly Thr Ala Ala
10 15 20

gtc gca ctg tca ctt ggt gtt gcg tct tgc tca aac gca gaa gat gct 211
Val Ala Leu Ser Leu Gly Val Ala Ser Cys Ser Asn Ala Glu Asp Ala
25 30 35

gtg gat agc gca aca gat gct gcc aac tct gca acc tcc gcc gcg gga 259
Val Asp Ser Ala Thr Asp Ala Ala Asn Ser Ala Thr Ser Ala Ala Gly
40 45 50

tct gca att aac gat gcc acc ggc act tcc agc gca tcc acc aca gag 307
Ser Ala Ile Asn Asp Ala Thr Gly Thr Ser Ser Ala Ser Thr Thr Glu
55 60 65

cct tcc gga acc tct gga tcc gac tcc ggg tct gac tct gct gga gga 355
Pro Ser Gly Thr Ser Gly Ser Asp Ser Gly Ser Asp Ser Ala Gly Gly
70 75 80 85

gac acc act gaa gta gaa agc gcc gat ggg tcc acc atc agc atc cca 403
Asp Thr Thr Glu Val Glu Ser Ala Asp Gly Ser Thr Ile Ser Ile Pro
90 95 100

act gcc gtc gtc acc gct gca aat gct gca gga ttc agt acc ccg gaa 451
Thr Ala Val Val Thr Ala Ala Asn Ala Ala Gly Phe Ser Thr Pro Glu
105 110 115

tcc gtg gaa gaa ggc ccg aat ggt gag tca ttg gtg acg ttc cct gaa 499
Ser Val Glu Glu Gly Pro Asn Gly Glu Ser Leu Val Thr Phe Pro Glu
120 125 130

ggc tac att gtt aac tct gca gaa ggt ggt gca caa gca ctg gtc ggc 547
Gly Tyr Ile Val Asn Ser Ala Glu Gly Gly Ala Gln Ala Leu Val Gly
135 140 145

atg atc ggt gaa acc tgg atc ggc gaa ggc gga cta tcc gcg gca gtg 595
Met Ile Gly Glu Thr Trp Ile Gly Glu Gly Gly Leu Ser Ala Ala Val
150 155 160 165

ggt ctc cca act ggg cct gaa gaa gca aca aca aat ggt tgg act caa 643
Gly Leu Pro Thr Gly Pro Glu Glu Ala Thr Thr Asn Gly Trp Thr Gln
170 175 180

cag ttc aca tct gga gta att agc tgg ctt gat gat gga tca gga cag 691
Gln Phe Thr Ser Gly Val Ile Ser Trp Leu Asp Asp Gly Ser Gly Gln
185 190 195

ttc gca gct tct gtt gaa cct gct taagggaatc tcacctggcc tcc 738
Phe Ala Ala Ser Val Glu Pro Ala
200 205

<210> 536
<211> 205
<212> PRT
<213> Corynebacterium glutamicum

<400> 536
Met His Val Ser Thr Leu Pro Asn Lys Lys Leu Arg Thr Arg Ile Phe
1 5 10 15

Ala Gly Thr Ala Ala Val Ala Leu Ser Leu Gly Val Ala Ser Cys Ser
20 25 30

Asn Ala Glu Asp Ala Val Asp Ser Ala Thr Asp Ala Ala Asn Ser Ala
35 40 45

Thr Ser Ala Ala Gly Ser Ala Ile Asn Asp Ala Thr Gly Thr Ser Ser
50 55 60

Ala Ser Thr Thr Glu Pro Ser Gly Thr Ser Gly Ser Asp Ser Gly Ser
65 70 75 80

Asp Ser Ala Gly Gly Asp Thr Thr Glu Val Glu Ser Ala Asp Gly Ser
85 90 95

Thr Ile Ser Ile Pro Thr Ala Val Val Thr Ala Ala Asn Ala Ala Gly
100 105 110

Phe Ser Thr Pro Glu Ser Val Glu Glu Gly Pro Asn Gly Glu Ser Leu
115 120 125

Val Thr Phe Pro Glu Gly Tyr Ile Val Asn Ser Ala Glu Gly Gly Ala
130 135 140

Gln Ala Leu Val Gly Met Ile Gly Glu Thr Trp Ile Gly Glu Gly Gly
145 150 155 160

Leu Ser Ala Ala Val Gly Leu Pro Thr Gly Pro Glu Glu Ala Thr Thr
165 170 175

Asn Gly Trp Thr Gln Gln Phe Thr Ser Gly Val Ile Ser Trp Leu Asp
180 185 190

Asp Gly Ser Gly Gln Phe Ala Ala Ser Val Glu Pro Ala
195 200 205

<210> 537
<211> 738
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(715)
<223> FRXA01173

<400> 537
agatctgttt ctatgtatta aagatcacac cgagtggtgg aatttcctca agtgatttac 60

ccacaatgga ctttgttgat acccaattcg agaaaggcca atg cac gtg agc act 115
Met His Val Ser Thr

```
                                                    1               5

ctt cca aac aag aaa ctg cgt act cgc att ttc gca ggc acc gct gcc   163
Leu Pro Asn Lys Lys Leu Arg Thr Arg Ile Phe Ala Gly Thr Ala Ala
                10                  15                  20

gtc gca ctg tca ctt ggt gtt gcg tct tgc tca aac gca gaa gat gct   211
Val Ala Leu Ser Leu Gly Val Ala Ser Cys Ser Asn Ala Glu Asp Ala
            25                  30                  35

gtg gat agc gca aca gat gct gcc aac tct gca acc tcc gcc gcg gga   259
Val Asp Ser Ala Thr Asp Ala Ala Asn Ser Ala Thr Ser Ala Ala Gly
        40                  45                  50

tct gca att aac gat gcc acc ggc act tcc agc gca tcc acc aca gag   307
Ser Ala Ile Asn Asp Ala Thr Gly Thr Ser Ser Ala Ser Thr Thr Glu
    55                  60                  65

cct tcc gga acc tct gga tcc gac tcc ggg tct gac tct gct gga gga   355
Pro Ser Gly Thr Ser Gly Ser Asp Ser Gly Ser Asp Ser Ala Gly Gly
70                  75                  80                  85

gac acc act gaa gta gaa agc gcc gat ggg tcc acc atc agc atc cca   403
Asp Thr Thr Glu Val Glu Ser Ala Asp Gly Ser Thr Ile Ser Ile Pro
                90                  95                  100

act gcc gtc gtc acc gct gca aat gct gca gga ttc agt acc ccg gaa   451
Thr Ala Val Val Thr Ala Ala Asn Ala Ala Gly Phe Ser Thr Pro Glu
            105                 110                 115

tcc gtg gaa gaa ggc ccg aat ggt gag tca ttg gtg acg ttc cct gaa   499
Ser Val Glu Glu Gly Pro Asn Gly Glu Ser Leu Val Thr Phe Pro Glu
        120                 125                 130

ggc tac att gtt aac tct gca gaa ggt ggt gca caa gca ctg gtc ggc   547
Gly Tyr Ile Val Asn Ser Ala Glu Gly Gly Ala Gln Ala Leu Val Gly
    135                 140                 145

atg atc ggt gaa acc tgg atc ggc gaa ggc gga cta tcc gcg gca gtg   595
Met Ile Gly Glu Thr Trp Ile Gly Glu Gly Gly Leu Ser Ala Ala Val
150                 155                 160                 165

ggt ctc cca act ggg cct gaa gaa gca aca aca aat ggt tgg act caa   643
Gly Leu Pro Thr Gly Pro Glu Glu Ala Thr Thr Asn Gly Trp Thr Gln
                170                 175                 180

cag ttc aca tct gga gta att agc tgg ctt gat gat gga tca gga cag   691
Gln Phe Thr Ser Gly Val Ile Ser Trp Leu Asp Asp Gly Ser Gly Gln
            185                 190                 195

ttc gca gct tct gtt gaa cct gct taagggaatc tcacctggcc tcc         738
Phe Ala Ala Ser Val Glu Pro Ala
        200                 205
```

<210> 538
<211> 205
<212> PRT
<213> Corynebacterium glutamicum

<400> 538

```
Met His Val Ser Thr Leu Pro Asn Lys Lys Leu Arg Thr Arg Ile Phe
  1               5                  10                  15

Ala Gly Thr Ala Ala Val Ala Leu Ser Leu Gly Val Ala Ser Cys Ser
             20                  25                  30

Asn Ala Glu Asp Ala Val Asp Ser Ala Thr Asp Ala Ala Asn Ser Ala
         35                  40                  45

Thr Ser Ala Ala Gly Ser Ala Ile Asn Asp Ala Thr Gly Thr Ser Ser
     50                  55                  60

Ala Ser Thr Thr Glu Pro Ser Gly Thr Ser Gly Ser Asp Ser Gly Ser
 65                  70                  75                  80

Asp Ser Ala Gly Gly Asp Thr Thr Glu Val Glu Ser Ala Asp Gly Ser
                 85                  90                  95

Thr Ile Ser Ile Pro Thr Ala Val Val Thr Ala Ala Asn Ala Ala Gly
            100                 105                 110

Phe Ser Thr Pro Glu Ser Val Glu Glu Gly Pro Asn Gly Glu Ser Leu
        115                 120                 125

Val Thr Phe Pro Glu Gly Tyr Ile Val Asn Ser Ala Glu Gly Gly Ala
    130                 135                 140

Gln Ala Leu Val Gly Met Ile Gly Glu Thr Trp Ile Gly Glu Gly Gly
145                 150                 155                 160

Leu Ser Ala Ala Val Gly Leu Pro Thr Gly Pro Glu Glu Ala Thr Thr
                165                 170                 175

Asn Gly Trp Thr Gln Gln Phe Thr Ser Gly Val Ile Ser Trp Leu Asp
            180                 185                 190

Asp Gly Ser Gly Gln Phe Ala Ala Ser Val Glu Pro Ala
        195                 200                 205
```

<210> 539
<211> 873
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(850)
<223> RXN01174

<400> 539
atatcgcaac cgctgttaat gaagaggaag aggctcgcga tatcgcgaag ctgtgccagg 60

agatggtgga attagctcgg aatattgaga agttgaggta atg agc aac atg cag 115
                                                Met Ser Asn Met Gln
                                                  1   5

gga aac gat tcc aag aaa tct agc ggc gcg agt cgt gcg gag agc cca 163
Gly Asn Asp Ser Lys Lys Ser Ser Gly Ala Ser Arg Ala Glu Ser Pro
                10   15   20

```
ctg atc aag ttc cgg aca ttg att atc gtc atc ttt gtc atc ttg atc   211
Leu Ile Lys Phe Arg Thr Leu Ile Ile Val Ile Phe Val Ile Leu Ile
            25                  30                  35

gtt ggt ttg gca tct att gca gtg gga cct gtc gtg tac cag ctc atc   259
Val Gly Leu Ala Ser Ile Ala Val Gly Pro Val Val Tyr Gln Leu Ile
        40                  45                  50

atg gga cct ggt gtg aaa acc gaa gga atc cag gct gat ggc gca gca   307
Met Gly Pro Gly Val Lys Thr Glu Gly Ile Gln Ala Asp Gly Ala Ala
    55                  60                  65

cct gcg tcc acc gac atg aac ggc acc tgg gat gtt gcc cca ggg agt   355
Pro Ala Ser Thr Asp Met Asn Gly Thr Trp Asp Val Ala Pro Gly Ser
70                  75                  80                  85

att cca aac acc acc tca gct gga ttc acc ttc gct gag atc ctg cca   403
Ile Pro Asn Thr Thr Ser Ala Gly Phe Thr Phe Ala Glu Ile Leu Pro
                90                  95                  100

ggc gaa gaa aag atc acc tcc ggc tca acc act ggt gtc act ggc gaa   451
Gly Glu Glu Lys Ile Thr Ser Gly Ser Thr Thr Gly Val Thr Gly Glu
            105                 110                 115

gtg gtc atc gag gat aac tcc ctg atc tct ggt ctg att acc gtc aac   499
Val Val Ile Glu Asp Asn Ser Leu Ile Ser Gly Leu Ile Thr Val Asn
        120                 125                 130

atg act cac atc acc acc gat cag gaa aag cgc gac atc aac gtg cgc   547
Met Thr His Ile Thr Thr Asp Gln Glu Lys Arg Asp Ile Asn Val Arg
    135                 140                 145

act aag ctc ttc cac acc gat cag tac cca gaa gca acc ttt gag gtt   595
Thr Lys Leu Phe His Thr Asp Gln Tyr Pro Glu Ala Thr Phe Glu Val
150                 155                 160                 165

acc gat tcc gtt gat ctt tct gcg ctc cca gac acc gga tcc att gct   643
Thr Asp Ser Val Asp Leu Ser Ala Leu Pro Asp Thr Gly Ser Ile Ala
                170                 175                 180

cag gtt gtc atc cca ggc gag ttg acc atc cac ggt gaa acc aag gct   691
Gln Val Val Ile Pro Gly Glu Leu Thr Ile His Gly Glu Thr Lys Ala
            185                 190                 195

gtg gag cct acc ttt gat gta ctt cgt act ggt gac caa gtt atc gtg   739
Val Glu Pro Thr Phe Asp Val Leu Arg Thr Gly Asp Gln Val Ile Val
        200                 205                 210

gct tcc gat atc gaa atc aac cgc ctc gac ttc ggt gta gaa acc cca   787
Ala Ser Asp Ile Glu Ile Asn Arg Leu Asp Phe Gly Val Glu Thr Pro
    215                 220                 225

gag ttc atc gcc gca aag atc aat gag acc ggc gag atc aac gtc cga   835
Glu Phe Ile Ala Ala Lys Ile Asn Glu Thr Gly Glu Ile Asn Val Arg
230                 235                 240                 245

atc gta ttg gag aaa taaaccatga tggcatcacg gat                    873
Ile Val Leu Glu Lys
                250
```

<210> 540
<211> 250
<212> PRT
<213> Corynebacterium glutamicum

<400> 540
Met Ser Asn Met Gln Gly Asn Asp Ser Lys Lys Ser Ser Gly Ala Ser
1 5 10 15

Arg Ala Glu Ser Pro Leu Ile Lys Phe Arg Thr Leu Ile Ile Val Ile
20 25 30

Phe Val Ile Leu Ile Val Gly Leu Ala Ser Ile Ala Val Gly Pro Val
35 40 45

Val Tyr Gln Leu Ile Met Gly Pro Gly Val Lys Thr Glu Gly Ile Gln
50 55 60

Ala Asp Gly Ala Ala Pro Ala Ser Thr Asp Met Asn Gly Thr Trp Asp
65 70 75 80

Val Ala Pro Gly Ser Ile Pro Asn Thr Thr Ser Ala Gly Phe Thr Phe
85 90 95

Ala Glu Ile Leu Pro Gly Glu Glu Lys Ile Thr Ser Gly Ser Thr Thr
100 105 110

Gly Val Thr Gly Glu Val Val Ile Glu Asp Asn Ser Leu Ile Ser Gly
115 120 125

Leu Ile Thr Val Asn Met Thr His Ile Thr Thr Asp Gln Glu Lys Arg
130 135 140

Asp Ile Asn Val Arg Thr Lys Leu Phe His Thr Asp Gln Tyr Pro Glu
145 150 155 160

Ala Thr Phe Glu Val Thr Asp Ser Val Asp Leu Ser Ala Leu Pro Asp
165 170 175

Thr Gly Ser Ile Ala Gln Val Val Ile Pro Gly Glu Leu Thr Ile His
180 185 190

Gly Glu Thr Lys Ala Val Glu Pro Thr Phe Asp Val Leu Arg Thr Gly
195 200 205

Asp Gln Val Ile Val Ala Ser Asp Ile Glu Ile Asn Arg Leu Asp Phe
210 215 220

Gly Val Glu Thr Pro Glu Phe Ile Ala Ala Lys Ile Asn Glu Thr Gly
225 230 235 240

Glu Ile Asn Val Arg Ile Val Leu Glu Lys
245 250

<210> 541
<211> 873
<212> DNA
<213> Corynebacterium glutamicum

<220>

<221> CDS
<222> (101)..(850)
<223> FRXA01174

<400> 541
atatcgcaac cgctgttaat gaagaggaag aggctcgcga tatcgcgaag ctgtgccagg 60

agatggtgga attagctcgg aatattgaga agttgaggta atg agc aac atg cag 115
Met Ser Asn Met Gln
1 5

gga aac gat tcc aag aaa tct agc ggc gcg agt cgt gcg gag agc cca 163
Gly Asn Asp Ser Lys Lys Ser Ser Gly Ala Ser Arg Ala Glu Ser Pro
10 15 20

ctg atc aag ttc cgg aca ttg att atc gtc atc ttt gtc atc ttg atc 211
Leu Ile Lys Phe Arg Thr Leu Ile Ile Val Ile Phe Val Ile Leu Ile
25 30 35

gtt ggt ttg gca tct att gca gtg gga cct gtc gtg tac cag ctc atc 259
Val Gly Leu Ala Ser Ile Ala Val Gly Pro Val Val Tyr Gln Leu Ile
40 45 50

atg gga cct ggt gtg aaa acc gaa gga atc cag gct gat ggc gca gca 307
Met Gly Pro Gly Val Lys Thr Glu Gly Ile Gln Ala Asp Gly Ala Ala
55 60 65

cct gcg tcc acc gac atg aac ggc acc tgg gat gtt gcc cca ggg agt 355
Pro Ala Ser Thr Asp Met Asn Gly Thr Trp Asp Val Ala Pro Gly Ser
70 75 80 85

att cca aac acc acc tca gct gga ttc acc ttc gct gag atc ctg cca 403
Ile Pro Asn Thr Thr Ser Ala Gly Phe Thr Phe Ala Glu Ile Leu Pro
90 95 100

ggc gaa gaa aag atc acc tcc ggc tca acc act ggt gtc act ggc gaa 451
Gly Glu Glu Lys Ile Thr Ser Gly Ser Thr Thr Gly Val Thr Gly Glu
105 110 115

gtg gtc atc gag gat aac tcc ctg atc tct ggt ctg att acc gtc aac 499
Val Val Ile Glu Asp Asn Ser Leu Ile Ser Gly Leu Ile Thr Val Asn
120 125 130

atg act cac atc acc acc gat cag gaa aag cgc gac atc aac gtg cgc 547
Met Thr His Ile Thr Thr Asp Gln Glu Lys Arg Asp Ile Asn Val Arg
135 140 145

act aag ctc ttc cac acc gat cag tac cca gaa gca acc ttt gag gtt 595
Thr Lys Leu Phe His Thr Asp Gln Tyr Pro Glu Ala Thr Phe Glu Val
150 155 160 165

acc gat tcc gtt gat ctt tct gcg ctc cca gac acc gga tcc att gct 643
Thr Asp Ser Val Asp Leu Ser Ala Leu Pro Asp Thr Gly Ser Ile Ala
170 175 180

cag gtt gtc atc cca ggc gag ttg acc atc cac ggt gaa acc aag gct 691
Gln Val Val Ile Pro Gly Glu Leu Thr Ile His Gly Glu Thr Lys Ala
185 190 195

gtg gag cct acc ttt gat gta ctt cgt act ggt gac caa gtt atc gtg 739
Val Glu Pro Thr Phe Asp Val Leu Arg Thr Gly Asp Gln Val Ile Val

```
        200                 205                 210

gct tcc gat atc gaa atc aac cgc ctc gac ttc ggt gta gaa acc cca   787
Ala Ser Asp Ile Glu Ile Asn Arg Leu Asp Phe Gly Val Glu Thr Pro
    215                 220                 225

gag ttc atc gcc gca aag atc aat gag acc ggc gag atc aac gtc cga   835
Glu Phe Ile Ala Ala Lys Ile Asn Glu Thr Gly Glu Ile Asn Val Arg
230                 235                 240                 245

atc gta ttg gag aaa taaaccatga tggcatcacg gat                     873
Ile Val Leu Glu Lys
                250
```

<210> 542
<211> 250
<212> PRT
<213> Corynebacterium glutamicum

<400> 542

```
Met Ser Asn Met Gln Gly Asn Asp Ser Lys Lys Ser Ser Gly Ala Ser
  1               5                  10                  15

Arg Ala Glu Ser Pro Leu Ile Lys Phe Arg Thr Leu Ile Ile Val Ile
             20                  25                  30

Phe Val Ile Leu Ile Val Gly Leu Ala Ser Ile Ala Val Gly Pro Val
         35                  40                  45

Val Tyr Gln Leu Ile Met Gly Pro Gly Val Lys Thr Glu Gly Ile Gln
     50                  55                  60

Ala Asp Gly Ala Ala Pro Ala Ser Thr Asp Met Asn Gly Thr Trp Asp
 65                  70                  75                  80

Val Ala Pro Gly Ser Ile Pro Asn Thr Thr Ser Ala Gly Phe Thr Phe
                 85                  90                  95

Ala Glu Ile Leu Pro Gly Glu Glu Lys Ile Thr Ser Gly Ser Thr Thr
            100                 105                 110

Gly Val Thr Gly Glu Val Val Ile Glu Asp Asn Ser Leu Ile Ser Gly
        115                 120                 125

Leu Ile Thr Val Asn Met Thr His Ile Thr Thr Asp Gln Glu Lys Arg
    130                 135                 140

Asp Ile Asn Val Arg Thr Lys Leu Phe His Thr Asp Gln Tyr Pro Glu
145                 150                 155                 160

Ala Thr Phe Glu Val Thr Asp Ser Val Asp Leu Ser Ala Leu Pro Asp
                165                 170                 175

Thr Gly Ser Ile Ala Gln Val Val Ile Pro Gly Glu Leu Thr Ile His
            180                 185                 190

Gly Glu Thr Lys Ala Val Glu Pro Thr Phe Asp Val Leu Arg Thr Gly
        195                 200                 205

Asp Gln Val Ile Val Ala Ser Asp Ile Glu Ile Asn Arg Leu Asp Phe
```

```
    210                 215                 220

Gly Val Glu Thr Pro Glu Phe Ile Ala Ala Lys Ile Asn Glu Thr Gly
225                 230                 235                 240

Glu Ile Asn Val Arg Ile Val Leu Glu Lys
                245                 250


<210> 543
<211> 1401
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1378)
<223> RXN01229

<400> 543
tagccccgaa agacggcgag ggttggctct gcttcgttgt gggaaaacta ggcccttaat 60

aagctgtgct atagggtctc cctgcaccga taaaggactg atg atc atc tcc act   115
                                              Met Ile Ile Ser Thr
                                                1               5

aac acc gct cac ccc ctg cac gaa ccg cac gta ccc agc cac cac aat   163
Asn Thr Ala His Pro Leu His Glu Pro His Val Pro Ser His His Asn
                10                  15                  20

cgt atg aat act ctg cgt gcc ggt gtg ctg ggt gct aat gac ggt atc   211
Arg Met Asn Thr Leu Arg Ala Gly Val Leu Gly Ala Asn Asp Gly Ile
            25                  30                  35

gtc tcc att gct gcg cta ctg ctc ggt gtg atc gcc acc ggc gcc agt   259
Val Ser Ile Ala Ala Leu Leu Leu Gly Val Ile Ala Thr Gly Ala Ser
        40                  45                  50

gac acc gtc gtg ttc ggc gct ggt ttg gcc tca acg atc gcg ggg gcg   307
Asp Thr Val Val Phe Gly Ala Gly Leu Ala Ser Thr Ile Ala Gly Ala
    55                  60                  65

gta tct atg gct ctc ggt gag tac gtc tct gtc tcc tca cag cgt gat   355
Val Ser Met Ala Leu Gly Glu Tyr Val Ser Val Ser Ser Gln Arg Asp
70                  75                  80                  85

acc gaa cgg gtg ctc atc gca aaa gaa gcg aag gag ctg gcc gaa gac   403
Thr Glu Arg Val Leu Ile Ala Lys Glu Ala Lys Glu Leu Ala Glu Asp
                90                  95                  100

ccg acg gcc gag cac gtc gag ctg tcg gag atc cta cac tcc tac ggc   451
Pro Thr Ala Glu His Val Glu Leu Ser Glu Ile Leu His Ser Tyr Gly
            105                 110                 115

atc tmc mmt gwg amt smr ras sms gcs rmm ayc grg awm ggg mas ggc   499
Ile Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Gly
        120                 125                 130

gac gcc ttg ggc gcc cac ctt cag ctc gag ctc ggt att gat aat gag   547
Asp Ala Leu Gly Ala His Leu Gln Leu Glu Leu Gly Ile Asp Asn Glu
    135                 140                 145
```

```
caa ctg acc agc ccc ttg gcc gcc gcc ttc tcc tcg gcc gtg gct ttc   595
Gln Leu Thr Ser Pro Leu Ala Ala Ala Phe Ser Ser Ala Val Ala Phe
150                 155                 160                 165

ctg ctc gga gca ctg ctg ccg atg gtg tyg gta ttc mty gcc ccy kca   643
Leu Leu Gly Ala Leu Leu Pro Met Val Xaa Val Phe Xaa Ala Xaa Xaa
                170                 175                 180

ggc tgg gac gcc ggc gtk gkc ttc gta gtc acg stg ctg gtc ctg gcg   691
Gly Trp Asp Ala Gly Xaa Xaa Phe Val Val Thr Xaa Leu Val Leu Ala
            185                 190                 195

gkk acc ggg ttc atc tca rcc cmg rtc ycg ggt acc tyc ccm atg cgc   739
Xaa Thr Gly Phe Ile Ser Xaa Xaa Xaa Xaa Gly Thr Xaa Xaa Met Arg
        200                 205                 210

gsg tgc sgg sgc ttk gkg rtc ggk ggt kcc ctc sgs cyg gcc ctg acc   787
Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Leu Xaa Xaa Ala Leu Thr
    215                 220                 225

mta ccg tct tgg aaw cwa tts kks gss gcm gyw ktm kgw gsy kcs ksr   835
Xaa Pro Ser Trp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
230                 235                 240                 245

rra mar arr rgg rrk rmk gsk kkt ktk gtg gyk gsk sgk ykt tkt cgw   883
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Val Xaa Xaa Xaa Xaa Xaa Xaa
                250                 255                 260

cgm cks sws ram gwr rts rkc gsc gmc swc cty syw gmm say cmk ssg   931
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            265                 270                 275

ssk scw kgr wss rcy gcy scm ssm ggs ksk csm swk wtr kks yss sks   979
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
        280                 285                 290

wsw mtw cky ktt tyy cyy csg smr gkw amc mmm myk gkk syw wkr rrw   1027
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
    295                 300                 305

tkt tty ykr rra rrm srm ywm csr rkw rgg cca cca ctg tca ggc gag   1075
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Pro Pro Leu Ser Gly Glu
310                 315                 320                 325

att ctg ctt gct ggc ctc ggc ggt gag ata ggc atg ggg gaa ccg agg   1123
Ile Leu Leu Ala Gly Leu Gly Gly Glu Ile Gly Met Gly Glu Pro Arg
                330                 335                 340

atc cca gtg act act ggt gac ctg gaa acc cgc ggt ctc cag tgc ctg   1171
Ile Pro Val Thr Thr Gly Asp Leu Glu Thr Arg Gly Leu Gln Cys Leu
            345                 350                 355

ggc aag ctc ggg cag tgg cca ccg gta ggc ggt ggc cac ggg atg ata   1219
Gly Lys Leu Gly Gln Trp Pro Pro Val Gly Gly Gly His Gly Met Ile
        360                 365                 370

cat cgg ttc cag aga agg ccc gga gaa aaa gga cat cag cag gcc acc   1267
His Arg Phe Gln Arg Arg Pro Gly Glu Lys Gly His Gln Gln Ala Thr
    375                 380                 385
```

```
acc atc ctc cac cgc cat ccg cag tgc gac cag ggc gtc ggg cag ctc   1315
Thr Ile Leu His Arg His Pro Gln Cys Asp Gln Gly Val Gly Gln Leu
390                 395                 400                 405

gcc cgg gcc cat gtg gat cag gga gta cca ggc caa cag gcc tgc cca   1363
Ala Arg Ala His Val Asp Gln Gly Val Pro Gly Gln Gln Ala Cys Pro
                410                 415                 420

gcg ctt cgg cga gtc tgagaggtcg gtaatagtgc cgt                     1401
Ala Leu Arg Arg Val
            425
```

<210> 544
<211> 426
<212> PRT
<213> Corynebacterium glutamicum

<400> 544

```
Met Ile Ile Ser Thr Asn Thr Ala His Pro Leu His Glu Pro His Val
  1               5                  10                  15

Pro Ser His His Asn Arg Met Asn Thr Leu Arg Ala Gly Val Leu Gly
             20                  25                  30

Ala Asn Asp Gly Ile Val Ser Ile Ala Ala Leu Leu Leu Gly Val Ile
         35                  40                  45

Ala Thr Gly Ala Ser Asp Thr Val Val Phe Gly Ala Gly Leu Ala Ser
     50                  55                  60

Thr Ile Ala Gly Ala Val Ser Met Ala Leu Gly Glu Tyr Val Ser Val
 65                  70                  75                  80

Ser Ser Gln Arg Asp Thr Glu Arg Val Leu Ile Ala Lys Glu Ala Lys
                 85                  90                  95

Glu Leu Ala Glu Asp Pro Thr Ala Glu His Val Glu Leu Ser Glu Ile
            100                 105                 110

Leu His Ser Tyr Gly Ile Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
        115                 120                 125

Xaa Xaa Gly Xaa Gly Asp Ala Leu Gly Ala His Leu Gln Leu Glu Leu
    130                 135                 140

Gly Ile Asp Asn Glu Gln Leu Thr Ser Pro Leu Ala Ala Ala Phe Ser
145                 150                 155                 160

Ser Ala Val Ala Phe Leu Leu Gly Ala Leu Leu Pro Met Val Xaa Val
                165                 170                 175

Phe Xaa Ala Xaa Xaa Gly Trp Asp Ala Gly Xaa Xaa Phe Val Val Thr
            180                 185                 190

Xaa Leu Val Leu Ala Xaa Thr Gly Phe Ile Ser Xaa Xaa Xaa Xaa Gly
        195                 200                 205

Thr Xaa Xaa Met Arg Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Leu
    210                 215                 220
```

```
Xaa Xaa Ala Leu Thr Xaa Pro Ser Trp Xaa Xaa Xaa Xaa Xaa Xaa Xaa
225                 230                 235                 240

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Val Xaa
                245                 250                 255

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            260                 265                 270

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
        275                 280                 285

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
    290                 295                 300

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Pro
305                 310                 315                 320

Pro Leu Ser Gly Glu Ile Leu Leu Ala Gly Leu Gly Gly Glu Ile Gly
                325                 330                 335

Met Gly Glu Pro Arg Ile Pro Val Thr Thr Gly Asp Leu Glu Thr Arg
            340                 345                 350

Gly Leu Gln Cys Leu Gly Lys Leu Gly Gln Trp Pro Pro Val Gly Gly
        355                 360                 365

Gly His Gly Met Ile His Arg Phe Gln Arg Arg Pro Gly Glu Lys Gly
    370                 375                 380

His Gln Gln Ala Thr Thr Ile Leu His Arg His Pro Gln Cys Asp Gln
385                 390                 395                 400

Gly Val Gly Gln Leu Ala Arg Ala His Val Asp Gln Gly Val Pro Gly
                405                 410                 415

Gln Gln Ala Cys Pro Ala Leu Arg Arg Val
            420                 425


<210> 545
<211> 793
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(793)
<223> FRXA01229

<400> 545
tagccccgaa agacggcgag ggttggctct gcttcgttgt gggaaaacta ggcccttaat 60

aagctgtgct tatagggtct cctgcaccga taaaggactg atg atc atc tcc act   115
                                            Met Ile Ile Ser Thr
                                              1               5

aac acc gct cac ccc ctg cac gaa ccg cac gta ccc agc cac cac aat   163
Asn Thr Ala His Pro Leu His Glu Pro His Val Pro Ser His His Asn
                 10                  15                  20
```

```
cgt atg aat act ctg cgt gcc ggt gtg ctg ggt gct aat gac ggt atc   211
Arg Met Asn Thr Leu Arg Ala Gly Val Leu Gly Ala Asn Asp Gly Ile
            25                  30                  35

gtc tcc att gct gcg cta ctg ctc ggt gtg atc gcc acc ggc gcc agt   259
Val Ser Ile Ala Ala Leu Leu Leu Gly Val Ile Ala Thr Gly Ala Ser
        40                  45                  50

gac acc gtc gtg ttc ggc gct ggt ttg gcc tca acg atc gcg ggg gcg   307
Asp Thr Val Val Phe Gly Ala Gly Leu Ala Ser Thr Ile Ala Gly Ala
    55                  60                  65

gta tct atg gct ctc ggt gag tac gtc tct gtc tcc tca cag cgt gat   355
Val Ser Met Ala Leu Gly Glu Tyr Val Ser Val Ser Ser Gln Arg Asp
70                  75                  80                  85

acc gaa cgg gtg ctc atc gca aaa gaa gcg aag gag ctg gcc gaa gac   403
Thr Glu Arg Val Leu Ile Ala Lys Glu Ala Lys Glu Leu Ala Glu Asp
                90                  95                  100

ccg acg gcc gag cac gtc gag ctg tcg gag atc cta cac tcc tac ggc   451
Pro Thr Ala Glu His Val Glu Leu Ser Glu Ile Leu His Ser Tyr Gly
            105                 110                 115

atc tcc cct gag act gcg aac cag gcg gcc acc gag atc ggg cag ggc   499
Ile Ser Pro Glu Thr Ala Asn Gln Ala Ala Thr Glu Ile Gly Gln Gly
        120                 125                 130

gac gcc ttg ggc gcc cac ctt cag ctc gag ctc ggt att gat aat gag   547
Asp Ala Leu Gly Ala His Leu Gln Leu Glu Leu Gly Ile Asp Asn Glu
    135                 140                 145

caa ctg acc agc ccc ttg gcc gcc gcc ttc tcc tcg gcc gtg gct ttc   595
Gln Leu Thr Ser Pro Leu Ala Ala Ala Phe Ser Ser Ala Val Ala Phe
150                 155                 160                 165

ctg ctc gga gca ctg ctg ccg atg gtg tcg gta ttc atc gcc cct gca   643
Leu Leu Gly Ala Leu Leu Pro Met Val Ser Val Phe Ile Ala Pro Ala
                170                 175                 180

ggc tgg gac gcc ggc gtg gtc ttc gta gtc acg ctg ctg gtc ctg gcg   691
Gly Trp Asp Ala Gly Val Val Phe Val Val Thr Leu Leu Val Leu Ala
            185                 190                 195

gtg acc ggg ttc atc tca gcc cag atc tcg ggt acc tcc cca atg cgc   739
Val Thr Gly Phe Ile Ser Ala Gln Ile Ser Gly Thr Ser Pro Met Arg
        200                 205                 210

gcg tgc ggg cgc ttg gtg atc ggt ggt gcc ctc ggc ctg gcc cta acc   787
Ala Cys Gly Arg Leu Val Ile Gly Gly Ala Leu Gly Leu Ala Leu Thr
    215                 220                 225

tac ggt                                                           793
Tyr Gly
230
```

Document Page 649 of 1300

<210> 546
<211> 231
<212> PRT
<213> Corynebacterium glutamicum

<400> 546
Met Ile Ile Ser Thr Asn Thr Ala His Pro Leu His Glu Pro His Val
1 5 10 15

Pro Ser His His Asn Arg Met Asn Thr Leu Arg Ala Gly Val Leu Gly
20 25 30

Ala Asn Asp Gly Ile Val Ser Ile Ala Ala Leu Leu Leu Gly Val Ile
35 40 45

Ala Thr Gly Ala Ser Asp Thr Val Val Phe Gly Ala Gly Leu Ala Ser
50 55 60

Thr Ile Ala Gly Ala Val Ser Met Ala Leu Gly Glu Tyr Val Ser Val
65 70 75 80

Ser Ser Gln Arg Asp Thr Glu Arg Val Leu Ile Ala Lys Glu Ala Lys
85 90 95

Glu Leu Ala Glu Asp Pro Thr Ala Glu His Val Glu Leu Ser Glu Ile
100 105 110

Leu His Ser Tyr Gly Ile Ser Pro Glu Thr Ala Asn Gln Ala Ala Thr
115 120 125

Glu Ile Gly Gln Gly Asp Ala Leu Gly Ala His Leu Gln Leu Glu Leu
130 135 140

Gly Ile Asp Asn Glu Gln Leu Thr Ser Pro Leu Ala Ala Ala Phe Ser
145 150 155 160

Ser Ala Val Ala Phe Leu Leu Gly Ala Leu Leu Pro Met Val Ser Val
165 170 175

Phe Ile Ala Pro Ala Gly Trp Asp Ala Gly Val Val Phe Val Val Thr
180 185 190

Leu Leu Val Leu Ala Val Thr Gly Phe Ile Ser Ala Gln Ile Ser Gly
195 200 205

Thr Ser Pro Met Arg Ala Cys Gly Arg Leu Val Ile Gly Gly Ala Leu
210 215 220

Gly Leu Ala Leu Thr Tyr Gly
225 230

<210> 547
<211> 630
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(607)
<223> RXN01246

<400> 547
gggaaggagg agaaggctgc tgtgagctct gcagcccccg tccgctgact ttcaatgctt 60

```
catggactcc ccgatacaca acctccgaaa gggaaccccc atg aag cgc act atc   115
                                            Met Lys Arg Thr Ile
                                              1               5

acc atc gcc gct ctc gcc ttg acc tcc acc ctg gtt ttg tcc gcc tgc   163
Thr Ile Ala Ala Leu Ala Leu Thr Ser Thr Leu Val Leu Ser Ala Cys
                 10                  15                  20

gca gat aac act gag gga gaa aac acc gac acc acg acc atc gcc act   211
Ala Asp Asn Thr Glu Gly Glu Asn Thr Asp Thr Thr Thr Ile Ala Thr
             25                  30                  35

acg tcc gcc ccc gac acc acc gaa acg acc ggg gcc acc acg gat cct   259
Thr Ser Ala Pro Asp Thr Thr Glu Thr Thr Gly Ala Thr Thr Asp Pro
         40                  45                  50

gag aca gag acg ggg gcg gcc gga gag gtc tcc gcc gag cac aat gat   307
Glu Thr Glu Thr Gly Ala Ala Gly Glu Val Ser Ala Glu His Asn Asp
     55                  60                  65

gcg gac atc atg ttc gcg cag atg atg atc ccg cat cac caa cag gcc   355
Ala Asp Ile Met Phe Ala Gln Met Met Ile Pro His His Gln Gln Ala
 70                  75                  80                  85

gtg gag atg agt gaa atc ctc ctg gcc aag gac gat atc ccg gcc gag   403
Val Glu Met Ser Glu Ile Leu Leu Ala Lys Asp Asp Ile Pro Ala Glu
                 90                  95                 100

gtc atc gag ttc acc cag ggt gtt atc gat gcc cag ggc ccg gag atc   451
Val Ile Glu Phe Thr Gln Gly Val Ile Asp Ala Gln Gly Pro Glu Ile
            105                 110                 115

gac cgg atg aat acc atg ctc gag acc tgg gaa gaa gat ccg gtc acc   499
Asp Arg Met Asn Thr Met Leu Glu Thr Trp Glu Glu Asp Pro Val Thr
        120                 125                 130

ggt gat atg ggt gag atg gac cat ggc ggg atg agt gga atg atg agc   547
Gly Asp Met Gly Glu Met Asp His Gly Gly Met Ser Gly Met Met Ser
    135                 140                 145

gag gag gac atg aca gcc ctc gag gac gcc cag ggc acc cga ggc tgc   595
Glu Glu Asp Met Thr Ala Leu Glu Asp Ala Gln Gly Thr Arg Gly Cys
150                 155                 160                 165

ccg gct cta cct tgagcagatg accgcccacc atg                        630
Pro Ala Leu Pro
```

<210> 548
<211> 169
<212> PRT
<213> Corynebacterium glutamicum

<400> 548

```
Met Lys Arg Thr Ile Thr Ile Ala Ala Leu Ala Leu Thr Ser Thr Leu
  1               5                  10                  15

Val Leu Ser Ala Cys Ala Asp Asn Thr Glu Gly Glu Asn Thr Asp Thr
             20                  25                  30
```

```
Thr Thr Ile Ala Thr Thr Ser Ala Pro Asp Thr Thr Glu Thr Thr Gly
         35                  40                  45

Ala Thr Thr Asp Pro Glu Thr Glu Thr Gly Ala Ala Gly Glu Val Ser
     50                  55                  60

Ala Glu His Asn Asp Ala Asp Ile Met Phe Ala Gln Met Met Ile Pro
 65                  70                  75                  80

His His Gln Gln Ala Val Glu Met Ser Glu Ile Leu Leu Ala Lys Asp
                 85                  90                  95

Asp Ile Pro Ala Glu Val Ile Glu Phe Thr Gln Gly Val Ile Asp Ala
            100                 105                 110

Gln Gly Pro Glu Ile Asp Arg Met Asn Thr Met Leu Glu Thr Trp Glu
        115                 120                 125

Glu Asp Pro Val Thr Gly Asp Met Gly Glu Met Asp His Gly Gly Met
    130                 135                 140

Ser Gly Met Met Ser Glu Glu Asp Met Thr Ala Leu Glu Asp Ala Gln
145                 150                 155                 160

Gly Thr Arg Gly Cys Pro Ala Leu Pro
                165
```

<210> 549
<211> 739
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(739)
<223> FRXA01246

<400> 549

```
gggaaggagg agaaggctgc tgtgagctct gcagcccccg tccgctgact ttcaatgctt 60

catggactcc ccgatacaca acctccgaaa gggaacccc atg aag cgc act atc   115
                                          Met Lys Arg Thr Ile
                                            1               5

acc atc gcc gct ctc gcc ttg acc tcc acc ctg gtt ttg tcc gcc tgc   163
Thr Ile Ala Ala Leu Ala Leu Thr Ser Thr Leu Val Leu Ser Ala Cys
                10                  15                  20

gca gat aac act gag gga gaa aac acc gac acc acg acc atc gcc act   211
Ala Asp Asn Thr Glu Gly Glu Asn Thr Asp Thr Thr Thr Ile Ala Thr
            25                  30                  35

acg tcc gcc ccc gac acc acc gaa acg acc ggg gcc acc acg gat cct   259
Thr Ser Ala Pro Asp Thr Thr Glu Thr Thr Gly Ala Thr Thr Asp Pro
        40                  45                  50

gag aca gag acg ggg gcg gcc gga gag gtc tcc gcc gag cac aat gat   307
Glu Thr Glu Thr Gly Ala Ala Gly Glu Val Ser Ala Glu His Asn Asp
    55                  60                  65
```

```
gcg gac atc atg ttc gcg cag atg atg atc ccg cat cac caa cag gcc   355
Ala Asp Ile Met Phe Ala Gln Met Met Ile Pro His His Gln Gln Ala
 70                  75                  80                  85

gtg gag atg agt gaa atc ctc ctg gcc aag gac gat atc ccg gcc gag   403
Val Glu Met Ser Glu Ile Leu Leu Ala Lys Asp Asp Ile Pro Ala Glu
                90                  95                 100

gtc atc gag ttc acc cag ggt gtt atc gat gcc cag ggc ccg gag atc   451
Val Ile Glu Phe Thr Gln Gly Val Ile Asp Ala Gln Gly Pro Glu Ile
            105                 110                 115

gac cgg atg aat acc atg ctc gag acc tgg gaa gaa gat ccg gtc acc   499
Asp Arg Met Asn Thr Met Leu Glu Thr Trp Glu Glu Asp Pro Val Thr
        120                 125                 130

ggt gat atg ggt gag atg gac cat ggc ggg atg agt gga atg atg agc   547
Gly Asp Met Gly Glu Met Asp His Gly Gly Met Ser Gly Met Met Ser
    135                 140                 145

gag gag gac atg aca gcc ctc gag gac gcc cag ggc acc gag gct gcc   595
Glu Glu Asp Met Thr Ala Leu Glu Asp Ala Gln Gly Thr Glu Ala Ala
150                 155                 160                 165

cgg ctc tac ctt gag cag atg acc gcc cac cat gag ggc gcg gtc gat   643
Arg Leu Tyr Leu Glu Gln Met Thr Ala His His Glu Gly Ala Val Asp
                170                 175                 180

atg gcc cgc gat gag gtc act gat ggc cag aac ccg cag gcc atc gct   691
Met Ala Arg Asp Glu Val Thr Asp Gly Gln Asn Pro Gln Ala Ile Ala
            185                 190                 195

ctg gct gag cag gtc att gaa gat cag gag gcc gag atc gcc gag att   739
Leu Ala Glu Gln Val Ile Glu Asp Gln Glu Ala Glu Ile Ala Glu Ile
        200                 205                 210


<210> 550
<211> 213
<212> PRT
<213> Corynebacterium glutamicum

<400> 550
Met Lys Arg Thr Ile Thr Ile Ala Ala Leu Ala Leu Thr Ser Thr Leu
  1               5                  10                  15

Val Leu Ser Ala Cys Ala Asp Asn Thr Glu Gly Glu Asn Thr Asp Thr
             20                  25                  30

Thr Thr Ile Ala Thr Thr Ser Ala Pro Asp Thr Thr Glu Thr Thr Gly
         35                  40                  45

Ala Thr Thr Asp Pro Glu Thr Glu Thr Gly Ala Ala Gly Glu Val Ser
     50                  55                  60

Ala Glu His Asn Asp Ala Asp Ile Met Phe Ala Gln Met Met Ile Pro
 65                  70                  75                  80

His His Gln Gln Ala Val Glu Met Ser Glu Ile Leu Leu Ala Lys Asp
                 85                  90                  95
```

```
Asp Ile Pro Ala Glu Val Ile Glu Phe Thr Gln Gly Val Ile Asp Ala
            100                 105                 110

Gln Gly Pro Glu Ile Asp Arg Met Asn Thr Met Leu Glu Thr Trp Glu
        115                 120                 125

Glu Asp Pro Val Thr Gly Asp Met Gly Glu Met Asp His Gly Gly Met
    130                 135                 140

Ser Gly Met Met Ser Glu Glu Asp Met Thr Ala Leu Glu Asp Ala Gln
145                 150                 155                 160

Gly Thr Glu Ala Ala Arg Leu Tyr Leu Glu Gln Met Thr Ala His His
                165                 170                 175

Glu Gly Ala Val Asp Met Ala Arg Asp Glu Val Thr Asp Gly Gln Asn
            180                 185                 190

Pro Gln Ala Ile Ala Leu Ala Glu Gln Val Ile Glu Asp Gln Glu Ala
        195                 200                 205

Glu Ile Ala Glu Ile
    210
```

Application as filed - Sequence Listing

<210> 551
<211> 471
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(471)
<223> RXN01249

<400> 551

```
tct cag att gtg gcg gtg tct tct cac ggt ctt acc acg atc cag gag   48
Ser Gln Ile Val Ala Val Ser Ser His Gly Leu Thr Thr Ile Gln Glu
  1               5                  10                  15

att gac gtg aaa cga gca gcg atc gca gcc gcc gcc ctt acc ctc gcc   96
Ile Asp Val Lys Arg Ala Ala Ile Ala Ala Ala Ala Leu Thr Leu Ala
             20                  25                  30

ctc acg ggg tgt tcg gcc gcc gac ccg gaa ccc acc gcc gac ggg acg   144
Leu Thr Gly Cys Ser Ala Ala Asp Pro Glu Pro Thr Ala Asp Gly Thr
         35                  40                  45

gtg tcc cag gat aca ttc ctg act acc cat ggc ctg gcc gcc atg gac   192
Val Ser Gln Asp Thr Phe Leu Thr Thr His Gly Leu Ala Ala Met Asp
     50                  55                  60

gcg gtg gag atc att gat cac ctc gac cgg cag aag gtc act gag cgt   240
Ala Val Glu Ile Ile Asp His Leu Asp Arg Gln Lys Val Thr Glu Arg
 65                  70                  75                  80

ccc acg gat ctg atc gcc tca gtg cgt gcc gat gaa ctg ctg ctc tcg   288
Pro Thr Asp Leu Ile Ala Ser Val Arg Ala Asp Glu Leu Leu Leu Ser
                 85                  90                  95

agc gat gac cag gaa gtc gtg gtc gat ctt ccc gac aat cag acg tat   336
```

```
Ser Asp Asp Gln Glu Val Val Val Asp Leu Pro Asp Asn Gln Thr Tyr
            100                 105                 110

gtc tcg atc gca ccc tac ctc aac tcc acc cac gac tgc ttc tac cac   384
Val Ser Ile Ala Pro Tyr Leu Asn Ser Thr His Asp Cys Phe Tyr His
        115                 120                 125

agc ctc acg acc tgc ctg ggg gat ctc gac aat gag gat atc cat gtc   432
Ser Leu Thr Thr Cys Leu Gly Asp Leu Asp Asn Glu Asp Ile His Val
    130                 135                 140

atg atc acc gat gaa gcg acc ggc gag gtc ctg ttc gat               471
Met Ile Thr Asp Glu Ala Thr Gly Glu Val Leu Phe Asp
145                 150                 155


<210> 552
<211> 157
<212> PRT
<213> Corynebacterium glutamicum

<400> 552
Ser Gln Ile Val Ala Val Ser Ser His Gly Leu Thr Thr Ile Gln Glu
  1               5                  10                  15

Ile Asp Val Lys Arg Ala Ala Ile Ala Ala Ala Ala Leu Thr Leu Ala
             20                  25                  30

Leu Thr Gly Cys Ser Ala Ala Asp Pro Glu Pro Thr Ala Asp Gly Thr
         35                  40                  45

Val Ser Gln Asp Thr Phe Leu Thr Thr His Gly Leu Ala Ala Met Asp
     50                  55                  60

Ala Val Glu Ile Ile Asp His Leu Asp Arg Gln Lys Val Thr Glu Arg
 65                  70                  75                  80

Pro Thr Asp Leu Ile Ala Ser Val Arg Ala Asp Glu Leu Leu Leu Ser
                 85                  90                  95

Ser Asp Asp Gln Glu Val Val Val Asp Leu Pro Asp Asn Gln Thr Tyr
            100                 105                 110

Val Ser Ile Ala Pro Tyr Leu Asn Ser Thr His Asp Cys Phe Tyr His
        115                 120                 125

Ser Leu Thr Thr Cys Leu Gly Asp Leu Asp Asn Glu Asp Ile His Val
    130                 135                 140

Met Ile Thr Asp Glu Ala Thr Gly Glu Val Leu Phe Asp
145                 150                 155


<210> 553
<211> 400
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(400)
```

<223> FRXA01249

<400> 553
gaattgacgt ggaaccgagc agcgatcgca gcccgccgcc cttaccctcg ccctcacggg 60

gtgttcggcc gccgacccgg aacccaccgc cgacgggacg gtg tcc cag gat aca 115
Val Ser Gln Asp Thr
1 5

ttc ctg act acc cat ggc ctg gcc gcc atg gac gcg gtg gag atc att 163
Phe Leu Thr Thr His Gly Leu Ala Ala Met Asp Ala Val Glu Ile Ile
10 15 20

gat cac ctc gac cgg cag aag gtc act gag cgt ccc acg gat ctg atc 211
Asp His Leu Asp Arg Gln Lys Val Thr Glu Arg Pro Thr Asp Leu Ile
25 30 35

gcc tca gtg cgt gcc gat gaa ctg ctg ctc tcg agc gat gac cag gaa 259
Ala Ser Val Arg Ala Asp Glu Leu Leu Leu Ser Ser Asp Asp Gln Glu
40 45 50

gtc gtg gtc gat ctt ccc gac aat cag acg tat gtc tcg atc gca ccc 307
Val Val Val Asp Leu Pro Asp Asn Gln Thr Tyr Val Ser Ile Ala Pro
55 60 65

tac ctc aac tcc acc cac gac tgc ttc tac cac agc ctc acg acc tgc 355
Tyr Leu Asn Ser Thr His Asp Cys Phe Tyr His Ser Leu Thr Thr Cys
70 75 80 85

ctg ggg gat ctc gac aat gag gat atc cat gtc atg atc acc gat 400
Leu Gly Asp Leu Asp Asn Glu Asp Ile His Val Met Ile Thr Asp
90 95 100

<210> 554
<211> 100
<212> PRT
<213> Corynebacterium glutamicum

<400> 554
Val Ser Gln Asp Thr Phe Leu Thr Thr His Gly Leu Ala Ala Met Asp
1 5 10 15

Ala Val Glu Ile Ile Asp His Leu Asp Arg Gln Lys Val Thr Glu Arg
20 25 30

Pro Thr Asp Leu Ile Ala Ser Val Arg Ala Asp Glu Leu Leu Leu Ser
35 40 45

Ser Asp Asp Gln Glu Val Val Val Asp Leu Pro Asp Asn Gln Thr Tyr
50 55 60

Val Ser Ile Ala Pro Tyr Leu Asn Ser Thr His Asp Cys Phe Tyr His
65 70 75 80

Ser Leu Thr Thr Cys Leu Gly Asp Leu Asp Asn Glu Asp Ile His Val
85 90 95

Met Ile Thr Asp
100

<210> 555
<211> 432
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(409)
<223> RXN01251

<400> 555
tgtaagccga gagcgaacct gccaaaagta aggggcgggt tcgcggtgac gtcggtagga 60

tcgagcgaag aaaccaacaa acttcttagg agccattctc atg acc cag cca gat 115
Met Thr Gln Pro Asp
1 5

atg tcc cag atc ctc gcc caa gct cag cag atg cag gct caa cta cag 163
Met Ser Gln Ile Leu Ala Gln Ala Gln Gln Met Gln Ala Gln Leu Gln
10 15 20

gcc gct cag cag gaa atc ctg gca acc acc gtt gtc gga aat gca gga 211
Ala Ala Gln Gln Glu Ile Leu Ala Thr Thr Val Val Gly Asn Ala Gly
25 30 35

aac ggg ctg gtt acc gtc act atg gcc ggc aac ggc gag gtc tcc gca 259
Asn Gly Leu Val Thr Val Thr Met Ala Gly Asn Gly Glu Val Ser Ala
40 45 50

gtg acc gtt gac cca aag gtc gtt gac cct gaa gat gtc gaa acc cta 307
Val Thr Val Asp Pro Lys Val Val Asp Pro Glu Asp Val Glu Thr Leu
55 60 65

cag gac ctt ctg ctc ggt gca ttc aag gat gcc cat aac aag gtc gca 355
Gln Asp Leu Leu Leu Gly Ala Phe Lys Asp Ala His Asn Lys Val Ala
70 75 80 85

aac gtt gct gaa gag aag atg ggc cca cta tcc cag ggc atg ggt ggc 403
Asn Val Ala Glu Glu Lys Met Gly Pro Leu Ser Gln Gly Met Gly Gly
90 95 100

ctc ttc taattagttg ctaaacgcag ggc 432
Leu Phe

<210> 556
<211> 103
<212> PRT
<213> Corynebacterium glutamicum

<400> 556
Met Thr Gln Pro Asp Met Ser Gln Ile Leu Ala Gln Ala Gln Gln Met
1 5 10 15

Gln Ala Gln Leu Gln Ala Ala Gln Gln Glu Ile Leu Ala Thr Thr Val
20 25 30

Val Gly Asn Ala Gly Asn Gly Leu Val Thr Val Thr Met Ala Gly Asn
35 40 45

```
Gly Glu Val Ser Ala Val Thr Val Asp Pro Lys Val Val Asp Pro Glu
     50                  55                  60

Asp Val Glu Thr Leu Gln Asp Leu Leu Leu Gly Ala Phe Lys Asp Ala
 65                  70                  75                  80

His Asn Lys Val Ala Asn Val Ala Glu Glu Lys Met Gly Pro Leu Ser
                 85                  90                  95

Gln Gly Met Gly Gly Leu Phe
            100


<210> 557
<211> 432
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(409)
<223> FRXA01251

<400> 557
tgtaagccga gagcgaacct gccaaaagta aggggcgggt tcgcggtgac gtcggtagga 60

tcgagcgaag aaaccaacaa acttcttagg agccattctc atg acc cag cca gat   115
                                            Met Thr Gln Pro Asp
                                              1               5

atg tcc cag atc ctc gcc caa gct cag cag atg cag gct caa cta cag   163
Met Ser Gln Ile Leu Ala Gln Ala Gln Gln Met Gln Ala Gln Leu Gln
                 10                  15                  20

gcc gct cag cag gaa atc ctg gca acc acc gtt gtc gga aat gca gga   211
Ala Ala Gln Gln Glu Ile Leu Ala Thr Thr Val Val Gly Asn Ala Gly
             25                  30                  35

aac ggg ctg gtt acc gtc act atg gcc ggc aac ggc gag gtc ttc gca   259
Asn Gly Leu Val Thr Val Thr Met Ala Gly Asn Gly Glu Val Phe Ala
         40                  45                  50

gtg acc gtt gac cca aag gtc gtt gac cct gaa gat gtc gaa acc cta   307
Val Thr Val Asp Pro Lys Val Val Asp Pro Glu Asp Val Glu Thr Leu
     55                  60                  65

cag gac ctt ctg ctc ggt gca ttc aag gat gcc cat aac aag gtc gca   355
Gln Asp Leu Leu Leu Gly Ala Phe Lys Asp Ala His Asn Lys Val Ala
 70                  75                  80                  85

aac gtt gct gaa gag aag atg ggc cca cta tcc cag ggc atg ggt ggc   403
Asn Val Ala Glu Glu Lys Met Gly Pro Leu Ser Gln Gly Met Gly Gly
                 90                  95                 100

ctc ttc taattagttg ctaaacgcag ggc                                432
Leu Phe


<210> 558
```

<211> 103
<212> PRT
<213> Corynebacterium glutamicum

<400> 558
Met Thr Gln Pro Asp Met Ser Gln Ile Leu Ala Gln Ala Gln Gln Met
1 5 10 15

Gln Ala Gln Leu Gln Ala Ala Gln Gln Glu Ile Leu Ala Thr Thr Val
20 25 30

Val Gly Asn Ala Gly Asn Gly Leu Val Thr Val Thr Met Ala Gly Asn
35 40 45

Gly Glu Val Phe Ala Val Thr Val Asp Pro Lys Val Val Asp Pro Glu
50 55 60

Asp Val Glu Thr Leu Gln Asp Leu Leu Leu Gly Ala Phe Lys Asp Ala
65 70 75 80

His Asn Lys Val Ala Asn Val Ala Glu Glu Lys Met Gly Pro Leu Ser
85 90 95

Gln Gly Met Gly Gly Leu Phe
100

<210> 559
<211> 1035
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1012)
<223> RXN01263

<400> 559
agtggccttt ggagttattt tgatgacggt atcggcgact gctgggatcc tcctcttttt 60

atctccaaat agaagccaag ctgcgccacc ccaatttagt ttg acc ccg tat gat 115
Leu Thr Pro Tyr Asp
1 5

cca acc gct gta aat aag gag tcg gaa aaa gaa gca gca aag aat ctg 163
Pro Thr Ala Val Asn Lys Glu Ser Glu Lys Glu Ala Ala Lys Asn Leu
10 15 20

ttt ggc gct gag gcg ttg aca gtg gat ccg gat gcc ggt gag gtt gtt 211
Phe Gly Ala Glu Ala Leu Thr Val Asp Pro Asp Ala Gly Glu Val Val
25 30 35

gat cga gta gat aat ttt tat ccg acg act gct aag gca aaa cga gat 259
Asp Arg Val Asp Asn Phe Tyr Pro Thr Thr Ala Lys Ala Lys Arg Asp
40 45 50

tac cca agt aac tat gca gcg ggt tgt cac caa gaa gtc aat gag act 307
Tyr Pro Ser Asn Tyr Ala Ala Gly Cys His Gln Glu Val Asn Glu Thr
55 60 65

agt cct gag tca tgt gtt tat ggt gat aaa aat tct gat ttt tct gta 355

```
Ser Pro Glu Ser Cys Val Tyr Gly Asp Lys Asn Ser Asp Phe Ser Val
 70                  75                  80                  85

gca ctt gtc ggt gac tcc cac gct ggt cat tgg ctt cct gcc ttg gaa   403
Ala Leu Val Gly Asp Ser His Ala Gly His Trp Leu Pro Ala Leu Glu
                90                  95                 100

cca att gct gaa gca cag ggg tgg aga ttg gaa gtt tat aca aag tca   451
Pro Ile Ala Glu Ala Gln Gly Trp Arg Leu Glu Val Tyr Thr Lys Ser
            105                 110                 115

cag tgt cca ctc ata agc act gcg atc aaa ctt ggt gaa act ttt tat   499
Gln Cys Pro Leu Ile Ser Thr Ala Ile Lys Leu Gly Glu Thr Phe Tyr
        120                 125                 130

gca gaa tgc tat gag tgg aat gaa aaa tta ctt gct aag cta act gga   547
Ala Glu Cys Tyr Glu Trp Asn Glu Lys Leu Leu Ala Lys Leu Thr Gly
    135                 140                 145

cct tct gca cca aat cat gtg att gta agt agc caa cgt tac gct tct   595
Pro Ser Ala Pro Asn His Val Ile Val Ser Ser Gln Arg Tyr Ala Ser
150                 155                 160                 165

gca aat ccg tta atc gat agt gtc gcg acg gga acc gtt tcc gaa gga   643
Ala Asn Pro Leu Ile Asp Ser Val Ala Thr Gly Thr Val Ser Glu Gly
                170                 175                 180

tat gaa atg gca tgg aat tca tta aaa gat gca ggt gtt tct att tct   691
Tyr Glu Met Ala Trp Asn Ser Leu Lys Asp Ala Gly Val Ser Ile Ser
            185                 190                 195

gta ctt ctt gat act cct cgg ccg caa att gat atc cca gaa tgt gta   739
Val Leu Leu Asp Thr Pro Arg Pro Gln Ile Asp Ile Pro Glu Cys Val
        200                 205                 210

gca tca aac cgc gat aat ctc tca gaa tgt tca gtt cac cgg agc gtt   787
Ala Ser Asn Arg Asp Asn Leu Ser Glu Cys Ser Val His Arg Ser Val
    215                 220                 225

gcg ctt ggg act gaa gct cat cct cag caa aaa act gca gct caa aat   835
Ala Leu Gly Thr Glu Ala His Pro Gln Gln Lys Thr Ala Ala Gln Asn
230                 235                 240                 245

ata gac gtg cct gta ttg gat ttg agt aat tgg att tgt ccg gaa gaa   883
Ile Asp Val Pro Val Leu Asp Leu Ser Asn Trp Ile Cys Pro Glu Glu
                250                 255                 260

tat tgc tcc gct gtt atc gga aat gtt ttg gta tac agg gat tca cat   931
Tyr Cys Ser Ala Val Ile Gly Asn Val Leu Val Tyr Arg Asp Ser His
            265                 270                 275

cat ttg acc gct acg tat gct cgt agt ctc tct agc gca tta tgg aat   979
His Leu Thr Ala Thr Tyr Ala Arg Ser Leu Ser Ser Ala Leu Trp Asn
        280                 285                 290

gag ttg gtt gcc tca aat ggt gag cct ttt aag taagaggtag ttgttcaagt 1032
Glu Leu Val Ala Ser Asn Gly Glu Pro Phe Lys
    295                 300

agc                                                               1035
```

<210> 560
<211> 304
<212> PRT
<213> Corynebacterium glutamicum

<400> 560
Leu Thr Pro Tyr Asp Pro Thr Ala Val Asn Lys Glu Ser Glu Lys Glu
1 5 10 15

Ala Ala Lys Asn Leu Phe Gly Ala Glu Ala Leu Thr Val Asp Pro Asp
20 25 30

Ala Gly Glu Val Val Asp Arg Val Asp Asn Phe Tyr Pro Thr Thr Ala
35 40 45

Lys Ala Lys Arg Asp Tyr Pro Ser Asn Tyr Ala Ala Gly Cys His Gln
50 55 60

Glu Val Asn Glu Thr Ser Pro Glu Ser Cys Val Tyr Gly Asp Lys Asn
65 70 75 80

Ser Asp Phe Ser Val Ala Leu Val Gly Asp Ser His Ala Gly His Trp
85 90 95

Leu Pro Ala Leu Glu Pro Ile Ala Glu Ala Gln Gly Trp Arg Leu Glu
100 105 110

Val Tyr Thr Lys Ser Gln Cys Pro Leu Ile Ser Thr Ala Ile Lys Leu
115 120 125

Gly Glu Thr Phe Tyr Ala Glu Cys Tyr Glu Trp Asn Glu Lys Leu Leu
130 135 140

Ala Lys Leu Thr Gly Pro Ser Ala Pro Asn His Val Ile Val Ser Ser
145 150 155 160

Gln Arg Tyr Ala Ser Ala Asn Pro Leu Ile Asp Ser Val Ala Thr Gly
165 170 175

Thr Val Ser Glu Gly Tyr Glu Met Ala Trp Asn Ser Leu Lys Asp Ala
180 185 190

Gly Val Ser Ile Ser Val Leu Leu Asp Thr Pro Arg Pro Gln Ile Asp
195 200 205

Ile Pro Glu Cys Val Ala Ser Asn Arg Asp Asn Leu Ser Glu Cys Ser
210 215 220

Val His Arg Ser Val Ala Leu Gly Thr Glu Ala His Pro Gln Gln Lys
225 230 235 240

Thr Ala Ala Gln Asn Ile Asp Val Pro Val Leu Asp Leu Ser Asn Trp
245 250 255

Ile Cys Pro Glu Glu Tyr Cys Ser Ala Val Ile Gly Asn Val Leu Val
260 265 270

Tyr Arg Asp Ser His His Leu Thr Ala Thr Tyr Ala Arg Ser Leu Ser
275 280 285

```
Ser Ala Leu Trp Asn Glu Leu Val Ala Ser Asn Gly Glu Pro Phe Lys
    290                 295                 300
```

<210> 561
<211> 1035
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1012)
<223> FRXA01263

<400> 561

```
agtggccttt ggagttattt tgatgacggt atcggcgact gctgggatcc tcctcttttt 60

atctccaaat agaagccaag ctgcgccacc ccaatttagt ttg acc ccg tat gat   115
                                            Leu Thr Pro Tyr Asp
                                              1               5

cca acc gct gta aat aag gag tcg gaa aaa gaa gca gca aag aat ctg   163
Pro Thr Ala Val Asn Lys Glu Ser Glu Lys Glu Ala Ala Lys Asn Leu
                10                  15                  20

ttt ggc gct gag gcg ttg aca gtg gat ccg gat gcc ggt gag gtt gtt   211
Phe Gly Ala Glu Ala Leu Thr Val Asp Pro Asp Ala Gly Glu Val Val
            25                  30                  35

gat cga gta gat aat ttt tat ccg acg act gct aag gca aaa cga gat   259
Asp Arg Val Asp Asn Phe Tyr Pro Thr Thr Ala Lys Ala Lys Arg Asp
        40                  45                  50

tac cca agt aac tat gca gcg ggt tgt cac caa gaa gtc aat gag act   307
Tyr Pro Ser Asn Tyr Ala Ala Gly Cys His Gln Glu Val Asn Glu Thr
    55                  60                  65

agt cct gag tca tgt gtt tat ggt gat aaa aat tct gat ttt tct gta   355
Ser Pro Glu Ser Cys Val Tyr Gly Asp Lys Asn Ser Asp Phe Ser Val
70                  75                  80                  85

gca ctt gtc ggt gac tcc cac gct ggt cat tgg ctt cct gcc ttg gaa   403
Ala Leu Val Gly Asp Ser His Ala Gly His Trp Leu Pro Ala Leu Glu
                90                  95                  100

cca att gct gaa gca cag ggg tgg aga ttg gaa gtt tat aca aag tca   451
Pro Ile Ala Glu Ala Gln Gly Trp Arg Leu Glu Val Tyr Thr Lys Ser
            105                 110                 115

cag tgt cca ctc ata agc act gcg atc aaa ctt ggt gaa act ttt tat   499
Gln Cys Pro Leu Ile Ser Thr Ala Ile Lys Leu Gly Glu Thr Phe Tyr
        120                 125                 130

gca gaa tgc tat gag tgg aat gaa aaa tta ctt gct aag cta act gga   547
Ala Glu Cys Tyr Glu Trp Asn Glu Lys Leu Leu Ala Lys Leu Thr Gly
    135                 140                 145

cct tct gca cca aat cat gtg att gta agt agc caa cgt tac gct tct   595
```

```
Pro Ser Ala Pro Asn His Val Ile Val Ser Ser Gln Arg Tyr Ala Ser
150                 155                 160                 165

gca aat ccg tta atc gat agt gtc gcg acg gga acc gtt tcc gaa gga   643
Ala Asn Pro Leu Ile Asp Ser Val Ala Thr Gly Thr Val Ser Glu Gly
                170                 175                 180

tat gaa atg gca tgg aat tca tta aaa gat gca ggt gtt tct att tct   691
Tyr Glu Met Ala Trp Asn Ser Leu Lys Asp Ala Gly Val Ser Ile Ser
            185                 190                 195

gta ctt ctt gat act cct cgg ccg caa att gat atc cca gaa tgt gta   739
Val Leu Leu Asp Thr Pro Arg Pro Gln Ile Asp Ile Pro Glu Cys Val
        200                 205                 210

gca tca aac cgc gat aat ctc tca gaa tgt tca gtt cac cgg agc gtt   787
Ala Ser Asn Arg Asp Asn Leu Ser Glu Cys Ser Val His Arg Ser Val
    215                 220                 225

gcg ctt ggg act gaa gct cat cct cag caa aaa act gca gct caa aat   835
Ala Leu Gly Thr Glu Ala His Pro Gln Gln Lys Thr Ala Ala Gln Asn
230                 235                 240                 245

ata gac gtg cct gta ttg gat ttg agt aat tgg att tgt ccg gaa gaa   883
Ile Asp Val Pro Val Leu Asp Leu Ser Asn Trp Ile Cys Pro Glu Glu
                250                 255                 260

tat tgc tcc gct gtt atc gga aat gtt ttg gta tac agg gat tca cat   931
Tyr Cys Ser Ala Val Ile Gly Asn Val Leu Val Tyr Arg Asp Ser His
            265                 270                 275

cat ttg acc gct acg tat gct cgt agt ctc tct agc gca tta tgg aat   979
His Leu Thr Ala Thr Tyr Ala Arg Ser Leu Ser Ser Ala Leu Trp Asn
        280                 285                 290

gag ttg gtt gcc tca aat ggt gag cct ttt aag taagaggtag ttgttcaagt 1032
Glu Leu Val Ala Ser Asn Gly Glu Pro Phe Lys
    295                 300

agc                                                               1035
```

<210> 562
<211> 304
<212> PRT
<213> Corynebacterium glutamicum

<400> 562

```
Leu Thr Pro Tyr Asp Pro Thr Ala Val Asn Lys Glu Ser Glu Lys Glu
  1               5                  10                  15

Ala Ala Lys Asn Leu Phe Gly Ala Glu Ala Leu Thr Val Asp Pro Asp
             20                  25                  30

Ala Gly Glu Val Val Asp Arg Val Asp Asn Phe Tyr Pro Thr Thr Ala
         35                  40                  45

Lys Ala Lys Arg Asp Tyr Pro Ser Asn Tyr Ala Ala Gly Cys His Gln
     50                  55                  60

Glu Val Asn Glu Thr Ser Pro Glu Ser Cys Val Tyr Gly Asp Lys Asn
```

```
 65                  70                  75                  80

Ser Asp Phe Ser Val Ala Leu Val Gly Asp Ser His Ala Gly His Trp
                 85                  90                  95

Leu Pro Ala Leu Glu Pro Ile Ala Glu Ala Gln Gly Trp Arg Leu Glu
            100                 105                 110

Val Tyr Thr Lys Ser Gln Cys Pro Leu Ile Ser Thr Ala Ile Lys Leu
        115                 120                 125

Gly Glu Thr Phe Tyr Ala Glu Cys Tyr Glu Trp Asn Glu Lys Leu Leu
    130                 135                 140

Ala Lys Leu Thr Gly Pro Ser Ala Pro Asn His Val Ile Val Ser Ser
145                 150                 155                 160

Gln Arg Tyr Ala Ser Ala Asn Pro Leu Ile Asp Ser Val Ala Thr Gly
                165                 170                 175

Thr Val Ser Glu Gly Tyr Glu Met Ala Trp Asn Ser Leu Lys Asp Ala
            180                 185                 190

Gly Val Ser Ile Ser Val Leu Leu Asp Thr Pro Arg Pro Gln Ile Asp
        195                 200                 205

Ile Pro Glu Cys Val Ala Ser Asn Arg Asp Asn Leu Ser Glu Cys Ser
    210                 215                 220

Val His Arg Ser Val Ala Leu Gly Thr Glu Ala His Pro Gln Gln Lys
225                 230                 235                 240

Thr Ala Ala Gln Asn Ile Asp Val Pro Val Leu Asp Leu Ser Asn Trp
                245                 250                 255

Ile Cys Pro Glu Glu Tyr Cys Ser Ala Val Ile Gly Asn Val Leu Val
            260                 265                 270

Tyr Arg Asp Ser His His Leu Thr Ala Thr Tyr Ala Arg Ser Leu Ser
        275                 280                 285

Ser Ala Leu Trp Asn Glu Leu Val Ala Ser Asn Gly Glu Pro Phe Lys
    290                 295                 300
```

Sequence Listing Page 664 of 1158

<210> 563
<211> 1158
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1135)
<223> RXN01266

<400> 563
gattgtgaag ttttatatct gtcatattct ggtgattttc gccctgctca tgaagtggcg 60

```
gacgagcaat ggcccgatat agatttagta aggaactaaa atg cca aaa gta agt   115
                                            Met Pro Lys Val Ser
                                              1               5

gtg gtt act ggt ttt tat aac cgc tgt gag cat tta gaa cga acc att   163
Val Val Thr Gly Phe Tyr Asn Arg Cys Glu His Leu Glu Arg Thr Ile
                 10                  15                  20

gag tct att ctt aac caa act tat agc gat ttt gaa tta att gtt ttt   211
Glu Ser Ile Leu Asn Gln Thr Tyr Ser Asp Phe Glu Leu Ile Val Phe
             25                  30                  35

gat gat gca tcg aca gat gga aca gct tca cga ttg tta gag tta aaa   259
Asp Asp Ala Ser Thr Asp Gly Thr Ala Ser Arg Leu Leu Glu Leu Lys
         40                  45                  50

gaa aaa tat gat gat ccg cgt ttc cga ttt atc att cat gaa gag aat   307
Glu Lys Tyr Asp Asp Pro Arg Phe Arg Phe Ile Ile His Glu Glu Asn
     55                  60                  65

aaa ggt ttc gta aaa ggg tta tca gaa gca att tct gga gct aaa ggg   355
Lys Gly Phe Val Lys Gly Leu Ser Glu Ala Ile Ser Gly Ala Lys Gly
 70                  75                  80                  85

cag tat att gca gtc cag gga tca ggc gat gta tct ctt cct cgc cgt   403
Gln Tyr Ile Ala Val Gln Gly Ser Gly Asp Val Ser Leu Pro Arg Arg
                 90                  95                 100

tta gag ctt cag gta gag ttt cta gac gcg aat cct tcg gta ggt gct   451
Leu Glu Leu Gln Val Glu Phe Leu Asp Ala Asn Pro Ser Val Gly Ala
            105                 110                 115

gtg ggt ggt gct atc tat aat att caa gaa gat acg gga aca cgc aac   499
Val Gly Gly Ala Ile Tyr Asn Ile Gln Glu Asp Thr Gly Thr Arg Asn
        120                 125                 130

cca cag aga ttt gaa aag cca att gct aca ttc gat gat tta ttg aca   547
Pro Gln Arg Phe Glu Lys Pro Ile Ala Thr Phe Asp Asp Leu Leu Thr
    135                 140                 145

tct aat ccg ttc act cac gga gaa gtg atg tat cgc tta gac ctt tat   595
Ser Asn Pro Phe Thr His Gly Glu Val Met Tyr Arg Leu Asp Leu Tyr
150                 155                 160                 165

aag agt ata ggt ggg tat cga agt ggc ttt act ttt gct caa gat cgt   643
Lys Ser Ile Gly Gly Tyr Arg Ser Gly Phe Thr Phe Ala Gln Asp Arg
                170                 175                 180

gat tta tgg ttg agg atg gcg aaa aaa gca gat ctg ggt atc att cca   691
Asp Leu Trp Leu Arg Met Ala Lys Lys Ala Asp Leu Gly Ile Ile Pro
            185                 190                 195

gat ttt ctt tat cac cgt tac aca ctt tta gat ggt gtc tct ttc gtc   739
Asp Phe Leu Tyr His Arg Tyr Thr Leu Leu Asp Gly Val Ser Phe Val
        200                 205                 210

ccg gat aaa act ata cgt cag cga tgc ttt tca gaa gct gcg gtg cga   787
Pro Asp Lys Thr Ile Arg Gln Arg Cys Phe Ser Glu Ala Ala Val Arg
    215                 220                 225

ctg gca tta atg cca gaa gag gaa gga gct tta gcc tac tct agg ctg   835
```

```
Leu Ala Leu Met Pro Glu Glu Glu Gly Ala Leu Ala Tyr Ser Arg Leu
230                 235                 240                 245

gaa gct gaa ggg cct act gcc gta gtt cct atc gct gat aga gct gtt   883
Glu Ala Glu Gly Pro Thr Ala Val Val Pro Ile Ala Asp Arg Ala Val
                250                 255                 260

cag aaa ttt gtc cct aaa gcg gct att cgc tta tgt cta tat ggt gct   931
Gln Lys Phe Val Pro Lys Ala Ala Ile Arg Leu Cys Leu Tyr Gly Ala
            265                 270                 275

ccg gaa act ggt tta cac atg gct cga gac tat atc cag aac cct ctg   979
Pro Glu Thr Gly Leu His Met Ala Arg Asp Tyr Ile Gln Asn Pro Leu
        280                 285                 290

cgc cgt acc ata gtt gta gtt ttg atc agc atc tat tcg tct aga tta   1027
Arg Arg Thr Ile Val Val Val Leu Ile Ser Ile Tyr Ser Ser Arg Leu
    295                 300                 305

att aag cct ctt caa gat att cta tat aag tct att ttt aag ggg gtc   1075
Ile Lys Pro Leu Gln Asp Ile Leu Tyr Lys Ser Ile Phe Lys Gly Val
310                 315                 320                 325

tcg att tct aaa cct att aag agt tca ctc gtg aag ttt aca aga aga   1123
Ser Ile Ser Lys Pro Ile Lys Ser Ser Leu Val Lys Phe Thr Arg Arg
                330                 335                 340

att caa ggg aag tagcgaaaaa ccgcatctac caa                        1158
Ile Gln Gly Lys
            345


<210> 564
<211> 345
<212> PRT
<213> Corynebacterium glutamicum

<400> 564
Met Pro Lys Val Ser Val Val Thr Gly Phe Tyr Asn Arg Cys Glu His
  1               5                  10                  15

Leu Glu Arg Thr Ile Glu Ser Ile Leu Asn Gln Thr Tyr Ser Asp Phe
             20                  25                  30

Glu Leu Ile Val Phe Asp Asp Ala Ser Thr Asp Gly Thr Ala Ser Arg
         35                  40                  45

Leu Leu Glu Leu Lys Glu Lys Tyr Asp Asp Pro Arg Phe Arg Phe Ile
     50                  55                  60

Ile His Glu Glu Asn Lys Gly Phe Val Lys Gly Leu Ser Glu Ala Ile
 65                  70                  75                  80

Ser Gly Ala Lys Gly Gln Tyr Ile Ala Val Gln Gly Ser Gly Asp Val
                 85                  90                  95

Ser Leu Pro Arg Arg Leu Glu Leu Gln Val Glu Phe Leu Asp Ala Asn
            100                 105                 110

Pro Ser Val Gly Ala Val Gly Gly Ala Ile Tyr Asn Ile Gln Glu Asp
        115                 120                 125
```

```
Thr Gly Thr Arg Asn Pro Gln Arg Phe Glu Lys Pro Ile Ala Thr Phe
    130                 135                 140

Asp Asp Leu Leu Thr Ser Asn Pro Phe Thr His Gly Glu Val Met Tyr
145                 150                 155                 160

Arg Leu Asp Leu Tyr Lys Ser Ile Gly Gly Tyr Arg Ser Gly Phe Thr
                165                 170                 175

Phe Ala Gln Asp Arg Asp Leu Trp Leu Arg Met Ala Lys Lys Ala Asp
            180                 185                 190

Leu Gly Ile Ile Pro Asp Phe Leu Tyr His Arg Tyr Thr Leu Leu Asp
        195                 200                 205

Gly Val Ser Phe Val Pro Asp Lys Thr Ile Arg Gln Arg Cys Phe Ser
    210                 215                 220

Glu Ala Ala Val Arg Leu Ala Leu Met Pro Glu Glu Glu Gly Ala Leu
225                 230                 235                 240

Ala Tyr Ser Arg Leu Glu Ala Glu Gly Pro Thr Ala Val Val Pro Ile
                245                 250                 255

Ala Asp Arg Ala Val Gln Lys Phe Val Pro Lys Ala Ala Ile Arg Leu
            260                 265                 270

Cys Leu Tyr Gly Ala Pro Glu Thr Gly Leu His Met Ala Arg Asp Tyr
        275                 280                 285

Ile Gln Asn Pro Leu Arg Arg Thr Ile Val Val Val Leu Ile Ser Ile
    290                 295                 300

Tyr Ser Ser Arg Leu Ile Lys Pro Leu Gln Asp Ile Leu Tyr Lys Ser
305                 310                 315                 320

Ile Phe Lys Gly Val Ser Ile Ser Lys Pro Ile Lys Ser Ser Leu Val
                325                 330                 335

Lys Phe Thr Arg Arg Ile Gln Gly Lys
            340                 345


<210> 565
<211> 1158
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1135)
<223> FRXA01266

<400> 565
gattgtgaag ttttatatct gtcatattct ggtgattttc gccctgctca tgaagtggcg 60

gacgagcaat ggcccgatat agatttagta aggaactaaa atg cca aaa gta agt   115
                                          Met Pro Lys Val Ser
                                            1               5
```

```
gtg gtt act ggt ttt tat aac cgc tgt gag cat tta gaa cga acc att   163
Val Val Thr Gly Phe Tyr Asn Arg Cys Glu His Leu Glu Arg Thr Ile
                10                  15                  20

gag tct att ctt aac caa act tat agc gat ttt gaa tta att gtt ttt   211
Glu Ser Ile Leu Asn Gln Thr Tyr Ser Asp Phe Glu Leu Ile Val Phe
            25                  30                  35

gat gat gca tcg aca gat gga aca gct tca cga ttg tta gag tta aaa   259
Asp Asp Ala Ser Thr Asp Gly Thr Ala Ser Arg Leu Leu Glu Leu Lys
        40                  45                  50

gaa aaa tat gat gat ccg cgt ttc cga ttt atc att cat gaa gag aat   307
Glu Lys Tyr Asp Asp Pro Arg Phe Arg Phe Ile Ile His Glu Glu Asn
    55                  60                  65

aaa ggt ttc gta aaa ggg tta tca gaa gca att tct gga gct aaa ggg   355
Lys Gly Phe Val Lys Gly Leu Ser Glu Ala Ile Ser Gly Ala Lys Gly
70                  75                  80                  85

cag tat att gca gtc cag gga tca ggc gat gta tct ctt cct cgc cgt   403
Gln Tyr Ile Ala Val Gln Gly Ser Gly Asp Val Ser Leu Pro Arg Arg
                90                  95                  100

tta gag ctt cag gta gag ttt cta gac gcg aat cct tcg gta ggt gct   451
Leu Glu Leu Gln Val Glu Phe Leu Asp Ala Asn Pro Ser Val Gly Ala
            105                 110                 115

gtg ggt ggt gct atc tat aat att caa gaa gat acg gga aca cgc aac   499
Val Gly Gly Ala Ile Tyr Asn Ile Gln Glu Asp Thr Gly Thr Arg Asn
        120                 125                 130

cca cag aga ttt gaa aag cca att gct aca ttc gat gat tta ttg aca   547
Pro Gln Arg Phe Glu Lys Pro Ile Ala Thr Phe Asp Asp Leu Leu Thr
    135                 140                 145

tct aat ccg ttc act cac gga gaa gtg atg tat cgc tta gac ctt tat   595
Ser Asn Pro Phe Thr His Gly Glu Val Met Tyr Arg Leu Asp Leu Tyr
150                 155                 160                 165

aag agt ata ggt ggg tat cga agt ggc ttt act ttt gct caa gat cgt   643
Lys Ser Ile Gly Gly Tyr Arg Ser Gly Phe Thr Phe Ala Gln Asp Arg
                170                 175                 180

gat tta tgg ttg agg atg gcg aaa aaa gca gat ctg ggt atc att cca   691
Asp Leu Trp Leu Arg Met Ala Lys Lys Ala Asp Leu Gly Ile Ile Pro
            185                 190                 195

gat ttt ctt tat cac cgt tac aca ctt tta gat ggt gtc tct ttc gtc   739
Asp Phe Leu Tyr His Arg Tyr Thr Leu Leu Asp Gly Val Ser Phe Val
        200                 205                 210

ccg gat aaa act ata cgt cag cga tgc ttt tca gaa gct gcg gtg cga   787
Pro Asp Lys Thr Ile Arg Gln Arg Cys Phe Ser Glu Ala Ala Val Arg
    215                 220                 225

ctg gca tta atg cca gaa gag gaa gga gct tta gcc tac tct agg ctg   835
Leu Ala Leu Met Pro Glu Glu Glu Gly Ala Leu Ala Tyr Ser Arg Leu
230                 235                 240                 245

gaa gct gaa ggg cct act gcc gta gtt cct atc gct gat aga gct gtt   883
```

```
Glu Ala Glu Gly Pro Thr Ala Val Val Pro Ile Ala Asp Arg Ala Val
                250                 255                 260

cag aaa ttt gtc cct aaa gcg gct att cgc tta tgt cta tat ggt gct   931
Gln Lys Phe Val Pro Lys Ala Ala Ile Arg Leu Cys Leu Tyr Gly Ala
            265                 270                 275

ccg gaa act ggt tta cac atg gct cga gac tat atc cag aac cct ctg   979
Pro Glu Thr Gly Leu His Met Ala Arg Asp Tyr Ile Gln Asn Pro Leu
        280                 285                 290

cgc cgt acc ata gtt gta gtt ttg atc agc atc tat tcg tct aga tta   1027
Arg Arg Thr Ile Val Val Val Leu Ile Ser Ile Tyr Ser Ser Arg Leu
    295                 300                 305

att aag cct ctt caa gat att cta tat aag tct att ttt aag ggg gtc   1075
Ile Lys Pro Leu Gln Asp Ile Leu Tyr Lys Ser Ile Phe Lys Gly Val
310                 315                 320                 325

tcg att tct aaa cct att aag agt tca ctc gtg aag ttt aca aga aga   1123
Ser Ile Ser Lys Pro Ile Lys Ser Ser Leu Val Lys Phe Thr Arg Arg
                330                 335                 340

att caa ggg aag tagcgaaaaa ccgcatctac caa                        1158
Ile Gln Gly Lys
            345



<210> 566
<211> 345
<212> PRT
<213> Corynebacterium glutamicum

<400> 566
Met Pro Lys Val Ser Val Val Thr Gly Phe Tyr Asn Arg Cys Glu His
  1               5                  10                  15

Leu Glu Arg Thr Ile Glu Ser Ile Leu Asn Gln Thr Tyr Ser Asp Phe
             20                  25                  30

Glu Leu Ile Val Phe Asp Asp Ala Ser Thr Asp Gly Thr Ala Ser Arg
         35                  40                  45

Leu Leu Glu Leu Lys Glu Lys Tyr Asp Asp Pro Arg Phe Arg Phe Ile
     50                  55                  60

Ile His Glu Glu Asn Lys Gly Phe Val Lys Gly Leu Ser Glu Ala Ile
 65                  70                  75                  80

Ser Gly Ala Lys Gly Gln Tyr Ile Ala Val Gln Gly Ser Gly Asp Val
                 85                  90                  95

Ser Leu Pro Arg Arg Leu Glu Leu Gln Val Glu Phe Leu Asp Ala Asn
            100                 105                 110

Pro Ser Val Gly Ala Val Gly Gly Ala Ile Tyr Asn Ile Gln Glu Asp
        115                 120                 125

Thr Gly Thr Arg Asn Pro Gln Arg Phe Glu Lys Pro Ile Ala Thr Phe
    130                 135                 140
```

```
Asp Asp Leu Leu Thr Ser Asn Pro Phe Thr His Gly Glu Val Met Tyr
145                 150                 155                 160

Arg Leu Asp Leu Tyr Lys Ser Ile Gly Gly Tyr Arg Ser Gly Phe Thr
                165                 170                 175

Phe Ala Gln Asp Arg Asp Leu Trp Leu Arg Met Ala Lys Lys Ala Asp
            180                 185                 190

Leu Gly Ile Ile Pro Asp Phe Leu Tyr His Arg Tyr Thr Leu Leu Asp
        195                 200                 205

Gly Val Ser Phe Val Pro Asp Lys Thr Ile Arg Gln Arg Cys Phe Ser
    210                 215                 220

Glu Ala Ala Val Arg Leu Ala Leu Met Pro Glu Glu Glu Gly Ala Leu
225                 230                 235                 240

Ala Tyr Ser Arg Leu Glu Ala Glu Gly Pro Thr Ala Val Val Pro Ile
                245                 250                 255

Ala Asp Arg Ala Val Gln Lys Phe Val Pro Lys Ala Ala Ile Arg Leu
            260                 265                 270

Cys Leu Tyr Gly Ala Pro Glu Thr Gly Leu His Met Ala Arg Asp Tyr
        275                 280                 285

Ile Gln Asn Pro Leu Arg Arg Thr Ile Val Val Leu Ile Ser Ile
    290                 295                 300

Tyr Ser Ser Arg Leu Ile Lys Pro Leu Gln Asp Ile Leu Tyr Lys Ser
305                 310                 315                 320

Ile Phe Lys Gly Val Ser Ile Ser Lys Pro Ile Lys Ser Ser Leu Val
                325                 330                 335

Lys Phe Thr Arg Arg Ile Gln Gly Lys
            340                 345


<210> 567
<211> 1041
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1018)
<223> RXN01275

<400> 567
cgccatacta ggctcggcct tttcgacggg aactcggata ggcttctgta aaaccatccc 60

cgttgaagag agactcgtgg ctgaaataac caccccatta atg gaa aaa att cgc   115
                                              Met Glu Lys Ile Arg
                                                1               5

tca ccc gca gtc caa tca gat gca ctg cag gtt ttt aaa tca gca ctt   163
Ser Pro Ala Val Gln Ser Asp Ala Leu Gln Val Phe Lys Ser Ala Leu
                10                  15                  20
```

```
gct gcg aca gtc acg tgg tgg att tcg gtt aac ctc ctt aac tcc caa   211
Ala Ala Thr Val Thr Trp Trp Ile Ser Val Asn Leu Leu Asn Ser Gln
            25                  30                  35

cta ccc ttt tta gct ccc tgg gta gcg tta atg acg atg caa ttc acc   259
Leu Pro Phe Leu Ala Pro Trp Val Ala Leu Met Thr Met Gln Phe Thr
        40                  45                  50

gtc tac cac acc ttt atc agt gga att cag act gca att gct tct gtc   307
Val Tyr His Thr Phe Ile Ser Gly Ile Gln Thr Ala Ile Ala Ser Val
    55                  60                  65

atc gga gtt gga ctt tcc ttt gtc ata ggc act tac tta gac gta agt   355
Ile Gly Val Gly Leu Ser Phe Val Ile Gly Thr Tyr Leu Asp Val Ser
70                  75                  80                  85

gtg tgg act ttt ggc ctt gca atg gtc ata gga tta ata ggt gca cga   403
Val Trp Thr Phe Gly Leu Ala Met Val Ile Gly Leu Ile Gly Ala Arg
                90                  95                  100

gta cca aag ctc cgc gcg gaa gga ata ggt att gct act aca tcc att   451
Val Pro Lys Leu Arg Ala Glu Gly Ile Gly Ile Ala Thr Thr Ser Ile
            105                 110                 115

ttt ctt ctt gcc tcc ggg ttt gat gat caa caa ccc ctt cta tac gac   499
Phe Leu Leu Ala Ser Gly Phe Asp Asp Gln Gln Pro Leu Leu Tyr Asp
        120                 125                 130

cgt att tta gag atc ctg ctc ggc gtg gct gtt gcc ata gcc atc aac   547
Arg Ile Leu Glu Ile Leu Leu Gly Val Ala Val Ala Ile Ala Ile Asn
    135                 140                 145

ctc atc atc ttt cct ccc tta cgc gac cag gag gca aac atg gtg gta   595
Leu Ile Ile Phe Pro Pro Leu Arg Asp Gln Glu Ala Asn Met Val Val
150                 155                 160                 165

gga aac tta gat cgg agg atg ggt gag gtt tta caa aaa atg gcc gat   643
Gly Asn Leu Asp Arg Arg Met Gly Glu Val Leu Gln Lys Met Ala Asp
                170                 175                 180

gag ctt gca gaa aag tgg aat atc gac aat gca gat gag tgg ctg gaa   691
Glu Leu Ala Glu Lys Trp Asn Ile Asp Asn Ala Asp Glu Trp Leu Glu
            185                 190                 195

gaa att aat tct att aac aat gac cta gaa aaa gcg tgg cac tcc gtg   739
Glu Ile Asn Ser Ile Asn Asn Asp Leu Glu Lys Ala Trp His Ser Val
        200                 205                 210

cgg ttc gtt cgc gaa agc cgt cga gtt aat cct cgt aaa atc cgc atc   787
Arg Phe Val Arg Glu Ser Arg Arg Val Asn Pro Arg Lys Ile Arg Ile
    215                 220                 225

caa gag ggc cgc ccc cag cct acg gaa aca agt tat gaa tca aac ctc   835
Gln Glu Gly Arg Pro Gln Pro Thr Glu Thr Ser Tyr Glu Ser Asn Leu
230                 235                 240                 245

acc agc att gat gaa ggg atc gct cat tta cgc cac ctt gcc cgt act   883
Thr Ser Ile Asp Glu Gly Ile Ala His Leu Arg His Leu Ala Arg Thr
                250                 255                 260

ctt cgt gat acc ccg att ata gat tcc gac tgg gga tcc agt att cca   931
```

```
Leu Arg Asp Thr Pro Ile Ile Asp Ser Asp Trp Gly Ser Ser Ile Pro
            265                 270                 275

gca aca gtg ggt atc cct tat gca cga tgc cgg agc ttt gct cgc aga   979
Ala Thr Val Gly Ile Pro Tyr Ala Arg Cys Arg Ser Phe Ala Arg Arg
        280                 285                 290

tcc gaa tca gga aat aga tcc tat ccg cga ccg gct ctc taaactttca   1028
Ser Glu Ser Gly Asn Arg Ser Tyr Pro Arg Pro Ala Leu
    295                 300                 305

agtgagatga gtg                                                  1041


<210> 568
<211> 306
<212> PRT
<213> Corynebacterium glutamicum

<400> 568
Met Glu Lys Ile Arg Ser Pro Ala Val Gln Ser Asp Ala Leu Gln Val
  1               5                  10                  15

Phe Lys Ser Ala Leu Ala Ala Thr Val Thr Trp Trp Ile Ser Val Asn
             20                  25                  30

Leu Leu Asn Ser Gln Leu Pro Phe Leu Ala Pro Trp Val Ala Leu Met
         35                  40                  45

Thr Met Gln Phe Thr Val Tyr His Thr Phe Ile Ser Gly Ile Gln Thr
     50                  55                  60

Ala Ile Ala Ser Val Ile Gly Val Gly Leu Ser Phe Val Ile Gly Thr
 65                  70                  75                  80

Tyr Leu Asp Val Ser Val Trp Thr Phe Gly Leu Ala Met Val Ile Gly
                 85                  90                  95

Leu Ile Gly Ala Arg Val Pro Lys Leu Arg Ala Glu Gly Ile Gly Ile
            100                 105                 110

Ala Thr Thr Ser Ile Phe Leu Leu Ala Ser Gly Phe Asp Asp Gln Gln
        115                 120                 125

Pro Leu Leu Tyr Asp Arg Ile Leu Glu Ile Leu Leu Gly Val Ala Val
    130                 135                 140

Ala Ile Ala Ile Asn Leu Ile Ile Phe Pro Pro Leu Arg Asp Gln Glu
145                 150                 155                 160

Ala Asn Met Val Val Gly Asn Leu Asp Arg Arg Met Gly Glu Val Leu
                165                 170                 175

Gln Lys Met Ala Asp Glu Leu Ala Glu Lys Trp Asn Ile Asp Asn Ala
            180                 185                 190

Asp Glu Trp Leu Glu Glu Ile Asn Ser Ile Asn Asn Asp Leu Glu Lys
        195                 200                 205

Ala Trp His Ser Val Arg Phe Val Arg Glu Ser Arg Arg Val Asn Pro
    210                 215                 220
```

```
Arg Lys Ile Arg Ile Gln Glu Gly Arg Pro Gln Pro Thr Glu Thr Ser
225                 230                 235                 240

Tyr Glu Ser Asn Leu Thr Ser Ile Asp Glu Gly Ile Ala His Leu Arg
                245                 250                 255

His Leu Ala Arg Thr Leu Arg Asp Thr Pro Ile Ile Asp Ser Asp Trp
            260                 265                 270

Gly Ser Ser Ile Pro Ala Thr Val Gly Ile Pro Tyr Ala Arg Cys Arg
        275                 280                 285

Ser Phe Ala Arg Arg Ser Glu Ser Gly Asn Arg Ser Tyr Pro Arg Pro
    290                 295                 300

Ala Leu
305
```

<210> 569
<211> 1041
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1018)
<223> FRXA01275

<400> 569

```
cgccatacta ggctcggcct tttcgacggg aactcggata ggcttctgta aaaccatccc 60

cgttgaagag agactcgtgg ctgaaataac caccccatta atg gaa aaa att cgc   115
                                            Met Glu Lys Ile Arg
                                              1               5

tca ccc gca gtc caa tca gat gca ctg cag gtt ttt aaa tca gca ctt   163
Ser Pro Ala Val Gln Ser Asp Ala Leu Gln Val Phe Lys Ser Ala Leu
                 10                  15                  20

gct gcg aca gtc acg tgg tgg att tcg gtt aac ctc ctt aac tcc caa   211
Ala Ala Thr Val Thr Trp Trp Ile Ser Val Asn Leu Leu Asn Ser Gln
             25                  30                  35

cta ccc ttt tta gct ccc tgg gta gcg tta atg acg atg caa ttc acc   259
Leu Pro Phe Leu Ala Pro Trp Val Ala Leu Met Thr Met Gln Phe Thr
         40                  45                  50

gtc tac cac acc ttt atc agt gga att cag act gca att gct tct gtc   307
Val Tyr His Thr Phe Ile Ser Gly Ile Gln Thr Ala Ile Ala Ser Val
     55                  60                  65

atc gga gtt gga ctt tcc ttt gtc ata ggc act tac tta gac gta agt   355
Ile Gly Val Gly Leu Ser Phe Val Ile Gly Thr Tyr Leu Asp Val Ser
 70                  75                  80                  85

gtg tgg act ttt ggc ctt gca atg gtc ata gga tta ata ggt gca cga   403
Val Trp Thr Phe Gly Leu Ala Met Val Ile Gly Leu Ile Gly Ala Arg
                 90                  95                 100
```

```
gta cca aag ctc cgc gcg gaa gga ata ggt att gct act aca tcc att   451
Val Pro Lys Leu Arg Ala Glu Gly Ile Gly Ile Ala Thr Thr Ser Ile
            105                 110                 115

ttt ctt ctt gcc tcc ggg ttt gat gat caa caa ccc ctt cta tac gac   499
Phe Leu Leu Ala Ser Gly Phe Asp Asp Gln Gln Pro Leu Leu Tyr Asp
        120                 125                 130

cgt att tta gag atc ctg ctc ggc gtg gct gtt gcc ata gcc atc aac   547
Arg Ile Leu Glu Ile Leu Leu Gly Val Ala Val Ala Ile Ala Ile Asn
    135                 140                 145

ctc atc atc ttt cct ccc tta cgc gac cag gag gca aac atg gtg gta   595
Leu Ile Ile Phe Pro Pro Leu Arg Asp Gln Glu Ala Asn Met Val Val
150                 155                 160                 165

gga aac tta gat cgg agg atg ggt gag gtt tta caa aaa atg gcc gat   643
Gly Asn Leu Asp Arg Arg Met Gly Glu Val Leu Gln Lys Met Ala Asp
                170                 175                 180

gag ctt gca gaa aag tgg aat atc gac aat gca gat gag tgg ctg gaa   691
Glu Leu Ala Glu Lys Trp Asn Ile Asp Asn Ala Asp Glu Trp Leu Glu
            185                 190                 195

gaa att aat tct att aac aat gac cta gaa aaa gcg tgg cac tcc gtg   739
Glu Ile Asn Ser Ile Asn Asn Asp Leu Glu Lys Ala Trp His Ser Val
        200                 205                 210

cgg ttc gtt cgc gaa agc cgt cga gtt aat cct cgt aaa atc cgc atc   787
Arg Phe Val Arg Glu Ser Arg Arg Val Asn Pro Arg Lys Ile Arg Ile
    215                 220                 225

caa gag ggc cgc ccc cag cct acg gaa aca agt tat gaa tca aac ctc   835
Gln Glu Gly Arg Pro Gln Pro Thr Glu Thr Ser Tyr Glu Ser Asn Leu
230                 235                 240                 245

acc agc att gat gaa ggg atc gct cat tta cgc cac ctt gcc cgt act   883
Thr Ser Ile Asp Glu Gly Ile Ala His Leu Arg His Leu Ala Arg Thr
                250                 255                 260

ctt cgt gat acc ccg att ata gat tcc gac tgg gga tcc agt att cca   931
Leu Arg Asp Thr Pro Ile Ile Asp Ser Asp Trp Gly Ser Ser Ile Pro
            265                 270                 275

gca aca gtg ggt atc cct tat gca cga tgc cgg agc ttt gct cgc aga   979
Ala Thr Val Gly Ile Pro Tyr Ala Arg Cys Arg Ser Phe Ala Arg Arg
        280                 285                 290

tcc gaa tca gga aat aga tcc tat ccg cga ccg gct ctc taaactttca   1028
Ser Glu Ser Gly Asn Arg Ser Tyr Pro Arg Pro Ala Leu
    295                 300                 305

agtgagatga gtg                                                  1041
```

<210> 570
<211> 306
<212> PRT
<213> Corynebacterium glutamicum

<400> 570

```
Met Glu Lys Ile Arg Ser Pro Ala Val Gln Ser Asp Ala Leu Gln Val
  1               5                  10                  15

Phe Lys Ser Ala Leu Ala Ala Thr Val Thr Trp Trp Ile Ser Val Asn
             20                  25                  30

Leu Leu Asn Ser Gln Leu Pro Phe Leu Ala Pro Trp Val Ala Leu Met
         35                  40                  45

Thr Met Gln Phe Thr Val Tyr His Thr Phe Ile Ser Gly Ile Gln Thr
     50                  55                  60

Ala Ile Ala Ser Val Ile Gly Val Gly Leu Ser Phe Val Ile Gly Thr
 65                  70                  75                  80

Tyr Leu Asp Val Ser Val Trp Thr Phe Gly Leu Ala Met Val Ile Gly
                 85                  90                  95

Leu Ile Gly Ala Arg Val Pro Lys Leu Arg Ala Glu Gly Ile Gly Ile
            100                 105                 110

Ala Thr Thr Ser Ile Phe Leu Leu Ala Ser Gly Phe Asp Asp Gln Gln
        115                 120                 125

Pro Leu Leu Tyr Asp Arg Ile Leu Glu Ile Leu Leu Gly Val Ala Val
    130                 135                 140

Ala Ile Ala Ile Asn Leu Ile Ile Phe Pro Pro Leu Arg Asp Gln Glu
145                 150                 155                 160

Ala Asn Met Val Val Gly Asn Leu Asp Arg Arg Met Gly Glu Val Leu
                165                 170                 175

Gln Lys Met Ala Asp Glu Leu Ala Glu Lys Trp Asn Ile Asp Asn Ala
            180                 185                 190

Asp Glu Trp Leu Glu Glu Ile Asn Ser Ile Asn Asn Asp Leu Glu Lys
        195                 200                 205

Ala Trp His Ser Val Arg Phe Val Arg Glu Ser Arg Arg Val Asn Pro
    210                 215                 220

Arg Lys Ile Arg Ile Gln Glu Gly Arg Pro Gln Pro Thr Glu Thr Ser
225                 230                 235                 240

Tyr Glu Ser Asn Leu Thr Ser Ile Asp Glu Gly Ile Ala His Leu Arg
                245                 250                 255

His Leu Ala Arg Thr Leu Arg Asp Thr Pro Ile Ile Asp Ser Asp Trp
            260                 265                 270

Gly Ser Ser Ile Pro Ala Thr Val Gly Ile Pro Tyr Ala Arg Cys Arg
        275                 280                 285

Ser Phe Ala Arg Arg Ser Glu Ser Gly Asn Arg Ser Tyr Pro Arg Pro
    290                 295                 300

Ala Leu
305
```

<210> 571
<211> 885
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(862)
<223> RXN01281

<400> 571
ggacaacctc atcaaatgca aacatgcgcc accgcgtccc ggaaaaccag gggcgatacc 60

gcgcttgagt gcgaggtgcc gtcaattccc aactacaaga gtg gga ctc agc cgt 115
Val Gly Leu Ser Arg
1 5

tca cat tat cag cta gcc gca gaa aac acc aaa tcc ctt gtt aga atg 163
Ser His Tyr Gln Leu Ala Ala Glu Asn Thr Lys Ser Leu Val Arg Met
10 15 20

gtt ccc atg act gtt cct caa gga aac gaa cca gca aag aag ctc gcc 211
Val Pro Met Thr Val Pro Gln Gly Asn Glu Pro Ala Lys Lys Leu Ala
25 30 35

act gac ctt aac cga aac caa gtc gtg gat gaa ctt tct gca gct gtt 259
Thr Asp Leu Asn Arg Asn Gln Val Val Asp Glu Leu Ser Ala Ala Val
40 45 50

tcc cga ggt caa ctc act ttg gag gaa ttt gaa gat cgc tcc tcc aaa 307
Ser Arg Gly Gln Leu Thr Leu Glu Glu Phe Glu Asp Arg Ser Ser Lys
55 60 65

gca tgg aat gcc cgc cac tta gac act ctt gta gag ctg atc tct gat 355
Ala Trp Asn Ala Arg His Leu Asp Thr Leu Val Glu Leu Ile Ser Asp
70 75 80 85

gtg aac gac aat ccc tac act ctg ctt ggt cag caa ttt ccc ggc gcc 403
Val Asn Asp Asn Pro Tyr Thr Leu Leu Gly Gln Gln Phe Pro Gly Ala
90 95 100

tcc tat gcg ccg gcg gcc tac gag acc act ccc cca gcg atg ccc aat 451
Ser Tyr Ala Pro Ala Ala Tyr Glu Thr Thr Pro Pro Ala Met Pro Asn
105 110 115

gtg tca gat cct gta aat att gtc cgc aac agg att acc ggc aac ccg 499
Val Ser Asp Pro Val Asn Ile Val Arg Asn Arg Ile Thr Gly Asn Pro
120 125 130

aat ggc tcc aaa atg tcg gtc tcg ttt atg ggt ggc acc gtg cgc aaa 547
Asn Gly Ser Lys Met Ser Val Ser Phe Met Gly Gly Thr Val Arg Lys
135 140 145

ggt gga tgg cat gtg cct aat gtt cac aca tcc ttc gcc atg atg ggc 595
Gly Gly Trp His Val Pro Asn Val His Thr Ser Phe Ala Met Met Gly
150 155 160 165

ggc aat cag atc gat ttg cgc gac gcc ttc ctg gaa agc gac cgc att 643
Gly Asn Gln Ile Asp Leu Arg Asp Ala Phe Leu Glu Ser Asp Arg Ile
170 175 180

```
cag atc aac gcc tac aca ttc atg ggt ggc atc gag att att gtt ccc   691
Gln Ile Asn Ala Tyr Thr Phe Met Gly Gly Ile Glu Ile Ile Val Pro
            185                 190                 195

gag ggt gtt ttt gtc att tgt gat ggc atg ggc att ttc ggc ggc ttc   739
Glu Gly Val Phe Val Ile Cys Asp Gly Met Gly Ile Phe Gly Gly Phe
        200                 205                 210

gaa cag tct gtg gac aag gcc ggt gca ctc aat ccc gcg cgc ctg cca   787
Glu Gln Ser Val Asp Lys Ala Gly Ala Leu Asn Pro Ala Arg Leu Pro
    215                 220                 225

agc aac gcg ccc acg gtc cac atc aaa ggc ctg gcg ttc atg ggc gga   835
Ser Asn Ala Pro Thr Val His Ile Lys Gly Leu Ala Phe Met Gly Gly
230                 235                 240                 245

gtc agc gta gtc acc aag aaa aac att taaaaagctt gtcgacgcgc         882
Val Ser Val Val Thr Lys Lys Asn Ile
                250

ccc                                                              885
```

Do not enter sequence data in this area

<210> 572
<211> 254
<212> PRT
<213> Corynebacterium glutamicum

<400> 572

```
Val Gly Leu Ser Arg Ser His Tyr Gln Leu Ala Ala Glu Asn Thr Lys
  1               5                  10                  15

Ser Leu Val Arg Met Val Pro Met Thr Val Pro Gln Gly Asn Glu Pro
             20                  25                  30

Ala Lys Lys Leu Ala Thr Asp Leu Asn Arg Asn Gln Val Val Asp Glu
         35                  40                  45

Leu Ser Ala Ala Val Ser Arg Gly Gln Leu Thr Leu Glu Glu Phe Glu
     50                  55                  60

Asp Arg Ser Ser Lys Ala Trp Asn Ala Arg His Leu Asp Thr Leu Val
 65                  70                  75                  80

Glu Leu Ile Ser Asp Val Asn Asp Asn Pro Tyr Thr Leu Leu Gly Gln
                 85                  90                  95

Gln Phe Pro Gly Ala Ser Tyr Ala Pro Ala Ala Tyr Glu Thr Thr Pro
            100                 105                 110

Pro Ala Met Pro Asn Val Ser Asp Pro Val Asn Ile Val Arg Asn Arg
        115                 120                 125

Ile Thr Gly Asn Pro Asn Gly Ser Lys Met Ser Val Ser Phe Met Gly
    130                 135                 140

Gly Thr Val Arg Lys Gly Gly Trp His Val Pro Asn Val His Thr Ser
145                 150                 155                 160

Phe Ala Met Met Gly Gly Asn Gln Ile Asp Leu Arg Asp Ala Phe Leu
                165                 170                 175
```

```
Glu Ser Asp Arg Ile Gln Ile Asn Ala Tyr Thr Phe Met Gly Gly Ile
            180                 185                 190

Glu Ile Ile Val Pro Glu Gly Val Phe Val Ile Cys Asp Gly Met Gly
        195                 200                 205

Ile Phe Gly Gly Phe Glu Gln Ser Val Asp Lys Ala Gly Ala Leu Asn
    210                 215                 220

Pro Ala Arg Leu Pro Ser Asn Ala Pro Thr Val His Ile Lys Gly Leu
225                 230                 235                 240

Ala Phe Met Gly Gly Val Ser Val Val Thr Lys Lys Asn Ile
                245                 250
```

<210> 573
<211> 885
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(862)
<223> FRXA01281

<400> 573

```
ggacaacctc atcaaatgca aacatgcgcc accgcgtccc ggaaaaccag gggcgatacc 60

gcgcttgagt gcgaggtgcc gtcaattccc aactacaaga gtg gga ctc agc cgt   115
                                              Val Gly Leu Ser Arg
                                                1               5

tca cat tat cag cta gcc gca gaa aac acc aaa tcc ctt gtt aga atg   163
Ser His Tyr Gln Leu Ala Ala Glu Asn Thr Lys Ser Leu Val Arg Met
                10                  15                  20

gtt ccc atg act gtt cct caa gga aac gaa cca gca aag aag ctc gcc   211
Val Pro Met Thr Val Pro Gln Gly Asn Glu Pro Ala Lys Lys Leu Ala
            25                  30                  35

act gac ctt aac cga aac caa gtc gtg gat gaa ctt tct gca gct gtt   259
Thr Asp Leu Asn Arg Asn Gln Val Val Asp Glu Leu Ser Ala Ala Val
        40                  45                  50

tcc cga ggt caa ctc act ttg gag gaa ttt gaa gat cgc tcc tcc aaa   307
Ser Arg Gly Gln Leu Thr Leu Glu Glu Phe Glu Asp Arg Ser Ser Lys
    55                  60                  65

gca tgg aat gcc cgc cac tta gac act ctt gta gag ctg atc tct gat   355
Ala Trp Asn Ala Arg His Leu Asp Thr Leu Val Glu Leu Ile Ser Asp
70                  75                  80                  85

gtg aac gac aat ccc tac act ctg ctt ggt cag caa ttt ccc ggc gcc   403
Val Asn Asp Asn Pro Tyr Thr Leu Leu Gly Gln Gln Phe Pro Gly Ala
                90                  95                 100

tcc tat gcg ccg gcg gcc tac gag acc act ccc cca gcg atg ccc aat   451
Ser Tyr Ala Pro Ala Ala Tyr Glu Thr Thr Pro Pro Ala Met Pro Asn
            105                 110                 115
```

```
gtg tca gat cct gta aat att gtc cgc aac agg att acc ggc aac ccg   499
Val Ser Asp Pro Val Asn Ile Val Arg Asn Arg Ile Thr Gly Asn Pro
        120                 125                 130

aat ggc tcc aaa atg tcg gtc tcg ttt atg ggt ggc acc gtg cgc aaa   547
Asn Gly Ser Lys Met Ser Val Ser Phe Met Gly Gly Thr Val Arg Lys
    135                 140                 145

ggt gga tgg cat gtg cct aat gtt cac aca tcc ttc gcc atg atg ggc   595
Gly Gly Trp His Val Pro Asn Val His Thr Ser Phe Ala Met Met Gly
150                 155                 160                 165

ggc aat cag atc gat ttg cgc gac gcc ttc ctg gaa agc gac cgc att   643
Gly Asn Gln Ile Asp Leu Arg Asp Ala Phe Leu Glu Ser Asp Arg Ile
                170                 175                 180

cag atc aac gcc tac aca ttc atg ggt ggc atc gag att att gtt ccc   691
Gln Ile Asn Ala Tyr Thr Phe Met Gly Gly Ile Glu Ile Ile Val Pro
            185                 190                 195

gag ggt gtt ttt gtc att tgt gat ggc atg ggc att ttc ggc ggc ttc   739
Glu Gly Val Phe Val Ile Cys Asp Gly Met Gly Ile Phe Gly Gly Phe
        200                 205                 210

gaa cag tct gtg gac aag gcc ggt gca ctc aat ccc gcg cgc ctg cca   787
Glu Gln Ser Val Asp Lys Ala Gly Ala Leu Asn Pro Ala Arg Leu Pro
    215                 220                 225

agc aac gcg ccc acg gtc cac atc aaa ggc ctg gcg ttc atg ggc gga   835
Ser Asn Ala Pro Thr Val His Ile Lys Gly Leu Ala Phe Met Gly Gly
230                 235                 240                 245

gtc agc gta gtc acc aag aaa aac att taaaaagctt gtcgacgcgc         882
Val Ser Val Val Thr Lys Lys Asn Ile
                250

ccc                                                              885
```

<210> 574
<211> 254
<212> PRT
<213> Corynebacterium glutamicum

<400> 574

```
Val Gly Leu Ser Arg Ser His Tyr Gln Leu Ala Ala Glu Asn Thr Lys
  1               5                  10                  15

Ser Leu Val Arg Met Val Pro Met Thr Val Pro Gln Gly Asn Glu Pro
             20                  25                  30

Ala Lys Lys Leu Ala Thr Asp Leu Asn Arg Asn Gln Val Val Asp Glu
         35                  40                  45

Leu Ser Ala Ala Val Ser Arg Gly Gln Leu Thr Leu Glu Glu Phe Glu
     50                  55                  60

Asp Arg Ser Ser Lys Ala Trp Asn Ala Arg His Leu Asp Thr Leu Val
 65                  70                  75                  80
```

```
Glu Leu Ile Ser Asp Val Asn Asp Asn Pro Tyr Thr Leu Leu Gly Gln
                85                  90                  95

Gln Phe Pro Gly Ala Ser Tyr Ala Pro Ala Ala Tyr Glu Thr Thr Pro
            100                 105                 110

Pro Ala Met Pro Asn Val Ser Asp Pro Val Asn Ile Val Arg Asn Arg
        115                 120                 125

Ile Thr Gly Asn Pro Asn Gly Ser Lys Met Ser Val Ser Phe Met Gly
    130                 135                 140

Gly Thr Val Arg Lys Gly Gly Trp His Val Pro Asn Val His Thr Ser
145                 150                 155                 160

Phe Ala Met Met Gly Gly Asn Gln Ile Asp Leu Arg Asp Ala Phe Leu
                165                 170                 175

Glu Ser Asp Arg Ile Gln Ile Asn Ala Tyr Thr Phe Met Gly Gly Ile
            180                 185                 190

Glu Ile Ile Val Pro Glu Gly Val Phe Val Ile Cys Asp Gly Met Gly
        195                 200                 205

Ile Phe Gly Gly Phe Glu Gln Ser Val Asp Lys Ala Gly Ala Leu Asn
    210                 215                 220

Pro Ala Arg Leu Pro Ser Asn Ala Pro Thr Val His Ile Lys Gly Leu
225                 230                 235                 240

Ala Phe Met Gly Gly Val Ser Val Val Thr Lys Lys Asn Ile
                245                 250
```

Sequence Listing - 2nd Edition - 2nd Edition

<210> 575
<211> 1206
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1183)
<223> RXN01296

<400> 575

```
taaaactcct gttcgaaatt gcccagacag gtgtccacca acactgctac attgcattgg 60

agatccagaa tcgatcactc tacgaccagg aaaaactttc atg tcc atc gag caa   115
                                            Met Ser Ile Glu Gln
                                              1               5

gca atc act tca ctc tcc gca aga gtg cgg gaa cta aag ccc atc atc   163
Ala Ile Thr Ser Leu Ser Ala Arg Val Arg Glu Leu Lys Pro Ile Ile
                 10                  15                  20

gag act gaa gaa gcc acc aaa acc gca ctg atc atc ccc ttt atc agc   211
Glu Thr Glu Glu Ala Thr Lys Thr Ala Leu Ile Ile Pro Phe Ile Ser
             25                  30                  35

aac gtt ctc ggc tac gac gtc act gat cct cgt gaa gtc att ccg gaa   259
Asn Val Leu Gly Tyr Asp Val Thr Asp Pro Arg Glu Val Ile Pro Glu
```

```
         40                  45                  50

tac act gct gat gtt ggc gtc aaa aag ggt gag aag gtc gac ttc gct   307
Tyr Thr Ala Asp Val Gly Val Lys Lys Gly Glu Lys Val Asp Phe Ala
     55                  60                  65

atc aaa acc ggc gat gat ttc cac ttc ctc atc gaa tgc aaa aag gtc   355
Ile Lys Thr Gly Asp Asp Phe His Phe Leu Ile Glu Cys Lys Lys Val
 70                  75                  80                  85

ggc tcc cca ctc agc ctc gat cac gct aac cag ctc gtc cgc tat ttc   403
Gly Ser Pro Leu Ser Leu Asp His Ala Asn Gln Leu Val Arg Tyr Phe
                 90                  95                 100

aat gtc aca gac acc gaa ttt gcc att ctc acc aac ggc gaa atc tac   451
Asn Val Thr Asp Thr Glu Phe Ala Ile Leu Thr Asn Gly Glu Ile Tyr
            105                 110                 115

caa ttc tat gga caa ctc gat gca gcc aac cgc atg gat gca aaa cca   499
Gln Phe Tyr Gly Gln Leu Asp Ala Ala Asn Arg Met Asp Ala Lys Pro
        120                 125                 130

ttc atg acc ttg gat ttg aac aat att gat gcc cgt cag ttc cct cat   547
Phe Met Thr Leu Asp Leu Asn Asn Ile Asp Ala Arg Gln Phe Pro His
    135                 140                 145

ttg gaa atg tgt acc cgc aag cat ttc aac cca caa gcg cta gcc gcc   595
Leu Glu Met Cys Thr Arg Lys His Phe Asn Pro Gln Ala Leu Ala Ala
150                 155                 160                 165

aac gct gaa gaa ctg aag tac att gct gaa ttg aag aaa gtc atc gcg   643
Asn Ala Glu Glu Leu Lys Tyr Ile Ala Glu Leu Lys Lys Val Ile Ala
                170                 175                 180

aat caa ttc caa gaa cct gac gta gaa atc gtc aag atg ctt gcg gcg   691
Asn Gln Phe Gln Glu Pro Asp Val Glu Ile Val Lys Met Leu Ala Ala
            185                 190                 195

aca gtc acc aca aag cgt atg act gca caa aat ctg gaa ttc ttc acc   739
Thr Val Thr Thr Lys Arg Met Thr Ala Gln Asn Leu Glu Phe Phe Thr
        200                 205                 210

cgc ttg gtt aat act gcg tct tcc cag ttc ctc aaa gac gag gtc aat   787
Arg Leu Val Asn Thr Ala Ser Ser Gln Phe Leu Lys Asp Glu Val Asn
    215                 220                 225

cgt aga ttg cgc tcc gcc caa gtc ttt gag gat cct gtc caa aca caa   835
Arg Arg Leu Arg Ser Ala Gln Val Phe Glu Asp Pro Val Gln Thr Gln
230                 235                 240                 245

ggt gct gat gca gaa aca cca gca gag gac gaa gca gta atc gaa gaa   883
Gly Ala Asp Ala Glu Thr Pro Ala Glu Asp Glu Ala Val Ile Glu Glu
                250                 255                 260

gtg gtt tca gaa atc gtg acg aca gaa gag gaa atc cac ggt cat tca   931
Val Val Ser Glu Ile Val Thr Thr Glu Glu Glu Ile His Gly His Ser
            265                 270                 275

att gtc cgt gca att tgc tgc tca gag gta tcg gca caa gaa atc acc   979
Ile Val Arg Ala Ile Cys Cys Ser Glu Val Ser Ala Gln Glu Ile Thr
        280                 285                 290
```

```
atg cgt gac gca aaa tcc tac tgc gct att ctc ttc caa gac aac aac   1027
Met Arg Asp Ala Lys Ser Tyr Cys Ala Ile Leu Phe Gln Asp Asn Asn
    295                 300                 305

cga aag cca atc gcc cgt ttc tac ttt gat cgc aag att cca cgc atc   1075
Arg Lys Pro Ile Ala Arg Phe Tyr Phe Asp Arg Lys Ile Pro Arg Ile
310                 315                 320                 325

ggc atc ttc aat gct gaa ggc gag cag gaa cac ttt gat ttg gaa tcc   1123
Gly Ile Phe Asn Ala Glu Gly Glu Gln Glu His Phe Asp Leu Glu Ser
                330                 335                 340

atc gaa gat atc tac aac cac gct gat ctt ctg cat tcc cgc gtc gta   1171
Ile Glu Asp Ile Tyr Asn His Ala Asp Leu Leu His Ser Arg Val Val
            345                 350                 355

gca ttg aac gct taagttctgc ctttagttct gca                        1206
Ala Leu Asn Ala
        360
```

<210> 576
<211> 361
<212> PRT
<213> Corynebacterium glutamicum

<400> 576

```
Met Ser Ile Glu Gln Ala Ile Thr Ser Leu Ser Ala Arg Val Arg Glu
  1               5                  10                  15

Leu Lys Pro Ile Ile Glu Thr Glu Glu Ala Thr Lys Thr Ala Leu Ile
             20                  25                  30

Ile Pro Phe Ile Ser Asn Val Leu Gly Tyr Asp Val Thr Asp Pro Arg
         35                  40                  45

Glu Val Ile Pro Glu Tyr Thr Ala Asp Val Gly Val Lys Lys Gly Glu
     50                  55                  60

Lys Val Asp Phe Ala Ile Lys Thr Gly Asp Asp Phe His Phe Leu Ile
 65                  70                  75                  80

Glu Cys Lys Lys Val Gly Ser Pro Leu Ser Leu Asp His Ala Asn Gln
                 85                  90                  95

Leu Val Arg Tyr Phe Asn Val Thr Asp Thr Glu Phe Ala Ile Leu Thr
            100                 105                 110

Asn Gly Glu Ile Tyr Gln Phe Tyr Gly Gln Leu Asp Ala Ala Asn Arg
        115                 120                 125

Met Asp Ala Lys Pro Phe Met Thr Leu Asp Leu Asn Asn Ile Asp Ala
    130                 135                 140

Arg Gln Phe Pro His Leu Glu Met Cys Thr Arg Lys His Phe Asn Pro
145                 150                 155                 160

Gln Ala Leu Ala Ala Asn Ala Glu Glu Leu Lys Tyr Ile Ala Glu Leu
                165                 170                 175
```

```
Lys Lys Val Ile Ala Asn Gln Phe Gln Glu Pro Asp Val Glu Ile Val
            180                 185                 190

Lys Met Leu Ala Ala Thr Val Thr Thr Lys Arg Met Thr Ala Gln Asn
        195                 200                 205

Leu Glu Phe Phe Thr Arg Leu Val Asn Thr Ala Ser Ser Gln Phe Leu
    210                 215                 220

Lys Asp Glu Val Asn Arg Arg Leu Arg Ser Ala Gln Val Phe Glu Asp
225                 230                 235                 240

Pro Val Gln Thr Gln Gly Ala Asp Ala Glu Thr Pro Ala Glu Asp Glu
                245                 250                 255

Ala Val Ile Glu Glu Val Val Ser Glu Ile Val Thr Thr Glu Glu Glu
            260                 265                 270

Ile His Gly His Ser Ile Val Arg Ala Ile Cys Cys Ser Glu Val Ser
        275                 280                 285

Ala Gln Glu Ile Thr Met Arg Asp Ala Lys Ser Tyr Cys Ala Ile Leu
    290                 295                 300

Phe Gln Asp Asn Asn Arg Lys Pro Ile Ala Arg Phe Tyr Phe Asp Arg
305                 310                 315                 320

Lys Ile Pro Arg Ile Gly Ile Phe Asn Ala Glu Gly Glu Gln Glu His
                325                 330                 335

Phe Asp Leu Glu Ser Ile Glu Asp Ile Tyr Asn His Ala Asp Leu Leu
            340                 345                 350

His Ser Arg Val Val Ala Leu Asn Ala
        355                 360


<210> 577
<211> 1206
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1183)
<223> FRXA01296

<400> 577
taaaactcct gttcgaaatt gcccagacag gtgtccacca acactgctac attgcattgg 60

agatccagaa tcgatcactc tacgaccagg aaaaactttc atg tcc atc gag caa   115
                                            Met Ser Ile Glu Gln
                                              1               5

gca atc act tca ctc tcc gca aga gtg cgg gaa cta aag ccc atc atc   163
Ala Ile Thr Ser Leu Ser Ala Arg Val Arg Glu Leu Lys Pro Ile Ile
                 10                  15                  20

gag act gaa gaa gcc acc aaa acc gca ctg atc atc ccc ttt atc agc   211
Glu Thr Glu Glu Ala Thr Lys Thr Ala Leu Ile Ile Pro Phe Ile Ser
             25                  30                  35
```

```
aac gtt ctc ggc tac gac gtc act gat cct cgt gaa gtc att ccg gaa   259
Asn Val Leu Gly Tyr Asp Val Thr Asp Pro Arg Glu Val Ile Pro Glu
         40                  45                  50

tac act gct gat gtt ggc gtc aaa aag ggt gag aag gtc gac ttc gct   307
Tyr Thr Ala Asp Val Gly Val Lys Lys Gly Glu Lys Val Asp Phe Ala
     55                  60                  65

atc aaa acc ggc gat gat ttc cac ttc ctc atc gaa tgc aaa aag gtc   355
Ile Lys Thr Gly Asp Asp Phe His Phe Leu Ile Glu Cys Lys Lys Val
 70                  75                  80                  85

ggc tcc cca ctc agc ctc gat cac gct aac cag ctc gtc cgc tat ttc   403
Gly Ser Pro Leu Ser Leu Asp His Ala Asn Gln Leu Val Arg Tyr Phe
                 90                  95                 100

aat gtc aca gac acc gaa ttt gcc att ctc acc aac ggc gaa atc tac   451
Asn Val Thr Asp Thr Glu Phe Ala Ile Leu Thr Asn Gly Glu Ile Tyr
            105                 110                 115

caa ttc tat gga caa ctc gat gca gcc aac cgc atg gat gca aaa cca   499
Gln Phe Tyr Gly Gln Leu Asp Ala Ala Asn Arg Met Asp Ala Lys Pro
        120                 125                 130

ttc atg acc ttg gat ttg aac aat att gat gcc cgt cag ttc cct cat   547
Phe Met Thr Leu Asp Leu Asn Asn Ile Asp Ala Arg Gln Phe Pro His
    135                 140                 145

ttg gaa atg tgt acc cgc aag cat ttc aac cca caa gcg cta gcc gcc   595
Leu Glu Met Cys Thr Arg Lys His Phe Asn Pro Gln Ala Leu Ala Ala
150                 155                 160                 165

aac gct gaa gaa ctg aag tac att gct gaa ttg aag aaa gtc atc gcg   643
Asn Ala Glu Glu Leu Lys Tyr Ile Ala Glu Leu Lys Lys Val Ile Ala
                170                 175                 180

aat caa ttc caa gaa cct gac gta gaa atc gtc aag atg ctt gcg gcg   691
Asn Gln Phe Gln Glu Pro Asp Val Glu Ile Val Lys Met Leu Ala Ala
            185                 190                 195

aca gtc acc aca aag cgt atg act gca caa aat ctg gaa ttc ttc acc   739
Thr Val Thr Thr Lys Arg Met Thr Ala Gln Asn Leu Glu Phe Phe Thr
        200                 205                 210

cgc ttg gtt aat act gcg tct tcc cag ttc ctc aaa gac gag gtc aat   787
Arg Leu Val Asn Thr Ala Ser Ser Gln Phe Leu Lys Asp Glu Val Asn
    215                 220                 225

cgt aga ttg cgc tcc gcc caa gtc ttt gag gat cct gtc caa aca caa   835
Arg Arg Leu Arg Ser Ala Gln Val Phe Glu Asp Pro Val Gln Thr Gln
230                 235                 240                 245

ggt gct gat gca gaa aca cca gca gag gac gaa gca gta atc gaa gaa   883
Gly Ala Asp Ala Glu Thr Pro Ala Glu Asp Glu Ala Val Ile Glu Glu
                250                 255                 260

gtg gtt tca gaa atc gtg acg aca gaa gag gaa atc cac ggt cat tca   931
Val Val Ser Glu Ile Val Thr Thr Glu Glu Glu Ile His Gly His Ser
            265                 270                 275
```

```
att gtc cgt gca att tgc tgc tca gag gta tcg gca caa gaa atc acc   979
Ile Val Arg Ala Ile Cys Cys Ser Glu Val Ser Ala Gln Glu Ile Thr
        280                 285                 290

atg cgt gac gca aaa tcc tac tgc gct att ctc ttc caa gac aac aac   1027
Met Arg Asp Ala Lys Ser Tyr Cys Ala Ile Leu Phe Gln Asp Asn Asn
    295                 300                 305

cga aag cca atc gcc cgt ttc tac ttt gat cgc aag att cca cgc atc   1075
Arg Lys Pro Ile Ala Arg Phe Tyr Phe Asp Arg Lys Ile Pro Arg Ile
310                 315                 320                 325

ggc atc ttc aat gct gaa ggc gag cag gaa cac ttt gat ttg gaa tcc   1123
Gly Ile Phe Asn Ala Glu Gly Glu Gln Glu His Phe Asp Leu Glu Ser
                330                 335                 340

atc gaa gat atc tac aac cac gct gat ctt ctg cat tcc cgc gtc gta   1171
Ile Glu Asp Ile Tyr Asn His Ala Asp Leu Leu His Ser Arg Val Val
            345                 350                 355

gca ttg aac gct taagttctgc ctttagttct gca                        1206
Ala Leu Asn Ala
        360
```

<210> 578
<211> 361
<212> PRT
<213> Corynebacterium glutamicum

<400> 578

```
Met Ser Ile Glu Gln Ala Ile Thr Ser Leu Ser Ala Arg Val Arg Glu
  1               5                  10                  15

Leu Lys Pro Ile Ile Glu Thr Glu Glu Ala Thr Lys Thr Ala Leu Ile
             20                  25                  30

Ile Pro Phe Ile Ser Asn Val Leu Gly Tyr Asp Val Thr Asp Pro Arg
         35                  40                  45

Glu Val Ile Pro Glu Tyr Thr Ala Asp Val Gly Val Lys Lys Gly Glu
     50                  55                  60

Lys Val Asp Phe Ala Ile Lys Thr Gly Asp Asp Phe His Phe Leu Ile
 65                  70                  75                  80

Glu Cys Lys Lys Val Gly Ser Pro Leu Ser Leu Asp His Ala Asn Gln
                 85                  90                  95

Leu Val Arg Tyr Phe Asn Val Thr Asp Thr Glu Phe Ala Ile Leu Thr
            100                 105                 110

Asn Gly Glu Ile Tyr Gln Phe Tyr Gly Gln Leu Asp Ala Ala Asn Arg
        115                 120                 125

Met Asp Ala Lys Pro Phe Met Thr Leu Asp Leu Asn Asn Ile Asp Ala
    130                 135                 140

Arg Gln Phe Pro His Leu Glu Met Cys Thr Arg Lys His Phe Asn Pro
145                 150                 155                 160
```

```
Gln Ala Leu Ala Ala Asn Ala Glu Glu Leu Lys Tyr Ile Ala Glu Leu
                165                 170                 175

Lys Lys Val Ile Ala Asn Gln Phe Gln Glu Pro Asp Val Glu Ile Val
            180                 185                 190

Lys Met Leu Ala Ala Thr Val Thr Thr Lys Arg Met Thr Ala Gln Asn
        195                 200                 205

Leu Glu Phe Phe Thr Arg Leu Val Asn Thr Ala Ser Ser Gln Phe Leu
    210                 215                 220

Lys Asp Glu Val Asn Arg Arg Leu Arg Ser Ala Gln Val Phe Glu Asp
225                 230                 235                 240

Pro Val Gln Thr Gln Gly Ala Asp Ala Glu Thr Pro Ala Glu Asp Glu
                245                 250                 255

Ala Val Ile Glu Glu Val Val Ser Glu Ile Val Thr Thr Glu Glu Glu
            260                 265                 270

Ile His Gly His Ser Ile Val Arg Ala Ile Cys Cys Ser Glu Val Ser
        275                 280                 285

Ala Gln Glu Ile Thr Met Arg Asp Ala Lys Ser Tyr Cys Ala Ile Leu
    290                 295                 300

Phe Gln Asp Asn Asn Arg Lys Pro Ile Ala Arg Phe Tyr Phe Asp Arg
305                 310                 315                 320

Lys Ile Pro Arg Ile Gly Ile Phe Asn Ala Glu Gly Glu Gln Glu His
                325                 330                 335

Phe Asp Leu Glu Ser Ile Glu Asp Ile Tyr Asn His Ala Asp Leu Leu
            340                 345                 350

His Ser Arg Val Val Ala Leu Asn Ala
        355                 360
```

Sequence Listing

<210> 579
<211> 1131
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1108)
<223> RXN01306

<400> 579

```
tgttttagag gtagagcgaa acgtgcctgt aaaactggcg ctcgctgtgc tcgaagacca 60

cccagacaat caccccgctc cgaaggagaa tcgctaagcc atg act gaa tgg tat   115
                                              Met Thr Glu Trp Tyr
                                                1               5

gtc gtt tta ccc gcc act att cta ctc atc gcg ctg tct gcg ttt ttc   163
Val Val Leu Pro Ala Thr Ile Leu Leu Ile Ala Leu Ser Ala Phe Phe
                10                  15                  20
```

```
gtc atc att gag ttc gct ttg ctt gca gct agg cgg aac cgg tta gag   211
Val Ile Ile Glu Phe Ala Leu Leu Ala Ala Arg Arg Asn Arg Leu Glu
             25                  30                  35

gag act gtg gaa acc tcg cgg tct tcc cgc gct gcg ttg cga agc ctc   259
Glu Thr Val Glu Thr Ser Arg Ser Ser Arg Ala Ala Leu Arg Ser Leu
         40                  45                  50

aat gaa ctt act ctc atg ctc gcg ggc gcg cag ttg gga atc acc atg   307
Asn Glu Leu Thr Leu Met Leu Ala Gly Ala Gln Leu Gly Ile Thr Met
     55                  60                  65

gtg act ttc gcg ttg ggt gct atc acg aag ccg tgg gtt cat tat gct   355
Val Thr Phe Ala Leu Gly Ala Ile Thr Lys Pro Trp Val His Tyr Ala
 70                  75                  80                  85

ttg atg ccg ctc ttc gaa tgg gcg cgt ata ccg ctg gtt atg gca gat   403
Leu Met Pro Leu Phe Glu Trp Ala Arg Ile Pro Leu Val Met Ala Asp
                 90                  95                 100

gtc att gcg ttt att ttg tcg ctg ttt atc gta acg ttt ctg cac ttg   451
Val Ile Ala Phe Ile Leu Ser Leu Phe Ile Val Thr Phe Leu His Leu
            105                 110                 115

gtc atc ggc gaa atg gct ccg aaa tcc tgg gca atc gcg cat ccg gag   499
Val Ile Gly Glu Met Ala Pro Lys Ser Trp Ala Ile Ala His Pro Glu
        120                 125                 130

acg gca ctt cga act atc gcg att ccc gca cgg ggc ttc att aac ctg   547
Thr Ala Leu Arg Thr Ile Ala Ile Pro Ala Arg Gly Phe Ile Asn Leu
    135                 140                 145

ttt cgt cca ttg ctg cag tgg atc aac aaa atg gcg aac gat ttg gtc   595
Phe Arg Pro Leu Leu Gln Trp Ile Asn Lys Met Ala Asn Asp Leu Val
150                 155                 160                 165

cgc aaa gtt ggt gaa act ccc gtt gat cga gct gca gct ggt ggc tat   643
Arg Lys Val Gly Glu Thr Pro Val Asp Arg Ala Ala Ala Gly Gly Tyr
                170                 175                 180

gac acc gat acc ctc cat gcc ctc att gag cat tcc cga gaa act ggc   691
Asp Thr Asp Thr Leu His Ala Leu Ile Glu His Ser Arg Glu Thr Gly
            185                 190                 195

gct ctg gat cag caa tcc gcc gcc caa atc agc gga att atc aag ctg   739
Ala Leu Asp Gln Gln Ser Ala Ala Gln Ile Ser Gly Ile Ile Lys Leu
        200                 205                 210

gat aaa atc acg gtc ggt caa acc ctg acc gca tct cca ttt acg cac   787
Asp Lys Ile Thr Val Gly Gln Thr Leu Thr Ala Ser Pro Phe Thr His
    215                 220                 225

agc gcc agc gcc acg gtt gct gag gtg caa gcc gca gct cag cgc agt   835
Ser Ala Ser Ala Thr Val Ala Glu Val Gln Ala Ala Ala Gln Arg Ser
230                 235                 240                 245

ggc agc ttg cgt gtg ctt atc gac gcc ccc tcc cac ctt ttc cca cac   883
Gly Ser Leu Arg Val Leu Ile Asp Ala Pro Ser His Leu Phe Pro His
                250                 255                 260

gtc att cat gtg cga gac acc ctt ggt gcc tcg cca gac gag aag gct   931
```

```
Val Ile His Val Arg Asp Thr Leu Gly Ala Ser Pro Asp Glu Lys Ala
            265                 270                 275

tcg aag tgg tct cgc cca atc ctc acc gtt gct gag acc gac acg tta   979
Ser Lys Trp Ser Arg Pro Ile Leu Thr Val Ala Glu Thr Asp Thr Leu
        280                 285                 290

cac caa gcg ctg gaa tac atg cgg gag cat aac gag cag atc agt gcg   1027
His Gln Ala Leu Glu Tyr Met Arg Glu His Asn Glu Gln Ile Ser Ala
    295                 300                 305

gtg ctt tcc gct gat ggg aaa acg gtg ctt ggt gta ata act tgg gat   1075
Val Leu Ser Ala Asp Gly Lys Thr Val Leu Gly Val Ile Thr Trp Asp
310                 315                 320                 325

cac atc ttg aaa tac ctg tgg cct gca tcg gtg tagctaattt gaggtgcgct 1128
His Ile Leu Lys Tyr Leu Trp Pro Ala Ser Val
                330                 335

gaa                                                               1131


<210> 580
<211> 336
<212> PRT
<213> Corynebacterium glutamicum

<400> 580
Met Thr Glu Trp Tyr Val Val Leu Pro Ala Thr Ile Leu Leu Ile Ala
  1               5                  10                  15

Leu Ser Ala Phe Phe Val Ile Ile Glu Phe Ala Leu Leu Ala Ala Arg
             20                  25                  30

Arg Asn Arg Leu Glu Glu Thr Val Glu Thr Ser Arg Ser Ser Arg Ala
         35                  40                  45

Ala Leu Arg Ser Leu Asn Glu Leu Thr Leu Met Leu Ala Gly Ala Gln
     50                  55                  60

Leu Gly Ile Thr Met Val Thr Phe Ala Leu Gly Ala Ile Thr Lys Pro
 65                  70                  75                  80

Trp Val His Tyr Ala Leu Met Pro Leu Phe Glu Trp Ala Arg Ile Pro
                 85                  90                  95

Leu Val Met Ala Asp Val Ile Ala Phe Ile Leu Ser Leu Phe Ile Val
            100                 105                 110

Thr Phe Leu His Leu Val Ile Gly Glu Met Ala Pro Lys Ser Trp Ala
        115                 120                 125

Ile Ala His Pro Glu Thr Ala Leu Arg Thr Ile Ala Ile Pro Ala Arg
    130                 135                 140

Gly Phe Ile Asn Leu Phe Arg Pro Leu Leu Gln Trp Ile Asn Lys Met
145                 150                 155                 160

Ala Asn Asp Leu Val Arg Lys Val Gly Glu Thr Pro Val Asp Arg Ala
                165                 170                 175
```

```
Ala Ala Gly Gly Tyr Asp Thr Asp Thr Leu His Ala Leu Ile Glu His
            180                 185                 190

Ser Arg Glu Thr Gly Ala Leu Asp Gln Gln Ser Ala Ala Gln Ile Ser
        195                 200                 205

Gly Ile Ile Lys Leu Asp Lys Ile Thr Val Gly Gln Thr Leu Thr Ala
    210                 215                 220

Ser Pro Phe Thr His Ser Ala Ser Ala Thr Val Ala Glu Val Gln Ala
225                 230                 235                 240

Ala Ala Gln Arg Ser Gly Ser Leu Arg Val Leu Ile Asp Ala Pro Ser
                245                 250                 255

His Leu Phe Pro His Val Ile His Val Arg Asp Thr Leu Gly Ala Ser
            260                 265                 270

Pro Asp Glu Lys Ala Ser Lys Trp Ser Arg Pro Ile Leu Thr Val Ala
        275                 280                 285

Glu Thr Asp Thr Leu His Gln Ala Leu Glu Tyr Met Arg Glu His Asn
    290                 295                 300

Glu Gln Ile Ser Ala Val Leu Ser Ala Asp Gly Lys Thr Val Leu Gly
305                 310                 315                 320

Val Ile Thr Trp Asp His Ile Leu Lys Tyr Leu Trp Pro Ala Ser Val
                325                 330                 335
```

US 2003/0175736 A1 Sep. 18, 2003

<210> 581
<211> 1107
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (77)..(1084)
<223> FRXA01306

<400> 581
cgtgcctgta aaatgcgctc gctctgctga agaccaccca gacaatcacc ccgctccgaa 60

```
ggagaatcga taagccatg act gaa tgg tat gtc gtt tta ccc gcc act att  112
                 Met Thr Glu Trp Tyr Val Val Leu Pro Ala Thr Ile
                   1               5                  10

cta ctc atc gcg ctg tct gcg ttt ttc gtc atc att gag ttc gct ttg   160
Leu Leu Ile Ala Leu Ser Ala Phe Phe Val Ile Ile Glu Phe Ala Leu
         15                  20                  25

ctt gca gct agg cgg aac cgg tta gag gag act gtg gaa acc tcg cgg   208
Leu Ala Ala Arg Arg Asn Arg Leu Glu Glu Thr Val Glu Thr Ser Arg
     30                  35                  40

tct tcc cgc gct gcg ttg cga agc ctc aat gaa ctt act ctc atg ctc   256
Ser Ser Arg Ala Ala Leu Arg Ser Leu Asn Glu Leu Thr Leu Met Leu
```

```
 45                  50                  55                  60

gcg ggc gcg cag ttg gga atc acc atg gtg act ttc gcg ttg ggt gct   304
Ala Gly Ala Gln Leu Gly Ile Thr Met Val Thr Phe Ala Leu Gly Ala
                65                  70                  75

atc acg aag ccg tgg gtt cat tat gct ttg atg ccg ctc ttc gaa tgg   352
Ile Thr Lys Pro Trp Val His Tyr Ala Leu Met Pro Leu Phe Glu Trp
            80                  85                  90

gcg cgt ata ccg ctg gtt atg gca gat gtc att gcg ttt att ttg tcg   400
Ala Arg Ile Pro Leu Val Met Ala Asp Val Ile Ala Phe Ile Leu Ser
        95                  100                 105

ctg ttt atc gta acg ttt ctg cac ttg gtc atc ggc gaa atg gct ccg   448
Leu Phe Ile Val Thr Phe Leu His Leu Val Ile Gly Glu Met Ala Pro
    110                 115                 120

aaa tcc tgg gca atc gcg cat ccg gag acg gca ctt cga act atc gcg   496
Lys Ser Trp Ala Ile Ala His Pro Glu Thr Ala Leu Arg Thr Ile Ala
125                 130                 135                 140

att ccc gca cgg ggc ttc att aac ctg ttt cgt cca ttg ctg cag tgg   544
Ile Pro Ala Arg Gly Phe Ile Asn Leu Phe Arg Pro Leu Leu Gln Trp
                145                 150                 155

atc aac aaa atg gcg aac gat ttg gtc cgc aaa gtt ggt gaa act ccc   592
Ile Asn Lys Met Ala Asn Asp Leu Val Arg Lys Val Gly Glu Thr Pro
            160                 165                 170

gtt gat cga gct gca gct ggt ggc tat gac acc gat acc ctc cat gcc   640
Val Asp Arg Ala Ala Ala Gly Gly Tyr Asp Thr Asp Thr Leu His Ala
        175                 180                 185

ctc att gag cat tcc cga gaa act ggc gct ctg gat cag caa tcc gcc   688
Leu Ile Glu His Ser Arg Glu Thr Gly Ala Leu Asp Gln Gln Ser Ala
    190                 195                 200

gcc caa atc agc gga att atc aag ctg gat aaa atc acg gtc ggt caa   736
Ala Gln Ile Ser Gly Ile Ile Lys Leu Asp Lys Ile Thr Val Gly Gln
205                 210                 215                 220

acc ctg acc gca tct cca ttt acg cac agc gcc agc gcc acg gtt gct   784
Thr Leu Thr Ala Ser Pro Phe Thr His Ser Ala Ser Ala Thr Val Ala
                225                 230                 235

gag gtg caa gcc gca gct cag cgc agt ggc agc ttg cgt gtg ctt atc   832
Glu Val Gln Ala Ala Ala Gln Arg Ser Gly Ser Leu Arg Val Leu Ile
            240                 245                 250

gac gcc ccc tcc cac ctt ttc cca cac gtc att cat gtg cga gac acc   880
Asp Ala Pro Ser His Leu Phe Pro His Val Ile His Val Arg Asp Thr
        255                 260                 265

ctt ggt gcc tcg cca gac gag aag gct tcg aag tgg tct cgc cca atc   928
Leu Gly Ala Ser Pro Asp Glu Lys Ala Ser Lys Trp Ser Arg Pro Ile
    270                 275                 280

ctc acc gtt gct gag acc gac acg tta cac caa gcg ctg gaa tac atg   976
Leu Thr Val Ala Glu Thr Asp Thr Leu His Gln Ala Leu Glu Tyr Met
285                 290                 295                 300
```

```
cgg gag cat aac gag cag atc agt gcg gtg ctt tcc gct gat ggg aaa   1024
Arg Glu His Asn Glu Gln Ile Ser Ala Val Leu Ser Ala Asp Gly Lys
                305                 310                 315

acg gtg ctt ggt gta ata act tgg gat cac atc ttg aaa tac ctg tgg   1072
Thr Val Leu Gly Val Ile Thr Trp Asp His Ile Leu Lys Tyr Leu Trp
            320                 325                 330

cct gca tcg gtg tagctaattt gaggtgcgct gaa                        1107
Pro Ala Ser Val
        335
```

<210> 582
<211> 336
<212> PRT
<213> Corynebacterium glutamicum

<400> 582

```
Met Thr Glu Trp Tyr Val Val Leu Pro Ala Thr Ile Leu Leu Ile Ala
  1               5                  10                  15

Leu Ser Ala Phe Phe Val Ile Ile Glu Phe Ala Leu Leu Ala Ala Arg
             20                  25                  30

Arg Asn Arg Leu Glu Glu Thr Val Glu Thr Ser Arg Ser Ser Arg Ala
         35                  40                  45

Ala Leu Arg Ser Leu Asn Glu Leu Thr Leu Met Leu Ala Gly Ala Gln
     50                  55                  60

Leu Gly Ile Thr Met Val Thr Phe Ala Leu Gly Ala Ile Thr Lys Pro
 65                  70                  75                  80

Trp Val His Tyr Ala Leu Met Pro Leu Phe Glu Trp Ala Arg Ile Pro
                 85                  90                  95

Leu Val Met Ala Asp Val Ile Ala Phe Ile Leu Ser Leu Phe Ile Val
            100                 105                 110

Thr Phe Leu His Leu Val Ile Gly Glu Met Ala Pro Lys Ser Trp Ala
        115                 120                 125

Ile Ala His Pro Glu Thr Ala Leu Arg Thr Ile Ala Ile Pro Ala Arg
    130                 135                 140

Gly Phe Ile Asn Leu Phe Arg Pro Leu Leu Gln Trp Ile Asn Lys Met
145                 150                 155                 160

Ala Asn Asp Leu Val Arg Lys Val Gly Glu Thr Pro Val Asp Arg Ala
                165                 170                 175

Ala Ala Gly Gly Tyr Asp Thr Asp Thr Leu His Ala Leu Ile Glu His
            180                 185                 190

Ser Arg Glu Thr Gly Ala Leu Asp Gln Gln Ser Ala Ala Gln Ile Ser
        195                 200                 205

Gly Ile Ile Lys Leu Asp Lys Ile Thr Val Gly Gln Thr Leu Thr Ala
    210                 215                 220
```

```
Ser Pro Phe Thr His Ser Ala Ser Ala Thr Val Ala Glu Val Gln Ala
225                 230                 235                 240

Ala Ala Gln Arg Ser Gly Ser Leu Arg Val Leu Ile Asp Ala Pro Ser
                245                 250                 255

His Leu Phe Pro His Val Ile His Val Arg Asp Thr Leu Gly Ala Ser
            260                 265                 270

Pro Asp Glu Lys Ala Ser Lys Trp Ser Arg Pro Ile Leu Thr Val Ala
        275                 280                 285

Glu Thr Asp Thr Leu His Gln Ala Leu Glu Tyr Met Arg Glu His Asn
    290                 295                 300

Glu Gln Ile Ser Ala Val Leu Ser Ala Asp Gly Lys Thr Val Leu Gly
305                 310                 315                 320

Val Ile Thr Trp Asp His Ile Leu Lys Tyr Leu Trp Pro Ala Ser Val
                325                 330                 335
```

Sequence Listing.ST25.txt

<210> 583
<211> 423
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(400)
<223> RXN01324

<400> 583
tcctcaaccc aatgcttgcc ggcattgcga tggccttcag ttcagttttc gtcgtctcca 60

attccttgcg tctgcgagga ttcaaagcaa ggagcaacta atg tcc aac agc gaa 115
                                    Met Ser Asn Ser Glu
                                      1   5

tgc cac acc cac ggt tac atc gaa gaa aag cag cgt tac ctc gca cgc 163
Cys His Thr His Gly Tyr Ile Glu Glu Lys Gln Arg Tyr Leu Ala Arg
                10   15   20

ctc aaa aga atc gaa ggc caa acc cga ggc att cac cgc atg atc gac 211
Leu Lys Arg Ile Glu Gly Gln Thr Arg Gly Ile His Arg Met Ile Asp
            25   30   35

gag gaa caa tac tgc atc gac atc ctc acg cag atc tcc gca gtg aac 259
Glu Glu Gln Tyr Cys Ile Asp Ile Leu Thr Gln Ile Ser Ala Val Asn
        40   45   50

tcc gca ctc aaa aac gtg gcg ttc ggc ctc ctc gac gat cac ctc gct 307
Ser Ala Leu Lys Asn Val Ala Phe Gly Leu Leu Asp Asp His Leu Ala
    55   60   65

cac tgt gtc aaa gaa gca gct gac ctc ggc ggc gac gaa ctc gac gca 355
His Cys Val Lys Glu Ala Ala Asp Leu Gly Gly Asp Glu Leu Asp Ala
```
```

```
 70                  75                  80                  85

aaa ctc aaa gaa gtt tcc gac gcc atc gcc cgc ttc agt aag gcc       400
Lys Leu Lys Glu Val Ser Asp Ala Ile Ala Arg Phe Ser Lys Ala
                90                  95                 100

taaacggatc cggtggcatt gga                                         423


<210> 584
<211> 100
<212> PRT
<213> Corynebacterium glutamicum

<400> 584
Met Ser Asn Ser Glu Cys His Thr His Gly Tyr Ile Glu Glu Lys Gln
  1               5                  10                  15

Arg Tyr Leu Ala Arg Leu Lys Arg Ile Glu Gly Gln Thr Arg Gly Ile
             20                  25                  30

His Arg Met Ile Asp Glu Glu Gln Tyr Cys Ile Asp Ile Leu Thr Gln
         35                  40                  45

Ile Ser Ala Val Asn Ser Ala Leu Lys Asn Val Ala Phe Gly Leu Leu
     50                  55                  60

Asp Asp His Leu Ala His Cys Val Lys Glu Ala Ala Asp Leu Gly Gly
 65                  70                  75                  80

Asp Glu Leu Asp Ala Lys Leu Lys Glu Val Ser Asp Ala Ile Ala Arg
                85                  90                  95

Phe Ser Lys Ala
            100


<210> 585
<211> 2520
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2497)
<223> RXN01331

<400> 585
ctaaactcgt ctctcgtatc tttcagtcat ttatgtctga taagcaggcg cgtgcgccac 60

acaattggca caatcacaag aaagtgaagt gggaacctag atg ctg acg aca cta   115
                                              Met Leu Thr Thr Leu
                                                1               5

tgg att gcg gtg ttg gta ttt acc gtt cca gga ttg gtc gtc tcg tgg   163
Trp Ile Ala Val Leu Val Phe Thr Val Pro Gly Leu Val Val Ser Trp
                10                  15                  20

gtt tct ggc ctt aaa gtg ccc tgg gct atc gca gcc tcc atc cca gcc   211
Val Ser Gly Leu Lys Val Pro Trp Ala Ile Ala Ala Ser Ile Pro Ala
            25                  30                  35
```

```
acc ttc ggt att tac ggc ctg tcc gcc tgg ttg ctg ggc ttg tgg gag   259
Thr Phe Gly Ile Tyr Gly Leu Ser Ala Trp Leu Leu Gly Leu Trp Glu
         40                  45                  50

atg cgt ttt gat ctc cat tct gta gtt att tcc aca ttg gtt ttc gct   307
Met Arg Phe Asp Leu His Ser Val Val Ile Ser Thr Leu Val Phe Ala
     55                  60                  65

gcg gtt gct ttg gta tgg cgc ttg ttt ttt gtc ggt ggt tgg ctt gta   355
Ala Val Ala Leu Val Trp Arg Leu Phe Phe Val Gly Gly Trp Leu Val
 70                  75                  80                  85

cgt cgg cgt aaa gca cgt atc cgc agg cag acg ctc gcg gat gaa gag   403
Arg Arg Arg Lys Ala Arg Ile Arg Arg Gln Thr Leu Ala Asp Glu Glu
                 90                  95                 100

cgg gca gaa aat gct gag gta tct gca ggg gag cct gcc gaa tcg agc   451
Arg Ala Glu Asn Ala Glu Val Ser Ala Gly Glu Pro Ala Glu Ser Ser
            105                 110                 115

aca aac gaa gca gcc gaa tct gaa tct gaa acc tcg gag cgt cgc gga   499
Thr Asn Glu Ala Ala Glu Ser Glu Ser Glu Thr Ser Glu Arg Arg Gly
        120                 125                 130

atc tgg cgc gtg atc ttt gat tac atg cgc gac ggt ggc atc ttg gat   547
Ile Trp Arg Val Ile Phe Asp Tyr Met Arg Asp Gly Gly Ile Leu Asp
    135                 140                 145

cac cgt tgg ctg ctg cct gcc gca ggt gct atc act ggt gcg tgg ctg   595
His Arg Trp Leu Leu Pro Ala Ala Gly Ala Ile Thr Gly Ala Trp Leu
150                 155                 160                 165

atc att gat cgt gcc gtt gat ctg ctc ttg agc acc gag cat ggt ttg   643
Ile Ile Asp Arg Ala Val Asp Leu Leu Leu Ser Thr Glu His Gly Leu
                170                 175                 180

ggc gat atc gtc caa ggc tgg gat gtc cat tgg cat gct tcg act gtc   691
Gly Asp Ile Val Gln Gly Trp Asp Val His Trp His Ala Ser Thr Val
            185                 190                 195

cgt ttt ata gat gag acc ggc att gcg tca tcc acg atg atg ggg cag   739
Arg Phe Ile Asp Glu Thr Gly Ile Ala Ser Ser Thr Met Met Gly Gln
        200                 205                 210

ctg cgc aat att gaa acg cag caa gat ctg ttc tac cca agc gca tgg   787
Leu Arg Asn Ile Glu Thr Gln Gln Asp Leu Phe Tyr Pro Ser Ala Trp
    215                 220                 225

cat gct ggt gca tgg gtg ctg tcg gat gtc gga aat ctg acg att gtt   835
His Ala Gly Ala Trp Val Leu Ser Asp Val Gly Asn Leu Thr Ile Val
230                 235                 240                 245

gaa gcc acc aac ctc act ggc att gtg ctg tcc gga ttg ttg ctg ccg   883
Glu Ala Thr Asn Leu Thr Gly Ile Val Leu Ser Gly Leu Leu Leu Pro
                250                 255                 260

tta gct gtt gca ctg att gca tgg cgg atg atc aac aat cgt gga ctg   931
Leu Ala Val Ala Leu Ile Ala Trp Arg Met Ile Asn Asn Arg Gly Leu
            265                 270                 275
```

```
acc gcg cag att ggt gcg ggc ttt gct gga ctg atc acc att gcc tct   979
Thr Ala Gln Ile Gly Ala Gly Phe Ala Gly Leu Ile Thr Ile Ala Ser
        280                 285                 290

ccg gta ctg ttc tgg gtt ggt aac tac gtg ggt gcg tgg cct tat gtt   1027
Pro Val Leu Phe Trp Val Gly Asn Tyr Val Gly Ala Trp Pro Tyr Val
    295                 300                 305

gct gcg atc ggt gct tca ggt gtg gtg ctt gcg ctg ttt atg tcc act   1075
Ala Ala Ile Gly Ala Ser Gly Val Val Leu Ala Leu Phe Met Ser Thr
310                 315                 320                 325

ccg tct gtg ccg gta aga atc ttt gcc gca gca ttg gcg ttc atg ggt   1123
Pro Ser Val Pro Val Arg Ile Phe Ala Ala Ala Leu Ala Phe Met Gly
                330                 335                 340

atg ttc cag ctg cat cca gcc cca tcc acc atc gtg atc atg gtg ttg   1171
Met Phe Gln Leu His Pro Ala Pro Ser Thr Ile Val Ile Met Val Leu
            345                 350                 355

ctg ctg tgg tgg ctg ctc aaa ctc gtg gtg gtt cca agc cag aaa gtg   1219
Leu Leu Trp Trp Leu Leu Lys Leu Val Val Val Pro Ser Gln Lys Val
        360                 365                 370

aag ggc tgg aag gcg ggc atc ggt atc cgt ttg aag gat gtc ggc atc   1267
Lys Gly Trp Lys Ala Gly Ile Gly Ile Arg Leu Lys Asp Val Gly Ile
    375                 380                 385

ctg gcc atc acg ggc atc atc ggt gtg ctc ttc atg ctg cct cag gtg   1315
Leu Ala Ile Thr Gly Ile Ile Gly Val Leu Phe Met Leu Pro Gln Val
390                 395                 400                 405

att tca ggt tcc gaa caa acc gaa gat gtg ctg tca tat tct gct gag   1363
Ile Ser Gly Ser Glu Gln Thr Glu Asp Val Leu Ser Tyr Ser Ala Glu
                410                 415                 420

gaa caa gtc acc cgc agc gag tcc tgg ttg gtg tct att ttc atg gag   1411
Glu Gln Val Thr Arg Ser Glu Ser Trp Leu Val Ser Ile Phe Met Glu
            425                 430                 435

acc cgc cat gtt gat ttc ttc gga aat att gac atc gtc cca gtg ctg   1459
Thr Arg His Val Asp Phe Phe Gly Asn Ile Asp Ile Val Pro Val Leu
        440                 445                 450

gta ttc gca gca atc ggt ggc gtg gtt gct ttg gtg tgg cgc gga aac   1507
Val Phe Ala Ala Ile Gly Gly Val Val Ala Leu Val Trp Arg Gly Asn
    455                 460                 465

ttg tgg gcg ccg gtg ttt tac ttc gcc agc gtt gcg ttg acc gct aac   1555
Leu Trp Ala Pro Val Phe Tyr Phe Ala Ser Val Ala Leu Thr Ala Asn
470                 475                 480                 485

tcg ctg aag cct ttt gaa gag ccg tgg ggt gat tgg ctc aac atc gtg   1603
Ser Leu Lys Pro Phe Glu Glu Pro Trp Gly Asp Trp Leu Asn Ile Val
                490                 495                 500

ggc ggt ctg cat tac tcc aca gga cac cgt ttg atc atg cct gtc gcc   1651
Gly Gly Leu His Tyr Ser Thr Gly His Arg Leu Ile Met Pro Val Ala
            505                 510                 515

atg ttc act ttt gct gcc gca ggt atc ggc gct gcc gca gtg atc cgt   1699
```

```
Met Phe Thr Phe Ala Ala Ala Gly Ile Gly Ala Ala Ala Val Ile Arg
        520                 525                 530

ttg atc tgc ttg gga cca ata aag aag ttc acc act gtt tcc ggt gtt   1747
Leu Ile Cys Leu Gly Pro Ile Lys Lys Phe Thr Thr Val Ser Gly Val
    535                 540                 545

gtt tct gtg gtg atg gct ctt gtt gtg gct gtg cca ttg cag act tgg   1795
Val Ser Val Val Met Ala Leu Val Val Ala Val Pro Leu Gln Thr Trp
550                 555                 560                 565

gcg aag gat ttt gta gag gaa gga tcc gaa acc aca atc ctt gcg cca   1843
Ala Lys Asp Phe Val Glu Glu Gly Ser Glu Thr Thr Ile Leu Ala Pro
                570                 575                 580

cac aat gat gaa cgt atg gtg agc aac aac gac ttg gct gcc tgg gac   1891
His Asn Asp Glu Arg Met Val Ser Asn Asn Asp Leu Ala Ala Trp Asp
            585                 590                 595

tgg tta atc caa cag cca ggt gga gct gac atg aac atc atg ggt gac   1939
Trp Leu Ile Gln Gln Pro Gly Gly Ala Asp Met Asn Ile Met Gly Asp
        600                 605                 610

ccc gca gat ggt aac ggc tgg atg tat gcc tac aac ggc ttg cac tcc   1987
Pro Ala Asp Gly Asn Gly Trp Met Tyr Ala Tyr Asn Gly Leu His Ser
    615                 620                 625

gtg gcc cgc cac tat gca tgg cca gca gca ggc gaa ggc tct gcc acc   2035
Val Ala Arg His Tyr Ala Trp Pro Ala Ala Gly Glu Gly Ser Ala Thr
630                 635                 640                 645

gcg atg ctg ttc tgg tgg cct caa ctt cta ggt gtg ggc acc gat gaa   2083
Ala Met Leu Phe Trp Trp Pro Gln Leu Leu Gly Val Gly Thr Asp Glu
                650                 655                 660

aac cca gat caa gtc aac gat gtg gat cag gct gct cgt gat ctc aac   2131
Asn Pro Asp Gln Val Asn Asp Val Asp Gln Ala Ala Arg Asp Leu Asn
            665                 670                 675

gtc ggc tac ttc atg atc agt ccg tgg acg ttc tgg gat ttc cag atc   2179
Val Gly Tyr Phe Met Ile Ser Pro Trp Thr Phe Trp Asp Phe Gln Ile
        680                 685                 690

ccc aac ttc cgc cag atc gat ctg ctg tgg caa acc cca ggc gtg aca   2227
Pro Asn Phe Arg Gln Ile Asp Leu Leu Trp Gln Thr Pro Gly Val Thr
    695                 700                 705

ccg gtg tgc aag aag ggc gac tcg gtg atc ttc gca gtc aac gat atg   2275
Pro Val Cys Lys Lys Gly Asp Ser Val Ile Phe Ala Val Asn Asp Met
710                 715                 720                 725

ttc act gac gcc gaa ctg gat cag atg cgt gca cct ggt aat tct cca   2323
Phe Thr Asp Ala Glu Leu Asp Gln Met Arg Ala Pro Gly Asn Ser Pro
                730                 735                 740

gaa cca ctg cca gag ctt cct acc ttg ggc gag ctt ggg ttg gct gaa   2371
Glu Pro Leu Pro Glu Leu Pro Thr Leu Gly Glu Leu Gly Leu Ala Glu
            745                 750                 755

act gaa gac gag gta gat cag act tat tac cat cgt cca acg gtt cct   2419
Thr Glu Asp Glu Val Asp Gln Thr Tyr Tyr His Arg Pro Thr Val Pro
```

```
        760                 765                 770

gct ggt gtg aac tca gag atg cct tca gcc gaa act ctg tat gca ccg   2467
Ala Gly Val Asn Ser Glu Met Pro Ser Ala Glu Thr Leu Tyr Ala Pro
    775                 780                 785

gat cca acg aag ccg cat acg gtc cct aac taatcacaaa gagtattcag     2517
Asp Pro Thr Lys Pro His Thr Val Pro Asn
790                 795

taa                                                               2520


<210> 586
<211> 799
<212> PRT
<213> Corynebacterium glutamicum

<400> 586
Met Leu Thr Thr Leu Trp Ile Ala Val Leu Val Phe Thr Val Pro Gly
  1               5                  10                  15

Leu Val Val Ser Trp Val Ser Gly Leu Lys Val Pro Trp Ala Ile Ala
             20                  25                  30

Ala Ser Ile Pro Ala Thr Phe Gly Ile Tyr Gly Leu Ser Ala Trp Leu
         35                  40                  45

Leu Gly Leu Trp Glu Met Arg Phe Asp Leu His Ser Val Val Ile Ser
     50                  55                  60

Thr Leu Val Phe Ala Ala Val Ala Leu Val Trp Arg Leu Phe Phe Val
 65                  70                  75                  80

Gly Gly Trp Leu Val Arg Arg Arg Lys Ala Arg Ile Arg Arg Gln Thr
                 85                  90                  95

Leu Ala Asp Glu Glu Arg Ala Glu Asn Ala Glu Val Ser Ala Gly Glu
            100                 105                 110

Pro Ala Glu Ser Ser Thr Asn Glu Ala Ala Glu Ser Glu Ser Glu Thr
        115                 120                 125

Ser Glu Arg Arg Gly Ile Trp Arg Val Ile Phe Asp Tyr Met Arg Asp
    130                 135                 140

Gly Gly Ile Leu Asp His Arg Trp Leu Leu Pro Ala Ala Gly Ala Ile
145                 150                 155                 160

Thr Gly Ala Trp Leu Ile Ile Asp Arg Ala Val Asp Leu Leu Leu Ser
                165                 170                 175

Thr Glu His Gly Leu Gly Asp Ile Val Gln Gly Trp Asp Val His Trp
            180                 185                 190

His Ala Ser Thr Val Arg Phe Ile Asp Glu Thr Gly Ile Ala Ser Ser
        195                 200                 205

Thr Met Met Gly Gln Leu Arg Asn Ile Glu Thr Gln Gln Asp Leu Phe
    210                 215                 220
```

```
Tyr Pro Ser Ala Trp His Ala Gly Ala Trp Val Leu Ser Asp Val Gly
225                 230                 235                 240

Asn Leu Thr Ile Val Glu Ala Thr Asn Leu Thr Gly Ile Val Leu Ser
                245                 250                 255

Gly Leu Leu Leu Pro Leu Ala Val Ala Leu Ile Ala Trp Arg Met Ile
            260                 265                 270

Asn Asn Arg Gly Leu Thr Ala Gln Ile Gly Ala Gly Phe Ala Gly Leu
        275                 280                 285

Ile Thr Ile Ala Ser Pro Val Leu Phe Trp Val Gly Asn Tyr Val Gly
    290                 295                 300

Ala Trp Pro Tyr Val Ala Ala Ile Gly Ala Ser Gly Val Val Leu Ala
305                 310                 315                 320

Leu Phe Met Ser Thr Pro Ser Val Pro Val Arg Ile Phe Ala Ala Ala
                325                 330                 335

Leu Ala Phe Met Gly Met Phe Gln Leu His Pro Ala Pro Ser Thr Ile
            340                 345                 350

Val Ile Met Val Leu Leu Leu Trp Trp Leu Leu Lys Leu Val Val Val
        355                 360                 365

Pro Ser Gln Lys Val Lys Gly Trp Lys Ala Gly Ile Gly Ile Arg Leu
    370                 375                 380

Lys Asp Val Gly Ile Leu Ala Ile Thr Gly Ile Ile Gly Val Leu Phe
385                 390                 395                 400

Met Leu Pro Gln Val Ile Ser Gly Ser Glu Gln Thr Glu Asp Val Leu
                405                 410                 415

Ser Tyr Ser Ala Glu Glu Gln Val Thr Arg Ser Glu Ser Trp Leu Val
            420                 425                 430

Ser Ile Phe Met Glu Thr Arg His Val Asp Phe Phe Gly Asn Ile Asp
        435                 440                 445

Ile Val Pro Val Leu Val Phe Ala Ala Ile Gly Gly Val Val Ala Leu
    450                 455                 460

Val Trp Arg Gly Asn Leu Trp Ala Pro Val Phe Tyr Phe Ala Ser Val
465                 470                 475                 480

Ala Leu Thr Ala Asn Ser Leu Lys Pro Phe Glu Glu Pro Trp Gly Asp
                485                 490                 495

Trp Leu Asn Ile Val Gly Gly Leu His Tyr Ser Thr Gly His Arg Leu
            500                 505                 510

Ile Met Pro Val Ala Met Phe Thr Phe Ala Ala Ala Gly Ile Gly Ala
        515                 520                 525

Ala Ala Val Ile Arg Leu Ile Cys Leu Gly Pro Ile Lys Lys Phe Thr
    530                 535                 540

Thr Val Ser Gly Val Val Ser Val Val Met Ala Leu Val Val Ala Val
```

```
545                 550                 555                 560

Pro Leu Gln Thr Trp Ala Lys Asp Phe Val Glu Glu Gly Ser Glu Thr
                565                 570                 575

Thr Ile Leu Ala Pro His Asn Asp Glu Arg Met Val Ser Asn Asn Asp
            580                 585                 590

Leu Ala Ala Trp Asp Trp Leu Ile Gln Gln Pro Gly Gly Ala Asp Met
        595                 600                 605

Asn Ile Met Gly Asp Pro Ala Asp Gly Asn Gly Trp Met Tyr Ala Tyr
    610                 615                 620

Asn Gly Leu His Ser Val Ala Arg His Tyr Ala Trp Pro Ala Ala Gly
625                 630                 635                 640

Glu Gly Ser Ala Thr Ala Met Leu Phe Trp Trp Pro Gln Leu Leu Gly
                645                 650                 655

Val Gly Thr Asp Glu Asn Pro Asp Gln Val Asn Asp Val Asp Gln Ala
            660                 665                 670

Ala Arg Asp Leu Asn Val Gly Tyr Phe Met Ile Ser Pro Trp Thr Phe
        675                 680                 685

Trp Asp Phe Gln Ile Pro Asn Phe Arg Gln Ile Asp Leu Leu Trp Gln
    690                 695                 700

Thr Pro Gly Val Thr Pro Val Cys Lys Lys Gly Asp Ser Val Ile Phe
705                 710                 715                 720

Ala Val Asn Asp Met Phe Thr Asp Ala Glu Leu Asp Gln Met Arg Ala
                725                 730                 735

Pro Gly Asn Ser Pro Glu Pro Leu Pro Glu Leu Pro Thr Leu Gly Glu
            740                 745                 750

Leu Gly Leu Ala Glu Thr Glu Asp Glu Val Asp Gln Thr Tyr Tyr His
        755                 760                 765

Arg Pro Thr Val Pro Ala Gly Val Asn Ser Glu Met Pro Ser Ala Glu
    770                 775                 780

Thr Leu Tyr Ala Pro Asp Pro Thr Lys Pro His Thr Val Pro Asn
785                 790                 795


<210> 587
<211> 638
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (40)..(615)
<223> FRXA01331

<400> 587
gcctcggact ggttaatcca acagccaggt ggagctgacatg aac atc atg ggt gac 57
                                                Met Asn Ile Met Gly Asp
```

```
                                                    1               5

ccc gca gat ggt aac ggc tgg atg tat gcc tac aac ggc ttg cac tcc   105
Pro Ala Asp Gly Asn Gly Trp Met Tyr Ala Tyr Asn Gly Leu His Ser
            10                  15                  20

gtg gcc cgc cac tat gca tgg cca gca gca ggc gaa ggc tct gcc acc   153
Val Ala Arg His Tyr Ala Trp Pro Ala Ala Gly Glu Gly Ser Ala Thr
        25                  30                  35

gcg atg ctg ttc tgg tgg cct caa ctt cta ggt gtg ggc acc gat gaa   201
Ala Met Leu Phe Trp Trp Pro Gln Leu Leu Gly Val Gly Thr Asp Glu
    40                  45                  50

aac cca gat caa gtc aac gat gtg gat cag gct gct cgt gat ctc aac   249
Asn Pro Asp Gln Val Asn Asp Val Asp Gln Ala Ala Arg Asp Leu Asn
55                  60                  65                  70

gtc ggc tac ttc atg atc agt ccg tgg acg ttc tgg gat ttc cag atc   297
Val Gly Tyr Phe Met Ile Ser Pro Trp Thr Phe Trp Asp Phe Gln Ile
                75                  80                  85

ccc aac ttc cgc cag atc gat ctg ctg tgg caa acc cca ggc gtg aca   345
Pro Asn Phe Arg Gln Ile Asp Leu Leu Trp Gln Thr Pro Gly Val Thr
            90                  95                  100

ccg gtg tgc aag aag ggc gac tcg gtg atc ttc gca gtc aac gat atg   393
Pro Val Cys Lys Lys Gly Asp Ser Val Ile Phe Ala Val Asn Asp Met
        105                 110                 115

ttc act gac gcc gaa ctg gat cag atg cgt gca cct ggt aat tct cca   441
Phe Thr Asp Ala Glu Leu Asp Gln Met Arg Ala Pro Gly Asn Ser Pro
    120                 125                 130

gaa cca ctg cca gag ctt cct acc ttg ggc gag ctt ggg ttg gct gaa   489
Glu Pro Leu Pro Glu Leu Pro Thr Leu Gly Glu Leu Gly Leu Ala Glu
135                 140                 145                 150

act gaa gac gag gta gat cag act tat tac cat cgt cca acg gtt cct   537
Thr Glu Asp Glu Val Asp Gln Thr Tyr Tyr His Arg Pro Thr Val Pro
                155                 160                 165

gct ggt gtg aac tca gag atg cct tca gcc gaa act ctg tat gca ccg   585
Ala Gly Val Asn Ser Glu Met Pro Ser Ala Glu Thr Leu Tyr Ala Pro
            170                 175                 180

gat cca acg aag ccg cat acg gtc cct aac taatcacaaa gagtattcag     635
Asp Pro Thr Lys Pro His Thr Val Pro Asn
        185                 190

taa                                                               638
```

<210> 588
<211> 192
<212> PRT
<213> Corynebacterium glutamicum

<400> 588

```
Met Asn Ile Met Gly Asp Pro Ala Asp Gly Asn Gly Trp Met Tyr Ala
  1               5                  10                  15
```

```
Tyr Asn Gly Leu His Ser Val Ala Arg His Tyr Ala Trp Pro Ala Ala
            20                  25                  30

Gly Glu Gly Ser Ala Thr Ala Met Leu Phe Trp Trp Pro Gln Leu Leu
        35                  40                  45

Gly Val Gly Thr Asp Glu Asn Pro Asp Gln Val Asn Asp Val Asp Gln
    50                  55                  60

Ala Ala Arg Asp Leu Asn Val Gly Tyr Phe Met Ile Ser Pro Trp Thr
65                  70                  75                  80

Phe Trp Asp Phe Gln Ile Pro Asn Phe Arg Gln Ile Asp Leu Leu Trp
                85                  90                  95

Gln Thr Pro Gly Val Thr Pro Val Cys Lys Lys Gly Asp Ser Val Ile
            100                 105                 110

Phe Ala Val Asn Asp Met Phe Thr Asp Ala Glu Leu Asp Gln Met Arg
        115                 120                 125

Ala Pro Gly Asn Ser Pro Glu Pro Leu Pro Glu Leu Pro Thr Leu Gly
    130                 135                 140

Glu Leu Gly Leu Ala Glu Thr Glu Asp Glu Val Asp Gln Thr Tyr Tyr
145                 150                 155                 160

His Arg Pro Thr Val Pro Ala Gly Val Asn Ser Glu Met Pro Ser Ala
                165                 170                 175

Glu Thr Leu Tyr Ala Pro Asp Pro Thr Lys Pro His Thr Val Pro Asn
            180                 185                 190
```

<210> 589
<211> 892
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(892)
<223> FRXA00668

<400> 589
ctaaactcgt ctctcgtatc tttcagtcat ttatgtctga taagcaggcg cgtgcgccac 60

acaattggca caatcacaag aaagtgaagt gggaacctag atg ctg acg aca cta 115
                                                Met Leu Thr Thr Leu
                                                  1   5

tgg att gcg gtg ttg gta ttt acc gtt cca gga ttg gtc gtc tcg tgg 163
Trp Ile Ala Val Leu Val Phe Thr Val Pro Gly Leu Val Val Ser Trp
                10   15   20

gtt tct ggc ctt aaa gtg ccc tgg gct atc gca gcc tcc atc cca gcc 211
Val Ser Gly Leu Lys Val Pro Trp Ala Ile Ala Ala Ser Ile Pro Ala

```
                25                  30                  35

acc ttc ggt att tac ggc ctg tcc gcc tgg ttg ctg ggc ttg tgg gag   259
Thr Phe Gly Ile Tyr Gly Leu Ser Ala Trp Leu Leu Gly Leu Trp Glu
         40                  45                  50

atg cgt ttt gat ctc cat tct gta gtt att tcc aca ttg gtt ttc gct   307
Met Arg Phe Asp Leu His Ser Val Val Ile Ser Thr Leu Val Phe Ala
     55                  60                  65

gcg gtt gct ttg gta tgg cgc ttg ttt ttt gtc ggt ggt tgg ctt gta   355
Ala Val Ala Leu Val Trp Arg Leu Phe Phe Val Gly Gly Trp Leu Val
 70                  75                  80                  85

cgt cgg cgt aaa gca cgt atc cgc agg cag acg ctc gcg gat gaa gag   403
Arg Arg Arg Lys Ala Arg Ile Arg Arg Gln Thr Leu Ala Asp Glu Glu
                 90                  95                 100

cgg gca gaa aat gct gag gta tct gca ggg gag cct gcc gaa tcg agc   451
Arg Ala Glu Asn Ala Glu Val Ser Ala Gly Glu Pro Ala Glu Ser Ser
            105                 110                 115

aca aac gaa gca gcc gaa tct gaa tct gaa acc tcg gag cgt cgc gga   499
Thr Asn Glu Ala Ala Glu Ser Glu Ser Glu Thr Ser Glu Arg Arg Gly
        120                 125                 130

atc tgg cgc gtg atc ttt gat tac atg cgc gac ggt ggc atc ttg gat   547
Ile Trp Arg Val Ile Phe Asp Tyr Met Arg Asp Gly Gly Ile Leu Asp
    135                 140                 145

cac cgt tgg ctg ctg cct gcc gca ggt gct atc act ggt gcg tgg ctg   595
His Arg Trp Leu Leu Pro Ala Ala Gly Ala Ile Thr Gly Ala Trp Leu
150                 155                 160                 165

atc att gat cgt gcc gtt gat ctg ctc ttg agc acc gag cat ggt ttg   643
Ile Ile Asp Arg Ala Val Asp Leu Leu Leu Ser Thr Glu His Gly Leu
                170                 175                 180

ggc gat atc gtc caa ggc tgg gat gtc cat tgg cat gct tcg act gtc   691
Gly Asp Ile Val Gln Gly Trp Asp Val His Trp His Ala Ser Thr Val
            185                 190                 195

cgt ttt ata gat gag acc ggc att gcg tca tcc acg atg atg ggg cag   739
Arg Phe Ile Asp Glu Thr Gly Ile Ala Ser Ser Thr Met Met Gly Gln
        200                 205                 210

ctg cgc aat att gaa acg cag caa gat ctg ttc tac cca agc gca tgg   787
Leu Arg Asn Ile Glu Thr Gln Gln Asp Leu Phe Tyr Pro Ser Ala Trp
    215                 220                 225

cat gct ggt gca tgg gtg ctg tcg gat gtc gga aat ctg acg att gtt   835
His Ala Gly Ala Trp Val Leu Ser Asp Val Gly Asn Leu Thr Ile Val
230                 235                 240                 245

gaa gcc acc aac ctc act ggc att gtg ctg tcc gga ttg ttg ctg ccg   883
Glu Ala Thr Asn Leu Thr Gly Ile Val Leu Ser Gly Leu Leu Leu Pro
                250                 255                 260

tta gct gtt                                                      892
Leu Ala Val
```

<210> 590
<211> 264
<212> PRT
<213> Corynebacterium glutamicum

<400> 590
Met Leu Thr Thr Leu Trp Ile Ala Val Leu Val Phe Thr Val Pro Gly
1 5 10 15

Leu Val Val Ser Trp Val Ser Gly Leu Lys Val Pro Trp Ala Ile Ala
20 25 30

Ala Ser Ile Pro Ala Thr Phe Gly Ile Tyr Gly Leu Ser Ala Trp Leu
35 40 45

Leu Gly Leu Trp Glu Met Arg Phe Asp Leu His Ser Val Val Ile Ser
50 55 60

Thr Leu Val Phe Ala Ala Val Ala Leu Val Trp Arg Leu Phe Phe Val
65 70 75 80

Gly Gly Trp Leu Val Arg Arg Arg Lys Ala Arg Ile Arg Arg Gln Thr
85 90 95

Leu Ala Asp Glu Glu Arg Ala Glu Asn Ala Glu Val Ser Ala Gly Glu
100 105 110

Pro Ala Glu Ser Ser Thr Asn Glu Ala Ala Glu Ser Glu Ser Glu Thr
115 120 125

Ser Glu Arg Arg Gly Ile Trp Arg Val Ile Phe Asp Tyr Met Arg Asp
130 135 140

Gly Gly Ile Leu Asp His Arg Trp Leu Leu Pro Ala Ala Gly Ala Ile
145 150 155 160

Thr Gly Ala Trp Leu Ile Ile Asp Arg Ala Val Asp Leu Leu Leu Ser
165 170 175

Thr Glu His Gly Leu Gly Asp Ile Val Gln Gly Trp Asp Val His Trp
180 185 190

His Ala Ser Thr Val Arg Phe Ile Asp Glu Thr Gly Ile Ala Ser Ser
195 200 205

Thr Met Met Gly Gln Leu Arg Asn Ile Glu Thr Gln Gln Asp Leu Phe
210 215 220

Tyr Pro Ser Ala Trp His Ala Gly Ala Trp Val Leu Ser Asp Val Gly
225 230 235 240

Asn Leu Thr Ile Val Glu Ala Thr Asn Leu Thr Gly Ile Val Leu Ser
245 250 255

Gly Leu Leu Leu Pro Leu Ala Val
260

<210> 591

<211> 750
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(750)
<223> FRXA00674

<400> 591

```
atc ttt gcc gca gca ttg gcg ttc atg ggt atg ttc cag ctg cat cca   48
Ile Phe Ala Ala Ala Leu Ala Phe Met Gly Met Phe Gln Leu His Pro
  1               5                  10                  15

gcc cca tcc acc atc gtg atc atg gtg ttg ctg ctg tgg tgg ctg ctc   96
Ala Pro Ser Thr Ile Val Ile Met Val Leu Leu Leu Trp Trp Leu Leu
             20                  25                  30

aaa ctc gtg gtg gtt cca agc cag aaa gtg aag ggc tgg aag gcg ggc   144
Lys Leu Val Val Val Pro Ser Gln Lys Val Lys Gly Trp Lys Ala Gly
         35                  40                  45

atc ggt atc cgt ttg aag gat gtc ggc atc ctg gcc atc acg ggc atc   192
Ile Gly Ile Arg Leu Lys Asp Val Gly Ile Leu Ala Ile Thr Gly Ile
     50                  55                  60

atc ggt gtg ctc ttc atg ctg cct cag gtg att tca ggt tcc gaa caa   240
Ile Gly Val Leu Phe Met Leu Pro Gln Val Ile Ser Gly Ser Glu Gln
 65                  70                  75                  80

acc gaa gat gtg ctg tca tat tct gct gag gaa caa gtc acc cgc agc   288
Thr Glu Asp Val Leu Ser Tyr Ser Ala Glu Glu Gln Val Thr Arg Ser
                 85                  90                  95

gag tcc tgg ttg gtg tct att ttc atg gag acc cgc cat gtt gat ttc   336
Glu Ser Trp Leu Val Ser Ile Phe Met Glu Thr Arg His Val Asp Phe
            100                 105                 110

ttc gga aat att gac atc gtc cca gtg ctg gta ttc gca gca atc ggt   384
Phe Gly Asn Ile Asp Ile Val Pro Val Leu Val Phe Ala Ala Ile Gly
        115                 120                 125

ggc gtg gtt gct ttg gtg tgg cgc gga aac ttg tgg gcg ccg gtg ttt   432
Gly Val Val Ala Leu Val Trp Arg Gly Asn Leu Trp Ala Pro Val Phe
    130                 135                 140

tac ttc gcc agc gtt gcg ttg acc gct aac tcg ctg aag cct ttt gaa   480
Tyr Phe Ala Ser Val Ala Leu Thr Ala Asn Ser Leu Lys Pro Phe Glu
145                 150                 155                 160

gag ccg tgg ggt gat tgg ctc aac atc gtg ggc ggt ctg cat tac tcc   528
Glu Pro Trp Gly Asp Trp Leu Asn Ile Val Gly Gly Leu His Tyr Ser
                165                 170                 175

aca gga cac cgt ttg atc atg cct gtc gcc atg ttc act ttt gct gcc   576
Thr Gly His Arg Leu Ile Met Pro Val Ala Met Phe Thr Phe Ala Ala
            180                 185                 190

gca ggt atc ggc gct gcc gca gtg atc cgt ttg atc tgc ttg gga cca   624
Ala Gly Ile Gly Ala Ala Ala Val Ile Arg Leu Ile Cys Leu Gly Pro
        195                 200                 205
```

```
ata aag aag ttc acc act gtt tcc ggt gtt gtt tct gtg gtg atg gct   672
Ile Lys Lys Phe Thr Thr Val Ser Gly Val Val Ser Val Val Met Ala
    210                 215                 220

ctt gtt gtg gct gtg cca ttg cag act tgg gcg aag gat ttt gta gag   720
Leu Val Val Ala Val Pro Leu Gln Thr Trp Ala Lys Asp Phe Val Glu
225                 230                 235                 240

gaa gga tcc gaa acc aca atc ctt gcg cca                          750
Glu Gly Ser Glu Thr Thr Ile Leu Ala Pro
                245                 250
```

<210> 592
<211> 250
<212> PRT
<213> Corynebacterium glutamicum

<400> 592

```
Ile Phe Ala Ala Ala Leu Ala Phe Met Gly Met Phe Gln Leu His Pro
  1               5                  10                  15

Ala Pro Ser Thr Ile Val Ile Met Val Leu Leu Leu Trp Trp Leu Leu
             20                  25                  30

Lys Leu Val Val Val Pro Ser Gln Lys Val Lys Gly Trp Lys Ala Gly
         35                  40                  45

Ile Gly Ile Arg Leu Lys Asp Val Gly Ile Leu Ala Ile Thr Gly Ile
     50                  55                  60

Ile Gly Val Leu Phe Met Leu Pro Gln Val Ile Ser Gly Ser Glu Gln
 65                  70                  75                  80

Thr Glu Asp Val Leu Ser Tyr Ser Ala Glu Glu Gln Val Thr Arg Ser
                 85                  90                  95

Glu Ser Trp Leu Val Ser Ile Phe Met Glu Thr Arg His Val Asp Phe
            100                 105                 110

Phe Gly Asn Ile Asp Ile Val Pro Val Leu Val Phe Ala Ala Ile Gly
        115                 120                 125

Gly Val Val Ala Leu Val Trp Arg Gly Asn Leu Trp Ala Pro Val Phe
    130                 135                 140

Tyr Phe Ala Ser Val Ala Leu Thr Ala Asn Ser Leu Lys Pro Phe Glu
145                 150                 155                 160

Glu Pro Trp Gly Asp Trp Leu Asn Ile Val Gly Gly Leu His Tyr Ser
                165                 170                 175

Thr Gly His Arg Leu Ile Met Pro Val Ala Met Phe Thr Phe Ala Ala
            180                 185                 190

Ala Gly Ile Gly Ala Ala Ala Val Ile Arg Leu Ile Cys Leu Gly Pro
        195                 200                 205

Ile Lys Lys Phe Thr Thr Val Ser Gly Val Val Ser Val Val Met Ala
    210                 215                 220
```

```
Leu Val Val Ala Val Pro Leu Gln Thr Trp Ala Lys Asp Phe Val Glu
225                 230                 235                 240

Glu Gly Ser Glu Thr Thr Ile Leu Ala Pro
                245                 250


<210> 593
<211> 1536
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1513)
<223> RXN01337

<400> 593
gctggctatc ctcaattccg ctcgggtcgc actgccacgc ggagcgatta gtgattttga 60

tacgcaagaa aaagtttctt agcagggtaa cctaaatgtc gtg aca ttt cga ggc   115
                                        Val Thr Phe Arg Gly
                                          1               5

gga aac act ggc gca aag cac gcg gtc gtt gtt ggt tct ggc ccc aat   163
Gly Asn Thr Gly Ala Lys His Ala Val Val Val Gly Ser Gly Pro Asn
                10                  15                  20

ggg ttg acc acg gcg gcg gtg ctg gcc aaa gca ggt tgg caa gta gat   211
Gly Leu Thr Thr Ala Ala Val Leu Ala Lys Ala Gly Trp Gln Val Asp
            25                  30                  35

gtg tat gag gcg gcg cca acc cct gga ggg gcg gcg cgc tca gaa agc   259
Val Tyr Glu Ala Ala Pro Thr Pro Gly Gly Ala Ala Arg Ser Glu Ser
        40                  45                  50

gtt ctg ggg gag ggg act atc agc gat ttg ggt gcc gca ggg cat cct   307
Val Leu Gly Glu Gly Thr Ile Ser Asp Leu Gly Ala Ala Gly His Pro
    55                  60                  65

ttc ggg gtg gca agc cca gct ttt cac tat ttg ggt ctg gaa gat cac   355
Phe Gly Val Ala Ser Pro Ala Phe His Tyr Leu Gly Leu Glu Asp His
70                  75                  80                  85

ggc ctg gaa tgg gcg tat tct ccc ttt gcg atg gcc cac ccg tta gat   403
Gly Leu Glu Trp Ala Tyr Ser Pro Phe Ala Met Ala His Pro Leu Asp
                90                  95                  100

tat ggc agg gcc gga ctg ctg gaa acg tca ctc cca gag acc gcc aaa   451
Tyr Gly Arg Ala Gly Leu Leu Glu Thr Ser Leu Pro Glu Thr Ala Lys
            105                 110                 115

aag ctt gga cct gat gca cgt cgt tgg aag aat ttg cac cag ggc tta   499
Lys Leu Gly Pro Asp Ala Arg Arg Trp Lys Asn Leu His Gln Gly Leu
        120                 125                 130

acc aaa aac att gat aaa cac ttg gcc aat cta tta ggg ccg gtg ctg   547
Thr Lys Asn Ile Asp Lys His Leu Ala Asn Leu Leu Gly Pro Val Leu
    135                 140                 145
```

```
aaa tgg cca gca cat ccg att cgg atg gca aag ttt ggc cca ttt gcg   595
Lys Trp Pro Ala His Pro Ile Arg Met Ala Lys Phe Gly Pro Phe Ala
150                 155                 160                 165

ttg ctg ccc gcg aaa cgt cta gcc agt gcc gct ttt gaa aca gaa gaa   643
Leu Leu Pro Ala Lys Arg Leu Ala Ser Ala Ala Phe Glu Thr Glu Glu
                170                 175                 180

gcc cga tcc ctg ttt atc ggt tcg gcg atg cac tcg gtg act cca cca   691
Ala Arg Ser Leu Phe Ile Gly Ser Ala Met His Ser Val Thr Pro Pro
            185                 190                 195

cac aag ccg atg acc gca tca ctt gga ttg ctt ttt ggc gct ctg ggg   739
His Lys Pro Met Thr Ala Ser Leu Gly Leu Leu Phe Gly Ala Leu Gly
        200                 205                 210

atg tcg cga gga tgg ccg gtt gca gtt ggg gga agc gga cgg atc gtc   787
Met Ser Arg Gly Trp Pro Val Ala Val Gly Gly Ser Gly Arg Ile Val
    215                 220                 225

gat gct ctg gtc aat gtc ata aac cat cac ggt ggc acc att cac tgc   835
Asp Ala Leu Val Asn Val Ile Asn His His Gly Gly Thr Ile His Cys
230                 235                 240                 245

gat tca cag att gat tcc ctc tca caa ttc cgc gac acc gat gcc att   883
Asp Ser Gln Ile Asp Ser Leu Ser Gln Phe Arg Asp Thr Asp Ala Ile
                250                 255                 260

att ctg aac caa acc ccc tca cag gtg ctg aaa ctc aaa gga act gac   931
Ile Leu Asn Gln Thr Pro Ser Gln Val Leu Lys Leu Lys Gly Thr Asp
            265                 270                 275

ctt aat gca ggg ctt ccg caa cgc atg agc acc tgg aaa cac gga cca   979
Leu Asn Ala Gly Leu Pro Gln Arg Met Ser Thr Trp Lys His Gly Pro
        280                 285                 290

agt tcc tac aaa gtg gac tac ctc ctt gac gaa cca att ccc tgg agc   1027
Ser Ser Tyr Lys Val Asp Tyr Leu Leu Asp Glu Pro Ile Pro Trp Ser
    295                 300                 305

aat ccc cag gta ggc cag gcc aca acc gtc cat gtg ggc gga agc tct   1075
Asn Pro Gln Val Gly Gln Ala Thr Thr Val His Val Gly Gly Ser Ser
310                 315                 320                 325

gag gaa atc gct ttc gca gaa gca gaa gtc gca gcg ggg cgg atg ccc   1123
Glu Glu Ile Ala Phe Ala Glu Ala Glu Val Ala Ala Gly Arg Met Pro
                330                 335                 340

gaa cgc ccg ttt atc att ttg tgc caa caa caa gtg gcg gat cct tca   1171
Glu Arg Pro Phe Ile Ile Leu Cys Gln Gln Gln Val Ala Asp Pro Ser
            345                 350                 355

cgc gcc cgg gag ggg cgc cac gtc gtg tgg gcc tac gcg cat gtg ccg   1219
Arg Ala Arg Glu Gly Arg His Val Val Trp Ala Tyr Ala His Val Pro
        360                 365                 370

cgg ggt ttc gtc gat aag cga gct gct tta tta atc act gcg cag att   1267
Arg Gly Phe Val Asp Lys Arg Ala Ala Leu Leu Ile Thr Ala Gln Ile
    375                 380                 385

gaa cgc ttc gcc ccc ggt ttc cgt gat cgc atc gtg cat tca gtg gat   1315
```

```
Glu Arg Phe Ala Pro Gly Phe Arg Asp Arg Ile Val His Ser Val Asp
390                 395                 400                 405

acc aac gcg gag gat tta gag gcg tgg aac ccc aat ctt gtt ggc gga   1363
Thr Asn Ala Glu Asp Leu Glu Ala Trp Asn Pro Asn Leu Val Gly Gly
                410                 415                 420

gac atc acc gca ggg tcc gcg ctg ctt cgg cga atg ccg acc aaa atc   1411
Asp Ile Thr Ala Gly Ser Ala Leu Leu Arg Arg Met Pro Thr Lys Ile
            425                 430                 435

ggc gag aaa acg tac atg gca tcc gcc tcc aac gcg ccg ggc ggg gga   1459
Gly Glu Lys Thr Tyr Met Ala Ser Ala Ser Asn Ala Pro Gly Gly Gly
        440                 445                 450

gtc cac gga atg ccc ggc tgg tgg gca gcg caa gcc gtt tta gca gat   1507
Val His Gly Met Pro Gly Trp Trp Ala Ala Gln Ala Val Leu Ala Asp
    455                 460                 465

cac agg tagaattgcg acatggagcc cac                                 1536
His Arg
470
```

[illegible]

```
<210> 594
<211> 471
<212> PRT
<213> Corynebacterium glutamicum

<400> 594
Val Thr Phe Arg Gly Gly Asn Thr Gly Ala Lys His Ala Val Val Val
  1               5                  10                  15

Gly Ser Gly Pro Asn Gly Leu Thr Thr Ala Ala Val Leu Ala Lys Ala
             20                  25                  30

Gly Trp Gln Val Asp Val Tyr Glu Ala Ala Pro Thr Pro Gly Gly Ala
         35                  40                  45

Ala Arg Ser Glu Ser Val Leu Gly Glu Gly Thr Ile Ser Asp Leu Gly
     50                  55                  60

Ala Ala Gly His Pro Phe Gly Val Ala Ser Pro Ala Phe His Tyr Leu
 65                  70                  75                  80

Gly Leu Glu Asp His Gly Leu Glu Trp Ala Tyr Ser Pro Phe Ala Met
                 85                  90                  95

Ala His Pro Leu Asp Tyr Gly Arg Ala Gly Leu Leu Glu Thr Ser Leu
            100                 105                 110

Pro Glu Thr Ala Lys Lys Leu Gly Pro Asp Ala Arg Arg Trp Lys Asn
        115                 120                 125

Leu His Gln Gly Leu Thr Lys Asn Ile Asp Lys His Leu Ala Asn Leu
    130                 135                 140

Leu Gly Pro Val Leu Lys Trp Pro Ala His Pro Ile Arg Met Ala Lys
145                 150                 155                 160

Phe Gly Pro Phe Ala Leu Leu Pro Ala Lys Arg Leu Ala Ser Ala Ala
```

```
                165                 170                 175

Phe Glu Thr Glu Glu Ala Arg Ser Leu Phe Ile Gly Ser Ala Met His
            180                 185                 190

Ser Val Thr Pro Pro His Lys Pro Met Thr Ala Ser Leu Gly Leu Leu
        195                 200                 205

Phe Gly Ala Leu Gly Met Ser Arg Gly Trp Pro Val Ala Val Gly Gly
    210                 215                 220

Ser Gly Arg Ile Val Asp Ala Leu Val Asn Val Ile Asn His His Gly
225                 230                 235                 240

Gly Thr Ile His Cys Asp Ser Gln Ile Asp Ser Leu Ser Gln Phe Arg
                245                 250                 255

Asp Thr Asp Ala Ile Ile Leu Asn Gln Thr Pro Ser Gln Val Leu Lys
            260                 265                 270

Leu Lys Gly Thr Asp Leu Asn Ala Gly Leu Pro Gln Arg Met Ser Thr
        275                 280                 285

Trp Lys His Gly Pro Ser Ser Tyr Lys Val Asp Tyr Leu Leu Asp Glu
    290                 295                 300

Pro Ile Pro Trp Ser Asn Pro Gln Val Gly Gln Ala Thr Thr Val His
305                 310                 315                 320

Val Gly Gly Ser Ser Glu Glu Ile Ala Phe Ala Glu Ala Glu Val Ala
                325                 330                 335

Ala Gly Arg Met Pro Glu Arg Pro Phe Ile Ile Leu Cys Gln Gln Gln
            340                 345                 350

Val Ala Asp Pro Ser Arg Ala Arg Glu Gly Arg His Val Val Trp Ala
        355                 360                 365

Tyr Ala His Val Pro Arg Gly Phe Val Asp Lys Arg Ala Ala Leu Leu
    370                 375                 380

Ile Thr Ala Gln Ile Glu Arg Phe Ala Pro Gly Phe Arg Asp Arg Ile
385                 390                 395                 400

Val His Ser Val Asp Thr Asn Ala Glu Asp Leu Glu Ala Trp Asn Pro
                405                 410                 415

Asn Leu Val Gly Gly Asp Ile Thr Ala Gly Ser Ala Leu Leu Arg Arg
            420                 425                 430

Met Pro Thr Lys Ile Gly Glu Lys Thr Tyr Met Ala Ser Ala Ser Asn
        435                 440                 445

Ala Pro Gly Gly Gly Val His Gly Met Pro Gly Trp Trp Ala Ala Gln
    450                 455                 460

Ala Val Leu Ala Asp His Arg
465                 470
```

<210> 595

<211> 1536
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1513)
<223> FRXA01337

<400> 595
gctggctatc ctcaattccg ctcgggtcgc actgccacgc ggagcgatta gtgattttga 60

tacgcaagaa aaagtttctt agcagggtaa cctaaatgtc gtg aca ttt cga ggc 115
Val Thr Phe Arg Gly
1 5

gga aac act ggc gca aag cac gcg gtc gtt gtt ggt tct ggc ccc aat 163
Gly Asn Thr Gly Ala Lys His Ala Val Val Val Gly Ser Gly Pro Asn
10 15 20

ggg ttg acc acg gcg gcg gtg ctg gcc aaa gca ggt tgg caa gta gat 211
Gly Leu Thr Thr Ala Ala Val Leu Ala Lys Ala Gly Trp Gln Val Asp
25 30 35

gtg tat gag gcg gcg cca acc cct gga ggg gcg gcg cgc tca gaa agc 259
Val Tyr Glu Ala Ala Pro Thr Pro Gly Gly Ala Ala Arg Ser Glu Ser
40 45 50

gtt ctg ggg gag ggg act atc agc gat ttg ggt gcc gca ggg cat cct 307
Val Leu Gly Glu Gly Thr Ile Ser Asp Leu Gly Ala Ala Gly His Pro
55 60 65

ttc ggg gtg gca agc cca gct ttt cac tat ttg ggt ctg gaa gat cac 355
Phe Gly Val Ala Ser Pro Ala Phe His Tyr Leu Gly Leu Glu Asp His
70 75 80 85

ggc ctg gaa tgg gcg tat tct ccc ttt gcg atg gcc cac ccg tta gat 403
Gly Leu Glu Trp Ala Tyr Ser Pro Phe Ala Met Ala His Pro Leu Asp
90 95 100

tat ggc agg gcc gga ctg ctg gaa acg tca ctc cca gag acc gcc aaa 451
Tyr Gly Arg Ala Gly Leu Leu Glu Thr Ser Leu Pro Glu Thr Ala Lys
105 110 115

aag ctt gga cct gat gca cgt cgt tgg aag aat ttg cac cag ggc tta 499
Lys Leu Gly Pro Asp Ala Arg Arg Trp Lys Asn Leu His Gln Gly Leu
120 125 130

acc aaa aac att gat aaa cac ttg gcc aat cta tta ggg ccg gtg ctg 547
Thr Lys Asn Ile Asp Lys His Leu Ala Asn Leu Leu Gly Pro Val Leu
135 140 145

aaa tgg cca gca cat ccg att cgg atg gca aag ttt ggc cca ttt gcg 595
Lys Trp Pro Ala His Pro Ile Arg Met Ala Lys Phe Gly Pro Phe Ala
150 155 160 165

ttg ctg ccc gcg aaa cgt cta gcc agt gcc gct ttt gaa aca gaa gaa 643
Leu Leu Pro Ala Lys Arg Leu Ala Ser Ala Ala Phe Glu Thr Glu Glu
170 175 180

gcc cga tcc ctg ttt atc ggt tcg gcg atg cac tcg gtg act cca cca 691

```
Ala Arg Ser Leu Phe Ile Gly Ser Ala Met His Ser Val Thr Pro Pro
            185                 190                 195

cac aag ccg atg acc gca tca ctt gga ttg ctt ttt ggc gct ctg ggg   739
His Lys Pro Met Thr Ala Ser Leu Gly Leu Leu Phe Gly Ala Leu Gly
        200                 205                 210

atg tcg cga gga tgg ccg gtt gca gtt ggg gga agc gga cgg atc gtc   787
Met Ser Arg Gly Trp Pro Val Ala Val Gly Gly Ser Gly Arg Ile Val
    215                 220                 225

gat gct ctg gtc aat gtc ata aac cat cac ggt ggc acc att cac tgc   835
Asp Ala Leu Val Asn Val Ile Asn His His Gly Gly Thr Ile His Cys
230                 235                 240                 245

gat tca cag att gat tcc ctc tca caa ttc cgc gac acc gat gcc att   883
Asp Ser Gln Ile Asp Ser Leu Ser Gln Phe Arg Asp Thr Asp Ala Ile
                250                 255                 260

att ctg aac caa acc ccc tca cag gtg ctg aaa ctc aaa gga act gac   931
Ile Leu Asn Gln Thr Pro Ser Gln Val Leu Lys Leu Lys Gly Thr Asp
            265                 270                 275

ctt aat gca ggg ctt ccg caa cgc atg agc acc tgg aaa cac gga cca   979
Leu Asn Ala Gly Leu Pro Gln Arg Met Ser Thr Trp Lys His Gly Pro
        280                 285                 290

agt tcc tac aaa gtg gac tac ctc ctt gac gaa cca att ccc tgg agc   1027
Ser Ser Tyr Lys Val Asp Tyr Leu Leu Asp Glu Pro Ile Pro Trp Ser
    295                 300                 305

aat ccc cag gta ggc cag gcc aca acc gtc cat gtg ggc gga agc tct   1075
Asn Pro Gln Val Gly Gln Ala Thr Thr Val His Val Gly Gly Ser Ser
310                 315                 320                 325

gag gaa atc gct ttc gca gaa gca gaa gtc gca gcg ggg cgg atg ccc   1123
Glu Glu Ile Ala Phe Ala Glu Ala Glu Val Ala Ala Gly Arg Met Pro
                330                 335                 340

gaa cgc ccg ttt atc att ttg tgc caa caa caa gtg gcg gat cct tca   1171
Glu Arg Pro Phe Ile Ile Leu Cys Gln Gln Gln Val Ala Asp Pro Ser
            345                 350                 355

cgc gcc cgg gag ggg cgc cac gtc gtg tgg gcc tac gcg cat gtg ccg   1219
Arg Ala Arg Glu Gly Arg His Val Val Trp Ala Tyr Ala His Val Pro
        360                 365                 370

cgg ggt ttc gtc gat aag cga gct gct tta tta atc act gcg cag att   1267
Arg Gly Phe Val Asp Lys Arg Ala Ala Leu Leu Ile Thr Ala Gln Ile
    375                 380                 385

gaa cgc ttc gcc ccc ggt ttc cgt gat cgc atc gtg cat tca gtg gat   1315
Glu Arg Phe Ala Pro Gly Phe Arg Asp Arg Ile Val His Ser Val Asp
390                 395                 400                 405

acc aac gcg gag gat tta gag gcg tgg aac ccc aat ctt gtt ggc gga   1363
Thr Asn Ala Glu Asp Leu Glu Ala Trp Asn Pro Asn Leu Val Gly Gly
                410                 415                 420

gac atc acc gca ggg tcc gcg ctg ctt cgg cga atg ccg acc aaa atc   1411
Asp Ile Thr Ala Gly Ser Ala Leu Leu Arg Arg Met Pro Thr Lys Ile
```

```
            425                 430                 435

ggc gag aaa acg tac atg gca tcc gcc tcc aac gcg ccg ggc ggg gga   1459
Gly Glu Lys Thr Tyr Met Ala Ser Ala Ser Asn Ala Pro Gly Gly Gly
        440                 445                 450

gtc cac gga atg ccc ggc tgg tgg gca gcg caa gcc gtt tta gca gat   1507
Val His Gly Met Pro Gly Trp Trp Ala Ala Gln Ala Val Leu Ala Asp
    455                 460                 465

cac agg tagaattgcg acatggagcc cac                                 1536
His Arg
470
```

<210> 596
<211> 471
<212> PRT
<213> Corynebacterium glutamicum

<400> 596

```
Val Thr Phe Arg Gly Gly Asn Thr Gly Ala Lys His Ala Val Val Val
  1               5                  10                  15

Gly Ser Gly Pro Asn Gly Leu Thr Thr Ala Ala Val Leu Ala Lys Ala
             20                  25                  30

Gly Trp Gln Val Asp Val Tyr Glu Ala Ala Pro Thr Pro Gly Gly Ala
         35                  40                  45

Ala Arg Ser Glu Ser Val Leu Gly Glu Gly Thr Ile Ser Asp Leu Gly
     50                  55                  60

Ala Ala Gly His Pro Phe Gly Val Ala Ser Pro Ala Phe His Tyr Leu
 65                  70                  75                  80

Gly Leu Glu Asp His Gly Leu Glu Trp Ala Tyr Ser Pro Phe Ala Met
                 85                  90                  95

Ala His Pro Leu Asp Tyr Gly Arg Ala Gly Leu Leu Glu Thr Ser Leu
            100                 105                 110

Pro Glu Thr Ala Lys Lys Leu Gly Pro Asp Ala Arg Arg Trp Lys Asn
        115                 120                 125

Leu His Gln Gly Leu Thr Lys Asn Ile Asp Lys His Leu Ala Asn Leu
    130                 135                 140

Leu Gly Pro Val Leu Lys Trp Pro Ala His Pro Ile Arg Met Ala Lys
145                 150                 155                 160

Phe Gly Pro Phe Ala Leu Leu Pro Ala Lys Arg Leu Ala Ser Ala Ala
                165                 170                 175

Phe Glu Thr Glu Glu Ala Arg Ser Leu Phe Ile Gly Ser Ala Met His
            180                 185                 190

Ser Val Thr Pro Pro His Lys Pro Met Thr Ala Ser Leu Gly Leu Leu
        195                 200                 205

Phe Gly Ala Leu Gly Met Ser Arg Gly Trp Pro Val Ala Val Gly Gly
```

```
    210                 215                 220

Ser Gly Arg Ile Val Asp Ala Leu Val Asn Val Ile Asn His His Gly
225                 230                 235                 240

Gly Thr Ile His Cys Asp Ser Gln Ile Asp Ser Leu Ser Gln Phe Arg
                245                 250                 255

Asp Thr Asp Ala Ile Ile Leu Asn Gln Thr Pro Ser Gln Val Leu Lys
            260                 265                 270

Leu Lys Gly Thr Asp Leu Asn Ala Gly Leu Pro Gln Arg Met Ser Thr
        275                 280                 285

Trp Lys His Gly Pro Ser Ser Tyr Lys Val Asp Tyr Leu Leu Asp Glu
    290                 295                 300

Pro Ile Pro Trp Ser Asn Pro Gln Val Gly Gln Ala Thr Thr Val His
305                 310                 315                 320

Val Gly Gly Ser Ser Glu Glu Ile Ala Phe Ala Glu Ala Glu Val Ala
                325                 330                 335

Ala Gly Arg Met Pro Glu Arg Pro Phe Ile Ile Leu Cys Gln Gln Gln
            340                 345                 350

Val Ala Asp Pro Ser Arg Ala Arg Glu Gly Arg His Val Val Trp Ala
        355                 360                 365

Tyr Ala His Val Pro Arg Gly Phe Val Asp Lys Arg Ala Ala Leu Leu
    370                 375                 380

Ile Thr Ala Gln Ile Glu Arg Phe Ala Pro Gly Phe Arg Asp Arg Ile
385                 390                 395                 400

Val His Ser Val Asp Thr Asn Ala Glu Asp Leu Glu Ala Trp Asn Pro
                405                 410                 415

Asn Leu Val Gly Gly Asp Ile Thr Ala Gly Ser Ala Leu Leu Arg Arg
            420                 425                 430

Met Pro Thr Lys Ile Gly Glu Lys Thr Tyr Met Ala Ser Ala Ser Asn
        435                 440                 445

Ala Pro Gly Gly Gly Val His Gly Met Pro Gly Trp Trp Ala Ala Gln
    450                 455                 460

Ala Val Leu Ala Asp His Arg
465                 470


<210> 597
<211> 708
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(685)
<223> RXN01351
```

<400> 597
ctggagattt ccgatttcca gcgcgcccgc atcgacgcga atgctcagga attgcaggcc 60

gagcgcgagg cagtgcgcga cttgctctaa tctttaacgc atg act tcg ctt ttc 115
Met Thr Ser Leu Phe
1 5

gac gcc cca acc ctc caa cgc gtc acc gtt ttc acg ggc tcg gcg ctc 163
Asp Ala Pro Thr Leu Gln Arg Val Thr Val Phe Thr Gly Ser Ala Leu
10 15 20

ggc agt tcc tcg ctg tac acg caa gcg gct caa acc ttg gcg aaa acc 211
Gly Ser Ser Ser Leu Tyr Thr Gln Ala Ala Gln Thr Leu Ala Lys Thr
25 30 35

gcg gta gac cgc ggc atc gac ttg gtt tac ggt ggc gga aaa gtg ggg 259
Ala Val Asp Arg Gly Ile Asp Leu Val Tyr Gly Gly Gly Lys Val Gly
40 45 50

ctc atg ggt atc gtc gcg gat gcg ttc ctg gaa tca ggt ggc gaa gcc 307
Leu Met Gly Ile Val Ala Asp Ala Phe Leu Glu Ser Gly Gly Glu Ala
55 60 65

ttt ggc gtc atc acg gaa tca ctt atg aag ggt gag ctt ggg cat gaa 355
Phe Gly Val Ile Thr Glu Ser Leu Met Lys Gly Glu Leu Gly His Glu
70 75 80 85

aag ctc acc gaa ctt gaa atc gtt cct gat atg cac atc cgc aag cgt 403
Lys Leu Thr Glu Leu Glu Ile Val Pro Asp Met His Ile Arg Lys Arg
90 95 100

cgc atg gca gaa ctt ggc gat ggt ttt atc gcc atg ccc ggt ggc gcc 451
Arg Met Ala Glu Leu Gly Asp Gly Phe Ile Ala Met Pro Gly Gly Ala
105 110 115

ggc acc ttg gaa gaa ctt ttc gag gtc tgg acc tgg caa cag ctg ggc 499
Gly Thr Leu Glu Glu Leu Phe Glu Val Trp Thr Trp Gln Gln Leu Gly
120 125 130

att cat caa aag ccc gtc gca ctt tat gat gtc gat ggt ttt tgg cag 547
Ile His Gln Lys Pro Val Ala Leu Tyr Asp Val Asp Gly Phe Trp Gln
135 140 145

ccc ctg ctg gaa atg ctt gag cag atg acc cag cgt gga ttt atc aag 595
Pro Leu Leu Glu Met Leu Glu Gln Met Thr Gln Arg Gly Phe Ile Lys
150 155 160 165

cga gac ttc ttt gag tgc ctc atc gtg gaa tcc gac ccg cat gcc ctg 643
Arg Asp Phe Phe Glu Cys Leu Ile Val Glu Ser Asp Pro His Ala Leu
170 175 180

cta aag gca atg cag acc tgg act cca cca gca cca aaa tgg 685
Leu Lys Ala Met Gln Thr Trp Thr Pro Pro Ala Pro Lys Trp
185 190 195

taactaaatt gtgtgctcga cgg 708

<210> 598
<211> 195
<212> PRT

<213> Corynebacterium glutamicum

<400> 598

```
Met Thr Ser Leu Phe Asp Ala Pro Thr Leu Gln Arg Val Thr Val Phe
  1               5                  10                  15

Thr Gly Ser Ala Leu Gly Ser Ser Ser Leu Tyr Thr Gln Ala Ala Gln
             20                  25                  30

Thr Leu Ala Lys Thr Ala Val Asp Arg Gly Ile Asp Leu Val Tyr Gly
         35                  40                  45

Gly Gly Lys Val Gly Leu Met Gly Ile Val Ala Asp Ala Phe Leu Glu
     50                  55                  60

Ser Gly Gly Glu Ala Phe Gly Val Ile Thr Glu Ser Leu Met Lys Gly
 65                  70                  75                  80

Glu Leu Gly His Glu Lys Leu Thr Glu Leu Glu Ile Val Pro Asp Met
                 85                  90                  95

His Ile Arg Lys Arg Arg Met Ala Glu Leu Gly Asp Gly Phe Ile Ala
            100                 105                 110

Met Pro Gly Gly Ala Gly Thr Leu Glu Glu Leu Phe Glu Val Trp Thr
        115                 120                 125

Trp Gln Gln Leu Gly Ile His Gln Lys Pro Val Ala Leu Tyr Asp Val
    130                 135                 140

Asp Gly Phe Trp Gln Pro Leu Leu Glu Met Leu Glu Gln Met Thr Gln
145                 150                 155                 160

Arg Gly Phe Ile Lys Arg Asp Phe Phe Glu Cys Leu Ile Val Glu Ser
                165                 170                 175

Asp Pro His Ala Leu Leu Lys Ala Met Gln Thr Trp Thr Pro Pro Ala
            180                 185                 190

Pro Lys Trp
        195
```

<210> 599
<211> 3677
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(3654)
<223> RXN01362

<400> 599

```
aaa tgg ctt ggc acg cct gcg cag agc tta ttc tta atc ccc cca gtt   48
Lys Trp Leu Gly Thr Pro Ala Gln Ser Leu Phe Leu Ile Pro Pro Val
  1               5                  10                  15

acc cag cat gct cgc acg ggc acc cac ctt tat gat tcc ctg cag ctg   96
Thr Gln His Ala Arg Thr Gly Thr His Leu Tyr Asp Ser Leu Gln Leu
             20                  25                  30
```

```
ctg ttc act ctg gtg gat aaa ggc cac cac cca aca gat gct aag gct   144
Leu Phe Thr Leu Val Asp Lys Gly His His Pro Thr Asp Ala Lys Ala
         35                  40                  45

gta gct ttt gat gcc gag gct gga gaa gaa ggc ctg cac ttc cgc aac   192
Val Ala Phe Asp Ala Glu Ala Gly Glu Glu Gly Leu His Phe Arg Asn
     50                  55                  60

ctt tca gcg gat ctc ttc ctc cct gca gcc aca gaa ctt att gat cga   240
Leu Ser Ala Asp Leu Phe Leu Pro Ala Ala Thr Glu Leu Ile Asp Arg
 65                  70                  75                  80

gtt ggt ctt tcc aat gaa gcc cta aac aag gtc ttg gaa aac ctc ctg   288
Val Gly Leu Ser Asn Glu Ala Leu Asn Lys Val Leu Glu Asn Leu Leu
                 85                  90                  95

ctc tcc cgg gtg caa tcc ggt aaa gac cgc ggc ttt atc tcc tat gcc   336
Leu Ser Arg Val Gln Ser Gly Lys Asp Arg Gly Phe Ile Ser Tyr Ala
            100                 105                 110

acc ttg ggt gtt acc gag ctt ggc caa gtt tat gag ggt ctg atg tcc   384
Thr Leu Gly Val Thr Glu Leu Gly Gln Val Tyr Glu Gly Leu Met Ser
        115                 120                 125

tat acc ggc ttt atc gcc cag gaa gat ctt ttt gag gtt gca cca cat   432
Tyr Thr Gly Phe Ile Ala Gln Glu Asp Leu Phe Glu Val Ala Pro His
    130                 135                 140

ggc aaa gcc gat aaa ggt tcc tgg atg ctc ccg gtc tca aag gct gat   480
Gly Lys Ala Asp Lys Gly Ser Trp Met Leu Pro Val Ser Lys Ala Asp
145                 150                 155                 160

gaa gtc cct gcc gat agc ttt atc gaa gtt gat caa gaa gcc cct ggt   528
Glu Val Pro Ala Asp Ser Phe Ile Glu Val Asp Gln Glu Ala Pro Gly
                165                 170                 175

ggc ggc gta atc aag gtg cgt aaa cgc cac ccg cgc gga tca ttt gtg   576
Gly Gly Val Ile Lys Val Arg Lys Arg His Pro Arg Gly Ser Phe Val
            180                 185                 190

ttc cgt cag tcc tct cgt gac cgc gaa cgc tca gcg tcc ttc tac acc   624
Phe Arg Gln Ser Ser Arg Asp Arg Glu Arg Ser Ala Ser Phe Tyr Thr
        195                 200                 205

cca caa gta ctc acc agc ttt act gtc acc cag gct att gaa gaa ctc   672
Pro Gln Val Leu Thr Ser Phe Thr Val Thr Gln Ala Ile Glu Glu Leu
    210                 215                 220

cag gca tca aag cgc atc acc aca gcc aat gat gtt ctc agc ctc acc   720
Gln Ala Ser Lys Arg Ile Thr Thr Ala Asn Asp Val Leu Ser Leu Thr
225                 230                 235                 240

atc tgt gaa cct gcc atg ggt tcc ggc gcc ttc gct gtg gaa gca gta   768
Ile Cys Glu Pro Ala Met Gly Ser Gly Ala Phe Ala Val Glu Ala Val
                245                 250                 255

cgc caa tta gca gag ctt tat ttg gaa ttg cgc caa gaa gaa cta gag   816
Arg Gln Leu Ala Glu Leu Tyr Leu Glu Leu Arg Gln Glu Glu Leu Glu
            260                 265                 270
```

```
cag cag att cca gcg gaa gac cgt gcc aag gaa ctc caa aag gtc aaa   864
Gln Gln Ile Pro Ala Glu Asp Arg Ala Lys Glu Leu Gln Lys Val Lys
        275                 280                 285

gcg cac att gcg ctg cac cag gtt tat ggt gtg gac ctt aac agc act   912
Ala His Ile Ala Leu His Gln Val Tyr Gly Val Asp Leu Asn Ser Thr
    290                 295                 300

gct gtg gag ttg gcg gaa atc tcg ctg tgg cta gac acc atg aat gca   960
Ala Val Glu Leu Ala Glu Ile Ser Leu Trp Leu Asp Thr Met Asn Ala
305                 310                 315                 320

gaa atg gac gca cct tgg tat ggc ctg cac ctg cgt aat ggt aac tcc   1008
Glu Met Asp Ala Pro Trp Tyr Gly Leu His Leu Arg Asn Gly Asn Ser
                325                 330                 335

ctc gtt ggt gcc acc cgt tcg ctg tat gca cct agt ctg ctt aat aaa   1056
Leu Val Gly Ala Thr Arg Ser Leu Tyr Ala Pro Ser Leu Leu Asn Lys
            340                 345                 350

aaa gcc tgg tta act gct act cca acc cgc tat cgg ctt gat gat atc   1104
Lys Ala Trp Leu Thr Ala Thr Pro Thr Arg Tyr Arg Leu Asp Asp Ile
        355                 360                 365

gcg cag gct att gat gaa aac aaa gca gaa ccc ctc ttc aac cac ggc   1152
Ala Gln Ala Ile Asp Glu Asn Lys Ala Glu Pro Leu Phe Asn His Gly
    370                 375                 380

atc cac cac ttc ctc ttg ccc tct act ggc tgg gga gcc act gca gat   1200
Ile His His Phe Leu Leu Pro Ser Thr Gly Trp Gly Ala Thr Ala Asp
385                 390                 395                 400

gcc aaa gat ctt aaa gat ctt atg gct act gaa atc aag gag ctt aaa   1248
Ala Lys Asp Leu Lys Asp Leu Met Ala Thr Glu Ile Lys Glu Leu Lys
                405                 410                 415

tct tgg cgt act tcc atc cgt gcg tct ttg agt aaa act cag att aag   1296
Ser Trp Arg Thr Ser Ile Arg Ala Ser Leu Ser Lys Thr Gln Ile Lys
            420                 425                 430

cag ctc aat aac ctt gcc cta cgc gtg gaa aca cta tgg cga ttt gtg   1344
Gln Leu Asn Asn Leu Ala Leu Arg Val Glu Thr Leu Trp Arg Phe Val
        435                 440                 445

ctg atg cgt att cgc att gca gaa tcc cag atc tca cgt agc act act   1392
Leu Met Arg Ile Arg Ile Ala Glu Ser Gln Ile Ser Arg Ser Thr Thr
    450                 455                 460

ctc tgg ggt caa gag cca gct gag gtt tcg gag gtt gtc aca cgt gag   1440
Leu Trp Gly Gln Glu Pro Ala Glu Val Ser Glu Val Val Thr Arg Glu
465                 470                 475                 480

caa att gaa caa gac ctc ttt ggc aat att gat ggt gca tat aac cgt   1488
Gln Ile Glu Gln Asp Leu Phe Gly Asn Ile Asp Gly Ala Tyr Asn Arg
                485                 490                 495

cta cgc ttg gtg atg gat gct tgg tgt gcg ctg tgg ttc tgg cct ttg   1536
Leu Arg Leu Val Met Asp Ala Trp Cys Ala Leu Trp Phe Trp Pro Leu
            500                 505                 510

gat gct gtt gct acc gct gag cat ccg gag cgt cca gcc ctt cca gat   1584
```

```
Asp Ala Val Ala Thr Ala Glu His Pro Glu Arg Pro Ala Leu Pro Asp
        515                 520                 525

ctt gat gag tgg cta gcc acc ctg acg gag att ctg ggt att gat ctc   1632
Leu Asp Glu Trp Leu Ala Thr Leu Thr Glu Ile Leu Gly Ile Asp Leu
    530                 535                 540

cct ctg aag tcc aaa aac gaa aat cag att gtc tta ggt cca gat acc   1680
Pro Leu Lys Ser Lys Asn Glu Asn Gln Ile Val Leu Gly Pro Asp Thr
545                 550                 555                 560

aat tgg cta gcc att aat gat gcc gag gct act gat ctt ggt ttt tct   1728
Asn Trp Leu Ala Ile Asn Asp Ala Glu Ala Thr Asp Leu Gly Phe Ser
                565                 570                 575

ggg gca ttg agc ttt gag cgt gtt agc gcg aat cac ccg tgg atc aat   1776
Gly Ala Leu Ser Phe Glu Arg Val Ser Ala Asn His Pro Trp Ile Asn
            580                 585                 590

gtt gcc cgc caa gtg gct aaa caa cag agc ttc ttc cac tgg gat cta   1824
Val Ala Arg Gln Val Ala Lys Gln Gln Ser Phe Phe His Trp Asp Leu
        595                 600                 605

gac ttc gcc cac gtt ttt gcc aag ggt gga ttt gat ctg cag gtt ggt   1872
Asp Phe Ala His Val Phe Ala Lys Gly Gly Phe Asp Leu Gln Val Gly
    610                 615                 620

aat cca cca tgg gtg cga cca gat gtg aac ttt gag gat ctg ctt gct   1920
Asn Pro Pro Trp Val Arg Pro Asp Val Asn Phe Glu Asp Leu Leu Ala
625                 630                 635                 640

gaa cat gat ccg tgg tgg gct gta atg agt aaa cca acc cag gca tcc   1968
Glu His Asp Pro Trp Trp Ala Val Met Ser Lys Pro Thr Gln Ala Ser
                645                 650                 655

aaa aaa gaa cgc cag aag aat ttt cac aac aat cct aag agc ctc gaa   2016
Lys Lys Glu Arg Gln Lys Asn Phe His Asn Asn Pro Lys Ser Leu Glu
            660                 665                 670

cat gtg gtc agt ggt gca ggt gaa ccc gtg gct act tct gcg atc ctc   2064
His Val Val Ser Gly Ala Gly Glu Pro Val Ala Thr Ser Ala Ile Leu
        675                 680                 685

ggt tcg gtt act ctc tat ccg cat ctt aaa gat caa cgc ccg gac ctc   2112
Gly Ser Val Thr Leu Tyr Pro His Leu Lys Asp Gln Arg Pro Asp Leu
    690                 695                 700

tac cgg ggc ttt atg gaa aag act tgg tct aat gcc tcc ccg gca ggt   2160
Tyr Arg Gly Phe Met Glu Lys Thr Trp Ser Asn Ala Ser Pro Ala Gly
705                 710                 715                 720

gcg atc tca ctg atc cac ccc gaa tcc cac ttc act gag aaa aaa gct   2208
Ala Ile Ser Leu Ile His Pro Glu Ser His Phe Thr Glu Lys Lys Ala
                725                 730                 735

gcc ccg cta cgt cgg gga gca tat gag cgt ctg cgc cgc cac tgg cag   2256
Ala Pro Leu Arg Arg Gly Ala Tyr Glu Arg Leu Arg Arg His Trp Gln
            740                 745                 750

ttc att aat gag ttg att ctt ttt gac gtc cac gac ttg gtt aaa tat   2304
Phe Ile Asn Glu Leu Ile Leu Phe Asp Val His Asp Leu Val Lys Tyr
```

```
        755                 760                 765

ggc gta cat gtc tat ggc gct ccg cag gaa tct att aac ttt tta agt   2352
Gly Val His Val Tyr Gly Ala Pro Gln Glu Ser Ile Asn Phe Leu Ser
    770                 775                 780

gct gcg tcg ctt tat cac cca caa aca gtg ctt gat tca ttt gat cat   2400
Ala Ala Ser Leu Tyr His Pro Gln Thr Val Leu Asp Ser Phe Asp His
785                 790                 795                 800

gac ggt tca ggt aat ctc cct ggt ctt aaa gac gac aat ggc aac tgg   2448
Asp Gly Ser Gly Asn Leu Pro Gly Leu Lys Asp Asp Asn Gly Asn Trp
                805                 810                 815

gac cgt cgc cca cac aag gac cgt atc caa ctg gtc aat gcc gat act   2496
Asp Arg Arg Pro His Lys Asp Arg Ile Gln Leu Val Asn Ala Asp Thr
            820                 825                 830

ttg acg gtg tgg aag tcc atc ctg gag gat gaa caa acg cca tac ttg   2544
Leu Thr Val Trp Lys Ser Ile Leu Glu Asp Glu Gln Thr Pro Tyr Leu
        835                 840                 845

gat acc cgc atg gtt tat acc gtc aac acg gaa gca gca gca gcg ttg   2592
Asp Thr Arg Met Val Tyr Thr Val Asn Thr Glu Ala Ala Ala Ala Leu
    850                 855                 860

gaa aag ttg gct tct gca cct cgt atc aaa gaa ctc ggg ctg cag ttc   2640
Glu Lys Leu Ala Ser Ala Pro Arg Ile Lys Glu Leu Gly Leu Gln Phe
865                 870                 875                 880

tcc agt ggc tgg aat gaa acc acc gat aag aaa aag gga tac ttt gac   2688
Ser Ser Gly Trp Asn Glu Thr Thr Asp Lys Lys Lys Gly Tyr Phe Asp
                885                 890                 895

gtt ggt tgg ggc tac cca gct tcc tgg tct gat gcc att ttg cag ggg   2736
Val Gly Trp Gly Tyr Pro Ala Ser Trp Ser Asp Ala Ile Leu Gln Gly
            900                 905                 910

ccg cac ctg ggt gtt gct aca cca atg atc aag cag ccc aat ccg aca   2784
Pro His Leu Gly Val Ala Thr Pro Met Ile Lys Gln Pro Asn Pro Thr
        915                 920                 925

atg aag cat aat caa gat tgg tct gaa att gat ttc gag gcc att cct   2832
Met Lys His Asn Gln Asp Trp Ser Glu Ile Asp Phe Glu Ala Ile Pro
    930                 935                 940

gca aac ttc ata cct gca acg gcg tac cag ccc gat cgc caa aca aag   2880
Ala Asn Phe Ile Pro Ala Thr Ala Tyr Gln Pro Asp Arg Gln Thr Lys
945                 950                 955                 960

ccc act tat gat gct gac tac ggc acc tgg act ttc ggg gac aag cag   2928
Pro Thr Tyr Asp Ala Asp Tyr Gly Thr Trp Thr Phe Gly Asp Lys Gln
                965                 970                 975

gta cca gtt gca gac act ttc cga att gca tgg agg gag atg gct gcc   2976
Val Pro Val Ala Asp Thr Phe Arg Ile Ala Trp Arg Glu Met Ala Ala
            980                 985                 990

acc acg gga ttt agg act gtc tac cca tca gta att cca ccg gga gcc   3024
Thr Thr Gly Phe Arg Thr Val Tyr Pro Ser Val Ile Pro Pro Gly Ala
        995                 1000                1005
```

```
aac cat gtg cac aca gtt aat agc gct gca tca cgt tca aac tta aaa   3072
Asn His Val His Thr Val Asn Ser Ala Ala Ser Arg Ser Asn Leu Lys
    1010                1015                1020

acc att ctc gtt gga gca cag ctt ggt gca att cta agt gac tat ttt   3120
Thr Ile Leu Val Gly Ala Gln Leu Gly Ala Ile Leu Ser Asp Tyr Phe
1025                1030                1035                1040

gct cgg tcc tcg ggt tca agc cac ata ttt aac gac att gtt cgc aag   3168
Ala Arg Ser Ser Gly Ser Ser His Ile Phe Asn Asp Ile Val Arg Lys
                1045                1050                1055

att cca ctt cca aat ttc aca tcc ttg gaa aag cag ttc gcc cgc aca   3216
Ile Pro Leu Pro Asn Phe Thr Ser Leu Glu Lys Gln Phe Ala Arg Thr
            1060                1065                1070

tac ctc cgc ctc aac tgc ctg acc tca gct tat gcc cca ttg tgg gaa   3264
Tyr Leu Arg Leu Asn Cys Leu Thr Ser Ala Tyr Ala Pro Leu Trp Glu
        1075                1080                1085

gag atc acc ggt gag ccg tgg gat gtt cag gtg cct ttg cgc aat gcc   3312
Glu Ile Thr Gly Glu Pro Trp Asp Val Gln Val Pro Leu Arg Asn Ala
    1090                1095                1100

gag caa cgt cga gca gcg caa aac gat att gat gcc atg gtg gca ttg   3360
Glu Gln Arg Arg Ala Ala Gln Asn Asp Ile Asp Ala Met Val Ala Leu
1105                1110                1115                1120

tct ttg ggt att agt gct gat gag ctg tgc atg att tat cgc act caa   3408
Ser Leu Gly Ile Ser Ala Asp Glu Leu Cys Met Ile Tyr Arg Thr Gln
                1125                1130                1135

ttc cca gtg atg cgt aga tat gat caa gaa gat cat ttt gat gcc aat   3456
Phe Pro Val Met Arg Arg Tyr Asp Gln Glu Asp His Phe Asp Ala Asn
            1140                1145                1150

ggc cgt aaa gtt cct aaa gag atc atc aag ctg cag cag aaa ctt aaa   3504
Gly Arg Lys Val Pro Lys Glu Ile Ile Lys Leu Gln Gln Lys Leu Lys
        1155                1160                1165

gat ggc caa gag ctc agc gtg gaa aag cgc acc tgg gtg cat ccc caa   3552
Asp Gly Gln Glu Leu Ser Val Glu Lys Arg Thr Trp Val His Pro Gln
    1170                1175                1180

tca gaa gtg tcc tat acc ttt gaa tat cct ttc cgg gtg ttg gat cgt   3600
Ser Glu Val Ser Tyr Thr Phe Glu Tyr Pro Phe Arg Val Leu Asp Arg
1185                1190                1195                1200

gaa gct gat ctg cgt gct gca tat gca aaa ttt gaa aac cag ctt aag   3648
Glu Ala Asp Leu Arg Ala Ala Tyr Ala Lys Phe Glu Asn Gln Leu Lys
                1205                1210                1215

gag cca tagagcgctt atgtcctcac tca                                3677
Glu Pro
```

<210> 600
<211> 1218
<212> PRT

<213> Corynebacterium glutamicum

<400> 600

```
Lys Trp Leu Gly Thr Pro Ala Gln Ser Leu Phe Leu Ile Pro Pro Val
  1               5                  10                  15

Thr Gln His Ala Arg Thr Gly Thr His Leu Tyr Asp Ser Leu Gln Leu
             20                  25                  30

Leu Phe Thr Leu Val Asp Lys Gly His His Pro Thr Asp Ala Lys Ala
         35                  40                  45

Val Ala Phe Asp Ala Glu Ala Gly Glu Glu Gly Leu His Phe Arg Asn
     50                  55                  60

Leu Ser Ala Asp Leu Phe Leu Pro Ala Ala Thr Glu Leu Ile Asp Arg
 65                  70                  75                  80

Val Gly Leu Ser Asn Glu Ala Leu Asn Lys Val Leu Glu Asn Leu Leu
                 85                  90                  95

Leu Ser Arg Val Gln Ser Gly Lys Asp Arg Gly Phe Ile Ser Tyr Ala
            100                 105                 110

Thr Leu Gly Val Thr Glu Leu Gly Gln Val Tyr Glu Gly Leu Met Ser
        115                 120                 125

Tyr Thr Gly Phe Ile Ala Gln Glu Asp Leu Phe Glu Val Ala Pro His
    130                 135                 140

Gly Lys Ala Asp Lys Gly Ser Trp Met Leu Pro Val Ser Lys Ala Asp
145                 150                 155                 160

Glu Val Pro Ala Asp Ser Phe Ile Glu Val Asp Gln Glu Ala Pro Gly
                165                 170                 175

Gly Gly Val Ile Lys Val Arg Lys Arg His Pro Arg Gly Ser Phe Val
            180                 185                 190

Phe Arg Gln Ser Ser Arg Asp Arg Glu Arg Ser Ala Ser Phe Tyr Thr
        195                 200                 205

Pro Gln Val Leu Thr Ser Phe Thr Val Thr Gln Ala Ile Glu Glu Leu
    210                 215                 220

Gln Ala Ser Lys Arg Ile Thr Thr Ala Asn Asp Val Leu Ser Leu Thr
225                 230                 235                 240

Ile Cys Glu Pro Ala Met Gly Ser Gly Ala Phe Ala Val Glu Ala Val
                245                 250                 255

Arg Gln Leu Ala Glu Leu Tyr Leu Glu Leu Arg Gln Glu Glu Leu Glu
            260                 265                 270

Gln Gln Ile Pro Ala Glu Asp Arg Ala Lys Glu Leu Gln Lys Val Lys
        275                 280                 285

Ala His Ile Ala Leu His Gln Val Tyr Gly Val Asp Leu Asn Ser Thr
    290                 295                 300

Ala Val Glu Leu Ala Glu Ile Ser Leu Trp Leu Asp Thr Met Asn Ala
```

```
305                 310                 315                 320

Glu Met Asp Ala Pro Trp Tyr Gly Leu His Leu Arg Asn Gly Asn Ser
                325                 330                 335

Leu Val Gly Ala Thr Arg Ser Leu Tyr Ala Pro Ser Leu Leu Asn Lys
            340                 345                 350

Lys Ala Trp Leu Thr Ala Thr Pro Thr Arg Tyr Arg Leu Asp Asp Ile
        355                 360                 365

Ala Gln Ala Ile Asp Glu Asn Lys Ala Glu Pro Leu Phe Asn His Gly
    370                 375                 380

Ile His His Phe Leu Leu Pro Ser Thr Gly Trp Gly Ala Thr Ala Asp
385                 390                 395                 400

Ala Lys Asp Leu Lys Asp Leu Met Ala Thr Glu Ile Lys Glu Leu Lys
                405                 410                 415

Ser Trp Arg Thr Ser Ile Arg Ala Ser Leu Ser Lys Thr Gln Ile Lys
            420                 425                 430

Gln Leu Asn Asn Leu Ala Leu Arg Val Glu Thr Leu Trp Arg Phe Val
        435                 440                 445

Leu Met Arg Ile Arg Ile Ala Glu Ser Gln Ile Ser Arg Ser Thr Thr
    450                 455                 460

Leu Trp Gly Gln Glu Pro Ala Glu Val Ser Glu Val Val Thr Arg Glu
465                 470                 475                 480

Gln Ile Glu Gln Asp Leu Phe Gly Asn Ile Asp Gly Ala Tyr Asn Arg
                485                 490                 495

Leu Arg Leu Val Met Asp Ala Trp Cys Ala Leu Trp Phe Trp Pro Leu
            500                 505                 510

Asp Ala Val Ala Thr Ala Glu His Pro Glu Arg Pro Ala Leu Pro Asp
        515                 520                 525

Leu Asp Glu Trp Leu Ala Thr Leu Thr Glu Ile Leu Gly Ile Asp Leu
    530                 535                 540

Pro Leu Lys Ser Lys Asn Glu Asn Gln Ile Val Leu Gly Pro Asp Thr
545                 550                 555                 560

Asn Trp Leu Ala Ile Asn Asp Ala Glu Ala Thr Asp Leu Gly Phe Ser
                565                 570                 575

Gly Ala Leu Ser Phe Glu Arg Val Ser Ala Asn His Pro Trp Ile Asn
            580                 585                 590

Val Ala Arg Gln Val Ala Lys Gln Gln Ser Phe Phe His Trp Asp Leu
        595                 600                 605

Asp Phe Ala His Val Phe Ala Lys Gly Gly Phe Asp Leu Gln Val Gly
    610                 615                 620

Asn Pro Pro Trp Val Arg Pro Asp Val Asn Phe Glu Asp Leu Leu Ala
625                 630                 635                 640
```

```
Glu His Asp Pro Trp Trp Ala Val Met Ser Lys Pro Thr Gln Ala Ser
                645                 650                 655

Lys Lys Glu Arg Gln Lys Asn Phe His Asn Asn Pro Lys Ser Leu Glu
            660                 665                 670

His Val Val Ser Gly Ala Gly Glu Pro Val Ala Thr Ser Ala Ile Leu
        675                 680                 685

Gly Ser Val Thr Leu Tyr Pro His Leu Lys Asp Gln Arg Pro Asp Leu
    690                 695                 700

Tyr Arg Gly Phe Met Glu Lys Thr Trp Ser Asn Ala Ser Pro Ala Gly
705                 710                 715                 720

Ala Ile Ser Leu Ile His Pro Glu Ser His Phe Thr Glu Lys Lys Ala
                725                 730                 735

Ala Pro Leu Arg Arg Gly Ala Tyr Glu Arg Leu Arg Arg His Trp Gln
            740                 745                 750

Phe Ile Asn Glu Leu Ile Leu Phe Asp Val His Asp Leu Val Lys Tyr
        755                 760                 765

Gly Val His Val Tyr Gly Ala Pro Gln Glu Ser Ile Asn Phe Leu Ser
    770                 775                 780

Ala Ala Ser Leu Tyr His Pro Gln Thr Val Leu Asp Ser Phe Asp His
785                 790                 795                 800

Asp Gly Ser Gly Asn Leu Pro Gly Leu Lys Asp Asp Asn Gly Asn Trp
                805                 810                 815

Asp Arg Arg Pro His Lys Asp Arg Ile Gln Leu Val Asn Ala Asp Thr
            820                 825                 830

Leu Thr Val Trp Lys Ser Ile Leu Glu Asp Glu Gln Thr Pro Tyr Leu
        835                 840                 845

Asp Thr Arg Met Val Tyr Thr Val Asn Thr Glu Ala Ala Ala Ala Leu
    850                 855                 860

Glu Lys Leu Ala Ser Ala Pro Arg Ile Lys Glu Leu Gly Leu Gln Phe
865                 870                 875                 880

Ser Ser Gly Trp Asn Glu Thr Thr Asp Lys Lys Lys Gly Tyr Phe Asp
                885                 890                 895

Val Gly Trp Gly Tyr Pro Ala Ser Trp Ser Asp Ala Ile Leu Gln Gly
            900                 905                 910

Pro His Leu Gly Val Ala Thr Pro Met Ile Lys Gln Pro Asn Pro Thr
        915                 920                 925

Met Lys His Asn Gln Asp Trp Ser Glu Ile Asp Phe Glu Ala Ile Pro
    930                 935                 940

Ala Asn Phe Ile Pro Ala Thr Ala Tyr Gln Pro Asp Arg Gln Thr Lys
945                 950                 955                 960
```

```
Pro Thr Tyr Asp Ala Asp Tyr Gly Thr Trp Thr Phe Gly Asp Lys Gln
                965                 970                 975

Val Pro Val Ala Asp Thr Phe Arg Ile Ala Trp Arg Glu Met Ala Ala
            980                 985                 990

Thr Thr Gly Phe Arg Thr Val Tyr Pro Ser Val Ile Pro Pro Gly Ala
        995                 1000                1005

Asn His Val His Thr Val Asn Ser Ala Ala Ser Arg Ser Asn Leu Lys
    1010                1015                1020

Thr Ile Leu Val Gly Ala Gln Leu Gly Ala Ile Leu Ser Asp Tyr Phe
1025                1030                1035                1040

Ala Arg Ser Ser Gly Ser Ser His Ile Phe Asn Asp Ile Val Arg Lys
                1045                1050                1055

Ile Pro Leu Pro Asn Phe Thr Ser Leu Glu Lys Gln Phe Ala Arg Thr
            1060                1065                1070

Tyr Leu Arg Leu Asn Cys Leu Thr Ser Ala Tyr Ala Pro Leu Trp Glu
        1075                1080                1085

Glu Ile Thr Gly Glu Pro Trp Asp Val Gln Val Pro Leu Arg Asn Ala
    1090                1095                1100

Glu Gln Arg Arg Ala Ala Gln Asn Asp Ile Asp Ala Met Val Ala Leu
1105                1110                1115                1120

Ser Leu Gly Ile Ser Ala Asp Glu Leu Cys Met Ile Tyr Arg Thr Gln
                1125                1130                1135

Phe Pro Val Met Arg Arg Tyr Asp Gln Glu Asp His Phe Asp Ala Asn
            1140                1145                1150

Gly Arg Lys Val Pro Lys Glu Ile Ile Lys Leu Gln Gln Lys Leu Lys
        1155                1160                1165

Asp Gly Gln Glu Leu Ser Val Glu Lys Arg Thr Trp Val His Pro Gln
    1170                1175                1180

Ser Glu Val Ser Tyr Thr Phe Glu Tyr Pro Phe Arg Val Leu Asp Arg
1185                1190                1195                1200

Glu Ala Asp Leu Arg Ala Ala Tyr Ala Lys Phe Glu Asn Gln Leu Lys
                1205                1210                1215

Glu Pro
```

<210> 601
<211> 1418
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1395)
<223> FRXA01362

<400> 601

```
att aat gag ttg att ctt ttt gac gta cac gac ttg gtt aaa tat ggc   48
Ile Asn Glu Leu Ile Leu Phe Asp Val His Asp Leu Val Lys Tyr Gly
  1               5                  10                  15

gta cat gtc tat ggc gct ccg cag gaa tct att aac ttt tta agt gct   96
Val His Val Tyr Gly Ala Pro Gln Glu Ser Ile Asn Phe Leu Ser Ala
            20                  25                  30

gcg tcg ctt tat cac cca caa aca gtg ctt gat tca ttt gat cat gac   144
Ala Ser Leu Tyr His Pro Gln Thr Val Leu Asp Ser Phe Asp His Asp
        35                  40                  45

ggt tca ggt aat ctc cct ggt ctt aaa gac gac aat ggc aac tgg gac   192
Gly Ser Gly Asn Leu Pro Gly Leu Lys Asp Asp Asn Gly Asn Trp Asp
    50                  55                  60

cgt cgc cca cac aag gac cgt atc caa ctg gtc aat gcc gat act ttg   240
Arg Arg Pro His Lys Asp Arg Ile Gln Leu Val Asn Ala Asp Thr Leu
65                  70                  75                  80

acg gtg tgg aag tcc atc ctg gag gat gaa caa acg cca tac ttg gat   288
Thr Val Trp Lys Ser Ile Leu Glu Asp Glu Gln Thr Pro Tyr Leu Asp
                85                  90                  95

acc cgc atg gtt tat acc gtc aac acg gaa gca gca gca gcg ttg gaa   336
Thr Arg Met Val Tyr Thr Val Asn Thr Glu Ala Ala Ala Ala Leu Glu
            100                 105                 110

aag ttg gct tct gca cct cgt atc aaa gaa ctc ggg ctg cag ttc tcc   384
Lys Leu Ala Ser Ala Pro Arg Ile Lys Glu Leu Gly Leu Gln Phe Ser
        115                 120                 125

agt ggc tgg aat gaa acc acc gat aag aaa aag gga tac ttt gac gtt   432
Ser Gly Trp Asn Glu Thr Thr Asp Lys Lys Lys Gly Tyr Phe Asp Val
    130                 135                 140

ggt tgg ggc tac cca gct tcc tgg tct gat gcc att ttg cag ggg ccg   480
Gly Trp Gly Tyr Pro Ala Ser Trp Ser Asp Ala Ile Leu Gln Gly Pro
145                 150                 155                 160

cac ctg ggt gtt gct aca cca atg atc aag cag ccc aat ccg aca atg   528
His Leu Gly Val Ala Thr Pro Met Ile Lys Gln Pro Asn Pro Thr Met
                165                 170                 175

aag cat aat caa gat tgg tct gaa att gat ttc gag gcc att cct gca   576
Lys His Asn Gln Asp Trp Ser Glu Ile Asp Phe Glu Ala Ile Pro Ala
            180                 185                 190

aac ttc ata cct gca acg gcg tac cag ccc gat cgc caa aca aag ccc   624
Asn Phe Ile Pro Ala Thr Ala Tyr Gln Pro Asp Arg Gln Thr Lys Pro
        195                 200                 205

act tat gat gct gac tac ggc acc tgg act ttc ggg gac aag cag gta   672
Thr Tyr Asp Ala Asp Tyr Gly Thr Trp Thr Phe Gly Asp Lys Gln Val
    210                 215                 220

cca gtt gca gac act ttc cga att gca tgg agg gag atg gct gcc acc   720
Pro Val Ala Asp Thr Phe Arg Ile Ala Trp Arg Glu Met Ala Ala Thr
225                 230                 235                 240
```

```
acg gga ttt agg act gtc tac cca tca gta att cca ccg gga gcc aac   768
Thr Gly Phe Arg Thr Val Tyr Pro Ser Val Ile Pro Pro Gly Ala Asn
                245                 250                 255

cat gtg cac aca gtt aat agc gct gca tca cgt tca aac tta aaa acc   816
His Val His Thr Val Asn Ser Ala Ala Ser Arg Ser Asn Leu Lys Thr
            260                 265                 270

att ctc gtt gga gca cag ctt ggt gca att cta agt gac tat ttt gct   864
Ile Leu Val Gly Ala Gln Leu Gly Ala Ile Leu Ser Asp Tyr Phe Ala
        275                 280                 285

cgg tcc tcg ggt tca agc cac ata ttt aac gac att gtt cgc aag att   912
Arg Ser Ser Gly Ser Ser His Ile Phe Asn Asp Ile Val Arg Lys Ile
    290                 295                 300

cca ctt cca aat ttc aca tcc ttg gaa aag cag ttc gcc cgc aca tac   960
Pro Leu Pro Asn Phe Thr Ser Leu Glu Lys Gln Phe Ala Arg Thr Tyr
305                 310                 315                 320

ctc cgc ctc aac tgc ctg acc tca gct tat gcc cca ttg tgg gaa gag   1008
Leu Arg Leu Asn Cys Leu Thr Ser Ala Tyr Ala Pro Leu Trp Glu Glu
                325                 330                 335

atc acc ggt gag ccg tgg gat gtt cag gtg cct ttg cgc aat gcc gag   1056
Ile Thr Gly Glu Pro Trp Asp Val Gln Val Pro Leu Arg Asn Ala Glu
            340                 345                 350

caa cgt cga gca gcg caa aac gat att gat gcc atg gtg gca ttg tct   1104
Gln Arg Arg Ala Ala Gln Asn Asp Ile Asp Ala Met Val Ala Leu Ser
        355                 360                 365

ttg ggt att agt gct gat gag ctg tgc atg att tat cgc act caa ttc   1152
Leu Gly Ile Ser Ala Asp Glu Leu Cys Met Ile Tyr Arg Thr Gln Phe
    370                 375                 380

cca gtg atg cgt aga tat gat caa gaa gat cat ttt gat gcc aat ggc   1200
Pro Val Met Arg Arg Tyr Asp Gln Glu Asp His Phe Asp Ala Asn Gly
385                 390                 395                 400

cgt aaa gtt cct aaa gag atc atc aag ctg cag cag aaa ctt aaa gat   1248
Arg Lys Val Pro Lys Glu Ile Ile Lys Leu Gln Gln Lys Leu Lys Asp
                405                 410                 415

ggc caa gag ctc agc gtg gaa aag cgc acc tgg gtg cat ccc caa tca   1296
Gly Gln Glu Leu Ser Val Glu Lys Arg Thr Trp Val His Pro Gln Ser
            420                 425                 430

gaa gtg tcc tat acc ttt gaa tat cct ttc cgg gtg ttg gat cgt gaa   1344
Glu Val Ser Tyr Thr Phe Glu Tyr Pro Phe Arg Val Leu Asp Arg Glu
        435                 440                 445

gct gat ctg cgt gct gca tat gca aaa ttt gaa aac cag ctt aag gag   1392
Ala Asp Leu Arg Ala Ala Tyr Ala Lys Phe Glu Asn Gln Leu Lys Glu
    450                 455                 460

cca tagagcgctt atgtcctcac tca                                    1418
Pro
465
```

<210> 602
<211> 465
<212> PRT
<213> Corynebacterium glutamicum

<400> 602

```
Ile Asn Glu Leu Ile Leu Phe Asp Val His Asp Leu Val Lys Tyr Gly
  1               5                  10                  15

Val His Val Tyr Gly Ala Pro Gln Glu Ser Ile Asn Phe Leu Ser Ala
             20                  25                  30

Ala Ser Leu Tyr His Pro Gln Thr Val Leu Asp Ser Phe Asp His Asp
         35                  40                  45

Gly Ser Gly Asn Leu Pro Gly Leu Lys Asp Asp Asn Gly Asn Trp Asp
     50                  55                  60

Arg Arg Pro His Lys Asp Arg Ile Gln Leu Val Asn Ala Asp Thr Leu
 65                  70                  75                  80

Thr Val Trp Lys Ser Ile Leu Glu Asp Glu Gln Thr Pro Tyr Leu Asp
                 85                  90                  95

Thr Arg Met Val Tyr Thr Val Asn Thr Glu Ala Ala Ala Ala Leu Glu
            100                 105                 110

Lys Leu Ala Ser Ala Pro Arg Ile Lys Glu Leu Gly Leu Gln Phe Ser
        115                 120                 125

Ser Gly Trp Asn Glu Thr Thr Asp Lys Lys Lys Gly Tyr Phe Asp Val
    130                 135                 140

Gly Trp Gly Tyr Pro Ala Ser Trp Ser Asp Ala Ile Leu Gln Gly Pro
145                 150                 155                 160

His Leu Gly Val Ala Thr Pro Met Ile Lys Gln Pro Asn Pro Thr Met
                165                 170                 175

Lys His Asn Gln Asp Trp Ser Glu Ile Asp Phe Glu Ala Ile Pro Ala
            180                 185                 190

Asn Phe Ile Pro Ala Thr Ala Tyr Gln Pro Asp Arg Gln Thr Lys Pro
        195                 200                 205

Thr Tyr Asp Ala Asp Tyr Gly Thr Trp Thr Phe Gly Asp Lys Gln Val
    210                 215                 220

Pro Val Ala Asp Thr Phe Arg Ile Ala Trp Arg Glu Met Ala Ala Thr
225                 230                 235                 240

Thr Gly Phe Arg Thr Val Tyr Pro Ser Val Ile Pro Pro Gly Ala Asn
                245                 250                 255

His Val His Thr Val Asn Ser Ala Ala Ser Arg Ser Asn Leu Lys Thr
            260                 265                 270

Ile Leu Val Gly Ala Gln Leu Gly Ala Ile Leu Ser Asp Tyr Phe Ala
        275                 280                 285
```

```
Arg Ser Ser Gly Ser Ser His Ile Phe Asn Asp Ile Val Arg Lys Ile
    290                 295                 300

Pro Leu Pro Asn Phe Thr Ser Leu Glu Lys Gln Phe Ala Arg Thr Tyr
305                 310                 315                 320

Leu Arg Leu Asn Cys Leu Thr Ser Ala Tyr Ala Pro Leu Trp Glu Glu
                325                 330                 335

Ile Thr Gly Glu Pro Trp Asp Val Gln Val Pro Leu Arg Asn Ala Glu
            340                 345                 350

Gln Arg Arg Ala Ala Gln Asn Asp Ile Asp Ala Met Val Ala Leu Ser
        355                 360                 365

Leu Gly Ile Ser Ala Asp Glu Leu Cys Met Ile Tyr Arg Thr Gln Phe
    370                 375                 380

Pro Val Met Arg Arg Tyr Asp Gln Glu Asp His Phe Asp Ala Asn Gly
385                 390                 395                 400

Arg Lys Val Pro Lys Glu Ile Ile Lys Leu Gln Gln Lys Leu Lys Asp
                405                 410                 415

Gly Gln Glu Leu Ser Val Glu Lys Arg Thr Trp Val His Pro Gln Ser
            420                 425                 430

Glu Val Ser Tyr Thr Phe Glu Tyr Pro Phe Arg Val Leu Asp Arg Glu
        435                 440                 445

Ala Asp Leu Arg Ala Ala Tyr Ala Lys Phe Glu Asn Gln Leu Lys Glu
    450                 455                 460

Pro
465
```

<210> 603
<211> 1866
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1866)
<223> FRXA01364

<400> 603

```
acg ggc acc cac ctt tat gat tcc ctg cag ctg ctg ttc act ctg gtg   48
Thr Gly Thr His Leu Tyr Asp Ser Leu Gln Leu Leu Phe Thr Leu Val
  1               5                  10                  15

gat aaa ggc cac cac cca aca gat gct aag gct gta gct ttt gat gcc   96
Asp Lys Gly His His Pro Thr Asp Ala Lys Ala Val Ala Phe Asp Ala
             20                  25                  30

gag gct gga gaa gaa ggc ctg cac ttc cgc aac ctt tca gcg gat ctc   144
Glu Ala Gly Glu Glu Gly Leu His Phe Arg Asn Leu Ser Ala Asp Leu
         35                  40                  45

ttc ctc cct gca gcc aca gaa ctt att gat cga gtt ggt ctt tcc aat   192
```

```
Phe Leu Pro Ala Ala Thr Glu Leu Ile Asp Arg Val Gly Leu Ser Asn
     50                  55                  60

gaa gcc cta aac aag gtc ttg gaa aac ctc ctg ctc tcc cgg gtg caa   240
Glu Ala Leu Asn Lys Val Leu Glu Asn Leu Leu Leu Ser Arg Val Gln
 65                  70                  75                  80

tcc ggt aaa gac cgc ggc ttt atc tcc tat gcc acc ttg ggt gtt acc   288
Ser Gly Lys Asp Arg Gly Phe Ile Ser Tyr Ala Thr Leu Gly Val Thr
                85                  90                  95

gag ctt ggc caa gtt tat gag ggt ctg atg tcc tat acc ggc ttt atc   336
Glu Leu Gly Gln Val Tyr Glu Gly Leu Met Ser Tyr Thr Gly Phe Ile
            100                 105                 110

gcc cag gaa gat ctt ttt gag gtt gca cca cat ggc aaa gcc gat aaa   384
Ala Gln Glu Asp Leu Phe Glu Val Ala Pro His Gly Lys Ala Asp Lys
        115                 120                 125

ggt tcc tgg atg ctc ccg gtc tca aag gct gat gaa gtc cct gcc gat   432
Gly Ser Trp Met Leu Pro Val Ser Lys Ala Asp Glu Val Pro Ala Asp
    130                 135                 140

agc ttt atc gaa gtt gat caa gaa gcc cct ggt ggc ggc gta atc aag   480
Ser Phe Ile Glu Val Asp Gln Glu Ala Pro Gly Gly Gly Val Ile Lys
145                 150                 155                 160

gtg cgt aaa cgc cac ccg cgc gga tca ttt gtg ttc cgt cag tcc tct   528
Val Arg Lys Arg His Pro Arg Gly Ser Phe Val Phe Arg Gln Ser Ser
                165                 170                 175

cgt gac cgc gaa cgc tca gcg tcc ttc tac acc cca caa gta ctc acc   576
Arg Asp Arg Glu Arg Ser Ala Ser Phe Tyr Thr Pro Gln Val Leu Thr
            180                 185                 190

agc ttt act gtc acc cag gct att gaa gaa ctc cag gca tca aag cgc   624
Ser Phe Thr Val Thr Gln Ala Ile Glu Glu Leu Gln Ala Ser Lys Arg
        195                 200                 205

atc acc aca gcc aat gat gtt ctc agc ctc acc atc tgt gaa cct gcc   672
Ile Thr Thr Ala Asn Asp Val Leu Ser Leu Thr Ile Cys Glu Pro Ala
    210                 215                 220

atg ggt tcc ggc gcc ttc gct gtg gaa gca gta cgc caa tta gca gag   720
Met Gly Ser Gly Ala Phe Ala Val Glu Ala Val Arg Gln Leu Ala Glu
225                 230                 235                 240

ctt tat ttg gaa ttg cgc caa gaa gaa cta gag cag cag att cca gcg   768
Leu Tyr Leu Glu Leu Arg Gln Glu Glu Leu Glu Gln Gln Ile Pro Ala
                245                 250                 255

gaa gac cgt gcc aag gaa ctc caa aag gtc aaa gcg cac att gcg ctg   816
Glu Asp Arg Ala Lys Glu Leu Gln Lys Val Lys Ala His Ile Ala Leu
            260                 265                 270

cac cag gtt tat ggt gtg gac ctt aac agc act gct gtg gag ttg gcg   864
His Gln Val Tyr Gly Val Asp Leu Asn Ser Thr Ala Val Glu Leu Ala
        275                 280                 285

gaa atc tcg ctg tgg cta gac acc atg aat gca gaa atg gac gca cct   912
Glu Ile Ser Leu Trp Leu Asp Thr Met Asn Ala Glu Met Asp Ala Pro
```

```
    290                 295                 300

tgg tat ggc ctg cac ctg cgt aat ggt aac tcc ctc gtt ggt gcc acc   960
Trp Tyr Gly Leu His Leu Arg Asn Gly Asn Ser Leu Val Gly Ala Thr
305                 310                 315                 320

cgt tcg ctg tat gca cct agt ctg ctt aat aaa aaa gcc tgg tta act   1008
Arg Ser Leu Tyr Ala Pro Ser Leu Leu Asn Lys Lys Ala Trp Leu Thr
                325                 330                 335

gct act cca acc cgc tat cgg ctt gat gat atc gcg cag gct att gat   1056
Ala Thr Pro Thr Arg Tyr Arg Leu Asp Asp Ile Ala Gln Ala Ile Asp
            340                 345                 350

gaa aac aaa gca gaa ccc ctc ttc aac cac ggc atc cac cac ttc ctc   1104
Glu Asn Lys Ala Glu Pro Leu Phe Asn His Gly Ile His His Phe Leu
        355                 360                 365

ttg ccc tct act ggc tgg gga gcc act gca gat gcc aaa gat ctt aaa   1152
Leu Pro Ser Thr Gly Trp Gly Ala Thr Ala Asp Ala Lys Asp Leu Lys
    370                 375                 380

gat ctt atg gct act gaa atc aag gag ctt aaa tct tgg cgt act tcc   1200
Asp Leu Met Ala Thr Glu Ile Lys Glu Leu Lys Ser Trp Arg Thr Ser
385                 390                 395                 400

atc cgt gcg tct ttg agt aaa act cag att aag cag ctc aat aac ctt   1248
Ile Arg Ala Ser Leu Ser Lys Thr Gln Ile Lys Gln Leu Asn Asn Leu
                405                 410                 415

gcc cta cgc gtg gaa aca cta tgg cga ttt gtg ctg atg cgt att cgc   1296
Ala Leu Arg Val Glu Thr Leu Trp Arg Phe Val Leu Met Arg Ile Arg
            420                 425                 430

att gca gaa tcc cag atc tca cgt agc act act ctc tgg ggt caa gag   1344
Ile Ala Glu Ser Gln Ile Ser Arg Ser Thr Thr Leu Trp Gly Gln Glu
        435                 440                 445

cca gct gag gtt tcg gag gtt gtc aca cgt gag caa att gaa caa gac   1392
Pro Ala Glu Val Ser Glu Val Val Thr Arg Glu Gln Ile Glu Gln Asp
    450                 455                 460

ctc ttt ggc aat att gat ggt gca tat aac cgt cta cgc ttg gtg atg   1440
Leu Phe Gly Asn Ile Asp Gly Ala Tyr Asn Arg Leu Arg Leu Val Met
465                 470                 475                 480

gat gct tgg tgt gcg ctg tgg ttc tgg cct ttg gat gct gtt gct acc   1488
Asp Ala Trp Cys Ala Leu Trp Phe Trp Pro Leu Asp Ala Val Ala Thr
                485                 490                 495

gct gag cat ccg gag cgt cca gcc ctt cca gat ctt gat gag tgg cta   1536
Ala Glu His Pro Glu Arg Pro Ala Leu Pro Asp Leu Asp Glu Trp Leu
            500                 505                 510

gcc acc ctg acg gag att ctg ggt att gat ctc cct ctg aag tcc aaa   1584
Ala Thr Leu Thr Glu Ile Leu Gly Ile Asp Leu Pro Leu Lys Ser Lys
        515                 520                 525

aac gaa aat cag att gtc tta ggt cca gat acc aat tgg cta gcc att   1632
Asn Glu Asn Gln Ile Val Leu Gly Pro Asp Thr Asn Trp Leu Ala Ile
    530                 535                 540
```

```
aat gat gcc gag gct act gat ctt ggt ttt tct ggg gca ttg agc ttt   1680
Asn Asp Ala Glu Ala Thr Asp Leu Gly Phe Ser Gly Ala Leu Ser Phe
545                 550                 555                 560

gag cgt gtt agc gcg aat cac ccg tgg atc aat gtt gcc cgc caa gtg   1728
Glu Arg Val Ser Ala Asn His Pro Trp Ile Asn Val Ala Arg Gln Val
                565                 570                 575

gct aaa caa cag agc ttc ttc cac tgg gat cta gac ttc gcc cac gtt   1776
Ala Lys Gln Gln Ser Phe Phe His Trp Asp Leu Asp Phe Ala His Val
            580                 585                 590

ttt gcc aag ggt gga ttt gat ctg cag gtt ggt aat cca cca tgg gtg   1824
Phe Ala Lys Gly Gly Phe Asp Leu Gln Val Gly Asn Pro Pro Trp Val
        595                 600                 605

cga cca gat gtg aac ttt gag gat ctg ctt gct gaa cat gat           1866
Arg Pro Asp Val Asn Phe Glu Asp Leu Leu Ala Glu His Asp
    610                 615                 620
```

<210> 604
<211> 622
<212> PRT
<213> Corynebacterium glutamicum

<400> 604

```
Thr Gly Thr His Leu Tyr Asp Ser Leu Gln Leu Leu Phe Thr Leu Val
  1               5                  10                  15

Asp Lys Gly His His Pro Thr Asp Ala Lys Ala Val Ala Phe Asp Ala
             20                  25                  30

Glu Ala Gly Glu Glu Gly Leu His Phe Arg Asn Leu Ser Ala Asp Leu
         35                  40                  45

Phe Leu Pro Ala Ala Thr Glu Leu Ile Asp Arg Val Gly Leu Ser Asn
     50                  55                  60

Glu Ala Leu Asn Lys Val Leu Glu Asn Leu Leu Leu Ser Arg Val Gln
 65                  70                  75                  80

Ser Gly Lys Asp Arg Gly Phe Ile Ser Tyr Ala Thr Leu Gly Val Thr
                 85                  90                  95

Glu Leu Gly Gln Val Tyr Glu Gly Leu Met Ser Tyr Thr Gly Phe Ile
            100                 105                 110

Ala Gln Glu Asp Leu Phe Glu Val Ala Pro His Gly Lys Ala Asp Lys
        115                 120                 125

Gly Ser Trp Met Leu Pro Val Ser Lys Ala Asp Glu Val Pro Ala Asp
    130                 135                 140

Ser Phe Ile Glu Val Asp Gln Glu Ala Pro Gly Gly Gly Val Ile Lys
145                 150                 155                 160

Val Arg Lys Arg His Pro Arg Gly Ser Phe Val Phe Arg Gln Ser Ser
                165                 170                 175
```

```
Arg Asp Arg Glu Arg Ser Ala Ser Phe Tyr Thr Pro Gln Val Leu Thr
            180                 185                 190

Ser Phe Thr Val Thr Gln Ala Ile Glu Glu Leu Gln Ala Ser Lys Arg
        195                 200                 205

Ile Thr Thr Ala Asn Asp Val Leu Ser Leu Thr Ile Cys Glu Pro Ala
    210                 215                 220

Met Gly Ser Gly Ala Phe Ala Val Glu Ala Val Arg Gln Leu Ala Glu
225                 230                 235                 240

Leu Tyr Leu Glu Leu Arg Gln Glu Glu Leu Glu Gln Gln Ile Pro Ala
                245                 250                 255

Glu Asp Arg Ala Lys Glu Leu Gln Lys Val Lys Ala His Ile Ala Leu
            260                 265                 270

His Gln Val Tyr Gly Val Asp Leu Asn Ser Thr Ala Val Glu Leu Ala
        275                 280                 285

Glu Ile Ser Leu Trp Leu Asp Thr Met Asn Ala Glu Met Asp Ala Pro
    290                 295                 300

Trp Tyr Gly Leu His Leu Arg Asn Gly Asn Ser Leu Val Gly Ala Thr
305                 310                 315                 320

Arg Ser Leu Tyr Ala Pro Ser Leu Leu Asn Lys Lys Ala Trp Leu Thr
                325                 330                 335

Ala Thr Pro Thr Arg Tyr Arg Leu Asp Asp Ile Ala Gln Ala Ile Asp
            340                 345                 350

Glu Asn Lys Ala Glu Pro Leu Phe Asn His Gly Ile His His Phe Leu
        355                 360                 365

Leu Pro Ser Thr Gly Trp Gly Ala Thr Ala Asp Ala Lys Asp Leu Lys
    370                 375                 380

Asp Leu Met Ala Thr Glu Ile Lys Glu Leu Lys Ser Trp Arg Thr Ser
385                 390                 395                 400

Ile Arg Ala Ser Leu Ser Lys Thr Gln Ile Lys Gln Leu Asn Asn Leu
                405                 410                 415

Ala Leu Arg Val Glu Thr Leu Trp Arg Phe Val Leu Met Arg Ile Arg
            420                 425                 430

Ile Ala Glu Ser Gln Ile Ser Arg Ser Thr Thr Leu Trp Gly Gln Glu
        435                 440                 445

Pro Ala Glu Val Ser Glu Val Val Thr Arg Glu Gln Ile Glu Gln Asp
    450                 455                 460

Leu Phe Gly Asn Ile Asp Gly Ala Tyr Asn Arg Leu Arg Leu Val Met
465                 470                 475                 480

Asp Ala Trp Cys Ala Leu Trp Phe Trp Pro Leu Asp Ala Val Ala Thr
                485                 490                 495

Ala Glu His Pro Glu Arg Pro Ala Leu Pro Asp Leu Asp Glu Trp Leu
```

```
            500                 505                 510

Ala Thr Leu Thr Glu Ile Leu Gly Ile Asp Leu Pro Leu Lys Ser Lys
        515                 520                 525

Asn Glu Asn Gln Ile Val Leu Gly Pro Asp Thr Asn Trp Leu Ala Ile
    530                 535                 540

Asn Asp Ala Glu Ala Thr Asp Leu Gly Phe Ser Gly Ala Leu Ser Phe
545                 550                 555                 560

Glu Arg Val Ser Ala Asn His Pro Trp Ile Asn Val Ala Arg Gln Val
                565                 570                 575

Ala Lys Gln Gln Ser Phe Phe His Trp Asp Leu Asp Phe Ala His Val
            580                 585                 590

Phe Ala Lys Gly Gly Phe Asp Leu Gln Val Gly Asn Pro Pro Trp Val
        595                 600                 605

Arg Pro Asp Val Asn Phe Glu Asp Leu Leu Ala Glu His Asp
    610                 615                 620
```

Patent Application Publication Dec. 27, 2007 Sheet 27 of 27 US 2007/0298488 A1

<210> 605
<211> 1042
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1042)
<223> RXN01379

<400> 605

```
cagaaattga gtaatgctct cgagccagac cgtgaactta ttaggccttt ggccgtcatt 60

cttccgcagc ccgcaacttt gaacaccgag gtttaacaca atg agt gca ttt gat   115
                                              Met Ser Ala Phe Asp
                                                1               5

tcg atc cta aat gtt gaa gag tgg atc agt gac cac tac ctc acc aat   163
Ser Ile Leu Asn Val Glu Glu Trp Ile Ser Asp His Tyr Leu Thr Asn
                10                  15                  20

gac gat gcc aaa ggt gcc tca ttt tcc aag cgg gtg cgc gag cgc att   211
Asp Asp Ala Lys Gly Ala Ser Phe Ser Lys Arg Val Arg Glu Arg Ile
            25                  30                  35

aaa gaa tgg aaa acc acc gag gac gca acc cag cag agt ggc cct tta   259
Lys Glu Trp Lys Thr Thr Glu Asp Ala Thr Gln Gln Ser Gly Pro Leu
        40                  45                  50

act cgt ttt tcc agc aac cgc ctg cag ttg cag cat gct ctt tct gag   307
Thr Arg Phe Ser Ser Asn Arg Leu Gln Leu Gln His Ala Leu Ser Glu
    55                  60                  65

ctt gac gac gcc acc acc gcc gcc agt tta gtg gcc tct gca ctg ggg   355
Leu Asp Asp Ala Thr Thr Ala Ala Ser Leu Val Ala Ser Ala Leu Gly
70                  75                  80                  85
```

```
tat ggt gtc ccc agc gcg cgc cac gcg cag cgc ggc tcc gac aca ata   403
Tyr Gly Val Pro Ser Ala Arg His Ala Gln Arg Gly Ser Asp Thr Ile
                 90                  95                 100

tcc tat tcc tct tgg gtg gga aat gcc ggc agt gtg gaa ttt ctt gca   451
Ser Tyr Ser Ser Trp Val Gly Asn Ala Gly Ser Val Glu Phe Leu Ala
            105                 110                 115

gcg act ccc gct gaa agc ttt gaa gag aac ttc cga tcc ctt ccc ctt   499
Ala Thr Pro Ala Glu Ser Phe Glu Glu Asn Phe Arg Ser Leu Pro Leu
        120                 125                 130

gag cca gta gcg gtc aat gac aag ccc cag gat atc acc gca gcc aaa   547
Glu Pro Val Ala Val Asn Asp Lys Pro Gln Asp Ile Thr Ala Ala Lys
    135                 140                 145

ttg gtg ggc cag att ttc ctt agt gat act ccc cct gct ttt gtt gtt   595
Leu Val Gly Gln Ile Phe Leu Ser Asp Thr Pro Pro Ala Phe Val Val
150                 155                 160                 165

atc acc gct ggt aaa tgg gtg gtt tta gcc gag cgt gaa acc tgg cct   643
Ile Thr Ala Gly Lys Trp Val Val Leu Ala Glu Arg Glu Thr Trp Pro
                170                 175                 180

cta ggc cgc cac cta gct att gat att tcc ctg gtg gtg gaa cgt aat   691
Leu Gly Arg His Leu Ala Ile Asp Ile Ser Leu Val Val Glu Arg Asn
            185                 190                 195

gac acc aaa gcc cag ggt gag atg cag cag acg gtc gta gca cta gcc   739
Asp Thr Lys Ala Gln Gly Glu Met Gln Gln Thr Val Val Ala Leu Ala
        200                 205                 210

cgc gaa aat acc gag cgt gcc gcc gat ggc acc acc tgg tgg gaa gaa   787
Arg Glu Asn Thr Glu Arg Ala Ala Asp Gly Thr Thr Trp Trp Glu Glu
    215                 220                 225

acc att gag caa tcc cgc gaa cat gct gtc aag gtt tct ggc gag cta   835
Thr Ile Glu Gln Ser Arg Glu His Ala Val Lys Val Ser Gly Glu Leu
230                 235                 240                 245

cgc agt gcg gtg cgt gaa tcc att gaa atc ctg ggc aat gac gtg ctc   883
Arg Ser Ala Val Arg Glu Ser Ile Glu Ile Leu Gly Asn Asp Val Leu
                250                 255                 260

aca cgc tat gaa gct aaa gag ctc tcc acc gct gag atc gac ggt ggc   931
Thr Arg Tyr Glu Ala Lys Glu Leu Ser Thr Ala Glu Ile Asp Gly Gly
            265                 270                 275

gag cta gct aag caa tct ttg cgc tat ctc tac cgc att ttg ttc ctg   979
Glu Leu Ala Lys Gln Ser Leu Arg Tyr Leu Tyr Arg Ile Leu Phe Leu
        280                 285                 290

ctt ttt gcc gag gct tca cca gag ctt gaa atc ctg cca acc ggc acc   1027
Leu Phe Ala Glu Ala Ser Pro Glu Leu Glu Ile Leu Pro Thr Gly Thr
    295                 300                 305

ccg gaa tat gac gag                                               1042
Pro Glu Tyr Asp Glu
310
```

<210> 606
<211> 314
<212> PRT
<213> Corynebacterium glutamicum

<400> 606
Met Ser Ala Phe Asp Ser Ile Leu Asn Val Glu Glu Trp Ile Ser Asp
1 5 10 15

His Tyr Leu Thr Asn Asp Asp Ala Lys Gly Ala Ser Phe Ser Lys Arg
20 25 30

Val Arg Glu Arg Ile Lys Glu Trp Lys Thr Thr Glu Asp Ala Thr Gln
35 40 45

Gln Ser Gly Pro Leu Thr Arg Phe Ser Ser Asn Arg Leu Gln Leu Gln
50 55 60

His Ala Leu Ser Glu Leu Asp Asp Ala Thr Thr Ala Ala Ser Leu Val
65 70 75 80

Ala Ser Ala Leu Gly Tyr Gly Val Pro Ser Ala Arg His Ala Gln Arg
85 90 95

Gly Ser Asp Thr Ile Ser Tyr Ser Ser Trp Val Gly Asn Ala Gly Ser
100 105 110

Val Glu Phe Leu Ala Ala Thr Pro Ala Glu Ser Phe Glu Glu Asn Phe
115 120 125

Arg Ser Leu Pro Leu Glu Pro Val Ala Val Asn Asp Lys Pro Gln Asp
130 135 140

Ile Thr Ala Ala Lys Leu Val Gly Gln Ile Phe Leu Ser Asp Thr Pro
145 150 155 160

Pro Ala Phe Val Val Ile Thr Ala Gly Lys Trp Val Val Leu Ala Glu
165 170 175

Arg Glu Thr Trp Pro Leu Gly Arg His Leu Ala Ile Asp Ile Ser Leu
180 185 190

Val Val Glu Arg Asn Asp Thr Lys Ala Gln Gly Glu Met Gln Gln Thr
195 200 205

Val Val Ala Leu Ala Arg Glu Asn Thr Glu Arg Ala Ala Asp Gly Thr
210 215 220

Thr Trp Trp Glu Glu Thr Ile Glu Gln Ser Arg Glu His Ala Val Lys
225 230 235 240

Val Ser Gly Glu Leu Arg Ser Ala Val Arg Glu Ser Ile Glu Ile Leu
245 250 255

Gly Asn Asp Val Leu Thr Arg Tyr Glu Ala Lys Glu Leu Ser Thr Ala
260 265 270

Glu Ile Asp Gly Gly Glu Leu Ala Lys Gln Ser Leu Arg Tyr Leu Tyr
275 280 285

Arg Ile Leu Phe Leu Leu Phe Ala Glu Ala Ser Pro Glu Leu Glu Ile

```
    290                 295                 300

Leu Pro Thr Gly Thr Pro Glu Tyr Asp Glu
305                 310


<210> 607
<211> 921
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(921)
<223> FRXA01379

<400> 607
cta aat gtt gaa gag tgg atc agt gac cac tac ctc acc aat gac gat   48
Leu Asn Val Glu Glu Trp Ile Ser Asp His Tyr Leu Thr Asn Asp Asp
  1               5                  10                  15

gcc aaa ggt gcc tca ttt tcc aag cgg gtg cgc gag cgc att aaa gaa   96
Ala Lys Gly Ala Ser Phe Ser Lys Arg Val Arg Glu Arg Ile Lys Glu
             20                  25                  30

tgg aaa acc acc gag gac gca acc cag cag agt ggc cct tta act cgt   144
Trp Lys Thr Thr Glu Asp Ala Thr Gln Gln Ser Gly Pro Leu Thr Arg
         35                  40                  45

ttt tcc agc aac cgc ctg cag ttg cag cat gct ctt tct gag ctt gac   192
Phe Ser Ser Asn Arg Leu Gln Leu Gln His Ala Leu Ser Glu Leu Asp
     50                  55                  60

gac gcc acc acc gcc gcc agt tta gtg gcc tct gca ctg ggg tat ggt   240
Asp Ala Thr Thr Ala Ala Ser Leu Val Ala Ser Ala Leu Gly Tyr Gly
 65                  70                  75                  80

gtc ccc agc gcg cgc cac gcg cag cgc ggc tcc gac aca ata tcc tat   288
Val Pro Ser Ala Arg His Ala Gln Arg Gly Ser Asp Thr Ile Ser Tyr
                 85                  90                  95

tcc tct tgg gtg gga aat gcc ggc agt gtg gaa ttt ctt gca gcg act   336
Ser Ser Trp Val Gly Asn Ala Gly Ser Val Glu Phe Leu Ala Ala Thr
            100                 105                 110

ccc gct gaa agc ttt gaa gag aac ttc cga tcc ctt ccc ctt gag cca   384
Pro Ala Glu Ser Phe Glu Glu Asn Phe Arg Ser Leu Pro Leu Glu Pro
        115                 120                 125

gta gcg gtc aat gac aag ccc cag gat atc acc gca gcc aaa ttg gtg   432
Val Ala Val Asn Asp Lys Pro Gln Asp Ile Thr Ala Ala Lys Leu Val
    130                 135                 140

ggc cag att ttc ctt agt gat act ccc cct gct ttt gtt gtt atc acc   480
Gly Gln Ile Phe Leu Ser Asp Thr Pro Pro Ala Phe Val Val Ile Thr
145                 150                 155                 160

gct ggt aaa tgg gtg gtt tta gcc gag cgt gaa acc tgg cct cta ggc   528
Ala Gly Lys Trp Val Val Leu Ala Glu Arg Glu Thr Trp Pro Leu Gly
                165                 170                 175
```

```
cgc cac cta gct att gat att tcc ctg gtg gtg gaa cgt aat gac acc   576
Arg His Leu Ala Ile Asp Ile Ser Leu Val Val Glu Arg Asn Asp Thr
            180                 185                 190

aaa gcc cag ggt gag atg cag cag acg gtc gta gca cta gcc cgc gaa   624
Lys Ala Gln Gly Glu Met Gln Gln Thr Val Val Ala Leu Ala Arg Glu
        195                 200                 205

aat acc gag cgt gcc gcc gat ggc acc acc tgg tgg gaa gaa acc att   672
Asn Thr Glu Arg Ala Ala Asp Gly Thr Thr Trp Trp Glu Glu Thr Ile
    210                 215                 220

gag caa tcc cgc gaa cat gct gtc aag gtt tct ggc gag cta cgc agt   720
Glu Gln Ser Arg Glu His Ala Val Lys Val Ser Gly Glu Leu Arg Ser
225                 230                 235                 240

gcg gtg cgt gaa tcc att gaa atc ctg ggc aat gac gtg ctc aca cgc   768
Ala Val Arg Glu Ser Ile Glu Ile Leu Gly Asn Asp Val Leu Thr Arg
                245                 250                 255

tat gaa gct aaa gag ctc tcc acc gct gag atc gac ggt ggc gag cta   816
Tyr Glu Ala Lys Glu Leu Ser Thr Ala Glu Ile Asp Gly Gly Glu Leu
            260                 265                 270

gct aag caa tct ttg cgc tat ctc tac cgc att ttg ttc ctg ctt ttt   864
Ala Lys Gln Ser Leu Arg Tyr Leu Tyr Arg Ile Leu Phe Leu Leu Phe
        275                 280                 285

gcc gag gct tca cca gag ctt gaa atc ctg cca acc ggc acc ccg gaa   912
Ala Glu Ala Ser Pro Glu Leu Glu Ile Leu Pro Thr Gly Thr Pro Glu
    290                 295                 300

tat gac gag                                                      921
Tyr Asp Glu
305
```

Sequence Listing

<210> 608
<211> 307
<212> PRT
<213> Corynebacterium glutamicum

<400> 608

```
Leu Asn Val Glu Glu Trp Ile Ser Asp His Tyr Leu Thr Asn Asp Asp
  1               5                  10                  15

Ala Lys Gly Ala Ser Phe Ser Lys Arg Val Arg Glu Arg Ile Lys Glu
             20                  25                  30

Trp Lys Thr Thr Glu Asp Ala Thr Gln Gln Ser Gly Pro Leu Thr Arg
         35                  40                  45

Phe Ser Ser Asn Arg Leu Gln Leu Gln His Ala Leu Ser Glu Leu Asp
     50                  55                  60

Asp Ala Thr Thr Ala Ala Ser Leu Val Ala Ser Ala Leu Gly Tyr Gly
 65                  70                  75                  80

Val Pro Ser Ala Arg His Ala Gln Arg Gly Ser Asp Thr Ile Ser Tyr
                 85                  90                  95
```

```
Ser Ser Trp Val Gly Asn Ala Gly Ser Val Glu Phe Leu Ala Ala Thr
            100                 105                 110

Pro Ala Glu Ser Phe Glu Glu Asn Phe Arg Ser Leu Pro Leu Glu Pro
        115                 120                 125

Val Ala Val Asn Asp Lys Pro Gln Asp Ile Thr Ala Ala Lys Leu Val
    130                 135                 140

Gly Gln Ile Phe Leu Ser Asp Thr Pro Pro Ala Phe Val Val Ile Thr
145                 150                 155                 160

Ala Gly Lys Trp Val Val Leu Ala Glu Arg Glu Thr Trp Pro Leu Gly
                165                 170                 175

Arg His Leu Ala Ile Asp Ile Ser Leu Val Val Glu Arg Asn Asp Thr
            180                 185                 190

Lys Ala Gln Gly Glu Met Gln Gln Thr Val Val Ala Leu Ala Arg Glu
        195                 200                 205

Asn Thr Glu Arg Ala Ala Asp Gly Thr Thr Trp Trp Glu Glu Thr Ile
    210                 215                 220

Glu Gln Ser Arg Glu His Ala Val Lys Val Ser Gly Glu Leu Arg Ser
225                 230                 235                 240

Ala Val Arg Glu Ser Ile Glu Ile Leu Gly Asn Asp Val Leu Thr Arg
                245                 250                 255

Tyr Glu Ala Lys Glu Leu Ser Thr Ala Glu Ile Asp Gly Gly Glu Leu
            260                 265                 270

Ala Lys Gln Ser Leu Arg Tyr Leu Tyr Arg Ile Leu Phe Leu Leu Phe
        275                 280                 285

Ala Glu Ala Ser Pro Glu Leu Glu Ile Leu Pro Thr Gly Thr Pro Glu
    290                 295                 300

Tyr Asp Glu
305
```

Confidential - Subject to Protective Order

<210> 609
<211> 780
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(757)
<223> RXN01390

<400> 609
cgtccagata atcaatctgc gaagccagtg gcttccgaag ctccaacaac tattacgccg 60

gcaagctctg gtgcattagc atccgatgct ccgacgtctt atg ttc agg cgc agc 115
                                                Met Phe Arg Arg Ser
                                                  1   5

ctt ccc agc aac aag aca tcc tca gca agt tcc gcc agc tcc gcc gac 163

```
Leu Pro Ser Asn Lys Thr Ser Ser Ala Ser Ser Ala Ser Ser Ala Asp
                10                  15                  20

aca agt tac tca gtc aga tta ggc cgt cct gaa gag cct ggt tac cag   211
Thr Ser Tyr Ser Val Arg Leu Gly Arg Pro Glu Glu Pro Gly Tyr Gln
            25                  30                  35

cca gaa ccg tct tat tcg gag cct tac act gac tct gat ttc gcg cca   259
Pro Glu Pro Ser Tyr Ser Glu Pro Tyr Thr Asp Ser Asp Phe Ala Pro
        40                  45                  50

gca ggt gcg gcc gct gcg gca gct gca gta gct cca cca atg att gcg   307
Ala Gly Ala Ala Ala Ala Ala Ala Ala Val Ala Pro Pro Met Ile Ala
    55                  60                  65

gaa cag cca caa att gtt gaa gat gcc cgc cga ggt acc ctc gat ttc   355
Glu Gln Pro Gln Ile Val Glu Asp Ala Arg Arg Gly Thr Leu Asp Phe
70                  75                  80                  85

ggc ctg ttg att atc cgc gca gtc att ggt gtc tat ttg atc gtc cgt   403
Gly Leu Leu Ile Ile Arg Ala Val Ile Gly Val Tyr Leu Ile Val Arg
                90                  95                  100

gga gtc ttt aca ttc ttc acc ctt gga gga tct gcc ggt ctt gct ggc   451
Gly Val Phe Thr Phe Phe Thr Leu Gly Gly Ser Ala Gly Leu Ala Gly
            105                 110                 115

ctc gag gca gag ttc gct ggt tac cag tgg cct gaa atc ctc gcg atc   499
Leu Glu Ala Glu Phe Ala Gly Tyr Gln Trp Pro Glu Ile Leu Ala Ile
        120                 125                 130

ctg ctt cca tct att gaa ctt gcg gct ggt gtc ttc ctg ctc ctt ggt   547
Leu Leu Pro Ser Ile Glu Leu Ala Ala Gly Val Phe Leu Leu Leu Gly
    135                 140                 145

ctg atg acc cca gtg gca gca gcg gta gcc acg gtg gcg aca tcc ttt   595
Leu Met Thr Pro Val Ala Ala Ala Val Ala Thr Val Ala Thr Ser Phe
150                 155                 160                 165

acc acc ctt cac caa gtc aac act cat gaa ggt ggt tgg ggt gaa ctt   643
Thr Thr Leu His Gln Val Asn Thr His Glu Gly Gly Trp Gly Glu Leu
                170                 175                 180

agt gag cca ttg atg ctg gca ctg atc ctc act atc gtg gtt gtc gga   691
Ser Glu Pro Leu Met Leu Ala Leu Ile Leu Thr Ile Val Val Val Gly
            185                 190                 195

ctt cag ttc acc ggc ccc ggc aag att tcc ctt gac tct ggc cga ggt   739
Leu Gln Phe Thr Gly Pro Gly Lys Ile Ser Leu Asp Ser Gly Arg Gly
        200                 205                 210

tgg caa agc gtc cac tgg tgagctcgtg gatcttcgtg gtc                 780
Trp Gln Ser Val His Trp
    215
```

<210> 610
<211> 219
<212> PRT
<213> Corynebacterium glutamicum

<400> 610
Met Phe Arg Arg Ser Leu Pro Ser Asn Lys Thr Ser Ser Ala Ser Ser
1 5 10 15

Ala Ser Ser Ala Asp Thr Ser Tyr Ser Val Arg Leu Gly Arg Pro Glu
20 25 30

Glu Pro Gly Tyr Gln Pro Glu Pro Ser Tyr Ser Glu Pro Tyr Thr Asp
35 40 45

Ser Asp Phe Ala Pro Ala Gly Ala Ala Ala Ala Ala Ala Ala Val Ala
50 55 60

Pro Pro Met Ile Ala Glu Gln Pro Gln Ile Val Glu Asp Ala Arg Arg
65 70 75 80

Gly Thr Leu Asp Phe Gly Leu Leu Ile Ile Arg Ala Val Ile Gly Val
85 90 95

Tyr Leu Ile Val Arg Gly Val Phe Thr Phe Phe Thr Leu Gly Gly Ser
100 105 110

Ala Gly Leu Ala Gly Leu Glu Ala Glu Phe Ala Gly Tyr Gln Trp Pro
115 120 125

Glu Ile Leu Ala Ile Leu Leu Pro Ser Ile Glu Leu Ala Ala Gly Val
130 135 140

Phe Leu Leu Leu Gly Leu Met Thr Pro Val Ala Ala Ala Val Ala Thr
145 150 155 160

Val Ala Thr Ser Phe Thr Thr Leu His Gln Val Asn Thr His Glu Gly
165 170 175

Gly Trp Gly Glu Leu Ser Glu Pro Leu Met Leu Ala Leu Ile Leu Thr
180 185 190

Ile Val Val Val Gly Leu Gln Phe Thr Gly Pro Gly Lys Ile Ser Leu
195 200 205

Asp Ser Gly Arg Gly Trp Gln Ser Val His Trp
210 215

<210> 611
<211> 780
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(757)
<223> FRXA01390

<400> 611
cgtccagata atcaatctgc gaagccagtg gcttccgaag ctccaacaac tattacgccg 60

gcaagctctg gtgcattagc atccgatgct ccgacgtctt atg ttc agg cgc agc 115
Met Phe Arg Arg Ser
1 5

```
ctt ccc agc aac aag aca tcc tca gca agt tcc gcc agc tcc gcc gac   163
Leu Pro Ser Asn Lys Thr Ser Ser Ala Ser Ser Ala Ser Ser Ala Asp
                10                  15                  20

aca agt tac tca gtc aga tta ggc cgt cct gaa gag cct ggt tac cag   211
Thr Ser Tyr Ser Val Arg Leu Gly Arg Pro Glu Glu Pro Gly Tyr Gln
            25                  30                  35

cca gaa ccg tct tat tcg gag cct tac act gac tct gat ttc gcg cca   259
Pro Glu Pro Ser Tyr Ser Glu Pro Tyr Thr Asp Ser Asp Phe Ala Pro
        40                  45                  50

gca ggt gcg gcc gct gcg gca gct gca gta gct cca cca atg att gcg   307
Ala Gly Ala Ala Ala Ala Ala Ala Ala Val Ala Pro Pro Met Ile Ala
    55                  60                  65

gaa cag cca caa att gtt gaa gat gcc cgc cga ggt acc ctc gat ttc   355
Glu Gln Pro Gln Ile Val Glu Asp Ala Arg Arg Gly Thr Leu Asp Phe
70                  75                  80                  85

ggc ctg ttg att atc cgc gca gtc att ggt gtc tat ttg atc gtc cgt   403
Gly Leu Leu Ile Ile Arg Ala Val Ile Gly Val Tyr Leu Ile Val Arg
                90                  95                  100

gga gtc ttt aca ttc ttc acc ctt gga gga tct gcc ggt ctt gct ggc   451
Gly Val Phe Thr Phe Phe Thr Leu Gly Gly Ser Ala Gly Leu Ala Gly
            105                 110                 115

ctc gag gca gag ttc gct ggt tac cag tgg cct gaa atc ctc gcg atc   499
Leu Glu Ala Glu Phe Ala Gly Tyr Gln Trp Pro Glu Ile Leu Ala Ile
        120                 125                 130

ctg ctt cca tct att gaa ctt gcg gct ggt gtc ttc ctg ctc ctt ggt   547
Leu Leu Pro Ser Ile Glu Leu Ala Ala Gly Val Phe Leu Leu Leu Gly
    135                 140                 145

ctg atg acc cca gtg gca gca gcg gta gcc acg gtg gcg aca tcc ttt   595
Leu Met Thr Pro Val Ala Ala Ala Val Ala Thr Val Ala Thr Ser Phe
150                 155                 160                 165

acc acc ctt cac caa gtc aac act cat gaa ggt ggt tgg ggt gaa ctt   643
Thr Thr Leu His Gln Val Asn Thr His Glu Gly Gly Trp Gly Glu Leu
                170                 175                 180

agt gag cca ttg atg ctg gca ctg atc ctc act atc gtg gtt gtc gga   691
Ser Glu Pro Leu Met Leu Ala Leu Ile Leu Thr Ile Val Val Val Gly
            185                 190                 195

ctt cag ttc acc ggc ccc ggc aag att tcc ctt gac tct ggc cga ggt   739
Leu Gln Phe Thr Gly Pro Gly Lys Ile Ser Leu Asp Ser Gly Arg Gly
        200                 205                 210

tgg caa agc gtc cac tgg tgagctcgtg gatcttcgtg gtc                 780
Trp Gln Ser Val His Trp
    215
```

<210> 612
<211> 219
<212> PRT
<213> Corynebacterium glutamicum

<400> 612
Met Phe Arg Arg Ser Leu Pro Ser Asn Lys Thr Ser Ser Ala Ser Ser
1 5 10 15

Ala Ser Ser Ala Asp Thr Ser Tyr Ser Val Arg Leu Gly Arg Pro Glu
20 25 30

Glu Pro Gly Tyr Gln Pro Glu Pro Ser Tyr Ser Glu Pro Tyr Thr Asp
35 40 45

Ser Asp Phe Ala Pro Ala Gly Ala Ala Ala Ala Ala Ala Ala Val Ala
50 55 60

Pro Pro Met Ile Ala Glu Gln Pro Gln Ile Val Glu Asp Ala Arg Arg
65 70 75 80

Gly Thr Leu Asp Phe Gly Leu Leu Ile Ile Arg Ala Val Ile Gly Val
85 90 95

Tyr Leu Ile Val Arg Gly Val Phe Thr Phe Phe Thr Leu Gly Gly Ser
100 105 110

Ala Gly Leu Ala Gly Leu Glu Ala Glu Phe Ala Gly Tyr Gln Trp Pro
115 120 125

Glu Ile Leu Ala Ile Leu Leu Pro Ser Ile Glu Leu Ala Ala Gly Val
130 135 140

Phe Leu Leu Leu Gly Leu Met Thr Pro Val Ala Ala Ala Val Ala Thr
145 150 155 160

Val Ala Thr Ser Phe Thr Thr Leu His Gln Val Asn Thr His Glu Gly
165 170 175

Gly Trp Gly Glu Leu Ser Glu Pro Leu Met Leu Ala Leu Ile Leu Thr
180 185 190

Ile Val Val Val Gly Leu Gln Phe Thr Gly Pro Gly Lys Ile Ser Leu
195 200 205

Asp Ser Gly Arg Gly Trp Gln Ser Val His Trp
210 215

<210> 613
<211> 813
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(790)
<223> RXN01391

<400> 613
atggtgtgaa accatcatgg ctcgatcaca aaaaagaaca cctgctatca ggtcaaccaa 60

aaaagttaaa agtgtaatat ccagcatcat cacgattgcc gtg gct gca gtc gct 115
Val Ala Ala Val Ala
1 5

```
ttt gca gct tac gtt ata gat ggt ggg gta gaa gag gcg tct gga aca   163
Phe Ala Ala Tyr Val Ile Asp Gly Gly Val Glu Glu Ala Ser Gly Thr
                 10                  15                  20

ccg acg tct tcg gaa agc tcg gta gcg gca act gct cca gcg gca tct   211
Pro Thr Ser Ser Glu Ser Ser Val Ala Ala Thr Ala Pro Ala Ala Ser
             25                  30                  35

agc gag act gcg gct gaa tac cgt gcg atg ctc gct tcc ctt gac gtt   259
Ser Glu Thr Ala Ala Glu Tyr Arg Ala Met Leu Ala Ser Leu Asp Val
         40                  45                  50

aaa ggt cgt gcg cca gga aca gga tat gac cgc gaa tta ttc gga cca   307
Lys Gly Arg Ala Pro Gly Thr Gly Tyr Asp Arg Glu Leu Phe Gly Pro
     55                  60                  65

gca tgg acc gac act gtt tcc gtg gaa tat gga cac aat ggc tgc gat   355
Ala Trp Thr Asp Thr Val Ser Val Glu Tyr Gly His Asn Gly Cys Asp
 70                  75                  80                  85

acc cgc aac gac atc ctg caa cgc gac ctg gat gac atc caa ctt cgc   403
Thr Arg Asn Asp Ile Leu Gln Arg Asp Leu Asp Asp Ile Gln Leu Arg
                 90                  95                 100

gaa ggc acc aag gat tgt atc gtc acg agc ggc ctg ctc agc gat cca   451
Glu Gly Thr Lys Asp Cys Ile Val Thr Ser Gly Leu Leu Ser Asp Pro
             105                 110                 115

ttt tct ggc gaa ctt att gat ttc gtt cgc ggt gaa cgt tcc ggc gac   499
Phe Ser Gly Glu Leu Ile Asp Phe Val Arg Gly Glu Arg Ser Gly Asp
         120                 125                 130

gtg cag atc gat cac ctg gtc cca tta cat gac gca tgg gtc aag gga   547
Val Gln Ile Asp His Leu Val Pro Leu His Asp Ala Trp Val Lys Gly
     135                 140                 145

gca cag cag tgg gat gag caa act cga aag aac ttt gcc aac gat ccc   595
Ala Gln Gln Trp Asp Glu Gln Thr Arg Lys Asn Phe Ala Asn Asp Pro
150                 155                 160                 165

gac aac ctt ctc gcc gtt aaa ggt acg ctt aac cag caa aaa ggt gca   643
Asp Asn Leu Leu Ala Val Lys Gly Thr Leu Asn Gln Gln Lys Gly Ala
                170                 175                 180

ggc gat gca gca acc tgg ctt cca cca aac aca gct ttt agg tgc gat   691
Gly Asp Ala Ala Thr Trp Leu Pro Pro Asn Thr Ala Phe Arg Cys Asp
             185                 190                 195

tac gca aag aaa atc atc acc gtt aaa gat cgc tac aac gtg tgg gtg   739
Tyr Ala Lys Lys Ile Ile Thr Val Lys Asp Arg Tyr Asn Val Trp Val
         200                 205                 210

act gag gct gaa gca agc gcc ctg gaa cgc caa tta gat acg tgt gct   787
Thr Glu Ala Glu Ala Ser Ala Leu Glu Arg Gln Leu Asp Thr Cys Ala
     215                 220                 225

gca taacagtcac ataagcattt ggg                                    813
Ala
230
```

<210> 614
<211> 230
<212> PRT
<213> Corynebacterium glutamicum

<400> 614
Val Ala Ala Val Ala Phe Ala Ala Tyr Val Ile Asp Gly Gly Val Glu
1 5 10 15

Glu Ala Ser Gly Thr Pro Thr Ser Ser Glu Ser Ser Val Ala Ala Thr
20 25 30

Ala Pro Ala Ala Ser Ser Glu Thr Ala Ala Glu Tyr Arg Ala Met Leu
35 40 45

Ala Ser Leu Asp Val Lys Gly Arg Ala Pro Gly Thr Gly Tyr Asp Arg
50 55 60

Glu Leu Phe Gly Pro Ala Trp Thr Asp Thr Val Ser Val Glu Tyr Gly
65 70 75 80

His Asn Gly Cys Asp Thr Arg Asn Asp Ile Leu Gln Arg Asp Leu Asp
85 90 95

Asp Ile Gln Leu Arg Glu Gly Thr Lys Asp Cys Ile Val Thr Ser Gly
100 105 110

Leu Leu Ser Asp Pro Phe Ser Gly Glu Leu Ile Asp Phe Val Arg Gly
115 120 125

Glu Arg Ser Gly Asp Val Gln Ile Asp His Leu Val Pro Leu His Asp
130 135 140

Ala Trp Val Lys Gly Ala Gln Gln Trp Asp Glu Gln Thr Arg Lys Asn
145 150 155 160

Phe Ala Asn Asp Pro Asp Asn Leu Leu Ala Val Lys Gly Thr Leu Asn
165 170 175

Gln Gln Lys Gly Ala Gly Asp Ala Ala Thr Trp Leu Pro Pro Asn Thr
180 185 190

Ala Phe Arg Cys Asp Tyr Ala Lys Lys Ile Ile Thr Val Lys Asp Arg
195 200 205

Tyr Asn Val Trp Val Thr Glu Ala Glu Ala Ser Ala Leu Glu Arg Gln
210 215 220

Leu Asp Thr Cys Ala Ala
225 230

<210> 615
<211> 813
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(790)

<223> FRXA01391

<400> 615

```
atggtgtgaa accatcatgg ctcgatcaca aaaaagaaca cctgctatca ggtcaaccaa 60

aaaagttaaa agtgtaatat ccagcatcat cacgattgcc gtg gct gca gtc gct   115
                                        Val Ala Ala Val Ala
                                          1               5

ttt gca gct tac gtt ata gat ggt ggg gta gaa gag gcg tct gga aca   163
Phe Ala Ala Tyr Val Ile Asp Gly Gly Val Glu Glu Ala Ser Gly Thr
                 10                  15                  20

ccg acg tct tcg gaa agc tcg gta gcg gca act gct cca gcg gca tct   211
Pro Thr Ser Ser Glu Ser Ser Val Ala Ala Thr Ala Pro Ala Ala Ser
             25                  30                  35

agc gag act gcg gct gaa tac cgt gcg atg ctc gct tcc ctt gac gtt   259
Ser Glu Thr Ala Ala Glu Tyr Arg Ala Met Leu Ala Ser Leu Asp Val
         40                  45                  50

aaa ggt cgt gcg cca gga aca gga tat gac cgc gaa tta ttc gga cca   307
Lys Gly Arg Ala Pro Gly Thr Gly Tyr Asp Arg Glu Leu Phe Gly Pro
     55                  60                  65

gca tgg acc gac act gtt tcc gtg gaa tat gga cac aat ggc tgc gat   355
Ala Trp Thr Asp Thr Val Ser Val Glu Tyr Gly His Asn Gly Cys Asp
 70                  75                  80                  85

acc cgc aac gac atc ctg caa cgc gac ctg gat gac atc caa ctt cgc   403
Thr Arg Asn Asp Ile Leu Gln Arg Asp Leu Asp Asp Ile Gln Leu Arg
                 90                  95                 100

gaa ggc acc aag gat tgt atc gtc acg agc ggc ctg ctc agc gat cca   451
Glu Gly Thr Lys Asp Cys Ile Val Thr Ser Gly Leu Leu Ser Asp Pro
            105                 110                 115

ttt tct ggc gaa ctt att gat ttc gtt cgc ggt gaa cgt tcc ggc gac   499
Phe Ser Gly Glu Leu Ile Asp Phe Val Arg Gly Glu Arg Ser Gly Asp
        120                 125                 130

gtg cag atc gat cac ctg gtc cca tta cat gac gca tgg gtc aag gga   547
Val Gln Ile Asp His Leu Val Pro Leu His Asp Ala Trp Val Lys Gly
    135                 140                 145

gca cag cag tgg gat gag caa act cga aag aac ttt gcc aac gat ccc   595
Ala Gln Gln Trp Asp Glu Gln Thr Arg Lys Asn Phe Ala Asn Asp Pro
150                 155                 160                 165

gac aac ctt ctc gcc gtt aaa ggt acg ctt aac cag caa aaa ggt gca   643
Asp Asn Leu Leu Ala Val Lys Gly Thr Leu Asn Gln Gln Lys Gly Ala
                170                 175                 180

ggc gat gca gca acc tgg ctt cca cca aac aca gct ttt agg tgc gat   691
Gly Asp Ala Ala Thr Trp Leu Pro Pro Asn Thr Ala Phe Arg Cys Asp
            185                 190                 195

tac gca aag aaa atc atc acc gtt aaa gat cgc tac aac gtg tgg gtg   739
Tyr Ala Lys Lys Ile Ile Thr Val Lys Asp Arg Tyr Asn Val Trp Val
        200                 205                 210
```

```
act gag gct gaa gca agc gcc ctg gaa cgc caa tta gat acg tgt gct   787
Thr Glu Ala Glu Ala Ser Ala Leu Glu Arg Gln Leu Asp Thr Cys Ala
    215                 220                 225

gca taacagtcac ataagcattt ggg                                   813
Ala
230
```

<210> 616
<211> 230
<212> PRT
<213> Corynebacterium glutamicum

<400> 616

```
Val Ala Ala Val Ala Phe Ala Ala Tyr Val Ile Asp Gly Gly Val Glu
  1               5                  10                  15

Glu Ala Ser Gly Thr Pro Thr Ser Ser Glu Ser Ser Val Ala Ala Thr
             20                  25                  30

Ala Pro Ala Ala Ser Ser Glu Thr Ala Ala Glu Tyr Arg Ala Met Leu
         35                  40                  45

Ala Ser Leu Asp Val Lys Gly Arg Ala Pro Gly Thr Gly Tyr Asp Arg
     50                  55                  60

Glu Leu Phe Gly Pro Ala Trp Thr Asp Thr Val Ser Val Glu Tyr Gly
 65                  70                  75                  80

His Asn Gly Cys Asp Thr Arg Asn Asp Ile Leu Gln Arg Asp Leu Asp
                 85                  90                  95

Asp Ile Gln Leu Arg Glu Gly Thr Lys Asp Cys Ile Val Thr Ser Gly
            100                 105                 110

Leu Leu Ser Asp Pro Phe Ser Gly Glu Leu Ile Asp Phe Val Arg Gly
        115                 120                 125

Glu Arg Ser Gly Asp Val Gln Ile Asp His Leu Val Pro Leu His Asp
    130                 135                 140

Ala Trp Val Lys Gly Ala Gln Gln Trp Asp Glu Gln Thr Arg Lys Asn
145                 150                 155                 160

Phe Ala Asn Asp Pro Asp Asn Leu Leu Ala Val Lys Gly Thr Leu Asn
                165                 170                 175

Gln Gln Lys Gly Ala Gly Asp Ala Ala Thr Trp Leu Pro Pro Asn Thr
            180                 185                 190

Ala Phe Arg Cys Asp Tyr Ala Lys Lys Ile Ile Thr Val Lys Asp Arg
        195                 200                 205

Tyr Asn Val Trp Val Thr Glu Ala Glu Ala Ser Ala Leu Glu Arg Gln
    210                 215                 220

Leu Asp Thr Cys Ala Ala
225                 230
```

<210> 617
<211> 1623
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1600)
<223> RXN01400

<400> 617
gagcagctat cacccttatg catcggctcc gggtgaggcg gtgccggtgt cctttgatca 60

gcaacgacat gtgggtgccg gcgagcgacc gggtagttgg atg gcg att agt gtt 115
Met Ala Ile Ser Val
1 5

tct atg cct aag gcg atc agc cgt gag gaa ttg gag cgc gcg tgg ctt 163
Ser Met Pro Lys Ala Ile Ser Arg Glu Glu Leu Glu Arg Ala Trp Leu
10 15 20

gaa gtg att gaa cgg cac ggc acc ttg cgc aca gta ttt agc acg gga 211
Glu Val Ile Glu Arg His Gly Thr Leu Arg Thr Val Phe Ser Thr Gly
25 30 35

atg ggt ggg gaa gtg cag caa cac cgc att gat gtg ggc ccg gga aaa 259
Met Gly Gly Glu Val Gln Gln His Arg Ile Asp Val Gly Pro Gly Lys
40 45 50

tgg att gac cac gcc gtt gcg cct ggt gag agc att aat gag gcg ttg 307
Trp Ile Asp His Ala Val Ala Pro Gly Glu Ser Ile Asn Glu Ala Leu
55 60 65

cgg gcg gtg ttg aat cgg cag tgt tcg ccg tac tcg agg cca tcg cat 355
Arg Ala Val Leu Asn Arg Gln Cys Ser Pro Tyr Ser Arg Pro Ser His
70 75 80 85

agt ttg tgc att att gat gcg cat ccg cgt ccc acg gtg att att ggt 403
Ser Leu Cys Ile Ile Asp Ala His Pro Arg Pro Thr Val Ile Ile Gly
90 95 100

agt gat cat tcg cat gtg gat atg tgg tcc atg ctg gtg att gtg cgc 451
Ser Asp His Ser His Val Asp Met Trp Ser Met Leu Val Ile Val Arg
105 110 115

gat ttg ttg gct gcg ctc gat atg gaa ctt ccc gtt gag ccg ccg ttg 499
Asp Leu Leu Ala Ala Leu Asp Met Glu Leu Pro Val Glu Pro Pro Leu
120 125 130

gcg ttt gaa tcg cac acc gcg gaa ctc ctc gcg gct cca cct gca ccg 547
Ala Phe Glu Ser His Thr Ala Glu Leu Leu Ala Ala Pro Pro Ala Pro
135 140 145

gag cgg att cac cag cgg tgg cgt gaa att ttg gaa gct ggt ggt gga 595
Glu Arg Ile His Gln Arg Trp Arg Glu Ile Leu Glu Ala Gly Gly Gly
150 155 160 165

aaa atg cct cag ttc ccg ctt ccg ctt ggc gat gcc atc tcc atg cct 643
Lys Met Pro Gln Phe Pro Leu Pro Leu Gly Asp Ala Ile Ser Met Pro
170 175 180

```
gaa cgc gtt gaa gtc cgc gac att ttc ggg gtc aat ggc ttg gcg att   691
Glu Arg Val Glu Val Arg Asp Ile Phe Gly Val Asn Gly Leu Ala Ile
            185                 190                 195

tac tcg gca cgc gcc cgc gca caa cag gta agc tcc ctg gcc ttg act   739
Tyr Ser Ala Arg Ala Arg Ala Gln Gln Val Ser Ser Leu Ala Leu Thr
        200                 205                 210

att tca gtg atg gct gat gtt acg gcg gcg ctg gcg gac ctt ccg ttg   787
Ile Ser Val Met Ala Asp Val Thr Ala Ala Leu Ala Asp Leu Pro Leu
    215                 220                 225

cgt gct gta ttc cca gtc cat agc cgt ttc gat cag cgc tgg cac gat   835
Arg Ala Val Phe Pro Val His Ser Arg Phe Asp Gln Arg Trp His Asp
230                 235                 240                 245

agt gtc ggg tgg ttt atc tcc aat tcg gtc att gag gtg cca gat tcc   883
Ser Val Gly Trp Phe Ile Ser Asn Ser Val Ile Glu Val Pro Asp Ser
                250                 255                 260

gat cct cac act gca gcc caa gct gtt cgc gag gct gtt tct ttg gga   931
Asp Pro His Thr Ala Ala Gln Ala Val Arg Glu Ala Val Ser Leu Gly
            265                 270                 275

agc tac ccg ctg gct gag ctg ctt gaa ccg tgg ggt ggc atg ccg gaa   979
Ser Tyr Pro Leu Ala Glu Leu Leu Glu Pro Trp Gly Gly Met Pro Glu
        280                 285                 290

acg cca gga atg ttt gct att tct tgg ctt gac ctg cgc cga ctc cca   1027
Thr Pro Gly Met Phe Ala Ile Ser Trp Leu Asp Leu Arg Arg Leu Pro
    295                 300                 305

gtg agc att gac gat att ggc ctc caa gcc cag tat gtc agc gct tca   1075
Val Ser Ile Asp Asp Ile Gly Leu Gln Ala Gln Tyr Val Ser Ala Ser
310                 315                 320                 325

ctg cgc acc gat ggt gtg atg ctg tgg ttt att ttg gat cgc tcc ggc   1123
Leu Arg Thr Asp Gly Val Met Leu Trp Phe Ile Leu Asp Arg Ser Gly
                330                 335                 340

gcg cac ctt cgc tgt cgt tat cct gac tct ttg gtg gcg cgg gaa aat   1171
Ala His Leu Arg Cys Arg Tyr Pro Asp Ser Leu Val Ala Arg Glu Asn
            345                 350                 355

gta ggc cgc tgg att gat gcg att gtt gct cag atg cgc gcc gaa gct   1219
Val Gly Arg Trp Ile Asp Ala Ile Val Ala Gln Met Arg Ala Glu Ala
        360                 365                 370

ggg acg gtg aat ctg cag gcc ggc ggg gaa cag ctg aca ctt cgg cat   1267
Gly Thr Val Asn Leu Gln Ala Gly Gly Glu Gln Leu Thr Leu Arg His
    375                 380                 385

gga act cgc gcc gat att tcc gag atc gcc ccg cta ctt gcc cga aac   1315
Gly Thr Arg Ala Asp Ile Ser Glu Ile Ala Pro Leu Leu Ala Arg Asn
390                 395                 400                 405

gca gct gac cct tgt gag ctg gtg gat ctt gaa cat gcc ctt gac ctg   1363
Ala Ala Asp Pro Cys Glu Leu Val Asp Leu Glu His Ala Leu Asp Leu
                410                 415                 420

ctg aca cac gag tct tcg cat ttc ctg gcg gtg gtt cga aac gct cgt   1411
```

```
Leu Thr His Glu Ser Ser His Phe Leu Ala Val Val Arg Asn Ala Arg
            425                 430                 435

ggc aag ata atc gca gcg atg cag ttg act att gtt ccg gag ttt tcc   1459
Gly Lys Ile Ile Ala Ala Met Gln Leu Thr Ile Val Pro Glu Phe Ser
        440                 445                 450

cgc ggt ggt gcg ctt cat ctt cac atc gag ggg ccg ttc att att ccg   1507
Arg Gly Gly Ala Leu His Leu His Ile Glu Gly Pro Phe Ile Ile Pro
    455                 460                 465

gaa tat cgc acc acc gat ttg gat aaa aag ctg cgc gcc tgg gct gtg   1555
Glu Tyr Arg Thr Thr Asp Leu Asp Lys Lys Leu Arg Ala Trp Ala Val
470                 475                 480                 485

gag cat ggg cgt gcg cga ggg gtg aag gtt gag gag gtg gtg gga       1600
Glu His Gly Arg Ala Arg Gly Val Lys Val Glu Glu Val Val Gly
                490                 495                 500

tagttggttt attggcgcct cgt                                        1623


<210> 618
<211> 500
<212> PRT
<213> Corynebacterium glutamicum

<400> 618
Met Ala Ile Ser Val Ser Met Pro Lys Ala Ile Ser Arg Glu Glu Leu
  1               5                  10                  15

Glu Arg Ala Trp Leu Glu Val Ile Glu Arg His Gly Thr Leu Arg Thr
             20                  25                  30

Val Phe Ser Thr Gly Met Gly Gly Glu Val Gln Gln His Arg Ile Asp
         35                  40                  45

Val Gly Pro Gly Lys Trp Ile Asp His Ala Val Ala Pro Gly Glu Ser
     50                  55                  60

Ile Asn Glu Ala Leu Arg Ala Val Leu Asn Arg Gln Cys Ser Pro Tyr
 65                  70                  75                  80

Ser Arg Pro Ser His Ser Leu Cys Ile Ile Asp Ala His Pro Arg Pro
                 85                  90                  95

Thr Val Ile Ile Gly Ser Asp His Ser His Val Asp Met Trp Ser Met
            100                 105                 110

Leu Val Ile Val Arg Asp Leu Leu Ala Ala Leu Asp Met Glu Leu Pro
        115                 120                 125

Val Glu Pro Pro Leu Ala Phe Glu Ser His Thr Ala Glu Leu Leu Ala
    130                 135                 140

Ala Pro Pro Ala Pro Glu Arg Ile His Gln Arg Trp Arg Glu Ile Leu
145                 150                 155                 160

Glu Ala Gly Gly Gly Lys Met Pro Gln Phe Pro Leu Pro Leu Gly Asp
                165                 170                 175
```

```
Ala Ile Ser Met Pro Glu Arg Val Glu Val Arg Asp Ile Phe Gly Val
            180                 185                 190

Asn Gly Leu Ala Ile Tyr Ser Ala Arg Ala Arg Ala Gln Gln Val Ser
        195                 200                 205

Ser Leu Ala Leu Thr Ile Ser Val Met Ala Asp Val Thr Ala Ala Leu
    210                 215                 220

Ala Asp Leu Pro Leu Arg Ala Val Phe Pro Val His Ser Arg Phe Asp
225                 230                 235                 240

Gln Arg Trp His Asp Ser Val Gly Trp Phe Ile Ser Asn Ser Val Ile
                245                 250                 255

Glu Val Pro Asp Ser Asp Pro His Thr Ala Ala Gln Ala Val Arg Glu
            260                 265                 270

Ala Val Ser Leu Gly Ser Tyr Pro Leu Ala Glu Leu Leu Glu Pro Trp
        275                 280                 285

Gly Gly Met Pro Glu Thr Pro Gly Met Phe Ala Ile Ser Trp Leu Asp
    290                 295                 300

Leu Arg Arg Leu Pro Val Ser Ile Asp Asp Ile Gly Leu Gln Ala Gln
305                 310                 315                 320

Tyr Val Ser Ala Ser Leu Arg Thr Asp Gly Val Met Leu Trp Phe Ile
                325                 330                 335

Leu Asp Arg Ser Gly Ala His Leu Arg Cys Arg Tyr Pro Asp Ser Leu
            340                 345                 350

Val Ala Arg Glu Asn Val Gly Arg Trp Ile Asp Ala Ile Val Ala Gln
        355                 360                 365

Met Arg Ala Glu Ala Gly Thr Val Asn Leu Gln Ala Gly Gly Glu Gln
    370                 375                 380

Leu Thr Leu Arg His Gly Thr Arg Ala Asp Ile Ser Glu Ile Ala Pro
385                 390                 395                 400

Leu Leu Ala Arg Asn Ala Ala Asp Pro Cys Glu Leu Val Asp Leu Glu
                405                 410                 415

His Ala Leu Asp Leu Leu Thr His Glu Ser Ser His Phe Leu Ala Val
            420                 425                 430

Val Arg Asn Ala Arg Gly Lys Ile Ile Ala Ala Met Gln Leu Thr Ile
        435                 440                 445

Val Pro Glu Phe Ser Arg Gly Gly Ala Leu His Leu His Ile Glu Gly
    450                 455                 460

Pro Phe Ile Ile Pro Glu Tyr Arg Thr Thr Asp Leu Asp Lys Lys Leu
465                 470                 475                 480

Arg Ala Trp Ala Val Glu His Gly Arg Ala Arg Gly Val Lys Val Glu
                485                 490                 495

Glu Val Val Gly
```

500

<210> 619
<211> 1623
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1600)
<223> FRXA01400

<400> 619
gagcagctat cacccttatg catcggctcc gggtgaggcg gtgccggtgt cctttgatca 60

gcaacgacat gtgggtgccg gcgagcgacc gggtagttgg atg gcg att agt gtt 115
Met Ala Ile Ser Val
1 5

tct atg cct aag gcg atc agc cgt gag gaa ttg gag cgc gcg tgg ctt 163
Ser Met Pro Lys Ala Ile Ser Arg Glu Glu Leu Glu Arg Ala Trp Leu
10 15 20

gaa gtg att gaa cgg cac ggc acc ttg cgc aca gta ttt agc acg gga 211
Glu Val Ile Glu Arg His Gly Thr Leu Arg Thr Val Phe Ser Thr Gly
25 30 35

atg ggt ggg gaa gtg cag caa cac cgc att gat gtg ggc ccg gga aaa 259
Met Gly Gly Glu Val Gln Gln His Arg Ile Asp Val Gly Pro Gly Lys
40 45 50

tgg att gac cac gcc gtt gcg cct ggt gag agc att aat gag gcg ttg 307
Trp Ile Asp His Ala Val Ala Pro Gly Glu Ser Ile Asn Glu Ala Leu
55 60 65

cgg gcg gtg ttg aat cgg cag tgt tcg ccg tac tcg agg cca tcg cat 355
Arg Ala Val Leu Asn Arg Gln Cys Ser Pro Tyr Ser Arg Pro Ser His
70 75 80 85

agt ttg tgc att att gat gcg cat ccg cgt ccc acg gtg att att ggt 403
Ser Leu Cys Ile Ile Asp Ala His Pro Arg Pro Thr Val Ile Ile Gly
90 95 100

agt gat cat tcg cat gtg gat atg tgg tcc atg ctg gtg att gtg cgc 451
Ser Asp His Ser His Val Asp Met Trp Ser Met Leu Val Ile Val Arg
105 110 115

gat ttg ttg gct gcg ctc gat atg gaa ctt ccc gtt gag ccg ccg ttg 499
Asp Leu Leu Ala Ala Leu Asp Met Glu Leu Pro Val Glu Pro Pro Leu
120 125 130

gcg ttt gaa tcg cac acc gcg gaa ctc ctc gcg gct cca cct gca ccg 547
Ala Phe Glu Ser His Thr Ala Glu Leu Leu Ala Ala Pro Pro Ala Pro
135 140 145

gag cgg att cac cag cgg tgg cgt gaa att ttg gaa gct ggt ggt gga 595
Glu Arg Ile His Gln Arg Trp Arg Glu Ile Leu Glu Ala Gly Gly Gly
150 155 160 165

aaa atg cct cag ttc ccg ctt ccg ctt ggc gat gcc atc tcc atg cct 643

```
Lys Met Pro Gln Phe Pro Leu Pro Leu Gly Asp Ala Ile Ser Met Pro
                170                 175                 180

gaa cgc gtt gaa gtc cgc gac att ttc ggg gtc aat ggc ttg gcg att   691
Glu Arg Val Glu Val Arg Asp Ile Phe Gly Val Asn Gly Leu Ala Ile
            185                 190                 195

tac tcg gca cgc gcc cgc gca caa cag gta agc tcc ctg gcc ttg act   739
Tyr Ser Ala Arg Ala Arg Ala Gln Gln Val Ser Ser Leu Ala Leu Thr
        200                 205                 210

att tca gtg atg gct gat gtt acg gcg gcg ctg gcg gac ctt ccg ttg   787
Ile Ser Val Met Ala Asp Val Thr Ala Ala Leu Ala Asp Leu Pro Leu
    215                 220                 225

cgt gct gta ttc cca gtc cat agc cgt ttc gat cag cgc tgg cac gat   835
Arg Ala Val Phe Pro Val His Ser Arg Phe Asp Gln Arg Trp His Asp
230                 235                 240                 245

agt gtc ggg tgg ttt atc tcc aat tcg gtc att gag gtg cca gat tcc   883
Ser Val Gly Trp Phe Ile Ser Asn Ser Val Ile Glu Val Pro Asp Ser
                250                 255                 260

gat cct cac act gca gcc caa gct gtt cgc gag gct gtt tct ttg gga   931
Asp Pro His Thr Ala Ala Gln Ala Val Arg Glu Ala Val Ser Leu Gly
            265                 270                 275

agc tac ccg ctg gct gag ctg ctt gaa ccg tgg ggt ggc atg ccg gaa   979
Ser Tyr Pro Leu Ala Glu Leu Leu Glu Pro Trp Gly Gly Met Pro Glu
        280                 285                 290

acg cca gga atg ttt gct att tct tgg ctt gac ctg cgc cga ctc cca   1027
Thr Pro Gly Met Phe Ala Ile Ser Trp Leu Asp Leu Arg Arg Leu Pro
    295                 300                 305

gtg agc att gac gat att ggc ctc caa gcc cag tat gtc agc gct tca   1075
Val Ser Ile Asp Asp Ile Gly Leu Gln Ala Gln Tyr Val Ser Ala Ser
310                 315                 320                 325

ctg cgc acc gat ggt gtg atg ctg tgg ttt att ttg gat cgc tcc ggc   1123
Leu Arg Thr Asp Gly Val Met Leu Trp Phe Ile Leu Asp Arg Ser Gly
                330                 335                 340

gcg cac ctt cgc tgt cgt tat cct gac tct ttg gtg gcg cgg gaa aat   1171
Ala His Leu Arg Cys Arg Tyr Pro Asp Ser Leu Val Ala Arg Glu Asn
            345                 350                 355

gta ggc cgc tgg att gat gcg att gtt gct cag atg cgc gcc gaa gct   1219
Val Gly Arg Trp Ile Asp Ala Ile Val Ala Gln Met Arg Ala Glu Ala
        360                 365                 370

ggg acg gtg aat ctg cag gcc ggc ggg gaa cag ctg aca ctt cgg cat   1267
Gly Thr Val Asn Leu Gln Ala Gly Gly Glu Gln Leu Thr Leu Arg His
    375                 380                 385

gga act cgc gcc gat att tcc gag atc gcc ccg cta ctt gcc cga aac   1315
Gly Thr Arg Ala Asp Ile Ser Glu Ile Ala Pro Leu Leu Ala Arg Asn
390                 395                 400                 405

gca gct gac cct tgt gag ctg gtg gat ctt gaa cat gcc ctt gac ctg   1363
Ala Ala Asp Pro Cys Glu Leu Val Asp Leu Glu His Ala Leu Asp Leu
```

```
                410                 415                 420

ctg aca cac gag tct tcg cat ttc ctg gcg gtg gtt cga aac gct cgt   1411
Leu Thr His Glu Ser Ser His Phe Leu Ala Val Val Arg Asn Ala Arg
            425                 430                 435

ggc aag ata atc gca gcg atg cag ttg act att gtt ccg gag ttt tcc   1459
Gly Lys Ile Ile Ala Ala Met Gln Leu Thr Ile Val Pro Glu Phe Ser
        440                 445                 450

cgc ggt ggt gcg ctt cat ctt cac atc gag ggg ccg ttc att att ccg   1507
Arg Gly Gly Ala Leu His Leu His Ile Glu Gly Pro Phe Ile Ile Pro
    455                 460                 465

gaa tat cgc acc acc gat ttg gat aaa aag ctg cgc gcc tgg gct gtg   1555
Glu Tyr Arg Thr Thr Asp Leu Asp Lys Lys Leu Arg Ala Trp Ala Val
470                 475                 480                 485

gag cat ggg cgt gcg cga ggg gtg aag gtt gag gag gtg gtg gga       1600
Glu His Gly Arg Ala Arg Gly Val Lys Val Glu Glu Val Val Gly
                490                 495                 500

tagttggttt attggcgcct cgt                                        1623


<210> 620
<211> 500
<212> PRT
<213> Corynebacterium glutamicum

<400> 620
Met Ala Ile Ser Val Ser Met Pro Lys Ala Ile Ser Arg Glu Glu Leu
  1               5                  10                  15

Glu Arg Ala Trp Leu Glu Val Ile Glu Arg His Gly Thr Leu Arg Thr
             20                  25                  30

Val Phe Ser Thr Gly Met Gly Gly Glu Val Gln Gln His Arg Ile Asp
         35                  40                  45

Val Gly Pro Gly Lys Trp Ile Asp His Ala Val Ala Pro Gly Glu Ser
     50                  55                  60

Ile Asn Glu Ala Leu Arg Ala Val Leu Asn Arg Gln Cys Ser Pro Tyr
 65                  70                  75                  80

Ser Arg Pro Ser His Ser Leu Cys Ile Ile Asp Ala His Pro Arg Pro
                 85                  90                  95

Thr Val Ile Ile Gly Ser Asp His Ser His Val Asp Met Trp Ser Met
            100                 105                 110

Leu Val Ile Val Arg Asp Leu Leu Ala Ala Leu Asp Met Glu Leu Pro
        115                 120                 125

Val Glu Pro Pro Leu Ala Phe Glu Ser His Thr Ala Glu Leu Leu Ala
    130                 135                 140

Ala Pro Pro Ala Pro Glu Arg Ile His Gln Arg Trp Arg Glu Ile Leu
145                 150                 155                 160
```

```
Glu Ala Gly Gly Gly Lys Met Pro Gln Phe Pro Leu Pro Leu Gly Asp
                165                 170                 175

Ala Ile Ser Met Pro Glu Arg Val Glu Val Arg Asp Ile Phe Gly Val
            180                 185                 190

Asn Gly Leu Ala Ile Tyr Ser Ala Arg Ala Arg Ala Gln Gln Val Ser
        195                 200                 205

Ser Leu Ala Leu Thr Ile Ser Val Met Ala Asp Val Thr Ala Ala Leu
    210                 215                 220

Ala Asp Leu Pro Leu Arg Ala Val Phe Pro Val His Ser Arg Phe Asp
225                 230                 235                 240

Gln Arg Trp His Asp Ser Val Gly Trp Phe Ile Ser Asn Ser Val Ile
                245                 250                 255

Glu Val Pro Asp Ser Asp Pro His Thr Ala Ala Gln Ala Val Arg Glu
            260                 265                 270

Ala Val Ser Leu Gly Ser Tyr Pro Leu Ala Glu Leu Leu Glu Pro Trp
        275                 280                 285

Gly Gly Met Pro Glu Thr Pro Gly Met Phe Ala Ile Ser Trp Leu Asp
    290                 295                 300

Leu Arg Arg Leu Pro Val Ser Ile Asp Asp Ile Gly Leu Gln Ala Gln
305                 310                 315                 320

Tyr Val Ser Ala Ser Leu Arg Thr Asp Gly Val Met Leu Trp Phe Ile
                325                 330                 335

Leu Asp Arg Ser Gly Ala His Leu Arg Cys Arg Tyr Pro Asp Ser Leu
            340                 345                 350

Val Ala Arg Glu Asn Val Gly Arg Trp Ile Asp Ala Ile Val Ala Gln
        355                 360                 365

Met Arg Ala Glu Ala Gly Thr Val Asn Leu Gln Ala Gly Gly Glu Gln
    370                 375                 380

Leu Thr Leu Arg His Gly Thr Arg Ala Asp Ile Ser Glu Ile Ala Pro
385                 390                 395                 400

Leu Leu Ala Arg Asn Ala Ala Asp Pro Cys Glu Leu Val Asp Leu Glu
                405                 410                 415

His Ala Leu Asp Leu Leu Thr His Glu Ser Ser His Phe Leu Ala Val
            420                 425                 430

Val Arg Asn Ala Arg Gly Lys Ile Ile Ala Ala Met Gln Leu Thr Ile
        435                 440                 445

Val Pro Glu Phe Ser Arg Gly Gly Ala Leu His Leu His Ile Glu Gly
    450                 455                 460

Pro Phe Ile Ile Pro Glu Tyr Arg Thr Thr Asp Leu Asp Lys Lys Leu
465                 470                 475                 480

Arg Ala Trp Ala Val Glu His Gly Arg Ala Arg Gly Val Lys Val Glu
```

```
                485                 490                 495

Glu Val Val Gly
            500


<210> 621
<211> 845
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(822)
<223> RXN01409

<400> 621
tgg gtg gat ttc ccc gac gtc acc gca cgt ttg ggg tat gaa tac atg   48
Trp Val Asp Phe Pro Asp Val Thr Ala Arg Leu Gly Tyr Glu Tyr Met
  1               5                  10                  15

cag ctg acc cct cat gta gat ttc ggt cct ttc ttc cgc cac ccc aag   96
Gln Leu Thr Pro His Val Asp Phe Gly Pro Phe Phe Arg His Pro Lys
             20                  25                  30

gca gac gat gat ctc gtg gca gcc ctg aaa aag cgt gcc aag gat gcc   144
Ala Asp Asp Asp Leu Val Ala Ala Leu Lys Lys Arg Ala Lys Asp Ala
         35                  40                  45

gga gtc acc att cct gca ctg ttg cca gtg cag cgt att tcc tgg ccg   192
Gly Val Thr Ile Pro Ala Leu Leu Pro Val Gln Arg Ile Ser Trp Pro
     50                  55                  60

gag gaa acc cag cgt gtt gca gca gta cgc aac atc aag cgc atc atc   240
Glu Glu Thr Gln Arg Val Ala Ala Val Arg Asn Ile Lys Arg Ile Ile
 65                  70                  75                  80

cag ttg gcc gtt gat ctg gaa gta gac acc ctc aac acg gag ttt tct   288
Gln Leu Ala Val Asp Leu Glu Val Asp Thr Leu Asn Thr Glu Phe Ser
                 85                  90                  95

gga cgc cca gaa cgc tcc gag gat tcc gaa gat gcc ttc tac cgc tcc   336
Gly Arg Pro Glu Arg Ser Glu Asp Ser Glu Asp Ala Phe Tyr Arg Ser
            100                 105                 110

atg gaa gaa ctc ctg cca atc ctg gaa aaa gag ggc atc aag ttc aac   384
Met Glu Glu Leu Leu Pro Ile Leu Glu Lys Glu Gly Ile Lys Phe Asn
        115                 120                 125

atc gac cca cac cct gat gat ttc gtg gaa aac ggt att gaa gca tgg   432
Ile Asp Pro His Pro Asp Asp Phe Val Glu Asn Gly Ile Glu Ala Trp
    130                 135                 140

cga gtc atc cgc ggt ctg aac tcc aag cag gtg ggc ttt gtt tac gtg   480
Arg Val Ile Arg Gly Leu Asn Ser Lys Gln Val Gly Phe Val Tyr Val
145                 150                 155                 160

gca cct cac tca ttc cac atg ggt gat cag gct gag gca atc ctg cca   528
Ala Pro His Ser Phe His Met Gly Asp Gln Ala Glu Ala Ile Leu Pro
                165                 170                 175
```

```
gca gta ggc gat cgc ctt ggg gct gtg tac ctg tca gat acc ttc gac   576
Ala Val Gly Asp Arg Leu Gly Ala Val Tyr Leu Ser Asp Thr Phe Asp
            180                 185                 190

cac cac aaa tcc cac ggc ctg cgc tac atc act aac cct cca ggc aac   624
His His Lys Ser His Gly Leu Arg Tyr Ile Thr Asn Pro Pro Gly Asn
        195                 200                 205

gca gtg cgc gtg cac cag cac cta aaa atc ggt gat ggc gat gtg aac   672
Ala Val Arg Val His Gln His Leu Lys Ile Gly Asp Gly Asp Val Asn
    210                 215                 220

ttt gaa gag atc ttc tca ctg ctg cgc tct acc ggt tac ctt gac cgt   720
Phe Glu Glu Ile Phe Ser Leu Leu Arg Ser Thr Gly Tyr Leu Asp Arg
225                 230                 235                 240

gaa gat gca ctg ttg gtc tcc aac gtg ttt gca gaa gat gaa gca gca   768
Glu Asp Ala Leu Leu Val Ser Asn Val Phe Ala Glu Asp Glu Ala Ala
                245                 250                 255

gat gaa gta tcc cgc tac cag ctg gag aaa atc cgc tca ctc atc gaa   816
Asp Glu Val Ser Arg Tyr Gln Leu Glu Lys Ile Arg Ser Leu Ile Glu
            260                 265                 270

aac gca tagagttatc tcgaaactac caa                                845
Asn Ala
```

<210> 622
<211> 274
<212> PRT
<213> Corynebacterium glutamicum

<400> 622

```
Trp Val Asp Phe Pro Asp Val Thr Ala Arg Leu Gly Tyr Glu Tyr Met
  1               5                  10                  15

Gln Leu Thr Pro His Val Asp Phe Gly Pro Phe Phe Arg His Pro Lys
             20                  25                  30

Ala Asp Asp Asp Leu Val Ala Ala Leu Lys Lys Arg Ala Lys Asp Ala
         35                  40                  45

Gly Val Thr Ile Pro Ala Leu Leu Pro Val Gln Arg Ile Ser Trp Pro
     50                  55                  60

Glu Glu Thr Gln Arg Val Ala Ala Val Arg Asn Ile Lys Arg Ile Ile
 65                  70                  75                  80

Gln Leu Ala Val Asp Leu Glu Val Asp Thr Leu Asn Thr Glu Phe Ser
                 85                  90                  95

Gly Arg Pro Glu Arg Ser Glu Asp Ser Glu Asp Ala Phe Tyr Arg Ser
            100                 105                 110

Met Glu Glu Leu Leu Pro Ile Leu Glu Lys Glu Gly Ile Lys Phe Asn
        115                 120                 125

Ile Asp Pro His Pro Asp Asp Phe Val Glu Asn Gly Ile Glu Ala Trp
    130                 135                 140
```

```
Arg Val Ile Arg Gly Leu Asn Ser Lys Gln Val Gly Phe Val Tyr Val
145                 150                 155                 160

Ala Pro His Ser Phe His Met Gly Asp Gln Ala Glu Ala Ile Leu Pro
                165                 170                 175

Ala Val Gly Asp Arg Leu Gly Ala Val Tyr Leu Ser Asp Thr Phe Asp
            180                 185                 190

His His Lys Ser His Gly Leu Arg Tyr Ile Thr Asn Pro Pro Gly Asn
        195                 200                 205

Ala Val Arg Val His Gln His Leu Lys Ile Gly Asp Gly Asp Val Asn
    210                 215                 220

Phe Glu Glu Ile Phe Ser Leu Leu Arg Ser Thr Gly Tyr Leu Asp Arg
225                 230                 235                 240

Glu Asp Ala Leu Leu Val Ser Asn Val Phe Ala Glu Asp Glu Ala Ala
                245                 250                 255

Asp Glu Val Ser Arg Tyr Gln Leu Glu Lys Ile Arg Ser Leu Ile Glu
            260                 265                 270

Asn Ala
```

Application Filed with the Chinese Patent Office

<210> 623
<211> 839
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(816)
<223> FRXA01409

<400> 623

```
gat ttc ccc gac gtc acc gca cgt ttg ggg tat gaa tac atg cag ctg   48
Asp Phe Pro Asp Val Thr Ala Arg Leu Gly Tyr Glu Tyr Met Gln Leu
  1               5                  10                  15

acc cct cat gta gat ttc ggt cct ttc ttc cgc cac ccc aag gca gac   96
Thr Pro His Val Asp Phe Gly Pro Phe Phe Arg His Pro Lys Ala Asp
             20                  25                  30

gat gat ctc gtg gca gcc ctg aaa aag cgt gcc aag gat gcc gga gtc  144
Asp Asp Leu Val Ala Ala Leu Lys Lys Arg Ala Lys Asp Ala Gly Val
         35                  40                  45

acc att cct gca ctg ttg cca gtg cag cgt att tcc tgg ccg gag gaa  192
Thr Ile Pro Ala Leu Leu Pro Val Gln Arg Ile Ser Trp Pro Glu Glu
     50                  55                  60

acc cag cgt gtt gca gca gta cgc aac atc aag cgc atc atc cag ttg  240
Thr Gln Arg Val Ala Ala Val Arg Asn Ile Lys Arg Ile Ile Gln Leu
 65                  70                  75                  80

gcc gtt gat ctg gaa gta gac acc ctc aac acg gag ttt tct gga cgc  288
```

```
Ala Val Asp Leu Glu Val Asp Thr Leu Asn Thr Glu Phe Ser Gly Arg
                 85                  90                  95

cca gaa cgc tcc gag gat tcc gaa gat gcc ttc tac cgc tcc atg gaa   336
Pro Glu Arg Ser Glu Asp Ser Glu Asp Ala Phe Tyr Arg Ser Met Glu
            100                 105                 110

gaa ctc ctg cca atc ctg gaa aaa gag ggc atc aag ttc aac atc gac   384
Glu Leu Leu Pro Ile Leu Glu Lys Glu Gly Ile Lys Phe Asn Ile Asp
        115                 120                 125

cca cac cct gat gat ttc gtg gaa aac ggt att gaa gca tgg cga gtc   432
Pro His Pro Asp Asp Phe Val Glu Asn Gly Ile Glu Ala Trp Arg Val
    130                 135                 140

atc cgc ggt ctg aac tcc aag cag gtg ggc ttt gtt tac gtg gca cct   480
Ile Arg Gly Leu Asn Ser Lys Gln Val Gly Phe Val Tyr Val Ala Pro
145                 150                 155                 160

cac tca ttc cac atg ggt gat cag gct gag gca atc ctg cca gca gta   528
His Ser Phe His Met Gly Asp Gln Ala Glu Ala Ile Leu Pro Ala Val
                165                 170                 175

ggc gat cgc ctt ggg gct gtg tac ctg tca gat acc ttc gac cac cac   576
Gly Asp Arg Leu Gly Ala Val Tyr Leu Ser Asp Thr Phe Asp His His
            180                 185                 190

aaa tcc cac ggc ctg cgc tac atc act aac cct cca ggc aac gca gtg   624
Lys Ser His Gly Leu Arg Tyr Ile Thr Asn Pro Pro Gly Asn Ala Val
        195                 200                 205

cgc gtg cac cag cac cta aaa atc ggt gat ggc gat gtg aac ttt gaa   672
Arg Val His Gln His Leu Lys Ile Gly Asp Gly Asp Val Asn Phe Glu
    210                 215                 220

gag atc ttc tca ctg ctg cgc tct acc ggt tac ctt gac cgt gaa gat   720
Glu Ile Phe Ser Leu Leu Arg Ser Thr Gly Tyr Leu Asp Arg Glu Asp
225                 230                 235                 240

gca ctg ttg gtc tcc aac gtg ttt gca gaa gat gaa gca gca gat gaa   768
Ala Leu Leu Val Ser Asn Val Phe Ala Glu Asp Glu Ala Ala Asp Glu
                245                 250                 255

gta tcc cgc tac cag ctg gag aaa atc cgc tca ctc atc gaa aac gca   816
Val Ser Arg Tyr Gln Leu Glu Lys Ile Arg Ser Leu Ile Glu Asn Ala
            260                 265                 270

tagagttatc tcgaaactac caa                                        839


<210> 624
<211> 272
<212> PRT
<213> Corynebacterium glutamicum

<400> 624
Asp Phe Pro Asp Val Thr Ala Arg Leu Gly Tyr Glu Tyr Met Gln Leu
  1               5                  10                  15

Thr Pro His Val Asp Phe Gly Pro Phe Phe Arg His Pro Lys Ala Asp
             20                  25                  30
```

```
Asp Asp Leu Val Ala Ala Leu Lys Lys Arg Ala Lys Asp Ala Gly Val
         35                  40                  45

Thr Ile Pro Ala Leu Leu Pro Val Gln Arg Ile Ser Trp Pro Glu Glu
     50                  55                  60

Thr Gln Arg Val Ala Ala Val Arg Asn Ile Lys Arg Ile Ile Gln Leu
 65                  70                  75                  80

Ala Val Asp Leu Glu Val Asp Thr Leu Asn Thr Glu Phe Ser Gly Arg
                 85                  90                  95

Pro Glu Arg Ser Glu Asp Ser Glu Asp Ala Phe Tyr Arg Ser Met Glu
            100                 105                 110

Glu Leu Leu Pro Ile Leu Glu Lys Glu Gly Ile Lys Phe Asn Ile Asp
        115                 120                 125

Pro His Pro Asp Asp Phe Val Glu Asn Gly Ile Glu Ala Trp Arg Val
    130                 135                 140

Ile Arg Gly Leu Asn Ser Lys Gln Val Gly Phe Val Tyr Val Ala Pro
145                 150                 155                 160

His Ser Phe His Met Gly Asp Gln Ala Glu Ala Ile Leu Pro Ala Val
                165                 170                 175

Gly Asp Arg Leu Gly Ala Val Tyr Leu Ser Asp Thr Phe Asp His His
            180                 185                 190

Lys Ser His Gly Leu Arg Tyr Ile Thr Asn Pro Pro Gly Asn Ala Val
        195                 200                 205

Arg Val His Gln His Leu Lys Ile Gly Asp Gly Asp Val Asn Phe Glu
    210                 215                 220

Glu Ile Phe Ser Leu Leu Arg Ser Thr Gly Tyr Leu Asp Arg Glu Asp
225                 230                 235                 240

Ala Leu Leu Val Ser Asn Val Phe Ala Glu Asp Glu Ala Ala Asp Glu
                245                 250                 255

Val Ser Arg Tyr Gln Leu Glu Lys Ile Arg Ser Leu Ile Glu Asn Ala
            260                 265                 270
```

<210> 625
<211> 3075
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(3052)
<223> RXN01434

<400> 625

```
ggtttcctgc gcaccgtgat gattggtgcg gcgctgtcgc cggccatcgc ttcggcgttc 60

aacactgcca acacgctgcc caacctgatc actggaaatc gtg ttg ggt gcg gtg   115
                                          Val Leu Gly Ala Val
                                            1               5

ctg aca tcg ctg gtt att ccg gtc ctt acc cgc gcg gaa aaa gaa gac   163
Leu Thr Ser Leu Val Ile Pro Val Leu Thr Arg Ala Glu Lys Glu Asp
                 10                  15                  20

gcc gac ggc ggt tcc ggg ttc ttc agg cgg ctg ctc acc ctg tcg gtg   211
Ala Asp Gly Gly Ser Gly Phe Phe Arg Arg Leu Leu Thr Leu Ser Val
             25                  30                  35

acg ctg ctg ggt ggt gtc acc atc ctg tcg att atc ggc gcg ccg ctg   259
Thr Leu Leu Gly Gly Val Thr Ile Leu Ser Ile Ile Gly Ala Pro Leu
         40                  45                  50

ctg aca cgg atg atg ctg tcc tct gag gga caa gtc aac gtg gtc atg   307
Leu Thr Arg Met Met Leu Ser Ser Glu Gly Gln Val Asn Val Val Met
     55                  60                  65

tcc acg gcc ttt gcg tat tgg ctg ctg cca cag att ttc ttc tac ggc   355
Ser Thr Ala Phe Ala Tyr Trp Leu Leu Pro Gln Ile Phe Phe Tyr Gly
 70                  75                  80                  85

ctg ttt gcc ctg ttc atg gct gtg ttg aac acc cgt gaa gtg ttc aaa   403
Leu Phe Ala Leu Phe Met Ala Val Leu Asn Thr Arg Glu Val Phe Lys
                 90                  95                 100

ccc ggc gcg tgg gca cct gtt gtc aac aat gtg atc acc ttg acc gtg   451
Pro Gly Ala Trp Ala Pro Val Val Asn Asn Val Ile Thr Leu Thr Val
            105                 110                 115

ctg ggc gtg tac atg gtg ctg cct gcg cgt ttg cac ccg cat gag cag   499
Leu Gly Val Tyr Met Val Leu Pro Ala Arg Leu His Pro His Glu Gln
        120                 125                 130

gtg ggc att ttt gat ccg cag atc att ttc ctc ggc gtg ggc acc acc   547
Val Gly Ile Phe Asp Pro Gln Ile Ile Phe Leu Gly Val Gly Thr Thr
    135                 140                 145

ctt ggt gtg gtt gca cag tgt cta atc atg att ccg tac ctg cgt cgc   595
Leu Gly Val Val Ala Gln Cys Leu Ile Met Ile Pro Tyr Leu Arg Arg
150                 155                 160                 165

gcg ggc att gat atg cgc cct ctg tgg ggt atc gat gcg cgt ttg aag   643
Ala Gly Ile Asp Met Arg Pro Leu Trp Gly Ile Asp Ala Arg Leu Lys
                170                 175                 180

caa ttc ggt ggc atg gcg atg gcg atc atc gtg tac gtg gca atc tcc   691
Gln Phe Gly Gly Met Ala Met Ala Ile Ile Val Tyr Val Ala Ile Ser
            185                 190                 195

cag ttc ggt tac atc atc acc act cgc att gcg tcg att gca gac gat   739
Gln Phe Gly Tyr Ile Ile Thr Thr Arg Ile Ala Ser Ile Ala Asp Asp
        200                 205                 210

gct gcg ccg ttt att tat cag cag cac tgg atg ttg ctg caa gtt cct   787
Ala Ala Pro Phe Ile Tyr Gln Gln His Trp Met Leu Leu Gln Val Pro
    215                 220                 225
```

```
tat ggc atc atc ggc gtc acc ttg ctc acc gcg att atg ccg cga ctg   835
Tyr Gly Ile Ile Gly Val Thr Leu Leu Thr Ala Ile Met Pro Arg Leu
230                 235                 240                 245

tcc cgc aac gcg gca gac ggc gat gat agg gca gta gtc tct gac ctt   883
Ser Arg Asn Ala Ala Asp Gly Asp Asp Arg Ala Val Val Ser Asp Leu
                250                 255                 260

cag ttg ggt tcc aag cta acc ttc atc gca ctg atc ccc atc gtg gtg   931
Gln Leu Gly Ser Lys Leu Thr Phe Ile Ala Leu Ile Pro Ile Val Val
            265                 270                 275

ttc ttc acc gcc ttc ggt gtc cct att gcc aat ggc ctt ttt gcc tac   979
Phe Phe Thr Ala Phe Gly Val Pro Ile Ala Asn Gly Leu Phe Ala Tyr
        280                 285                 290

ggc caa ttc gat gcc aac gcc gcc aac atc ctt ggt tgg act ctg agc   1027
Gly Gln Phe Asp Ala Asn Ala Ala Asn Ile Leu Gly Trp Thr Leu Ser
    295                 300                 305

ttc tct gct ttc acg ctg att cct tac gct ttg gtg ctg cta cat ctg   1075
Phe Ser Ala Phe Thr Leu Ile Pro Tyr Ala Leu Val Leu Leu His Leu
310                 315                 320                 325

cgt gtg ttt tat gcg cgt gaa gag gtc tgg acc cca acc ttc atc atc   1123
Arg Val Phe Tyr Ala Arg Glu Glu Val Trp Thr Pro Thr Phe Ile Ile
                330                 335                 340

gcc ggc atc acc gcc acc aag gtc gtg ctt tcc ctg ttg gca ccg ctg   1171
Ala Gly Ile Thr Ala Thr Lys Val Val Leu Ser Leu Leu Ala Pro Leu
            345                 350                 355

ctg tcg agc tcc ccg gag cgt gtg gtg gtg ctt ctt ggt gcg gcc aac   1219
Leu Ser Ser Ser Pro Glu Arg Val Val Val Leu Leu Gly Ala Ala Asn
        360                 365                 370

ggt ttc agt ttc atc acc ggc gcg gtc atc ggc gcg tat ctg ttg cgc   1267
Gly Phe Ser Phe Ile Thr Gly Ala Val Ile Gly Ala Tyr Leu Leu Arg
    375                 380                 385

aac aaa ctc ggc ctg ttg ggt atg cgc tct ttg gct aaa acc tcc ctg   1315
Asn Lys Leu Gly Leu Leu Gly Met Arg Ser Leu Ala Lys Thr Ser Leu
390                 395                 400                 405

tgg gcg ttg ggc tct gcg gcg gtt ggt gca gca gca gca tgg gcg ttg   1363
Trp Ala Leu Gly Ser Ala Ala Val Gly Ala Ala Ala Ala Trp Ala Leu
                410                 415                 420

ggg tgg ctg att caa gcc gtc gtg ggc gat ttc ttg ctg ggc act cta   1411
Gly Trp Leu Ile Gln Ala Val Val Gly Asp Phe Leu Leu Gly Thr Leu
            425                 430                 435

agc tcc gta ggc tac ttg ttg aac ctg gct gtg ttg ggt gtc ttc ttc   1459
Ser Ser Val Gly Tyr Leu Leu Asn Leu Ala Val Leu Gly Val Phe Phe
        440                 445                 450

atc ttc gtc acc ggc atc gtg ttg tca cgt tct ggt ttg ccg gag gtc   1507
Ile Phe Val Thr Gly Ile Val Leu Ser Arg Ser Gly Leu Pro Glu Val
    455                 460                 465
```

```
caa aac ttg ggc cag gca ctg acc cgc atc cca ggt ttg agc cgg ttt   1555
Gln Asn Leu Gly Gln Ala Leu Thr Arg Ile Pro Gly Leu Ser Arg Phe
470                 475                 480                 485

att cgc ccg aat acc aag atc tct ttg gat gtc ggc gaa gtc tcc gag   1603
Ile Arg Pro Asn Thr Lys Ile Ser Leu Asp Val Gly Glu Val Ser Glu
                490                 495                 500

cag gat ttc tcc acc cag ctg gtc gcg cca agc gag ttc gca gca acc   1651
Gln Asp Phe Ser Thr Gln Leu Val Ala Pro Ser Glu Phe Ala Ala Thr
            505                 510                 515

cct gtg ccg cca ccg atg tcc gcc ggt att gtc cgc gga cct cgc ctg   1699
Pro Val Pro Pro Pro Met Ser Ala Gly Ile Val Arg Gly Pro Arg Leu
        520                 525                 530

gtt ccc ggc gcc cca gtc ggc gac ggt cgt ttc cgt ctg ctc gcc gat   1747
Val Pro Gly Ala Pro Val Gly Asp Gly Arg Phe Arg Leu Leu Ala Asp
    535                 540                 545

cac ggc ggc gtc caa ggc gcg cgt ttc tgg cag gcc cgc gag atc gcc   1795
His Gly Gly Val Gln Gly Ala Arg Phe Trp Gln Ala Arg Glu Ile Ala
550                 555                 560                 565

acc ggc aag gaa gtc gcg ctg atc ttt gtg gat act tcc ggc aac gcc   1843
Thr Gly Lys Glu Val Ala Leu Ile Phe Val Asp Thr Ser Gly Asn Ala
                570                 575                 580

cca ttt gcg cca ctg tct tcg gca gcc gca gcg ggc atc gcc tac gag   1891
Pro Phe Ala Pro Leu Ser Ser Ala Ala Ala Ala Gly Ile Ala Tyr Glu
            585                 590                 595

gtg cag cgc cgc acc aag aag ctg gcc agc ttg ggc agc ttg gcg gta   1939
Val Gln Arg Arg Thr Lys Lys Leu Ala Ser Leu Gly Ser Leu Ala Val
        600                 605                 610

gcc ccc aac atc cac tcc gag gcg tac cgc aac ggt tgc ctc att gtg   1987
Ala Pro Asn Ile His Ser Glu Ala Tyr Arg Asn Gly Cys Leu Ile Val
    615                 620                 625

gcc gat tgg gtg cct ggc tcc agc ttg agc gcc gtc gcg gaa tcc ggt   2035
Ala Asp Trp Val Pro Gly Ser Ser Leu Ser Ala Val Ala Glu Ser Gly
630                 635                 640                 645

gcc gat ccc cgc gcc gcc gcg ttc gcg ctc gcg gaa cta act gaa acc   2083
Ala Asp Pro Arg Ala Ala Ala Phe Ala Leu Ala Glu Leu Thr Glu Thr
                650                 655                 660

atc ggc gag gcc cac gag atg ggt atc ccg gcc ggc ttg gac aac aag   2131
Ile Gly Glu Ala His Glu Met Gly Ile Pro Ala Gly Leu Asp Asn Lys
            665                 670                 675

tgc cga att cgt atc aac acc gac ggc cat gcc gtc ctc gcc ttg ccg   2179
Cys Arg Ile Arg Ile Asn Thr Asp Gly His Ala Val Leu Ala Leu Pro
        680                 685                 690

gcg att ttg ccc gat gcc tca gag ctc cgc gac gcc aag tcc ctg gcc   2227
Ala Ile Leu Pro Asp Ala Ser Glu Leu Arg Asp Ala Lys Ser Leu Ala
    695                 700                 705

tcg gcc gcc gag atg ctt atc gac gcg acc ctc gct ccc agc gac gtc   2275
```

```
Ser Ala Ala Glu Met Leu Ile Asp Ala Thr Leu Ala Pro Ser Asp Val
710                 715                 720                 725

aag gca atg gtc act gaa gcc cag ggg cta gct aca gaa gac aat ccc   2323
Lys Ala Met Val Thr Glu Ala Gln Gly Leu Ala Thr Glu Asp Asn Pro
                730                 735                 740

gat tac gca tca ctt gcc atg gcg atg cgc acc tgc gga ctg ttc acc   2371
Asp Tyr Ala Ser Leu Ala Met Ala Met Arg Thr Cys Gly Leu Phe Thr
            745                 750                 755

gag gaa cca acc cac ctt gtg gtg aag aag gaa aag aca cca aag cct   2419
Glu Glu Pro Thr His Leu Val Val Lys Lys Glu Lys Thr Pro Lys Pro
        760                 765                 770

gcg aca cgt gat ggt ttc ggt gcc tcc gac tac acc gtc aag ggc atg   2467
Ala Thr Arg Asp Gly Phe Gly Ala Ser Asp Tyr Thr Val Lys Gly Met
    775                 780                 785

gca gcc atc gcc gct gtg gtg atc atc ttg gtt tcc ctg gtg gcc gcc   2515
Ala Ala Ile Ala Ala Val Val Ile Ile Leu Val Ser Leu Val Ala Ala
790                 795                 800                 805

ggt acc gcg ttc ctc acc agc ttc ttc ggc agc agc acc aac gaa caa   2563
Gly Thr Ala Phe Leu Thr Ser Phe Phe Gly Ser Ser Thr Asn Glu Gln
                810                 815                 820

tcc ccg ttg gcc tct gtt gaa gcc acc acc tct gca aca cca gaa cct   2611
Ser Pro Leu Ala Ser Val Glu Ala Thr Thr Ser Ala Thr Pro Glu Pro
            825                 830                 835

gtg ggg cca ccg gtc tac ctg gat ctg gat caa gcc cgc acg tgg gat   2659
Val Gly Pro Pro Val Tyr Leu Asp Leu Asp Gln Ala Arg Thr Trp Asp
        840                 845                 850

gac ggt gca gga aca gat gtc acc gac gtc acc gac ggc aac acc tcc   2707
Asp Gly Ala Gly Thr Asp Val Thr Asp Val Thr Asp Gly Asn Thr Ser
    855                 860                 865

acc gca tgg acc tcc acc ggc ggc gac ggc ctc cta gtt gac ctg tcc   2755
Thr Ala Trp Thr Ser Thr Gly Gly Asp Gly Leu Leu Val Asp Leu Ser
870                 875                 880                 885

acg cct gcc cgc ctc gac cgc gtc atc ttg acc acc ggc acc ggc tcc   2803
Thr Pro Ala Arg Leu Asp Arg Val Ile Leu Thr Thr Gly Thr Gly Ser
                890                 895                 900

gac agc aac gtg acc tcg acc gtg aag atc tac gca ttc aac gac gcc   2851
Asp Ser Asn Val Thr Ser Thr Val Lys Ile Tyr Ala Phe Asn Asp Ala
            905                 910                 915

tca cca cac tcc ctg tcg gaa ggc atc gag atc ggc acc gtg gat tat   2899
Ser Pro His Ser Leu Ser Glu Gly Ile Glu Ile Gly Thr Val Asp Tyr
        920                 925                 930

tcc ggc cgc agt ctc agc cac agc atc cgc gat tcc tcc aag ctt ccg   2947
Ser Gly Arg Ser Leu Ser His Ser Ile Arg Asp Ser Ser Lys Leu Pro
    935                 940                 945

ggt cag gtg gaa tcc gtg gtg att ctg gtc gat gag gtt cgt tcc tca   2995
Gly Gln Val Glu Ser Val Val Ile Leu Val Asp Glu Val Arg Ser Ser
```

```
950                 955                 960                 965

caa acc tca gac acc aat cca cag atg cag atc gct gaa gta caa ctt   3043
Gln Thr Ser Asp Thr Asn Pro Gln Met Gln Ile Ala Glu Val Gln Leu
                970                 975                 980

gtt ggt tgg taaattacgc gtttgtgatt gac                             3075
Val Gly Trp
```

<210> 626
<211> 984
<212> PRT
<213> Corynebacterium glutamicum

<400> 626

```
Val Leu Gly Ala Val Leu Thr Ser Leu Val Ile Pro Val Leu Thr Arg
  1               5                  10                  15

Ala Glu Lys Glu Asp Ala Asp Gly Gly Ser Gly Phe Phe Arg Arg Leu
             20                  25                  30

Leu Thr Leu Ser Val Thr Leu Leu Gly Gly Val Thr Ile Leu Ser Ile
         35                  40                  45

Ile Gly Ala Pro Leu Leu Thr Arg Met Met Leu Ser Ser Glu Gly Gln
     50                  55                  60

Val Asn Val Val Met Ser Thr Ala Phe Ala Tyr Trp Leu Leu Pro Gln
 65                  70                  75                  80

Ile Phe Phe Tyr Gly Leu Phe Ala Leu Phe Met Ala Val Leu Asn Thr
                 85                  90                  95

Arg Glu Val Phe Lys Pro Gly Ala Trp Ala Pro Val Val Asn Asn Val
            100                 105                 110

Ile Thr Leu Thr Val Leu Gly Val Tyr Met Val Leu Pro Ala Arg Leu
        115                 120                 125

His Pro His Glu Gln Val Gly Ile Phe Asp Pro Gln Ile Ile Phe Leu
    130                 135                 140

Gly Val Gly Thr Thr Leu Gly Val Val Ala Gln Cys Leu Ile Met Ile
145                 150                 155                 160

Pro Tyr Leu Arg Arg Ala Gly Ile Asp Met Arg Pro Leu Trp Gly Ile
                165                 170                 175

Asp Ala Arg Leu Lys Gln Phe Gly Gly Met Ala Met Ala Ile Ile Val
            180                 185                 190

Tyr Val Ala Ile Ser Gln Phe Gly Tyr Ile Ile Thr Thr Arg Ile Ala
        195                 200                 205

Ser Ile Ala Asp Asp Ala Ala Pro Phe Ile Tyr Gln Gln His Trp Met
    210                 215                 220

Leu Leu Gln Val Pro Tyr Gly Ile Ile Gly Val Thr Leu Leu Thr Ala
225                 230                 235                 240
```

```
Ile Met Pro Arg Leu Ser Arg Asn Ala Ala Asp Gly Asp Asp Arg Ala
                245                 250                 255

Val Val Ser Asp Leu Gln Leu Gly Ser Lys Leu Thr Phe Ile Ala Leu
            260                 265                 270

Ile Pro Ile Val Val Phe Phe Thr Ala Phe Gly Val Pro Ile Ala Asn
        275                 280                 285

Gly Leu Phe Ala Tyr Gly Gln Phe Asp Ala Asn Ala Ala Asn Ile Leu
    290                 295                 300

Gly Trp Thr Leu Ser Phe Ser Ala Phe Thr Leu Ile Pro Tyr Ala Leu
305                 310                 315                 320

Val Leu Leu His Leu Arg Val Phe Tyr Ala Arg Glu Glu Val Trp Thr
                325                 330                 335

Pro Thr Phe Ile Ile Ala Gly Ile Thr Ala Thr Lys Val Val Leu Ser
            340                 345                 350

Leu Leu Ala Pro Leu Leu Ser Ser Ser Pro Glu Arg Val Val Val Leu
        355                 360                 365

Leu Gly Ala Ala Asn Gly Phe Ser Phe Ile Thr Gly Ala Val Ile Gly
    370                 375                 380

Ala Tyr Leu Leu Arg Asn Lys Leu Gly Leu Leu Gly Met Arg Ser Leu
385                 390                 395                 400

Ala Lys Thr Ser Leu Trp Ala Leu Gly Ser Ala Ala Val Gly Ala Ala
                405                 410                 415

Ala Ala Trp Ala Leu Gly Trp Leu Ile Gln Ala Val Val Gly Asp Phe
            420                 425                 430

Leu Leu Gly Thr Leu Ser Ser Val Gly Tyr Leu Leu Asn Leu Ala Val
        435                 440                 445

Leu Gly Val Phe Phe Ile Phe Val Thr Gly Ile Val Leu Ser Arg Ser
    450                 455                 460

Gly Leu Pro Glu Val Gln Asn Leu Gly Gln Ala Leu Thr Arg Ile Pro
465                 470                 475                 480

Gly Leu Ser Arg Phe Ile Arg Pro Asn Thr Lys Ile Ser Leu Asp Val
                485                 490                 495

Gly Glu Val Ser Glu Gln Asp Phe Ser Thr Gln Leu Val Ala Pro Ser
            500                 505                 510

Glu Phe Ala Ala Thr Pro Val Pro Pro Pro Met Ser Ala Gly Ile Val
        515                 520                 525

Arg Gly Pro Arg Leu Val Pro Gly Ala Pro Val Gly Asp Gly Arg Phe
    530                 535                 540

Arg Leu Leu Ala Asp His Gly Gly Val Gln Gly Ala Arg Phe Trp Gln
545                 550                 555                 560
```

Sequence Listing - 2005-05-26 - 15:55:34

```
Ala Arg Glu Ile Ala Thr Gly Lys Glu Val Ala Leu Ile Phe Val Asp
                565                 570                 575

Thr Ser Gly Asn Ala Pro Phe Ala Pro Leu Ser Ser Ala Ala Ala Ala
            580                 585                 590

Gly Ile Ala Tyr Glu Val Gln Arg Arg Thr Lys Lys Leu Ala Ser Leu
        595                 600                 605

Gly Ser Leu Ala Val Ala Pro Asn Ile His Ser Glu Ala Tyr Arg Asn
    610                 615                 620

Gly Cys Leu Ile Val Ala Asp Trp Val Pro Gly Ser Ser Leu Ser Ala
625                 630                 635                 640

Val Ala Glu Ser Gly Ala Asp Pro Arg Ala Ala Ala Phe Ala Leu Ala
                645                 650                 655

Glu Leu Thr Glu Thr Ile Gly Glu Ala His Glu Met Gly Ile Pro Ala
            660                 665                 670

Gly Leu Asp Asn Lys Cys Arg Ile Arg Ile Asn Thr Asp Gly His Ala
        675                 680                 685

Val Leu Ala Leu Pro Ala Ile Leu Pro Asp Ala Ser Glu Leu Arg Asp
    690                 695                 700

Ala Lys Ser Leu Ala Ser Ala Ala Glu Met Leu Ile Asp Ala Thr Leu
705                 710                 715                 720

Ala Pro Ser Asp Val Lys Ala Met Val Thr Glu Ala Gln Gly Leu Ala
                725                 730                 735

Thr Glu Asp Asn Pro Asp Tyr Ala Ser Leu Ala Met Ala Met Arg Thr
            740                 745                 750

Cys Gly Leu Phe Thr Glu Glu Pro Thr His Leu Val Val Lys Lys Glu
        755                 760                 765

Lys Thr Pro Lys Pro Ala Thr Arg Asp Gly Phe Gly Ala Ser Asp Tyr
    770                 775                 780

Thr Val Lys Gly Met Ala Ala Ile Ala Ala Val Val Ile Ile Leu Val
785                 790                 795                 800

Ser Leu Val Ala Ala Gly Thr Ala Phe Leu Thr Ser Phe Phe Gly Ser
                805                 810                 815

Ser Thr Asn Glu Gln Ser Pro Leu Ala Ser Val Glu Ala Thr Thr Ser
            820                 825                 830

Ala Thr Pro Glu Pro Val Gly Pro Pro Val Tyr Leu Asp Leu Asp Gln
        835                 840                 845

Ala Arg Thr Trp Asp Asp Gly Ala Gly Thr Asp Val Thr Asp Val Thr
    850                 855                 860

Asp Gly Asn Thr Ser Thr Ala Trp Thr Ser Thr Gly Gly Asp Gly Leu
865                 870                 875                 880

Leu Val Asp Leu Ser Thr Pro Ala Arg Leu Asp Arg Val Ile Leu Thr
```

```
                885                 890                 895

Thr Gly Thr Gly Ser Asp Ser Asn Val Thr Ser Thr Val Lys Ile Tyr
            900                 905                 910

Ala Phe Asn Asp Ala Ser Pro His Ser Leu Ser Glu Gly Ile Glu Ile
        915                 920                 925

Gly Thr Val Asp Tyr Ser Gly Arg Ser Leu Ser His Ser Ile Arg Asp
    930                 935                 940

Ser Ser Lys Leu Pro Gly Gln Val Glu Ser Val Val Ile Leu Val Asp
945                 950                 955                 960

Glu Val Arg Ser Ser Gln Thr Ser Asp Thr Asn Pro Gln Met Gln Ile
                965                 970                 975

Ala Glu Val Gln Leu Val Gly Trp
            980
```

<210> 627
<211> 389
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(366)
<223> FRXA01434

<400> 627

```
gtc acc gac ggc aac acc tcc acc gca tgg acc tcc acc ggc ggc gac   48
Val Thr Asp Gly Asn Thr Ser Thr Ala Trp Thr Ser Thr Gly Gly Asp
  1               5                  10                  15

ggc ctc cta gtt gac ctg tcc acg cct gcc cgc ctc gac cgc gtc atc   96
Gly Leu Leu Val Asp Leu Ser Thr Pro Ala Arg Leu Asp Arg Val Ile
             20                  25                  30

ttg acc acc ggc acc ggc tcc gac agc aac gtg acc tcg acc gtg aag   144
Leu Thr Thr Gly Thr Gly Ser Asp Ser Asn Val Thr Ser Thr Val Lys
         35                  40                  45

atc tac gca ttc aac gac gcc tca cca cac tcc ctg tcg gaa ggc atc   192
Ile Tyr Ala Phe Asn Asp Ala Ser Pro His Ser Leu Ser Glu Gly Ile
     50                  55                  60

gag atc ggc acc gtg gat tat tcc ggc cgc agt ctc agc cac agc atc   240
Glu Ile Gly Thr Val Asp Tyr Ser Gly Arg Ser Leu Ser His Ser Ile
 65                  70                  75                  80

cgc gat tcc tcc aag ctt ccg ggt cag gtg gaa tcc gtg gtg att ctg   288
Arg Asp Ser Ser Lys Leu Pro Gly Gln Val Glu Ser Val Val Ile Leu
                 85                  90                  95

gtc gat gag gtt cgt tcc tca caa acc tca gac acc aat cca cag atg   336
Val Asp Glu Val Arg Ser Ser Gln Thr Ser Asp Thr Asn Pro Gln Met
            100                 105                 110

cag atc gct gaa gta caa ctt gtt ggt tgg taaattacgc gtttgtgatt     386
```

```
Gln Ile Ala Glu Val Gln Leu Val Gly Trp
        115                 120

gac                                                                    389


<210> 628
<211> 122
<212> PRT
<213> Corynebacterium glutamicum

<400> 628
Val Thr Asp Gly Asn Thr Ser Thr Ala Trp Thr Ser Thr Gly Gly Asp
  1               5                  10                  15

Gly Leu Leu Val Asp Leu Ser Thr Pro Ala Arg Leu Asp Arg Val Ile
             20                  25                  30

Leu Thr Thr Gly Thr Gly Ser Asp Ser Asn Val Thr Ser Thr Val Lys
         35                  40                  45

Ile Tyr Ala Phe Asn Asp Ala Ser Pro His Ser Leu Ser Glu Gly Ile
     50                  55                  60

Glu Ile Gly Thr Val Asp Tyr Ser Gly Arg Ser Leu Ser His Ser Ile
 65                  70                  75                  80

Arg Asp Ser Ser Lys Leu Pro Gly Gln Val Glu Ser Val Val Ile Leu
                 85                  90                  95

Val Asp Glu Val Arg Ser Ser Gln Thr Ser Asp Thr Asn Pro Gln Met
            100                 105                 110

Gln Ile Ala Glu Val Gln Leu Val Gly Trp
        115                 120


<210> 629
<211> 1290
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1267)
<223> RXN01448

<400> 629
gtaatctcag cagttaaaaa gggcagttcc gcatcagggg gactgccctt tttcgtgtct 60

tctcatgctc ttgtgaatat gcatagctaa tcttgaggcc atg gca aag aag aaa   115
                                            Met Ala Lys Lys Lys
                                              1               5

ctg ggg act gtc gcc aga ctg tct gaa ctg gat aag tcc ctg cgc aat   163
Leu Gly Thr Val Ala Arg Leu Ser Glu Leu Asp Lys Ser Leu Arg Asn
                10                  15                  20

aga ttg ctg cgg gtt cgt tcc cga ctg ctg ttt att gtt cat tcc gca   211
Arg Leu Leu Arg Val Arg Ser Arg Leu Leu Phe Ile Val His Ser Ala
            25                  30                  35
```

```
att ggt gcg ggt gtg gcg tat tgg atc gcc gtg gaa gtg atc aaa cac   259
Ile Gly Ala Gly Val Ala Tyr Trp Ile Ala Val Glu Val Ile Lys His
         40                  45                  50

gga caa ccg ttt ttc gca ccg atg tcc gcg gtg att att ttg ggt ctc   307
Gly Gln Pro Phe Phe Ala Pro Met Ser Ala Val Ile Ile Leu Gly Leu
     55                  60                  65

tcc gga gga gac cgc atc aaa aga gcc acg gaa ctc acc ctg ggc tgt   355
Ser Gly Gly Asp Arg Ile Lys Arg Ala Thr Glu Leu Thr Leu Gly Cys
 70                  75                  80                  85

gct tta ggc gtt ggt ttg ggt gat tta ctg atc atg caa atc ggc acg   403
Ala Leu Gly Val Gly Leu Gly Asp Leu Leu Ile Met Gln Ile Gly Thr
                 90                  95                 100

ggc tat tgg cag ata ttt gtg gta gtt gga tta gcg ctg ctg gtg gcc   451
Gly Tyr Trp Gln Ile Phe Val Val Val Gly Leu Ala Leu Leu Val Ala
            105                 110                 115

tcg ttt gtt tca ccg gca ccg ttg gtg agt aat cag atg gcc att ggt   499
Ser Phe Val Ser Pro Ala Pro Leu Val Ser Asn Gln Met Ala Ile Gly
        120                 125                 130

ggc att ttg att gcc acg atg ttc ccg cca ggt gat ggt gga agc att   547
Gly Ile Leu Ile Ala Thr Met Phe Pro Pro Gly Asp Gly Gly Ser Ile
    135                 140                 145

gac cgt atg atc gac gcc ttc att ggt ggt ggc gtg gga att ttg gtc   595
Asp Arg Met Ile Asp Ala Phe Ile Gly Gly Gly Val Gly Ile Leu Val
150                 155                 160                 165

atc gca ctt ctt ccc tca tct cct ctt gac gca ggc cgg cat caa gtg   643
Ile Ala Leu Leu Pro Ser Ser Pro Leu Asp Ala Gly Arg His Gln Val
                170                 175                 180

gcc aac gtt ttg ggg atc gca gct agt gtg ctg gaa gac gtg gca gct   691
Ala Asn Val Leu Gly Ile Ala Ala Ser Val Leu Glu Asp Val Ala Ala
            185                 190                 195

tcc cta aaa gcc aag gat gca gcc aaa ctc aac aat gct ttg gaa gca   739
Ser Leu Lys Ala Lys Asp Ala Ala Lys Leu Asn Asn Ala Leu Glu Ala
        200                 205                 210

ttg aga agg tcg cag gcg tcg gtg aac aag ctg gaa act gcg gca tct   787
Leu Arg Arg Ser Gln Ala Ser Val Asn Lys Leu Glu Thr Ala Ala Ser
    215                 220                 225

tca ggc aag gaa gca acc acc gta tcg cca ttt tta tgg gga gat agg   835
Ser Gly Lys Glu Ala Thr Thr Val Ser Pro Phe Leu Trp Gly Asp Arg
230                 235                 240                 245

gcc cgc gtg aga tcg ctg tat cgc att ctg gcg cca gtg gac aac gtc   883
Ala Arg Val Arg Ser Leu Tyr Arg Ile Leu Ala Pro Val Asp Asn Val
                250                 255                 260

atc cga aat gct cga gtc ctt gcg cga cgg gca gtg gtg ctg acc gaa   931
Ile Arg Asn Ala Arg Val Leu Ala Arg Arg Ala Val Val Leu Thr Glu
            265                 270                 275
```

```
gac aat gac acc gtc agt gat gaa caa atc cac gtg att gag gaa atc   979
Asp Asn Asp Thr Val Ser Asp Glu Gln Ile His Val Ile Glu Glu Ile
        280                 285                 290

gca gac att gca ctg cga ctg tca gac ctt tat gag cac cac aaa gaa   1027
Ala Asp Ile Ala Leu Arg Leu Ser Asp Leu Tyr Glu His His Lys Glu
    295                 300                 305

atc agt gaa gca ctg gaa att cct gag ttg gtt aac cga ctg cgt caa   1075
Ile Ser Glu Ala Leu Glu Ile Pro Glu Leu Val Asn Arg Leu Arg Gln
310                 315                 320                 325

ctg ggc agt gaa gtg ggc gag gac atc gcc gaa gat cga gtg cta tcc   1123
Leu Gly Ser Glu Val Gly Glu Asp Ile Ala Glu Asp Arg Val Leu Ser
                330                 335                 340

gca caa gta att ttg gcg caa tcg cga tcc atc att gtg gac ctg ttg   1171
Ala Gln Val Ile Leu Ala Gln Ser Arg Ser Ile Ile Val Asp Leu Leu
            345                 350                 355

cag atc tgc ggc atg tcc agg gaa tct gcg gtg gca gtg ttg gtt ccg   1219
Gln Ile Cys Gly Met Ser Arg Glu Ser Ala Val Ala Val Leu Val Pro
        360                 365                 370

acc tca gag agt ccg gct tac cct ccg gag ctg tgg gat gac gaa gac   1267
Thr Ser Glu Ser Pro Ala Tyr Pro Pro Glu Leu Trp Asp Asp Glu Asp
    375                 380                 385

tagcctttta tcgcggttcg gtt                                        1290


<210> 630
<211> 389
<212> PRT
<213> Corynebacterium glutamicum

<400> 630
Met Ala Lys Lys Lys Leu Gly Thr Val Ala Arg Leu Ser Glu Leu Asp
  1               5                  10                  15

Lys Ser Leu Arg Asn Arg Leu Leu Arg Val Arg Ser Arg Leu Leu Phe
             20                  25                  30

Ile Val His Ser Ala Ile Gly Ala Gly Val Ala Tyr Trp Ile Ala Val
         35                  40                  45

Glu Val Ile Lys His Gly Gln Pro Phe Phe Ala Pro Met Ser Ala Val
     50                  55                  60

Ile Ile Leu Gly Leu Ser Gly Gly Asp Arg Ile Lys Arg Ala Thr Glu
 65                  70                  75                  80

Leu Thr Leu Gly Cys Ala Leu Gly Val Gly Leu Gly Asp Leu Leu Ile
                 85                  90                  95

Met Gln Ile Gly Thr Gly Tyr Trp Gln Ile Phe Val Val Val Gly Leu
            100                 105                 110

Ala Leu Leu Val Ala Ser Phe Val Ser Pro Ala Pro Leu Val Ser Asn
        115                 120                 125
```

```
Gln Met Ala Ile Gly Gly Ile Leu Ile Ala Thr Met Phe Pro Pro Gly
    130                 135                 140

Asp Gly Gly Ser Ile Asp Arg Met Ile Asp Ala Phe Ile Gly Gly Gly
145                 150                 155                 160

Val Gly Ile Leu Val Ile Ala Leu Leu Pro Ser Ser Pro Leu Asp Ala
                165                 170                 175

Gly Arg His Gln Val Ala Asn Val Leu Gly Ile Ala Ala Ser Val Leu
            180                 185                 190

Glu Asp Val Ala Ala Ser Leu Lys Ala Lys Asp Ala Ala Lys Leu Asn
        195                 200                 205

Asn Ala Leu Glu Ala Leu Arg Arg Ser Gln Ala Ser Val Asn Lys Leu
    210                 215                 220

Glu Thr Ala Ala Ser Ser Gly Lys Glu Ala Thr Thr Val Ser Pro Phe
225                 230                 235                 240

Leu Trp Gly Asp Arg Ala Arg Val Arg Ser Leu Tyr Arg Ile Leu Ala
                245                 250                 255

Pro Val Asp Asn Val Ile Arg Asn Ala Arg Val Leu Ala Arg Arg Ala
            260                 265                 270

Val Val Leu Thr Glu Asp Asn Asp Thr Val Ser Asp Glu Gln Ile His
        275                 280                 285

Val Ile Glu Glu Ile Ala Asp Ile Ala Leu Arg Leu Ser Asp Leu Tyr
    290                 295                 300

Glu His His Lys Glu Ile Ser Glu Ala Leu Glu Ile Pro Glu Leu Val
305                 310                 315                 320

Asn Arg Leu Arg Gln Leu Gly Ser Glu Val Gly Glu Asp Ile Ala Glu
                325                 330                 335

Asp Arg Val Leu Ser Ala Gln Val Ile Leu Ala Gln Ser Arg Ser Ile
            340                 345                 350

Ile Val Asp Leu Leu Gln Ile Cys Gly Met Ser Arg Glu Ser Ala Val
        355                 360                 365

Ala Val Leu Val Pro Thr Ser Glu Ser Pro Ala Tyr Pro Pro Glu Leu
    370                 375                 380

Trp Asp Asp Glu Asp
385
```

<210> 631
<211> 842
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (40)..(819)
<223> FRXA01448

<400> 631
gcctcgtttg tttcaccggc accgttggtg agtaatcagatg gcc att ggt ggc att 57
Met Ala Ile Gly Gly Ile
1 5

ttg att gcc acg atg ttc ccg cca ggt gat ggt gga agc att gac cgt 105
Leu Ile Ala Thr Met Phe Pro Pro Gly Asp Gly Gly Ser Ile Asp Arg
10 15 20

atg atc gac gcc ttc att ggt ggt ggc gtg gga att ttg gtc atc gca 153
Met Ile Asp Ala Phe Ile Gly Gly Gly Val Gly Ile Leu Val Ile Ala
25 30 35

ctt ctt ccc tca tct cct ctt gac gca ggc cgg cat caa gtg gcc aac 201
Leu Leu Pro Ser Ser Pro Leu Asp Ala Gly Arg His Gln Val Ala Asn
40 45 50

gtt ttg ggg atc gca gct agt gtg ctg gaa gac gtg gca gct tcc cta 249
Val Leu Gly Ile Ala Ala Ser Val Leu Glu Asp Val Ala Ala Ser Leu
55 60 65 70

aaa gcc aag gat gca gcc aaa ctc aac aat gct ttg gaa gca ttg aga 297
Lys Ala Lys Asp Ala Ala Lys Leu Asn Asn Ala Leu Glu Ala Leu Arg
75 80 85

agg tcg cag gcg tcg gtg aac aag ctg gaa act gcg gca tct tca ggc 345
Arg Ser Gln Ala Ser Val Asn Lys Leu Glu Thr Ala Ala Ser Ser Gly
90 95 100

aag gaa gca acc acc gta tcg cca ttt tta tgg gga gat agg gcc cgc 393
Lys Glu Ala Thr Thr Val Ser Pro Phe Leu Trp Gly Asp Arg Ala Arg
105 110 115

gtg aga tcg ctg tat cgc att ctg gcg cca gtg gac aac gtc atc cga 441
Val Arg Ser Leu Tyr Arg Ile Leu Ala Pro Val Asp Asn Val Ile Arg
120 125 130

aat gct cga gtc ctt gcg cga cgg gca gtg gtg ctg acc gaa gac aat 489
Asn Ala Arg Val Leu Ala Arg Arg Ala Val Val Leu Thr Glu Asp Asn
135 140 145 150

gac acc gtc agt gat gaa caa atc cac gtg att gag gaa atc gca gac 537
Asp Thr Val Ser Asp Glu Gln Ile His Val Ile Glu Glu Ile Ala Asp
155 160 165

att gca ctg cga ctg tca gac ctt tat gag cac cac aaa gaa atc agt 585
Ile Ala Leu Arg Leu Ser Asp Leu Tyr Glu His His Lys Glu Ile Ser
170 175 180

gaa gca ctg gaa att cct gag ttg gtt aac cga ctg cgt caa ctg ggc 633
Glu Ala Leu Glu Ile Pro Glu Leu Val Asn Arg Leu Arg Gln Leu Gly
185 190 195

agt gaa gtg ggc gag gac atc gcc gaa gat cga gtg cta tcc gca caa 681
Ser Glu Val Gly Glu Asp Ile Ala Glu Asp Arg Val Leu Ser Ala Gln
200 205 210

gta att ttg gcg caa tcg cga tcc atc att gtg gac ctg ttg cag atc 729
Val Ile Leu Ala Gln Ser Arg Ser Ile Ile Val Asp Leu Leu Gln Ile
215 220 225 230

```
tgc ggc atg tcc agg gaa tct gcg gtg gca gtg ttg gtt ccg acc tca   777
Cys Gly Met Ser Arg Glu Ser Ala Val Ala Val Leu Val Pro Thr Ser
                235                 240                 245

gag agt ccg gct tac cct ccg gag ctg tgg gat gac gaa gac           819
Glu Ser Pro Ala Tyr Pro Pro Glu Leu Trp Asp Asp Glu Asp
            250                 255                 260

tagcctttta tcgcggttcg gtt                                        842


<210> 632
<211> 260
<212> PRT
<213> Corynebacterium glutamicum

<400> 632
Met Ala Ile Gly Gly Ile Leu Ile Ala Thr Met Phe Pro Pro Gly Asp
  1               5                  10                  15

Gly Gly Ser Ile Asp Arg Met Ile Asp Ala Phe Ile Gly Gly Gly Val
             20                  25                  30

Gly Ile Leu Val Ile Ala Leu Leu Pro Ser Ser Pro Leu Asp Ala Gly
         35                  40                  45

Arg His Gln Val Ala Asn Val Leu Gly Ile Ala Ala Ser Val Leu Glu
     50                  55                  60

Asp Val Ala Ala Ser Leu Lys Ala Lys Asp Ala Ala Lys Leu Asn Asn
 65                  70                  75                  80

Ala Leu Glu Ala Leu Arg Arg Ser Gln Ala Ser Val Asn Lys Leu Glu
                 85                  90                  95

Thr Ala Ala Ser Ser Gly Lys Glu Ala Thr Thr Val Ser Pro Phe Leu
            100                 105                 110

Trp Gly Asp Arg Ala Arg Val Arg Ser Leu Tyr Arg Ile Leu Ala Pro
        115                 120                 125

Val Asp Asn Val Ile Arg Asn Ala Arg Val Leu Ala Arg Arg Ala Val
    130                 135                 140

Val Leu Thr Glu Asp Asn Asp Thr Val Ser Asp Glu Gln Ile His Val
145                 150                 155                 160

Ile Glu Glu Ile Ala Asp Ile Ala Leu Arg Leu Ser Asp Leu Tyr Glu
                165                 170                 175

His His Lys Glu Ile Ser Glu Ala Leu Glu Ile Pro Glu Leu Val Asn
            180                 185                 190

Arg Leu Arg Gln Leu Gly Ser Glu Val Gly Glu Asp Ile Ala Glu Asp
        195                 200                 205

Arg Val Leu Ser Ala Gln Val Ile Leu Ala Gln Ser Arg Ser Ile Ile
    210                 215                 220

Val Asp Leu Leu Gln Ile Cys Gly Met Ser Arg Glu Ser Ala Val Ala
```

```
225                 230                 235                 240

Val Leu Val Pro Thr Ser Glu Ser Pro Ala Tyr Pro Pro Glu Leu Trp
                245                 250                 255

Asp Asp Glu Asp
            260


<210> 633
<211> 933
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(910)
<223> RXN01459

<400> 633
gattcggcga ttcacgaata tccaccctac aacctgtgtt cgcttacagc gttgttcgga 60

tcgtagcaat aggaaatagt tgccttgtag attggtaaat atg aac tct aat ggc   115
                                            Met Asn Ser Asn Gly
                                              1               5

ttt ggt ttc tct ttt ggc aac aac gat gac gac gat gac aaa aac cgc   163
Phe Gly Phe Ser Phe Gly Asn Asn Asp Asp Asp Asp Lys Asn Arg
                10                  15                  20

aac aac gac cca ttc ggc ctt ttc ggt ggc aac ttc gga ttc gga gga   211
Asn Asn Asp Pro Phe Gly Leu Phe Gly Gly Asn Phe Gly Phe Gly Gly
            25                  30                  35

caa ggt ggc gct ggt ggc ccc ggc gga tta ggc gat att tta aac cag   259
Gln Gly Gly Ala Gly Gly Pro Gly Gly Leu Gly Asp Ile Leu Asn Gln
        40                  45                  50

ttc ggc cag atg ctg tcc gga atg gga gat tcg atg aac tcc ccc gaa   307
Phe Gly Gln Met Leu Ser Gly Met Gly Asp Ser Met Asn Ser Pro Glu
    55                  60                  65

gca gca ggc ccg gtt aat tat gat tta gca gca cgc atc gcc cgc cag   355
Ala Ala Gly Pro Val Asn Tyr Asp Leu Ala Ala Arg Ile Ala Arg Gln
70                  75                  80                  85

cag att ggt cgc gta gcg ccg gtg aag gat tct gag aag gaa gca gtc   403
Gln Ile Gly Arg Val Ala Pro Val Lys Asp Ser Glu Lys Glu Ala Val
                90                  95                  100

gaa gag tcc ctt cgc ctt gct gaa ctc tgg ctc gat aac gcc acc cag   451
Glu Glu Ser Leu Arg Leu Ala Glu Leu Trp Leu Asp Asn Ala Thr Gln
            105                 110                 115

ctc ccc act tcc ggg cac cgc gtc gaa gcg tgg aat cca gaa aac tgg   499
Leu Pro Thr Ser Gly His Arg Val Glu Ala Trp Asn Pro Glu Asn Trp
        120                 125                 130

tta gaa aac acc ctg cct gtg tgg aag cgt ctt gtc tcc cct gtt gcg   547
Leu Glu Asn Thr Leu Pro Val Trp Lys Arg Leu Val Ser Pro Val Ala
    135                 140                 145
```

```
gag caa atg aac aaa gcc caa tta gaa aac ctc cct gaa gaa gcc cgc   595
Glu Gln Met Asn Lys Ala Gln Leu Glu Asn Leu Pro Glu Glu Ala Arg
150                 155                 160                 165

gag atg atg ggc ccg atg tct tct ttg atg aac tcc atg tct tcg atg   643
Glu Met Met Gly Pro Met Ser Ser Leu Met Asn Ser Met Ser Ser Met
                170                 175                 180

aac ttc gga gtt caa tta gga aat gcg ctg ggc gac ctc gca aag cag   691
Asn Phe Gly Val Gln Leu Gly Asn Ala Leu Gly Asp Leu Ala Lys Gln
            185                 190                 195

acc ctc acc ggc tct gac ttc ggt ttg cct atc tcc cca gtc ggc gta   739
Thr Leu Thr Gly Ser Asp Phe Gly Leu Pro Ile Ser Pro Val Gly Val
        200                 205                 210

tct gcc gtc ctg ccc ggc aac atc gcc gaa gca tcc aaa ggc ctc aac   787
Ser Ala Val Leu Pro Gly Asn Ile Ala Glu Ala Ser Lys Gly Leu Asn
    215                 220                 225

gtg gca ccg caa gaa atg ctc gtt tac atc tgt gcc cgc gaa gcc gcc   835
Val Ala Pro Gln Glu Met Leu Val Tyr Ile Cys Ala Arg Glu Ala Ala
230                 235                 240                 245

gcc aac gcc tct tca agc acg tgc cgt ggc ttg tcg agc gcc tcg ttt   883
Ala Asn Ala Ser Ser Ser Thr Cys Arg Gly Leu Ser Ser Ala Ser Phe
                250                 255                 260

cct ccg ttg agg aat acg ccg tcg gcc tagaaatcga cacctcacac         930
Pro Pro Leu Arg Asn Thr Pro Ser Ala
            265                 270

att                                                               933
```

<210> 634
<211> 270
<212> PRT
<213> Corynebacterium glutamicum

<400> 634

```
Met Asn Ser Asn Gly Phe Gly Phe Ser Phe Gly Asn Asn Asp Asp Asp
  1               5                  10                  15

Asp Asp Lys Asn Arg Asn Asn Asp Pro Phe Gly Leu Phe Gly Gly Asn
             20                  25                  30

Phe Gly Phe Gly Gly Gln Gly Gly Ala Gly Gly Pro Gly Gly Leu Gly
         35                  40                  45

Asp Ile Leu Asn Gln Phe Gly Gln Met Leu Ser Gly Met Gly Asp Ser
     50                  55                  60

Met Asn Ser Pro Glu Ala Ala Gly Pro Val Asn Tyr Asp Leu Ala Ala
 65                  70                  75                  80

Arg Ile Ala Arg Gln Gln Ile Gly Arg Val Ala Pro Val Lys Asp Ser
                 85                  90                  95

Glu Lys Glu Ala Val Glu Glu Ser Leu Arg Leu Ala Glu Leu Trp Leu
```

```
            100                 105                 110

Asp Asn Ala Thr Gln Leu Pro Thr Ser Gly His Arg Val Glu Ala Trp
        115                 120                 125

Asn Pro Glu Asn Trp Leu Glu Asn Thr Leu Pro Val Trp Lys Arg Leu
    130                 135                 140

Val Ser Pro Val Ala Glu Gln Met Asn Lys Ala Gln Leu Glu Asn Leu
145                 150                 155                 160

Pro Glu Glu Ala Arg Glu Met Met Gly Pro Met Ser Ser Leu Met Asn
                165                 170                 175

Ser Met Ser Ser Met Asn Phe Gly Val Gln Leu Gly Asn Ala Leu Gly
            180                 185                 190

Asp Leu Ala Lys Gln Thr Leu Thr Gly Ser Asp Phe Gly Leu Pro Ile
        195                 200                 205

Ser Pro Val Gly Val Ser Ala Val Leu Pro Gly Asn Ile Ala Glu Ala
    210                 215                 220

Ser Lys Gly Leu Asn Val Ala Pro Gln Glu Met Leu Val Tyr Ile Cys
225                 230                 235                 240

Ala Arg Glu Ala Ala Ala Asn Ala Ser Ser Ser Thr Cys Arg Gly Leu
                245                 250                 255

Ser Ser Ala Ser Phe Pro Pro Leu Arg Asn Thr Pro Ser Ala
            260                 265                 270


<210> 635
<211> 933
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(910)
<223> FRXA01459

<400> 635
gattcggcga ttcacgaata tccaccctac aacctgtgtt cgcttacagc gttgttcgga 60

tcgtagcaat aggaaatagt tgccttgtag attggtaaat atg aac tct aat ggc   115
                                            Met Asn Ser Asn Gly
                                              1               5

ttt ggt ttc tct ttt ggc aac aac gat gac gac gat gac aaa aac cgc   163
Phe Gly Phe Ser Phe Gly Asn Asn Asp Asp Asp Asp Asp Lys Asn Arg
                10                  15                  20

aac aac gac cca ttc ggc ctt ttc ggt ggc aac ttc gga ttc gga gga   211
Asn Asn Asp Pro Phe Gly Leu Phe Gly Gly Asn Phe Gly Phe Gly Gly
            25                  30                  35

caa ggt ggc gct ggt ggc ccc ggc gga tta ggc gat att tta aac cag   259
Gln Gly Gly Ala Gly Gly Pro Gly Gly Leu Gly Asp Ile Leu Asn Gln
        40                  45                  50
```

```
ttc ggc cag atg ctg tcc gga atg gga gat tcg atg aac tcc ccc gaa   307
Phe Gly Gln Met Leu Ser Gly Met Gly Asp Ser Met Asn Ser Pro Glu
     55                  60                  65

gca gca ggc ccg gtt aat tat gat tta gca gca cgc atc gcc cgc cag   355
Ala Ala Gly Pro Val Asn Tyr Asp Leu Ala Ala Arg Ile Ala Arg Gln
 70                  75                  80                  85

cag att ggt cgc gta gcg ccg gtg aag gat tct gag aag gaa gca gtc   403
Gln Ile Gly Arg Val Ala Pro Val Lys Asp Ser Glu Lys Glu Ala Val
                 90                  95                 100

gaa gag tcc ctt cgc ctt gct gaa ctc tgg ctc gat aac gcc acc cag   451
Glu Glu Ser Leu Arg Leu Ala Glu Leu Trp Leu Asp Asn Ala Thr Gln
            105                 110                 115

ctc ccc act tcc ggg cac cgc gtc gaa gcg tgg aat cca gaa aac tgg   499
Leu Pro Thr Ser Gly His Arg Val Glu Ala Trp Asn Pro Glu Asn Trp
        120                 125                 130

tta gaa aac acc ctg cct gtg tgg aag cgt ctt gtc tcc cct gtt gcg   547
Leu Glu Asn Thr Leu Pro Val Trp Lys Arg Leu Val Ser Pro Val Ala
    135                 140                 145

gag caa atg aac aaa gcc caa tta gaa aac ctc cct gaa gaa gcc cgc   595
Glu Gln Met Asn Lys Ala Gln Leu Glu Asn Leu Pro Glu Glu Ala Arg
150                 155                 160                 165

gag atg atg ggc ccg atg tct tct ttg atg aac tcc atg tct tcg atg   643
Glu Met Met Gly Pro Met Ser Ser Leu Met Asn Ser Met Ser Ser Met
                170                 175                 180

aac ttc gga gtt caa tta gga aat gcg ctg ggc gac ctc gca aag cag   691
Asn Phe Gly Val Gln Leu Gly Asn Ala Leu Gly Asp Leu Ala Lys Gln
            185                 190 *               195

acc ctc acc ggc tct gac ttc ggt ttg cct atc tcc cca gtc ggc gta   739
Thr Leu Thr Gly Ser Asp Phe Gly Leu Pro Ile Ser Pro Val Gly Val
        200                 205                 210

tct gcc gtc ctg ccc ggc aac atc gcc gaa gca tcc aaa ggc ctc aac   787
Ser Ala Val Leu Pro Gly Asn Ile Ala Glu Ala Ser Lys Gly Leu Asn
    215                 220                 225

gtg gca ccg caa gaa atg ctc gtt tac atc tgt gcc cgc gaa gcc gcc   835
Val Ala Pro Gln Glu Met Leu Val Tyr Ile Cys Ala Arg Glu Ala Ala
230                 235                 240                 245

gcc aac gcc tct tca agc acg tgc cgt ggc ttg tcg agc gcc tcg ttt   883
Ala Asn Ala Ser Ser Ser Thr Cys Arg Gly Leu Ser Ser Ala Ser Phe
                250                 255                 260

cct ccg ttg agg aat acg ccg tcg gcc tagaaatcga cacctcacac         930
Pro Pro Leu Arg Asn Thr Pro Ser Ala
            265                 270

att                                                               933
```

<210> 636

<211> 270
<212> PRT
<213> Corynebacterium glutamicum

<400> 636

```
Met Asn Ser Asn Gly Phe Gly Phe Ser Phe Gly Asn Asn Asp Asp Asp
  1               5                  10                  15

Asp Asp Lys Asn Arg Asn Asn Asp Pro Phe Gly Leu Phe Gly Gly Asn
             20                  25                  30

Phe Gly Phe Gly Gly Gln Gly Gly Ala Gly Gly Pro Gly Gly Leu Gly
         35                  40                  45

Asp Ile Leu Asn Gln Phe Gly Gln Met Leu Ser Gly Met Gly Asp Ser
     50                  55                  60

Met Asn Ser Pro Glu Ala Ala Gly Pro Val Asn Tyr Asp Leu Ala Ala
 65                  70                  75                  80

Arg Ile Ala Arg Gln Gln Ile Gly Arg Val Ala Pro Val Lys Asp Ser
                 85                  90                  95

Glu Lys Glu Ala Val Glu Glu Ser Leu Arg Leu Ala Glu Leu Trp Leu
            100                 105                 110

Asp Asn Ala Thr Gln Leu Pro Thr Ser Gly His Arg Val Glu Ala Trp
        115                 120                 125

Asn Pro Glu Asn Trp Leu Glu Asn Thr Leu Pro Val Trp Lys Arg Leu
    130                 135                 140

Val Ser Pro Val Ala Glu Gln Met Asn Lys Ala Gln Leu Glu Asn Leu
145                 150                 155                 160

Pro Glu Glu Ala Arg Glu Met Met Gly Pro Met Ser Ser Leu Met Asn
                165                 170                 175

Ser Met Ser Ser Met Asn Phe Gly Val Gln Leu Gly Asn Ala Leu Gly
            180                 185                 190

Asp Leu Ala Lys Gln Thr Leu Thr Gly Ser Asp Phe Gly Leu Pro Ile
        195                 200                 205

Ser Pro Val Gly Val Ser Ala Val Leu Pro Gly Asn Ile Ala Glu Ala
    210                 215                 220

Ser Lys Gly Leu Asn Val Ala Pro Gln Glu Met Leu Val Tyr Ile Cys
225                 230                 235                 240

Ala Arg Glu Ala Ala Ala Asn Ala Ser Ser Ser Thr Cys Arg Gly Leu
                245                 250                 255

Ser Ser Ala Ser Phe Pro Pro Leu Arg Asn Thr Pro Ser Ala
            260                 265                 270
```

<210> 637
<211> 417
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(394)
<223> RXN01460

<400> 637
gcaacatcgc cgaagcatcc aaaggcctca acgtggcacc gcaagaaatg ctcgtttaca 60

tctgtgcccg cgaagccgcc gccaacgcct cttcaagcac gtg ccg tgg ctt gtc 115
Val Pro Trp Leu Val
1 5

gag cgc ctc gtt tcc tcc gtt gag gaa tac gcc gtc ggc cta gaa atc 163
Glu Arg Leu Val Ser Ser Val Glu Glu Tyr Ala Val Gly Leu Glu Ile
10 15 20

gac acc tca cac att caa gag gcc atg ggc aac ttc caa atg gac aac 211
Asp Thr Ser His Ile Gln Glu Ala Met Gly Asn Phe Gln Met Asp Asn
25 30 35

cca gat cct gaa cgc ctc cag gaa atg atg aac gaa ctc caa ggt atg 259
Pro Asp Pro Glu Arg Leu Gln Glu Met Met Asn Glu Leu Gln Gly Met
40 45 50

gac ctg tcc cca cgc atc gga tcc cgc aac gcc aac gca gta tcc cgc 307
Asp Leu Ser Pro Arg Ile Gly Ser Arg Asn Ala Asn Ala Val Ser Arg
55 60 65

ctg gaa act ctc ctc gca ctc gtc gaa ggc tgg gtc gac atc gta gtt 355
Leu Glu Thr Leu Leu Ala Leu Val Glu Gly Trp Val Asp Ile Val Val
70 75 80 85

acc caa gcc ctg agc gaa cgc att cca tca ccg acg cca tgaacgaagc 404
Thr Gln Ala Leu Ser Glu Arg Ile Pro Ser Pro Thr Pro
90 95

ctggaagcgc cgc 417

<210> 638
<211> 98
<212> PRT
<213> Corynebacterium glutamicum

<400> 638
Val Pro Trp Leu Val Glu Arg Leu Val Ser Ser Val Glu Glu Tyr Ala
1 5 10 15

Val Gly Leu Glu Ile Asp Thr Ser His Ile Gln Glu Ala Met Gly Asn
20 25 30

Phe Gln Met Asp Asn Pro Asp Pro Glu Arg Leu Gln Glu Met Met Asn
35 40 45

Glu Leu Gln Gly Met Asp Leu Ser Pro Arg Ile Gly Ser Arg Asn Ala
50 55 60

Asn Ala Val Ser Arg Leu Glu Thr Leu Leu Ala Leu Val Glu Gly Trp
65 70 75 80

```
Val Asp Ile Val Val Thr Gln Ala Leu Ser Glu Arg Ile Pro Ser Pro
                 85                  90                  95

Thr Pro



<210> 639
<211> 417
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(394)
<223> FRXA01460

<400> 639
gcaacatcgc cgaagcatcc aaaggcctca acgtggcacc gcaagaaatg ctcgtttaca 60

tctgtgcccg cgaagccgcc gccaacgcct cttcaagcac gtg ccg tgg ctt gtc   115
                                          Val Pro Trp Leu Val
                                            1               5

gag cgc ctc gtt tcc tcc gtt gag gaa tac gcc gtc ggc cta gaa atc   163
Glu Arg Leu Val Ser Ser Val Glu Glu Tyr Ala Val Gly Leu Glu Ile
                10                  15                  20

gac acc tca cac att caa gag gcc atg ggc aac ttc caa atg gac aac   211
Asp Thr Ser His Ile Gln Glu Ala Met Gly Asn Phe Gln Met Asp Asn
            25                  30                  35

cca gat cct gaa cgc ctc cag gaa atg atg aac gaa ctc caa ggt atg   259
Pro Asp Pro Glu Arg Leu Gln Glu Met Met Asn Glu Leu Gln Gly Met
        40                  45                  50

gac ctg tcc cca cgc atc gga tcc cgc aac gcc aac gca gta tcc cgc   307
Asp Leu Ser Pro Arg Ile Gly Ser Arg Asn Ala Asn Ala Val Ser Arg
    55                  60                  65

ctg gaa act ctc ctc gca ctc gtc gaa ggc tgg gtc gac atc gta gtt   355
Leu Glu Thr Leu Leu Ala Leu Val Glu Gly Trp Val Asp Ile Val Val
70                  75                  80                  85

acc caa gcc ctg agc gaa cgc att cca tca ccg acg cca tgaacgaagc    404
Thr Gln Ala Leu Ser Glu Arg Ile Pro Ser Pro Thr Pro
                90                  95

ctggaagcgc cgc                                                   417


<210> 640
<211> 98
<212> PRT
<213> Corynebacterium glutamicum

<400> 640
Val Pro Trp Leu Val Glu Arg Leu Val Ser Ser Val Glu Glu Tyr Ala
  1               5                  10                  15

Val Gly Leu Glu Ile Asp Thr Ser His Ile Gln Glu Ala Met Gly Asn
```

```
            20                  25                  30

Phe Gln Met Asp Asn Pro Asp Pro Glu Arg Leu Gln Glu Met Met Asn
         35                  40                  45

Glu Leu Gln Gly Met Asp Leu Ser Pro Arg Ile Gly Ser Arg Asn Ala
     50                  55                  60

Asn Ala Val Ser Arg Leu Glu Thr Leu Leu Ala Leu Val Glu Gly Trp
 65                  70                  75                  80

Val Asp Ile Val Val Thr Gln Ala Leu Ser Glu Arg Ile Pro Ser Pro
                 85                  90                  95

Thr Pro
```

<210> 641
<211> 930
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(907)
<223> RXN01471

<400> 641

```
cctccaacca gagctataaa aaaggttgta gaagaaattt cttaacatac atcgttgtgt 60

tgccaggggt ttaacagatt agttgctaag gtctgtctcc atg cag agt ttt aag   115
                                           Met Gln Ser Phe Lys
                                             1               5

acg ctt gaa tct tgg cct gtc gac aat gtt tcg gcc agt gtc atc tcc   163
Thr Leu Glu Ser Trp Pro Val Asp Asn Val Ser Ala Ser Val Ile Ser
                 10                  15                  20

gac ggc gcc gtg cac ttt tac ggc gac gtc gat cgt gtt ttt gaa ctc   211
Asp Gly Ala Val His Phe Tyr Gly Asp Val Asp Arg Val Phe Glu Leu
             25                  30                  35

atg agt gtg aca aaa ctc ctg gcc acc tac ggt ttc ctt gtt gcc atc   259
Met Ser Val Thr Lys Leu Leu Ala Thr Tyr Gly Phe Leu Val Ala Ile
         40                  45                  50

gaa gaa ggt gtt ttt gag ctc gat tca ccg atg ggt cct gaa gga tcc   307
Glu Glu Gly Val Phe Glu Leu Asp Ser Pro Met Gly Pro Glu Gly Ser
     55                  60                  65

aca gtg agg cat ctg ctc tca cat gct tcc ggc gtg gca ttc gat aag   355
Thr Val Arg His Leu Leu Ser His Ala Ser Gly Val Ala Phe Asp Lys
 70                  75                  80                  85

ccg gta gcg gaa aag gga gtg ggg gag cgc cgc att tac tcc tct gct   403
Pro Val Ala Glu Lys Gly Val Gly Glu Arg Arg Ile Tyr Ser Ser Ala
                 90                  95                 100

ggc atg gac atc ttg gcg gat gct gtt gcc gct gaa gct gaa atg ccg   451
Gly Met Asp Ile Leu Ala Asp Ala Val Ala Ala Glu Ala Glu Met Pro
```

```
            105                 110                 115

ttt gca gag tat ctc cgc gag gct gtg ttc gag cct ttg gga atg gag   499
Phe Ala Glu Tyr Leu Arg Glu Ala Val Phe Glu Pro Leu Gly Met Glu
        120                 125                 130

aac tct gaa cta tgg ggt tct gcg ggc cac gag gcg cgc agc aca gtg   547
Asn Ser Glu Leu Trp Gly Ser Ala Gly His Glu Ala Arg Ser Thr Val
    135                 140                 145

gct gat ctg acc aag ttc ggc caa gag ctc acc gca cca act ctg atc   595
Ala Asp Leu Thr Lys Phe Gly Gln Glu Leu Thr Ala Pro Thr Leu Ile
150                 155                 160                 165

tca cca gaa acc ctt gca gag gct ttc cag gtg caa ttc ccg gaa ctg   643
Ser Pro Glu Thr Leu Ala Glu Ala Phe Gln Val Gln Phe Pro Glu Leu
                170                 175                 180

att ggc acc gtc ccc ggt tat ggc atg cag aag ccg tgt ccg tgg gga   691
Ile Gly Thr Val Pro Gly Tyr Gly Met Gln Lys Pro Cys Pro Trp Gly
            185                 190                 195

ttg ggc ttt gaa att aag gga cag aag tcg ccg cac tgg aca ggt gac   739
Leu Gly Phe Glu Ile Lys Gly Gln Lys Ser Pro His Trp Thr Gly Asp
        200                 205                 210

ttg atg ccg gag aac act gct gga cac ttt gga cag tcg gga aca ttc   787
Leu Met Pro Glu Asn Thr Ala Gly His Phe Gly Gln Ser Gly Thr Phe
    215                 220                 225

ttt tgg act gtt cca ggc tca ggt caa gtc ggg gtt gtt ttg act gac   835
Phe Trp Thr Val Pro Gly Ser Gly Gln Val Gly Val Val Leu Thr Asp
230                 235                 240                 245

cga aat ttc ggt cct tgg gct aaa ccg ttg tgg act gcc ttc aat gac   883
Arg Asn Phe Gly Pro Trp Ala Lys Pro Leu Trp Thr Ala Phe Asn Asp
                250                 255                 260

gaa gtc tgg gcc gag tta aat tca taaacttttg ccgtaattac ggt         930
Glu Val Trp Ala Glu Leu Asn Ser
            265
```

[illegible]

<210> 642
<211> 269
<212> PRT
<213> Corynebacterium glutamicum

<400> 642

```
Met Gln Ser Phe Lys Thr Leu Glu Ser Trp Pro Val Asp Asn Val Ser
  1               5                  10                  15

Ala Ser Val Ile Ser Asp Gly Ala Val His Phe Tyr Gly Asp Val Asp
             20                  25                  30

Arg Val Phe Glu Leu Met Ser Val Thr Lys Leu Leu Ala Thr Tyr Gly
         35                  40                  45

Phe Leu Val Ala Ile Glu Glu Gly Val Phe Glu Leu Asp Ser Pro Met
     50                  55                  60
```

```
Gly Pro Glu Gly Ser Thr Val Arg His Leu Leu Ser His Ala Ser Gly
 65                  70                  75                  80

Val Ala Phe Asp Lys Pro Val Ala Glu Lys Gly Val Gly Glu Arg Arg
                85                  90                  95

Ile Tyr Ser Ser Ala Gly Met Asp Ile Leu Ala Asp Ala Val Ala Ala
            100                 105                 110

Glu Ala Glu Met Pro Phe Ala Glu Tyr Leu Arg Glu Ala Val Phe Glu
        115                 120                 125

Pro Leu Gly Met Glu Asn Ser Glu Leu Trp Gly Ser Ala Gly His Glu
    130                 135                 140

Ala Arg Ser Thr Val Ala Asp Leu Thr Lys Phe Gly Gln Glu Leu Thr
145                 150                 155                 160

Ala Pro Thr Leu Ile Ser Pro Glu Thr Leu Ala Glu Ala Phe Gln Val
                165                 170                 175

Gln Phe Pro Glu Leu Ile Gly Thr Val Pro Gly Tyr Gly Met Gln Lys
            180                 185                 190

Pro Cys Pro Trp Gly Leu Gly Phe Glu Ile Lys Gly Gln Lys Ser Pro
        195                 200                 205

His Trp Thr Gly Asp Leu Met Pro Glu Asn Thr Ala Gly His Phe Gly
    210                 215                 220

Gln Ser Gly Thr Phe Phe Trp Thr Val Pro Gly Ser Gly Gln Val Gly
225                 230                 235                 240

Val Val Leu Thr Asp Arg Asn Phe Gly Pro Trp Ala Lys Pro Leu Trp
                245                 250                 255

Thr Ala Phe Asn Asp Glu Val Trp Ala Glu Leu Asn Ser
            260                 265
```

Sequence Listing - 2005-12-22 - 2005-12-22

<210> 643
<211> 930
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(907)
<223> FRXA01471

<400> 643
cctccaacca gagctataaa aaaggttgta gaagaaattt cttaacatac atcgttgtgt 60

```
tgccaggggt ttaacagatt agttgctaag gtctgtctcc atg cag agt ttt aag   115
                                               Met Gln Ser Phe Lys
                                                 1               5

acg ctt gaa tct tgg cct gtc gac aat gtt tcg gcc agt gtc atc tcc   163
Thr Leu Glu Ser Trp Pro Val Asp Asn Val Ser Ala Ser Val Ile Ser
                10                  15                  20
```

```
gac ggc gcc gtg cac ttt tac ggc gac gtc gat cgt gtt ttt gaa ctc   211
Asp Gly Ala Val His Phe Tyr Gly Asp Val Asp Arg Val Phe Glu Leu
            25                  30                  35

atg agt gtg aca aaa ctc ctg gcc acc tac ggt ttc ctt gtt gcc atc   259
Met Ser Val Thr Lys Leu Leu Ala Thr Tyr Gly Phe Leu Val Ala Ile
        40                  45                  50

gaa gaa ggt gtt ttt gag ctc gat tca ccg atg ggt cct gaa gga tcc   307
Glu Glu Gly Val Phe Glu Leu Asp Ser Pro Met Gly Pro Glu Gly Ser
    55                  60                  65

aca gtg agg cat ctg ctc tca cat gct tcc ggc gtg gca ttc gat aag   355
Thr Val Arg His Leu Leu Ser His Ala Ser Gly Val Ala Phe Asp Lys
70                  75                  80                  85

ccg gta gcg gaa aag gga gtg ggg gag cgc cgc att tac tcc tct gct   403
Pro Val Ala Glu Lys Gly Val Gly Glu Arg Arg Ile Tyr Ser Ser Ala
                90                  95                  100

ggc atg gac atc ttg gcg gat gct gtt gcc gct gaa gct gaa atg ccg   451
Gly Met Asp Ile Leu Ala Asp Ala Val Ala Ala Glu Ala Glu Met Pro
            105                 110                 115

ttt gca gag tat ctc cgc gag gct gtg ttc gag cct ttg gga atg gag   499
Phe Ala Glu Tyr Leu Arg Glu Ala Val Phe Glu Pro Leu Gly Met Glu
        120                 125                 130

aac tct gaa cta tgg ggt tct gcg ggc cac gag gcg cgc agc aca gtg   547
Asn Ser Glu Leu Trp Gly Ser Ala Gly His Glu Ala Arg Ser Thr Val
    135                 140                 145

gct gat ctg acc aag ttc ggc caa gag ctc acc gca cca act ctg atc   595
Ala Asp Leu Thr Lys Phe Gly Gln Glu Leu Thr Ala Pro Thr Leu Ile
150                 155                 160                 165

tca cca gaa acc ctt gca gag gct ttc cag gtg caa ttc ccg gaa ctg   643
Ser Pro Glu Thr Leu Ala Glu Ala Phe Gln Val Gln Phe Pro Glu Leu
                170                 175                 180

att ggc acc gtc ccc ggt tat ggc atg cag aag ccg tgt ccg tgg gga   691
Ile Gly Thr Val Pro Gly Tyr Gly Met Gln Lys Pro Cys Pro Trp Gly
            185                 190                 195

ttg ggc ttt gaa att aag gga cag aag tcg ccg cac tgg aca ggt gac   739
Leu Gly Phe Glu Ile Lys Gly Gln Lys Ser Pro His Trp Thr Gly Asp
        200                 205                 210

ttg atg ccg gag aac act gct gga cac ttt gga cag tcg gga aca ttc   787
Leu Met Pro Glu Asn Thr Ala Gly His Phe Gly Gln Ser Gly Thr Phe
    215                 220                 225

ttt tgg act gtt cca ggc tca ggt caa gtc ggg gtt gtt ttg act gac   835
Phe Trp Thr Val Pro Gly Ser Gly Gln Val Gly Val Val Leu Thr Asp
230                 235                 240                 245

cga aat ttc ggt cct tgg gct aaa ccg ttg tgg act gcc ttc aat gac   883
Arg Asn Phe Gly Pro Trp Ala Lys Pro Leu Trp Thr Ala Phe Asn Asp
                250                 255                 260

gaa gtc tgg gcc gag tta aat tca taaacttttg ccgtaattac ggt         930
```

Glu Val Trp Ala Glu Leu Asn Ser
265

<210> 644
<211> 269
<212> PRT
<213> Corynebacterium glutamicum

<400> 644
Met Gln Ser Phe Lys Thr Leu Glu Ser Trp Pro Val Asp Asn Val Ser
1 5 10 15

Ala Ser Val Ile Ser Asp Gly Ala Val His Phe Tyr Gly Asp Val Asp
20 25 30

Arg Val Phe Glu Leu Met Ser Val Thr Lys Leu Leu Ala Thr Tyr Gly
35 40 45

Phe Leu Val Ala Ile Glu Glu Gly Val Phe Glu Leu Asp Ser Pro Met
50 55 60

Gly Pro Glu Gly Ser Thr Val Arg His Leu Leu Ser His Ala Ser Gly
65 70 75 80

Val Ala Phe Asp Lys Pro Val Ala Glu Lys Gly Val Gly Glu Arg Arg
85 90 95

Ile Tyr Ser Ser Ala Gly Met Asp Ile Leu Ala Asp Ala Val Ala Ala
100 105 110

Glu Ala Glu Met Pro Phe Ala Glu Tyr Leu Arg Glu Ala Val Phe Glu
115 120 125

Pro Leu Gly Met Glu Asn Ser Glu Leu Trp Gly Ser Ala Gly His Glu
130 135 140

Ala Arg Ser Thr Val Ala Asp Leu Thr Lys Phe Gly Gln Glu Leu Thr
145 150 155 160

Ala Pro Thr Leu Ile Ser Pro Glu Thr Leu Ala Glu Ala Phe Gln Val
165 170 175

Gln Phe Pro Glu Leu Ile Gly Thr Val Pro Gly Tyr Gly Met Gln Lys
180 185 190

Pro Cys Pro Trp Gly Leu Gly Phe Glu Ile Lys Gly Gln Lys Ser Pro
195 200 205

His Trp Thr Gly Asp Leu Met Pro Glu Asn Thr Ala Gly His Phe Gly
210 215 220

Gln Ser Gly Thr Phe Phe Trp Thr Val Pro Gly Ser Gly Gln Val Gly
225 230 235 240

Val Val Leu Thr Asp Arg Asn Phe Gly Pro Trp Ala Lys Pro Leu Trp
245 250 255

Thr Ala Phe Asn Asp Glu Val Trp Ala Glu Leu Asn Ser
260 265

<210> 645
<211> 363
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(340)
<223> RXN01479

<400> 645
agcgctgccc gtgccataaa tttcgaagaa gcgcgaaaca ggtagagtct aaggtgtcat 60

tcttggtaca agttttatat ttagggagag ttatccacac atg atc cag tta gtg 115
Met Ile Gln Leu Val
1 5

ata ggc gct gca gca ggc tac gtg ctt ggc aca aag gcc ggc cgc aag 163
Ile Gly Ala Ala Ala Gly Tyr Val Leu Gly Thr Lys Ala Gly Arg Lys
10 15 20

cgt tac cac cag atc aaa aag gga tat gag gca gcg att aac tcc cct 211
Arg Tyr His Gln Ile Lys Lys Gly Tyr Glu Ala Ala Ile Asn Ser Pro
25 30 35

gcc acc aaa tct gca gta aac gcc gcc cgc aaa gcc att gcc aac aag 259
Ala Thr Lys Ser Ala Val Asn Ala Ala Arg Lys Ala Ile Ala Asn Lys
40 45 50

ctg gat ccg cag ccc cgc atg aag gaa gta aaa aac ctg cgg act gcg 307
Leu Asp Pro Gln Pro Arg Met Lys Glu Val Lys Asn Leu Arg Thr Ala
55 60 65

gac ggg cat gaa gtc ctc gag caa gac cag gac taaattaccc tctaaacgcc 360
Asp Gly His Glu Val Leu Glu Gln Asp Gln Asp
70 75 80

cgg 363

<210> 646
<211> 80
<212> PRT
<213> Corynebacterium glutamicum

<400> 646
Met Ile Gln Leu Val Ile Gly Ala Ala Ala Gly Tyr Val Leu Gly Thr
1 5 10 15

Lys Ala Gly Arg Lys Arg Tyr His Gln Ile Lys Lys Gly Tyr Glu Ala
20 25 30

Ala Ile Asn Ser Pro Ala Thr Lys Ser Ala Val Asn Ala Ala Arg Lys
35 40 45

Ala Ile Ala Asn Lys Leu Asp Pro Gln Pro Arg Met Lys Glu Val Lys
50 55 60

Asn Leu Arg Thr Ala Asp Gly His Glu Val Leu Glu Gln Asp Gln Asp
65 70 75 80

<210> 647
<211> 351
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(328)
<223> FRXA01479

<400> 647
gccataaatt tcgaagaagc gcgaaacagg tagagtctaa ggtgtcattc ttggtacaag 60

ttttatattt agggagagtt atccacacat gatccagtta gtg ata ggc gct gca 115
Val Ile Gly Ala Ala
1 5

gca ggc tac gtg ctt ggc aca aag gcc ggc cgc aag cgt tac cac cag 163
Ala Gly Tyr Val Leu Gly Thr Lys Ala Gly Arg Lys Arg Tyr His Gln
10 15 20

atc aaa aag gga tat gag gca gcg att aac tcc cct gcc acc aaa tct 211
Ile Lys Lys Gly Tyr Glu Ala Ala Ile Asn Ser Pro Ala Thr Lys Ser
25 30 35

gca gta aac gcc gcc cgc aaa gcc att gcc aac aag ctg gat ccg cag 259
Ala Val Asn Ala Ala Arg Lys Ala Ile Ala Asn Lys Leu Asp Pro Gln
40 45 50

ccc cgc atg aag gaa gta aaa aac ctg cgg act gcg gac ggg cat gaa 307
Pro Arg Met Lys Glu Val Lys Asn Leu Arg Thr Ala Asp Gly His Glu
55 60 65

gtc ctc gag caa gac cag gac taaattaccc tctaaacgcc cgg 351
Val Leu Glu Gln Asp Gln Asp
70 75

<210> 648
<211> 76
<212> PRT
<213> Corynebacterium glutamicum

<400> 648
Val Ile Gly Ala Ala Ala Gly Tyr Val Leu Gly Thr Lys Ala Gly Arg
1 5 10 15

Lys Arg Tyr His Gln Ile Lys Lys Gly Tyr Glu Ala Ala Ile Asn Ser
20 25 30

Pro Ala Thr Lys Ser Ala Val Asn Ala Ala Arg Lys Ala Ile Ala Asn
35 40 45

Lys Leu Asp Pro Gln Pro Arg Met Lys Glu Val Lys Asn Leu Arg Thr
50 55 60

Ala Asp Gly His Glu Val Leu Glu Gln Asp Gln Asp
65 70 75

<210> 649
<211> 669
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(646)
<223> RXN01484

<400> 649
gagtttactc ttaaccgcag tagtgcagcc agccctgagg gtggtggcgt attcgatgct 60

cagaacgcct aataatcggc acaaaattga ttcaattttg gtg ttg ggc aca gct 115
Val Leu Gly Thr Ala
1 5

caa tat gat gga gtt cca tcg agg cag ttt gct gct cgt ttg agg cat 163
Gln Tyr Asp Gly Val Pro Ser Arg Gln Phe Ala Ala Arg Leu Arg His
10 15 20

gcc gcg aag ctg tgg cgt ctt cat gaa atc cag cat gta tat act gtc 211
Ala Ala Lys Leu Trp Arg Leu His Glu Ile Gln His Val Tyr Thr Val
25 30 35

ggc gga aaa ctt cct ggc gat cgt ttc acc gaa gca gaa gtc gcg cgg 259
Gly Gly Lys Leu Pro Gly Asp Arg Phe Thr Glu Ala Glu Val Ala Arg
40 45 50

gag tat ttg atc aaa gag ggc gtg gat ccg gat ctg att ttt gtc tct 307
Glu Tyr Leu Ile Lys Glu Gly Val Asp Pro Asp Leu Ile Phe Val Ser
55 60 65

gca gtt ggc aat gac act gtc tcc tcc tat gag gcg ctt gat ccg gaa 355
Ala Val Gly Asn Asp Thr Val Ser Ser Tyr Glu Ala Leu Asp Pro Glu
70 75 80 85

aag ctt ggt cgg gtg ctg att gtt act gat ccg aac cat tcg tat cgg 403
Lys Leu Gly Arg Val Leu Ile Val Thr Asp Pro Asn His Ser Tyr Arg
90 95 100

gcg gtg cgc atc gcg cga cgc atg ggc ttt gac gcg aaa cct tcc ccg 451
Ala Val Arg Ile Ala Arg Arg Met Gly Phe Asp Ala Lys Pro Ser Pro
105 110 115

aca acc tat agt ccc gcg aag ttt ccg tcg ata gtt tat ttt ctg acc 499
Thr Thr Tyr Ser Pro Ala Lys Phe Pro Ser Ile Val Tyr Phe Leu Thr
120 125 130

ttg tcc cat gag tgg ggc ggg gta gta gta cag gac gtg tcg cgg ctc 547
Leu Ser His Glu Trp Gly Gly Val Val Val Gln Asp Val Ser Arg Leu
135 140 145

ttg ggt gaa cgg gtg ccc gat aag gtg aag cat ctt tgc gcg caa tcc 595
Leu Gly Glu Arg Val Pro Asp Lys Val Lys His Leu Cys Ala Gln Ser
150 155 160 165

```
aag gtc tgc tgc gcc ctt cgc ggc gtg cac gcc atg agc aac ttc gga   643
Lys Val Cys Cys Ala Leu Arg Gly Val His Ala Met Ser Asn Phe Gly
                170                 175                 180

ggc tgaaaaagta gatgtacccc tat                                     669
Gly
```

<210> 650
<211> 182
<212> PRT
<213> Corynebacterium glutamicum

<400> 650

```
Val Leu Gly Thr Ala Gln Tyr Asp Gly Val Pro Ser Arg Gln Phe Ala
  1               5                  10                  15

Ala Arg Leu Arg His Ala Ala Lys Leu Trp Arg Leu His Glu Ile Gln
             20                  25                  30

His Val Tyr Thr Val Gly Gly Lys Leu Pro Gly Asp Arg Phe Thr Glu
         35                  40                  45

Ala Glu Val Ala Arg Glu Tyr Leu Ile Lys Glu Gly Val Asp Pro Asp
     50                  55                  60

Leu Ile Phe Val Ser Ala Val Gly Asn Asp Thr Val Ser Ser Tyr Glu
 65                  70                  75                  80

Ala Leu Asp Pro Glu Lys Leu Gly Arg Val Leu Ile Val Thr Asp Pro
                 85                  90                  95

Asn His Ser Tyr Arg Ala Val Arg Ile Ala Arg Arg Met Gly Phe Asp
            100                 105                 110

Ala Lys Pro Ser Pro Thr Thr Tyr Ser Pro Ala Lys Phe Pro Ser Ile
        115                 120                 125

Val Tyr Phe Leu Thr Leu Ser His Glu Trp Gly Gly Val Val Val Gln
    130                 135                 140

Asp Val Ser Arg Leu Leu Gly Glu Arg Val Pro Asp Lys Val Lys His
145                 150                 155                 160

Leu Cys Ala Gln Ser Lys Val Cys Cys Ala Leu Arg Gly Val His Ala
                165                 170                 175

Met Ser Asn Phe Gly Gly
            180
```

<210> 651
<211> 669
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(646)
<223> FRXA01484

<400> 651
gagtttactc ttaaccgcag tagtgcagcc agccctgagg gtggtggcgt attcgatgct 60

cagaacgcct aataatcggc acaaaattga ttcaattttg gtg ttg ggc aca gct 115
Val Leu Gly Thr Ala
1 5

caa tat gat gga gtt cca tcg agg cag ttt gct gct cgt ttg agg cat 163
Gln Tyr Asp Gly Val Pro Ser Arg Gln Phe Ala Ala Arg Leu Arg His
10 15 20

gcc gcg aag ctg tgg cgt ctt cat gaa atc cag cat gta tat act gtc 211
Ala Ala Lys Leu Trp Arg Leu His Glu Ile Gln His Val Tyr Thr Val
25 30 35

ggc gga aaa ctt cct ggc gat cgt ttc acc gaa gca gaa gtc gcg cgg 259
Gly Gly Lys Leu Pro Gly Asp Arg Phe Thr Glu Ala Glu Val Ala Arg
40 45 50

gag tat ttg atc aaa gag ggc gtg gat ccg gat ctg att ttt gtc tct 307
Glu Tyr Leu Ile Lys Glu Gly Val Asp Pro Asp Leu Ile Phe Val Ser
55 60 65

gca gtt ggc aat gac act gtc tcc tcc tat gag gcg ctt gat ccg gaa 355
Ala Val Gly Asn Asp Thr Val Ser Ser Tyr Glu Ala Leu Asp Pro Glu
70 75 80 85

aag ctt ggt cgg gtg ctg att gtt act gat ccg aac cat tcg tat cgg 403
Lys Leu Gly Arg Val Leu Ile Val Thr Asp Pro Asn His Ser Tyr Arg
90 95 100

gcg gtg cgc atc gcg cga cgc atg ggc ttt gac gcg aaa cct tcc ccg 451
Ala Val Arg Ile Ala Arg Arg Met Gly Phe Asp Ala Lys Pro Ser Pro
105 110 115

aca acc tat agt ccc gcg aag ttt ccg tcg ata gtt tat ttt ctg acc 499
Thr Thr Tyr Ser Pro Ala Lys Phe Pro Ser Ile Val Tyr Phe Leu Thr
120 125 130

ttg tcc cat gag tgg ggc ggg gta gta gta cag gac gtg tcg cgg ctc 547
Leu Ser His Glu Trp Gly Gly Val Val Val Gln Asp Val Ser Arg Leu
135 140 145

ttg ggt gaa cgg gtg ccc gat aag gtg aag cat ctt tgc gcg caa tcc 595
Leu Gly Glu Arg Val Pro Asp Lys Val Lys His Leu Cys Ala Gln Ser
150 155 160 165

aag gtc tgc tgc gcc ctt cgc ggc gtg cac gcc atg agc aac ttc gga 643
Lys Val Cys Cys Ala Leu Arg Gly Val His Ala Met Ser Asn Phe Gly
170 175 180

ggc tgaaaaagta gatgtacccc tat 669
Gly

<210> 652
<211> 182
<212> PRT
<213> Corynebacterium glutamicum

<400> 652
Val Leu Gly Thr Ala Gln Tyr Asp Gly Val Pro Ser Arg Gln Phe Ala
1 5 10 15

Ala Arg Leu Arg His Ala Ala Lys Leu Trp Arg Leu His Glu Ile Gln
20 25 30

His Val Tyr Thr Val Gly Gly Lys Leu Pro Gly Asp Arg Phe Thr Glu
35 40 45

Ala Glu Val Ala Arg Glu Tyr Leu Ile Lys Glu Gly Val Asp Pro Asp
50 55 60

Leu Ile Phe Val Ser Ala Val Gly Asn Asp Thr Val Ser Ser Tyr Glu
65 70 75 80

Ala Leu Asp Pro Glu Lys Leu Gly Arg Val Leu Ile Val Thr Asp Pro
85 90 95

Asn His Ser Tyr Arg Ala Val Arg Ile Ala Arg Arg Met Gly Phe Asp
100 105 110

Ala Lys Pro Ser Pro Thr Thr Tyr Ser Pro Ala Lys Phe Pro Ser Ile
115 120 125

Val Tyr Phe Leu Thr Leu Ser His Glu Trp Gly Gly Val Val Val Gln
130 135 140

Asp Val Ser Arg Leu Leu Gly Glu Arg Val Pro Asp Lys Val Lys His
145 150 155 160

Leu Cys Ala Gln Ser Lys Val Cys Cys Ala Leu Arg Gly Val His Ala
165 170 175

Met Ser Asn Phe Gly Gly
180

<210> 653
<211> 2175
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2152)
<223> RXN01485

<400> 653
ctcagggctg gctgcactac tgcggttaag agtaaactct tggctaaaaa tcttctcacg 60

ttaactagtg tgccagctgg actcgtctaa ggtggggacc atg aac ttt agt ttg 115
Met Asn Phe Ser Leu
1 5

gtg cat ctt cgg gaa aac gtc cgc cgt gta tcg gtc act gtg gca att 163
Val His Leu Arg Glu Asn Val Arg Arg Val Ser Val Thr Val Ala Ile
10 15 20

gga gct ggc gcg ctc ctt atc agt gga cca ttt ttt act gct cac act 211

```
Gly Ala Gly Ala Leu Leu Ile Ser Gly Pro Phe Phe Thr Ala His Thr
            25                  30                  35

gca gaa gcc aca gaa aca tat gtc ttg gct gaa tca cca gaa ttt tac   259
Ala Glu Ala Thr Glu Thr Tyr Val Leu Ala Glu Ser Pro Glu Phe Tyr
        40                  45                  50

caa gac aat gtc act gac tac acc ggc cag att tcc tcg tcc gat atc   307
Gln Asp Asn Val Thr Asp Tyr Thr Gly Gln Ile Ser Ser Ser Asp Ile
    55                  60                  65

acc aac att cag gct gcc atc gat gat gta aag gca tct gaa caa aag   355
Thr Asn Ile Gln Ala Ala Ile Asp Asp Val Lys Ala Ser Glu Gln Lys
70                  75                  80                  85

gtt att ttc gtt gtt ttc cta agc tct ttc gac gga gtt gac cct gaa   403
Val Ile Phe Val Val Phe Leu Ser Ser Phe Asp Gly Val Asp Pro Glu
                90                  95                  100

acg tgg acg cag caa gca ctc caa gcc aac ggc ggc gga aac gtc ttg   451
Thr Trp Thr Gln Gln Ala Leu Gln Ala Asn Gly Gly Gly Asn Val Leu
            105                 110                 115

att tat gca ctc gct ccc gag gaa cgg cag tac ggc atc caa ggt ggt   499
Ile Tyr Ala Leu Ala Pro Glu Glu Arg Gln Tyr Gly Ile Gln Gly Gly
        120                 125                 130

act caa tgg acc gac gct gaa ctc gac gcc gcc aac aac gct gct ttc   547
Thr Gln Trp Thr Asp Ala Glu Leu Asp Ala Ala Asn Asn Ala Ala Phe
    135                 140                 145

cag gca ctt tcc caa gaa gat tgg gca ggc tct gca cta gcg ctg gca   595
Gln Ala Leu Ser Gln Glu Asp Trp Ala Gly Ser Ala Leu Ala Leu Ala
150                 155                 160                 165

gaa tca gtt ggt tct agt tct tcc agc tct tcg ggc tcg tcc agc tct   643
Glu Ser Val Gly Ser Ser Ser Ser Ser Ser Ser Gly Ser Ser Ser Ser
                170                 175                 180

tcc gat ttt tcc ggc gct tgg ttg gct gct gcg ggc gtt ggc aca gtg   691
Ser Asp Phe Ser Gly Ala Trp Leu Ala Ala Ala Gly Val Gly Thr Val
            185                 190                 195

gcc gct ggt ggc gga att tgg gcc tat tcc cgc agc cgc aag aag aaa   739
Ala Ala Gly Gly Gly Ile Trp Ala Tyr Ser Arg Ser Arg Lys Lys Lys
        200                 205                 210

aca agt gct gca acc ttg gaa gat gca cgc gaa atc gac ccg cgc gat   787
Thr Ser Ala Ala Thr Leu Glu Asp Ala Arg Glu Ile Asp Pro Arg Asp
    215                 220                 225

acc aac cgc ctc atg cag ctt ccc atg gaa act ctc gaa cac ctt gcc   835
Thr Asn Arg Leu Met Gln Leu Pro Met Glu Thr Leu Glu His Leu Ala
230                 235                 240                 245

caa gaa gag ctc acc tcc act gat gac tcc atc cgt cgc gga aaa gaa   883
Gln Glu Glu Leu Thr Ser Thr Asp Asp Ser Ile Arg Arg Gly Lys Glu
                250                 255                 260

gag ctc gct atc gct acc tcc gag ttc gga cca gag cgc acc cgc agc   931
Glu Leu Ala Ile Ala Thr Ser Glu Phe Gly Pro Glu Arg Thr Arg Ser
```

```
            265                 270                 275

ttc aac cgc gcc atg aac cac tcc acc ggc acc ctg caa aaa gcc ttt   979
Phe Asn Arg Ala Met Asn His Ser Thr Gly Thr Leu Gln Lys Ala Phe
        280                 285                 290

gag att cag cag cgc ctc aac gat tct atc cca gaa tcc gaa gcc gaa   1027
Glu Ile Gln Gln Arg Leu Asn Asp Ser Ile Pro Glu Ser Glu Ala Glu
    295                 300                 305

cgt caa tcc atg ctg gta gaa atc att tca tcc tgt ggc caa gcc gac   1075
Arg Gln Ser Met Leu Val Glu Ile Ile Ser Ser Cys Gly Gln Ala Asp
310                 315                 320                 325

gat gcc ctc gac gcc gaa gcc caa aac ttt gcc gat atg cgc aac ctg   1123
Asp Ala Leu Asp Ala Glu Ala Gln Asn Phe Ala Asp Met Arg Asn Leu
                330                 335                 340

ctg atc aac gcg ggc agc aaa ttg gat gct ctc acc caa aaa tcc gtc   1171
Leu Ile Asn Ala Gly Ser Lys Leu Asp Ala Leu Thr Gln Lys Ser Val
            345                 350                 355

gac ctg cgc acc cgc ctc ccc aag gcc caa gaa aca ctc gct ggc ctg   1219
Asp Leu Arg Thr Arg Leu Pro Lys Ala Gln Glu Thr Leu Ala Gly Leu
        360                 365                 370

cgc act cgc tac tca gca gag gtc ctt gaa agc atc gac gac aac gtc   1267
Arg Thr Arg Tyr Ser Ala Glu Val Leu Glu Ser Ile Asp Asp Asn Val
    375                 380                 385

gac ctc gcc agc gct tcg ctc gac gaa gca gaa gaa gtc ctg cca cag   1315
Asp Leu Ala Ser Ala Ser Leu Asp Glu Ala Glu Glu Val Leu Pro Gln
390                 395                 400                 405

gcg tac gag ata gag tcc atg ccc gca ggc gag cag ggc ggg ctt atc   1363
Ala Tyr Glu Ile Glu Ser Met Pro Ala Gly Glu Gln Gly Gly Leu Ile
                410                 415                 420

gac gcg atc cgt cac atc gag cac gcc atc act acc gca gac aaa ctc   1411
Asp Ala Ile Arg His Ile Glu His Ala Ile Thr Thr Ala Asp Lys Leu
            425                 430                 435

ctc gcg ggc gtc gag cat gcc gat gaa aac atc tcc aca gcc aaa gca   1459
Leu Ala Gly Val Glu His Ala Asp Glu Asn Ile Ser Thr Ala Lys Ala
        440                 445                 450

aac gtt gcc gat ctg atc caa gaa atc tca gac gaa atc aac gaa gcc   1507
Asn Val Ala Asp Leu Ile Gln Glu Ile Ser Asp Glu Ile Asn Glu Ala
    455                 460                 465

ggc caa ctc aaa caa agc gca gga gcc gac ggt gcc cgt gcc gac tgg   1555
Gly Gln Leu Lys Gln Ser Ala Gly Ala Asp Gly Ala Arg Ala Asp Trp
470                 475                 480                 485

gcc tcc ctc gac gat gct gtc cgc gca gcc agc gca gca cta atc acc   1603
Ala Ser Leu Asp Asp Ala Val Arg Ala Ala Ser Ala Ala Leu Ile Thr
                490                 495                 500

gca tca gca gac gcc gaa aag gat ccg ctc gga acc tac aca gaa ctt   1651
Ala Ser Ala Asp Ala Glu Lys Asp Pro Leu Gly Thr Tyr Thr Glu Leu
            505                 510                 515
```

```
gtc gat gtc gac tcc gcc ctc gac act caa ctt gac aca ctt cgc gcc   1699
Val Asp Val Asp Ser Ala Leu Asp Thr Gln Leu Asp Thr Leu Arg Ala
        520                 525                 530

acc gca gct gat caa gcc cgc cag cta cgc gta ttc gac caa cag ctg   1747
Thr Ala Ala Asp Gln Ala Arg Gln Leu Arg Val Phe Asp Gln Gln Leu
    535                 540                 545

caa tct gca aga agc caa atc caa aag gcc gaa gac ctc atc tcc acc   1795
Gln Ser Ala Arg Ser Gln Ile Gln Lys Ala Glu Asp Leu Ile Ser Thr
550                 555                 560                 565

cgc ggt cgc atc gta aaa tcc gaa gcc cgc acc cac ctg gcc aac gca   1843
Arg Gly Arg Ile Val Lys Ser Glu Ala Arg Thr His Leu Ala Asn Ala
                570                 575                 580

caa aag ctg tac gcc atg gca caa caa aac cgc acc cgc gac acc cgt   1891
Gln Lys Leu Tyr Ala Met Ala Gln Gln Asn Arg Thr Arg Asp Thr Arg
            585                 590                 595

gca gga att gat tac gga cgt caa gca gca gtc gca gcc caa cgc gcc   1939
Ala Gly Ile Asp Tyr Gly Arg Gln Ala Ala Val Ala Ala Gln Arg Ala
        600                 605                 610

agc aag tca gca caa aac gac atc acc acc tac aac aat cgc cac aat   1987
Ser Lys Ser Ala Gln Asn Asp Ile Thr Thr Tyr Asn Asn Arg His Asn
    615                 620                 625

tcc ggt ggc gga acc acc ggt gcg att gtc acc ggc atg gtg atc aac   2035
Ser Gly Gly Gly Thr Thr Gly Ala Ile Val Thr Gly Met Val Ile Asn
630                 635                 640                 645

tcg att ctc aac agc ggc cgc ggt ggc ggt ttc tgt gga ggc gga ggc   2083
Ser Ile Leu Asn Ser Gly Arg Gly Gly Gly Phe Cys Gly Gly Gly Gly
                650                 655                 660

ttt ggt gga ggc ggt ggc ggc ttc agc ggt ggt ggc ggt ggc gga gga   2131
Phe Gly Gly Gly Gly Gly Gly Phe Ser Gly Gly Gly Gly Gly Gly Gly
            665                 670                 675

ggg ttc cgc gga ggc cgc ttc tagcctgaaa cgagcaaaac caa             2175
Gly Phe Arg Gly Gly Arg Phe
        680
```

<210> 654
<211> 684
<212> PRT
<213> Corynebacterium glutamicum

<400> 654

```
Met Asn Phe Ser Leu Val His Leu Arg Glu Asn Val Arg Arg Val Ser
  1               5                  10                  15

Val Thr Val Ala Ile Gly Ala Gly Ala Leu Leu Ile Ser Gly Pro Phe
             20                  25                  30

Phe Thr Ala His Thr Ala Glu Ala Thr Glu Thr Tyr Val Leu Ala Glu
         35                  40                  45
```

```
Ser Pro Glu Phe Tyr Gln Asp Asn Val Thr Asp Tyr Thr Gly Gln Ile
     50                  55                  60

Ser Ser Ser Asp Ile Thr Asn Ile Gln Ala Ala Ile Asp Asp Val Lys
 65                  70                  75                  80

Ala Ser Glu Gln Lys Val Ile Phe Val Val Phe Leu Ser Ser Phe Asp
                 85                  90                  95

Gly Val Asp Pro Glu Thr Trp Thr Gln Gln Ala Leu Gln Ala Asn Gly
            100                 105                 110

Gly Gly Asn Val Leu Ile Tyr Ala Leu Ala Pro Glu Glu Arg Gln Tyr
        115                 120                 125

Gly Ile Gln Gly Gly Thr Gln Trp Thr Asp Ala Glu Leu Asp Ala Ala
    130                 135                 140

Asn Asn Ala Ala Phe Gln Ala Leu Ser Gln Glu Asp Trp Ala Gly Ser
145                 150                 155                 160

Ala Leu Ala Leu Ala Glu Ser Val Gly Ser Ser Ser Ser Ser Ser Ser
                165                 170                 175

Gly Ser Ser Ser Ser Ser Asp Phe Ser Gly Ala Trp Leu Ala Ala Ala
            180                 185                 190

Gly Val Gly Thr Val Ala Ala Gly Gly Gly Ile Trp Ala Tyr Ser Arg
        195                 200                 205

Ser Arg Lys Lys Lys Thr Ser Ala Ala Thr Leu Glu Asp Ala Arg Glu
    210                 215                 220

Ile Asp Pro Arg Asp Thr Asn Arg Leu Met Gln Leu Pro Met Glu Thr
225                 230                 235                 240

Leu Glu His Leu Ala Gln Glu Glu Leu Thr Ser Thr Asp Asp Ser Ile
                245                 250                 255

Arg Arg Gly Lys Glu Glu Leu Ala Ile Ala Thr Ser Glu Phe Gly Pro
            260                 265                 270

Glu Arg Thr Arg Ser Phe Asn Arg Ala Met Asn His Ser Thr Gly Thr
        275                 280                 285

Leu Gln Lys Ala Phe Glu Ile Gln Gln Arg Leu Asn Asp Ser Ile Pro
    290                 295                 300

Glu Ser Glu Ala Glu Arg Gln Ser Met Leu Val Glu Ile Ile Ser Ser
305                 310                 315                 320

Cys Gly Gln Ala Asp Asp Ala Leu Asp Ala Glu Ala Gln Asn Phe Ala
                325                 330                 335

Asp Met Arg Asn Leu Leu Ile Asn Ala Gly Ser Lys Leu Asp Ala Leu
            340                 345                 350

Thr Gln Lys Ser Val Asp Leu Arg Thr Arg Leu Pro Lys Ala Gln Glu
        355                 360                 365

Thr Leu Ala Gly Leu Arg Thr Arg Tyr Ser Ala Glu Val Leu Glu Ser
```

370 375 380

Ile Asp Asp Asn Val Asp Leu Ala Ser Ala Ser Leu Asp Glu Ala Glu
385 390 395 400

Glu Val Leu Pro Gln Ala Tyr Glu Ile Glu Ser Met Pro Ala Gly Glu
405 410 415

Gln Gly Gly Leu Ile Asp Ala Ile Arg His Ile Glu His Ala Ile Thr
420 425 430

Thr Ala Asp Lys Leu Leu Ala Gly Val Glu His Ala Asp Glu Asn Ile
435 440 445

Ser Thr Ala Lys Ala Asn Val Ala Asp Leu Ile Gln Glu Ile Ser Asp
450 455 460

Glu Ile Asn Glu Ala Gly Gln Leu Lys Gln Ser Ala Gly Ala Asp Gly
465 470 475 480

Ala Arg Ala Asp Trp Ala Ser Leu Asp Asp Ala Val Arg Ala Ala Ser
485 490 495

Ala Ala Leu Ile Thr Ala Ser Ala Asp Ala Glu Lys Asp Pro Leu Gly
500 505 510

Thr Tyr Thr Glu Leu Val Asp Val Asp Ser Ala Leu Asp Thr Gln Leu
515 520 525

Asp Thr Leu Arg Ala Thr Ala Ala Asp Gln Ala Arg Gln Leu Arg Val
530 535 540

Phe Asp Gln Gln Leu Gln Ser Ala Arg Ser Gln Ile Gln Lys Ala Glu
545 550 555 560

Asp Leu Ile Ser Thr Arg Gly Arg Ile Val Lys Ser Glu Ala Arg Thr
565 570 575

His Leu Ala Asn Ala Gln Lys Leu Tyr Ala Met Ala Gln Gln Asn Arg
580 585 590

Thr Arg Asp Thr Arg Ala Gly Ile Asp Tyr Gly Arg Gln Ala Ala Val
595 600 605

Ala Ala Gln Arg Ala Ser Lys Ser Ala Gln Asn Asp Ile Thr Thr Tyr
610 615 620

Asn Asn Arg His Asn Ser Gly Gly Gly Thr Thr Gly Ala Ile Val Thr
625 630 635 640

Gly Met Val Ile Asn Ser Ile Leu Asn Ser Gly Arg Gly Gly Gly Phe
645 650 655

Cys Gly Gly Gly Gly Phe Gly Gly Gly Gly Gly Gly Phe Ser Gly Gly
660 665 670

Gly Gly Gly Gly Gly Gly Phe Arg Gly Gly Arg Phe
675 680

<210> 655

<211> 2175
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2152)
<223> FRXA01485

<400> 655
ctcagggctg gctgcactac tgcggttaag agtaaactct tggctaaaaa tcttctcacg 60

ttaactagtg tgccagctgg actcgtctaa ggtggggacc atg aac ttt agt ttg 115
Met Asn Phe Ser Leu
1 5

gtg cat ctt cgg gaa aac gtc cgc cgt gta tcg gtc act gtg gca att 163
Val His Leu Arg Glu Asn Val Arg Arg Val Ser Val Thr Val Ala Ile
10 15 20

gga gct ggc gcg ctc ctt atc agt gga cca ttt ttt act gct cac act 211
Gly Ala Gly Ala Leu Leu Ile Ser Gly Pro Phe Phe Thr Ala His Thr
25 30 35

gca gaa gcc aca gaa aca tat gtc ttg gct gaa tca cca gaa ttt tac 259
Ala Glu Ala Thr Glu Thr Tyr Val Leu Ala Glu Ser Pro Glu Phe Tyr
40 45 50

caa gac aat gtc act gac tac acc ggc cag att tcc tcg tcc gat atc 307
Gln Asp Asn Val Thr Asp Tyr Thr Gly Gln Ile Ser Ser Ser Asp Ile
55 60 65

acc aac att cag gct gcc atc gat gat gta aag gca tct gaa caa aag 355
Thr Asn Ile Gln Ala Ala Ile Asp Asp Val Lys Ala Ser Glu Gln Lys
70 75 80 85

gtt att ttc gtt gtt ttc cta agc tct ttc gac gga gtt gac cct gaa 403
Val Ile Phe Val Val Phe Leu Ser Ser Phe Asp Gly Val Asp Pro Glu
90 95 100

acg tgg acg cag caa gca ctc caa gcc aac ggc ggc gga aac gtc ttg 451
Thr Trp Thr Gln Gln Ala Leu Gln Ala Asn Gly Gly Gly Asn Val Leu
105 110 115

att tat gca ctc gct ccc gag gaa cgg cag tac ggc atc caa ggt ggt 499
Ile Tyr Ala Leu Ala Pro Glu Glu Arg Gln Tyr Gly Ile Gln Gly Gly
120 125 130

act caa tgg acc gac gct gaa ctc gac gcc gcc aac aac gct gct ttc 547
Thr Gln Trp Thr Asp Ala Glu Leu Asp Ala Ala Asn Asn Ala Ala Phe
135 140 145

cag gca ctt tcc caa gaa gat tgg gca ggc tct gca cta gcg ctg gca 595
Gln Ala Leu Ser Gln Glu Asp Trp Ala Gly Ser Ala Leu Ala Leu Ala
150 155 160 165

gaa tca gtt ggt tct agt tct tcc agc tct tcg ggc tcg tcc agc tct 643
Glu Ser Val Gly Ser Ser Ser Ser Ser Ser Ser Gly Ser Ser Ser Ser
170 175 180

tcc gat ttt tcc ggc gct tgg ttg gct gct gcg ggc gtt ggc aca gtg 691

```
Ser Asp Phe Ser Gly Ala Trp Leu Ala Ala Ala Gly Val Gly Thr Val
            185                 190                 195

gcc gct ggt ggc gga att tgg gcc tat tcc cgc agc cgc aag aag aaa   739
Ala Ala Gly Gly Gly Ile Trp Ala Tyr Ser Arg Ser Arg Lys Lys Lys
        200                 205                 210

aca agt gct gca acc ttg gaa gat gca cgc gaa atc gac ccg cgc gat   787
Thr Ser Ala Ala Thr Leu Glu Asp Ala Arg Glu Ile Asp Pro Arg Asp
    215                 220                 225

acc aac cgc ctc atg cag ctt ccc atg gaa act ctc gaa cac ctt gcc   835
Thr Asn Arg Leu Met Gln Leu Pro Met Glu Thr Leu Glu His Leu Ala
230                 235                 240                 245

caa gaa gag ctc acc tcc act gat gac tcc atc cgt cgc gga aaa gaa   883
Gln Glu Glu Leu Thr Ser Thr Asp Asp Ser Ile Arg Arg Gly Lys Glu
                250                 255                 260

gag ctc gct atc gct acc tcc gag ttc gga cca gag cgc acc cgc agc   931
Glu Leu Ala Ile Ala Thr Ser Glu Phe Gly Pro Glu Arg Thr Arg Ser
            265                 270                 275

ttc aac cgc gcc atg aac cac tcc acc ggc acc ctg caa aaa gcc ttt   979
Phe Asn Arg Ala Met Asn His Ser Thr Gly Thr Leu Gln Lys Ala Phe
        280                 285                 290

gag att cag cag cgc ctc aac gat tct atc cca gaa tcc gaa gcc gaa   1027
Glu Ile Gln Gln Arg Leu Asn Asp Ser Ile Pro Glu Ser Glu Ala Glu
    295                 300                 305

cgt caa tcc atg ctg gta gaa atc att tca tcc tgt ggc caa gcc gac   1075
Arg Gln Ser Met Leu Val Glu Ile Ile Ser Ser Cys Gly Gln Ala Asp
310                 315                 320                 325

gat gcc ctc gac gcc gaa gcc caa aac ttt gcc gat atg cgc aac ctg   1123
Asp Ala Leu Asp Ala Glu Ala Gln Asn Phe Ala Asp Met Arg Asn Leu
                330                 335                 340

ctg atc aac gcg ggc agc aaa ttg gat gct ctc acc caa aaa tcc gtc   1171
Leu Ile Asn Ala Gly Ser Lys Leu Asp Ala Leu Thr Gln Lys Ser Val
            345                 350                 355

gac ctg cgc acc cgc ctc ccc aag gcc caa gaa aca ctc gct ggc ctg   1219
Asp Leu Arg Thr Arg Leu Pro Lys Ala Gln Glu Thr Leu Ala Gly Leu
        360                 365                 370

cgc act cgc tac tca gca gag gtc ctt gaa agc atc gac gac aac gtc   1267
Arg Thr Arg Tyr Ser Ala Glu Val Leu Glu Ser Ile Asp Asp Asn Val
    375                 380                 385

gac ctc gcc agc gct tcg ctc gac gaa gca gaa gaa gtc ctg cca cag   1315
Asp Leu Ala Ser Ala Ser Leu Asp Glu Ala Glu Glu Val Leu Pro Gln
390                 395                 400                 405

gcg tac gag ata gag tcc atg ccc gca ggc gag cag ggc ggg ctt atc   1363
Ala Tyr Glu Ile Glu Ser Met Pro Ala Gly Glu Gln Gly Gly Leu Ile
                410                 415                 420

gac gcg atc cgt cac atc gag cac gcc atc act acc gca gac aaa ctc   1411
Asp Ala Ile Arg His Ile Glu His Ala Ile Thr Thr Ala Asp Lys Leu
```

```
            425                 430                 435

ctc gcg ggc gtc gag cat gcc gat gaa aac atc tcc aca gcc aaa gca   1459
Leu Ala Gly Val Glu His Ala Asp Glu Asn Ile Ser Thr Ala Lys Ala
        440                 445                 450

aac gtt gcc gat ctg atc caa gaa atc tca gac gaa atc aac gaa gcc   1507
Asn Val Ala Asp Leu Ile Gln Glu Ile Ser Asp Glu Ile Asn Glu Ala
    455                 460                 465

ggc caa ctc aaa caa agc gca gga gcc gac ggt gcc cgt gcc gac tgg   1555
Gly Gln Leu Lys Gln Ser Ala Gly Ala Asp Gly Ala Arg Ala Asp Trp
470                 475                 480                 485

gcc tcc ctc gac gat gct gtc cgc gca gcc agc gca gca cta atc acc   1603
Ala Ser Leu Asp Asp Ala Val Arg Ala Ala Ser Ala Ala Leu Ile Thr
                490                 495                 500

gca tca gca gac gcc gaa aag gat ccg ctc gga acc tac aca gaa ctt   1651
Ala Ser Ala Asp Ala Glu Lys Asp Pro Leu Gly Thr Tyr Thr Glu Leu
            505                 510                 515

gtc gat gtc gac tcc gcc ctc gac act caa ctt gac aca ctt cgc gcc   1699
Val Asp Val Asp Ser Ala Leu Asp Thr Gln Leu Asp Thr Leu Arg Ala
        520                 525                 530

acc gca gct gat caa gcc cgc cag cta cgc gta ttc gac caa cag ctg   1747
Thr Ala Ala Asp Gln Ala Arg Gln Leu Arg Val Phe Asp Gln Gln Leu
    535                 540                 545

caa tct gca aga agc caa atc caa aag gcc gaa gac ctc atc tcc acc   1795
Gln Ser Ala Arg Ser Gln Ile Gln Lys Ala Glu Asp Leu Ile Ser Thr
550                 555                 560                 565

cgc ggt cgc atc gta aaa tcc gaa gcc cgc acc cac ctg gcc aac gca   1843
Arg Gly Arg Ile Val Lys Ser Glu Ala Arg Thr His Leu Ala Asn Ala
                570                 575                 580

caa aag ctg tac gcc atg gca caa caa aac cgc acc cgc gac acc cgt   1891
Gln Lys Leu Tyr Ala Met Ala Gln Gln Asn Arg Thr Arg Asp Thr Arg
            585                 590                 595

gca gga att gat tac gga cgt caa gca gca gtc gca gcc caa cgc gcc   1939
Ala Gly Ile Asp Tyr Gly Arg Gln Ala Ala Val Ala Ala Gln Arg Ala
        600                 605                 610

agc aag tca gca caa aac gac atc acc acc tac aac aat cgc cac aat   1987
Ser Lys Ser Ala Gln Asn Asp Ile Thr Thr Tyr Asn Asn Arg His Asn
    615                 620                 625

tcc ggt ggc gga acc acc ggt gcg att gtc acc ggc atg gtg atc aac   2035
Ser Gly Gly Gly Thr Thr Gly Ala Ile Val Thr Gly Met Val Ile Asn
630                 635                 640                 645

tcg att ctc aac agc ggc cgc ggt ggc ggt ttc tgt gga ggc gga ggc   2083
Ser Ile Leu Asn Ser Gly Arg Gly Gly Gly Phe Cys Gly Gly Gly Gly
                650                 655                 660

ttt ggt gga ggc ggt ggc ggc ttc agc ggt ggt ggc ggt ggc gga gga   2131
Phe Gly Gly Gly Gly Gly Gly Phe Ser Gly Gly Gly Gly Gly Gly Gly
            665                 670                 675
```

ggg ttc cgc gga ggc cgc ttc tagcctgaaa cgagcaaaac caa 2175
Gly Phe Arg Gly Gly Arg Phe
680

<210> 656
<211> 684
<212> PRT
<213> Corynebacterium glutamicum

<400> 656
Met Asn Phe Ser Leu Val His Leu Arg Glu Asn Val Arg Arg Val Ser
1 5 10 15

Val Thr Val Ala Ile Gly Ala Gly Ala Leu Leu Ile Ser Gly Pro Phe
20 25 30

Phe Thr Ala His Thr Ala Glu Ala Thr Glu Thr Tyr Val Leu Ala Glu
35 40 45

Ser Pro Glu Phe Tyr Gln Asp Asn Val Thr Asp Tyr Thr Gly Gln Ile
50 55 60

Ser Ser Ser Asp Ile Thr Asn Ile Gln Ala Ala Ile Asp Asp Val Lys
65 70 75 80

Ala Ser Glu Gln Lys Val Ile Phe Val Val Phe Leu Ser Ser Phe Asp
85 90 95

Gly Val Asp Pro Glu Thr Trp Thr Gln Gln Ala Leu Gln Ala Asn Gly
100 105 110

Gly Gly Asn Val Leu Ile Tyr Ala Leu Ala Pro Glu Glu Arg Gln Tyr
115 120 125

Gly Ile Gln Gly Gly Thr Gln Trp Thr Asp Ala Glu Leu Asp Ala Ala
130 135 140

Asn Asn Ala Ala Phe Gln Ala Leu Ser Gln Glu Asp Trp Ala Gly Ser
145 150 155 160

Ala Leu Ala Leu Ala Glu Ser Val Gly Ser Ser Ser Ser Ser Ser Ser
165 170 175

Gly Ser Ser Ser Ser Ser Asp Phe Ser Gly Ala Trp Leu Ala Ala Ala
180 185 190

Gly Val Gly Thr Val Ala Ala Gly Gly Gly Ile Trp Ala Tyr Ser Arg
195 200 205

Ser Arg Lys Lys Lys Thr Ser Ala Ala Thr Leu Glu Asp Ala Arg Glu
210 215 220

Ile Asp Pro Arg Asp Thr Asn Arg Leu Met Gln Leu Pro Met Glu Thr
225 230 235 240

Leu Glu His Leu Ala Gln Glu Glu Leu Thr Ser Thr Asp Asp Ser Ile
245 250 255

Arg Arg Gly Lys Glu Glu Leu Ala Ile Ala Thr Ser Glu Phe Gly Pro

260 265 270

Glu Arg Thr Arg Ser Phe Asn Arg Ala Met Asn His Ser Thr Gly Thr
275 280 285

Leu Gln Lys Ala Phe Glu Ile Gln Gln Arg Leu Asn Asp Ser Ile Pro
290 295 300

Glu Ser Glu Ala Glu Arg Gln Ser Met Leu Val Glu Ile Ile Ser Ser
305 310 315 320

Cys Gly Gln Ala Asp Asp Ala Leu Asp Ala Glu Ala Gln Asn Phe Ala
325 330 335

Asp Met Arg Asn Leu Leu Ile Asn Ala Gly Ser Lys Leu Asp Ala Leu
340 345 350

Thr Gln Lys Ser Val Asp Leu Arg Thr Arg Leu Pro Lys Ala Gln Glu
355 360 365

Thr Leu Ala Gly Leu Arg Thr Arg Tyr Ser Ala Glu Val Leu Glu Ser
370 375 380

Ile Asp Asp Asn Val Asp Leu Ala Ser Ala Ser Leu Asp Glu Ala Glu
385 390 395 400

Glu Val Leu Pro Gln Ala Tyr Glu Ile Glu Ser Met Pro Ala Gly Glu
405 410 415

Gln Gly Gly Leu Ile Asp Ala Ile Arg His Ile Glu His Ala Ile Thr
420 425 430

Thr Ala Asp Lys Leu Leu Ala Gly Val Glu His Ala Asp Glu Asn Ile
435 440 445

Ser Thr Ala Lys Ala Asn Val Ala Asp Leu Ile Gln Glu Ile Ser Asp
450 455 460

Glu Ile Asn Glu Ala Gly Gln Leu Lys Gln Ser Ala Gly Ala Asp Gly
465 470 475 480

Ala Arg Ala Asp Trp Ala Ser Leu Asp Asp Ala Val Arg Ala Ala Ser
485 490 495

Ala Ala Leu Ile Thr Ala Ser Ala Asp Ala Glu Lys Asp Pro Leu Gly
500 505 510

Thr Tyr Thr Glu Leu Val Asp Val Asp Ser Ala Leu Asp Thr Gln Leu
515 520 525

Asp Thr Leu Arg Ala Thr Ala Ala Asp Gln Ala Arg Gln Leu Arg Val
530 535 540

Phe Asp Gln Gln Leu Gln Ser Ala Arg Ser Gln Ile Gln Lys Ala Glu
545 550 555 560

Asp Leu Ile Ser Thr Arg Gly Arg Ile Val Lys Ser Glu Ala Arg Thr
565 570 575

His Leu Ala Asn Ala Gln Lys Leu Tyr Ala Met Ala Gln Gln Asn Arg
580 585 590

```
Thr Arg Asp Thr Arg Ala Gly Ile Asp Tyr Gly Arg Gln Ala Ala Val
        595                 600                 605

Ala Ala Gln Arg Ala Ser Lys Ser Ala Gln Asn Asp Ile Thr Thr Tyr
    610                 615                 620

Asn Asn Arg His Asn Ser Gly Gly Gly Thr Thr Gly Ala Ile Val Thr
625                 630                 635                 640

Gly Met Val Ile Asn Ser Ile Leu Asn Ser Gly Arg Gly Gly Gly Phe
                645                 650                 655

Cys Gly Gly Gly Gly Phe Gly Gly Gly Gly Gly Gly Phe Ser Gly Gly
            660                 665                 670

Gly Gly Gly Gly Gly Gly Phe Arg Gly Gly Arg Phe
        675                 680
```

<210> 657
<211> 927
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(904)
<223> RXN01492

<400> 657

```
tgaagtgggc gcgttagctt cggcgcgtgg caaaccacat ttgctggact gcaggcataa 60

tggacaaaga cttttagcaa caactatgtg gaggtgacag gtg acc aca act ctg   115
                                               Val Thr Thr Thr Leu
                                                 1               5

tgg gcg gtt tct gac ctc cat gca gcg gtg aaa gct aac gct gat cca   163
Trp Ala Val Ser Asp Leu His Ala Ala Val Lys Ala Asn Ala Asp Pro
                10                  15                  20

att gag aat att cag cct aag gat ccg tct gac tgg ttg att gtt gca   211
Ile Glu Asn Ile Gln Pro Lys Asp Pro Ser Asp Trp Leu Ile Val Ala
            25                  30                  35

ggt gac gtg gcg gaa cgt acc gaa ttg gtg ctg gaa att ttg gca cgt   259
Gly Asp Val Ala Glu Arg Thr Glu Leu Val Leu Glu Ile Leu Ala Arg
        40                  45                  50

ttg cgc agg cgc ttt gcc aag gtg atc tgg gtt ccg ggt aac cat gag   307
Leu Arg Arg Arg Phe Ala Lys Val Ile Trp Val Pro Gly Asn His Glu
    55                  60                  65

ttg ttt tct cgc tcc gcg gac cgc tat cag ggg cgc gat aag tac tct   355
Leu Phe Ser Arg Ser Ala Asp Arg Tyr Gln Gly Arg Asp Lys Tyr Ser
70                  75                  80                  85

gaa ctc gtt gaa ggc tgc cgc aag att gat gtg ttg act ccg gag gac   403
Glu Leu Val Glu Gly Cys Arg Lys Ile Asp Val Leu Thr Pro Glu Asp
                90                  95                  100
```

```
cct tac tta acc ttt ggt ggg gtt act atc gtt ccg ttg ttt aca ctc   451
Pro Tyr Leu Thr Phe Gly Gly Val Thr Ile Val Pro Leu Phe Thr Leu
            105                 110                 115

tat gac tac tcg ttc cgt cga cct ggt ttc acc gtg gag cag gct gtg   499
Tyr Asp Tyr Ser Phe Arg Arg Pro Gly Phe Thr Val Glu Gln Ala Val
        120                 125                 130

caa gcg gcg cgg gat cgt caa gtg atg atg act gat gag ttt tct att   547
Gln Ala Ala Arg Asp Arg Gln Val Met Met Thr Asp Glu Phe Ser Ile
    135                 140                 145

gcg cct ttt gtt gat atc cga gcg tgg tgc tgg gat cgc tta gcc tat   595
Ala Pro Phe Val Asp Ile Arg Ala Trp Cys Trp Asp Arg Leu Ala Tyr
150                 155                 160                 165

tcc att aag cgt ttg agc aag atc aac ggg cca aca att ttg att aac   643
Ser Ile Lys Arg Leu Ser Lys Ile Asn Gly Pro Thr Ile Leu Ile Asn
                170                 175                 180

cac tgg ccg ctg gtg gtg gaa ccg act tat cag atg cgc tgg cag gaa   691
His Trp Pro Leu Val Val Glu Pro Thr Tyr Gln Met Arg Trp Gln Glu
            185                 190                 195

ctt gca ttg tgg tgc ggt act cgc cac acc agg gga tgg gcc gaa cgc   739
Leu Ala Leu Trp Cys Gly Thr Arg His Thr Arg Gly Trp Ala Glu Arg
        200                 205                 210

tac aac gcg gaa gcc gtt att tac ggt cat ctg cat atg ccc gga ata   787
Tyr Asn Ala Glu Ala Val Ile Tyr Gly His Leu His Met Pro Gly Ile
    215                 220                 225

acc aac gtc aac ggt gtg aaa cac att gaa gtg tcg ttg ggt tat ccg   835
Thr Asn Val Asn Gly Val Lys His Ile Glu Val Ser Leu Gly Tyr Pro
230                 235                 240                 245

cgc gaa tgg gag cat tgg tct ggg cag cat gtg tgg cca tat cca gtg   883
Arg Glu Trp Glu His Trp Ser Gly Gln His Val Trp Pro Tyr Pro Val
                250                 255                 260

atg gag gtg gac aat gct gga tgagtctttg tttccaaatt cgg             927
Met Glu Val Asp Asn Ala Gly
            265
```

<210> 658
<211> 268
<212> PRT
<213> Corynebacterium glutamicum

<400> 658

```
Val Thr Thr Thr Leu Trp Ala Val Ser Asp Leu His Ala Ala Val Lys
  1               5                  10                  15

Ala Asn Ala Asp Pro Ile Glu Asn Ile Gln Pro Lys Asp Pro Ser Asp
             20                  25                  30

Trp Leu Ile Val Ala Gly Asp Val Ala Glu Arg Thr Glu Leu Val Leu
         35                  40                  45

Glu Ile Leu Ala Arg Leu Arg Arg Arg Phe Ala Lys Val Ile Trp Val
```

```
     50                  55                  60

Pro Gly Asn His Glu Leu Phe Ser Arg Ser Ala Asp Arg Tyr Gln Gly
 65                  70                  75                  80

Arg Asp Lys Tyr Ser Glu Leu Val Glu Gly Cys Arg Lys Ile Asp Val
                 85                  90                  95

Leu Thr Pro Glu Asp Pro Tyr Leu Thr Phe Gly Gly Val Thr Ile Val
            100                 105                 110

Pro Leu Phe Thr Leu Tyr Asp Tyr Ser Phe Arg Arg Pro Gly Phe Thr
        115                 120                 125

Val Glu Gln Ala Val Gln Ala Ala Arg Asp Arg Gln Val Met Met Thr
    130                 135                 140

Asp Glu Phe Ser Ile Ala Pro Phe Val Asp Ile Arg Ala Trp Cys Trp
145                 150                 155                 160

Asp Arg Leu Ala Tyr Ser Ile Lys Arg Leu Ser Lys Ile Asn Gly Pro
                165                 170                 175

Thr Ile Leu Ile Asn His Trp Pro Leu Val Val Glu Pro Thr Tyr Gln
            180                 185                 190

Met Arg Trp Gln Glu Leu Ala Leu Trp Cys Gly Thr Arg His Thr Arg
        195                 200                 205

Gly Trp Ala Glu Arg Tyr Asn Ala Glu Ala Val Ile Tyr Gly His Leu
    210                 215                 220

His Met Pro Gly Ile Thr Asn Val Asn Gly Val Lys His Ile Glu Val
225                 230                 235                 240

Ser Leu Gly Tyr Pro Arg Glu Trp Glu His Trp Ser Gly Gln His Val
                245                 250                 255

Trp Pro Tyr Pro Val Met Glu Val Asp Asn Ala Gly
            260                 265


<210> 659
<211> 927
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(904)
<223> FRXA01492

<400> 659
tgaagtgggc gcgttagctt cggcgcgtgg caaaccacat ttgctggact gcaggcataa 60

tggacaaaga cttttagcaa caactatgtg gaggtgacag gtg acc aca act ctg   115
                                               Val Thr Thr Thr Leu
                                                 1               5

tgg gcg gtt tct gac ctc cat gca gcg gtg aaa gct aac gct gat cca   163
Trp Ala Val Ser Asp Leu His Ala Ala Val Lys Ala Asn Ala Asp Pro
```

```
                  10                  15                  20

att gag aat att cag cct aag gat ccg tct gac tgg ttg att gtt gca   211
Ile Glu Asn Ile Gln Pro Lys Asp Pro Ser Asp Trp Leu Ile Val Ala
             25                  30                  35

ggt gac gtg gcg gaa cgt acc gaa ttg gtg ctg gaa att ttg gca cgt   259
Gly Asp Val Ala Glu Arg Thr Glu Leu Val Leu Glu Ile Leu Ala Arg
         40                  45                  50

ttg cgc agg cgc ttt gcc aag gtg atc tgg gtt ccg ggt aac cat gag   307
Leu Arg Arg Arg Phe Ala Lys Val Ile Trp Val Pro Gly Asn His Glu
     55                  60                  65

ttg ttt tct cgc tcc gcg gac cgc tat cag ggg cgc gat aag tac tct   355
Leu Phe Ser Arg Ser Ala Asp Arg Tyr Gln Gly Arg Asp Lys Tyr Ser
 70                  75                  80                  85

gaa ctc gtt gaa ggc tgc cgc aag att gat gtg ttg act ccg gag gac   403
Glu Leu Val Glu Gly Cys Arg Lys Ile Asp Val Leu Thr Pro Glu Asp
                 90                  95                 100

cct tac tta acc ttt ggt ggg gtt act atc gtt ccg ttg ttt aca ctc   451
Pro Tyr Leu Thr Phe Gly Gly Val Thr Ile Val Pro Leu Phe Thr Leu
            105                 110                 115

tat gac tac tcg ttc cgt cga cct ggt ttc acc gtg gag cag gct gtg   499
Tyr Asp Tyr Ser Phe Arg Arg Pro Gly Phe Thr Val Glu Gln Ala Val
        120                 125                 130

caa gcg gcg cgg gat cgt caa gtg atg atg act gat gag ttt tct att   547
Gln Ala Ala Arg Asp Arg Gln Val Met Met Thr Asp Glu Phe Ser Ile
    135                 140                 145

gcg cct ttt gtt gat atc cga gcg tgg tgc tgg gat cgc tta gcc tat   595
Ala Pro Phe Val Asp Ile Arg Ala Trp Cys Trp Asp Arg Leu Ala Tyr
150                 155                 160                 165

tcc att aag cgt ttg agc aag atc aac ggg cca aca att ttg att aac   643
Ser Ile Lys Arg Leu Ser Lys Ile Asn Gly Pro Thr Ile Leu Ile Asn
                170                 175                 180

cac tgg ccg ctg gtg gtg gaa ccg act tat cag atg cgc tgg cag gaa   691
His Trp Pro Leu Val Val Glu Pro Thr Tyr Gln Met Arg Trp Gln Glu
            185                 190                 195

ctt gca ttg tgg tgc ggt act cgc cac acc agg gga tgg gcc gaa cgc   739
Leu Ala Leu Trp Cys Gly Thr Arg His Thr Arg Gly Trp Ala Glu Arg
        200                 205                 210

tac aac gcg gaa gcc gtt att tac ggt cat ctg cat atg ccc gga ata   787
Tyr Asn Ala Glu Ala Val Ile Tyr Gly His Leu His Met Pro Gly Ile
    215                 220                 225

acc aac gtc aac ggt gtg aaa cac att gaa gtg tcg ttg ggt tat ccg   835
Thr Asn Val Asn Gly Val Lys His Ile Glu Val Ser Leu Gly Tyr Pro
230                 235                 240                 245

cgc gaa tgg gag cat tgg tct ggg cag cat gtg tgg cca tat cca gtg   883
Arg Glu Trp Glu His Trp Ser Gly Gln His Val Trp Pro Tyr Pro Val
                250                 255                 260
```

```
atg gag gtg gac aat gct gga tgagtctttg tttccaaatt cgg                927
Met Glu Val Asp Asn Ala Gly
            265


<210> 660
<211> 268
<212> PRT
<213> Corynebacterium glutamicum

<400> 660
Val Thr Thr Thr Leu Trp Ala Val Ser Asp Leu His Ala Ala Val Lys
  1               5                  10                  15

Ala Asn Ala Asp Pro Ile Glu Asn Ile Gln Pro Lys Asp Pro Ser Asp
             20                  25                  30

Trp Leu Ile Val Ala Gly Asp Val Ala Glu Arg Thr Glu Leu Val Leu
         35                  40                  45

Glu Ile Leu Ala Arg Leu Arg Arg Arg Phe Ala Lys Val Ile Trp Val
     50                  55                  60

Pro Gly Asn His Glu Leu Phe Ser Arg Ser Ala Asp Arg Tyr Gln Gly
 65                  70                  75                  80

Arg Asp Lys Tyr Ser Glu Leu Val Glu Gly Cys Arg Lys Ile Asp Val
                 85                  90                  95

Leu Thr Pro Glu Asp Pro Tyr Leu Thr Phe Gly Gly Val Thr Ile Val
            100                 105                 110

Pro Leu Phe Thr Leu Tyr Asp Tyr Ser Phe Arg Arg Pro Gly Phe Thr
        115                 120                 125

Val Glu Gln Ala Val Gln Ala Ala Arg Asp Arg Gln Val Met Met Thr
    130                 135                 140

Asp Glu Phe Ser Ile Ala Pro Phe Val Asp Ile Arg Ala Trp Cys Trp
145                 150                 155                 160

Asp Arg Leu Ala Tyr Ser Ile Lys Arg Leu Ser Lys Ile Asn Gly Pro
                165                 170                 175

Thr Ile Leu Ile Asn His Trp Pro Leu Val Val Glu Pro Thr Tyr Gln
            180                 185                 190

Met Arg Trp Gln Glu Leu Ala Leu Trp Cys Gly Thr Arg His Thr Arg
        195                 200                 205

Gly Trp Ala Glu Arg Tyr Asn Ala Glu Ala Val Ile Tyr Gly His Leu
    210                 215                 220

His Met Pro Gly Ile Thr Asn Val Asn Gly Val Lys His Ile Glu Val
225                 230                 235                 240

Ser Leu Gly Tyr Pro Arg Glu Trp Glu His Trp Ser Gly Gln His Val
                245                 250                 255

Trp Pro Tyr Pro Val Met Glu Val Asp Asn Ala Gly
```

260 265

<210> 661
<211> 597
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(574)
<223> RXN01518

<400> 661
agcagaacct gatgccgtcc tgcacggcac gaccattgca gaacatgtgg ataatcttga 60

tcccacagac attgaaggtg tcaccaagat ttaaggagtc gtg gct ttc atg cag 115
Val Ala Phe Met Gln
1 5

aaa acg tca gcg ggt tgg ttg atc gca acg gga ggt ttc ctc gcc gct 163
Lys Thr Ser Ala Gly Trp Leu Ile Ala Thr Gly Gly Phe Leu Ala Ala
10 15 20

gtg tcc gcc att ttg acg tgg cgt ttt tat gga tcc atg acc tct att 211
Val Ser Ala Ile Leu Thr Trp Arg Phe Tyr Gly Ser Met Thr Ser Ile
25 30 35

tcc atc acg gta tcc atc act ttt tgg ttg ttg gcc gtg gtg tgt ggt 259
Ser Ile Thr Val Ser Ile Thr Phe Trp Leu Leu Ala Val Val Cys Gly
40 45 50

ttc gca ggt gtg aag gtc caa ggt cgc ctc gat gag ggg ctg atc ggc 307
Phe Ala Gly Val Lys Val Gln Gly Arg Leu Asp Glu Gly Leu Ile Gly
55 60 65

cag gac aaa tcc caa atg aac ccc gtg acc att gcc tat ctg gcc atg 355
Gln Asp Lys Ser Gln Met Asn Pro Val Thr Ile Ala Tyr Leu Ala Met
70 75 80 85

ctg ggt cga gcg tgt gcg tgg ggt ggc gca att ttc ggc ggc gtt tat 403
Leu Gly Arg Ala Cys Ala Trp Gly Gly Ala Ile Phe Gly Gly Val Tyr
90 95 100

gtg gga att ggc agt tat gta atc cca cgc gcc ggt gag ttg tcc gca 451
Val Gly Ile Gly Ser Tyr Val Ile Pro Arg Ala Gly Glu Leu Ser Ala
105 110 115

gca tcg aat gat ctt ccg gga gtt att gcc tgt gcg ctg ggc gga atc 499
Ala Ser Asn Asp Leu Pro Gly Val Ile Ala Cys Ala Leu Gly Gly Ile
120 125 130

gca ctc tca gct gcc gga ctt tat tta gag cga agc tgt gag gct ccg 547
Ala Leu Ser Ala Ala Gly Leu Tyr Leu Glu Arg Ser Cys Glu Ala Pro
135 140 145

cct ccc caa tct ggc gaa gcg atc agc tagattggaa ttcatgaatc 594
Pro Pro Gln Ser Gly Glu Ala Ile Ser
150 155

aag 597

<210> 662
<211> 158
<212> PRT
<213> Corynebacterium glutamicum

<400> 662
Val Ala Phe Met Gln Lys Thr Ser Ala Gly Trp Leu Ile Ala Thr Gly
1 5 10 15

Gly Phe Leu Ala Ala Val Ser Ala Ile Leu Thr Trp Arg Phe Tyr Gly
20 25 30

Ser Met Thr Ser Ile Ser Ile Thr Val Ser Ile Thr Phe Trp Leu Leu
35 40 45

Ala Val Val Cys Gly Phe Ala Gly Val Lys Val Gln Gly Arg Leu Asp
50 55 60

Glu Gly Leu Ile Gly Gln Asp Lys Ser Gln Met Asn Pro Val Thr Ile
65 70 75 80

Ala Tyr Leu Ala Met Leu Gly Arg Ala Cys Ala Trp Gly Gly Ala Ile
85 90 95

Phe Gly Gly Val Tyr Val Gly Ile Gly Ser Tyr Val Ile Pro Arg Ala
100 105 110

Gly Glu Leu Ser Ala Ala Ser Asn Asp Leu Pro Gly Val Ile Ala Cys
115 120 125

Ala Leu Gly Gly Ile Ala Leu Ser Ala Ala Gly Leu Tyr Leu Glu Arg
130 135 140

Ser Cys Glu Ala Pro Pro Pro Gln Ser Gly Glu Ala Ile Ser
145 150 155

<210> 663
<211> 597
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(574)
<223> FRXA01518

<400> 663
agcagaacct gatgccgtcc tgcacggcac gaccattgca gaacatgtgg ataatcttga 60

tcccacagac attgaaggtg tcaccaagat ttaaggagtc gtg gct ttc atg cag 115
Val Ala Phe Met Gln
1 5

aaa acg tca gcg ggt tgg ttg atc gca acg gga ggt ttc ctc gcc gct 163
Lys Thr Ser Ala Gly Trp Leu Ile Ala Thr Gly Gly Phe Leu Ala Ala
10 15 20

gtg tcc gcc att ttg acg tgg cgt ttt tat gga tcc atg acc tct att 211

```
Val Ser Ala Ile Leu Thr Trp Arg Phe Tyr Gly Ser Met Thr Ser Ile
            25                  30                  35

tcc atc acg gta tcc atc act ttt tgg ttg ttg gcc gtg gtg tgt ggt   259
Ser Ile Thr Val Ser Ile Thr Phe Trp Leu Leu Ala Val Val Cys Gly
        40                  45                  50

ttc gca ggt gtg aag gtc caa ggt cgc ctc gat gag ggg ctg atc ggc   307
Phe Ala Gly Val Lys Val Gln Gly Arg Leu Asp Glu Gly Leu Ile Gly
    55                  60                  65

cag gac aaa tcc caa atg aac ccc gtg acc att gcc tat ctg gcc atg   355
Gln Asp Lys Ser Gln Met Asn Pro Val Thr Ile Ala Tyr Leu Ala Met
70                  75                  80                  85

ctg ggt cga gcg tgt gcg tgg ggt ggc gca att ttc ggc ggc gtt tat   403
Leu Gly Arg Ala Cys Ala Trp Gly Gly Ala Ile Phe Gly Gly Val Tyr
                90                  95                  100

gtg gga att ggc agt tat gta atc cca cgc gcc ggt gag ttg tcc gca   451
Val Gly Ile Gly Ser Tyr Val Ile Pro Arg Ala Gly Glu Leu Ser Ala
            105                 110                 115

gca tcg aat gat ctt ccg gga gtt att gcc tgt gcg ctg ggc gga atc   499
Ala Ser Asn Asp Leu Pro Gly Val Ile Ala Cys Ala Leu Gly Gly Ile
        120                 125                 130

gca ctc tca gct gcc gga ctt tat tta gag cga agc tgt gag gct ccg   547
Ala Leu Ser Ala Ala Gly Leu Tyr Leu Glu Arg Ser Cys Glu Ala Pro
    135                 140                 145

cct ccc caa tct ggc gaa gcg atc agc tagattggaa ttcatgaatc         594
Pro Pro Gln Ser Gly Glu Ala Ile Ser
150                 155

aag                                                               597


<210> 664
<211> 158
<212> PRT
<213> Corynebacterium glutamicum

<400> 664
Val Ala Phe Met Gln Lys Thr Ser Ala Gly Trp Leu Ile Ala Thr Gly
  1               5                  10                  15

Gly Phe Leu Ala Ala Val Ser Ala Ile Leu Thr Trp Arg Phe Tyr Gly
            20                  25                  30

Ser Met Thr Ser Ile Ser Ile Thr Val Ser Ile Thr Phe Trp Leu Leu
        35                  40                  45

Ala Val Val Cys Gly Phe Ala Gly Val Lys Val Gln Gly Arg Leu Asp
    50                  55                  60

Glu Gly Leu Ile Gly Gln Asp Lys Ser Gln Met Asn Pro Val Thr Ile
65                  70                  75                  80

Ala Tyr Leu Ala Met Leu Gly Arg Ala Cys Ala Trp Gly Gly Ala Ile
                85                  90                  95
```

```
Phe Gly Gly Val Tyr Val Gly Ile Gly Ser Tyr Val Ile Pro Arg Ala
            100                 105                 110

Gly Glu Leu Ser Ala Ala Ser Asn Asp Leu Pro Gly Val Ile Ala Cys
        115                 120                 125

Ala Leu Gly Gly Ile Ala Leu Ser Ala Ala Gly Leu Tyr Leu Glu Arg
    130                 135                 140

Ser Cys Glu Ala Pro Pro Pro Gln Ser Gly Glu Ala Ile Ser
145                 150                 155


<210> 665
<211> 1727
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (46)..(1704)
<223> RXN01549

<400> 665
tgaattccgt ttctagattt tttttattga ttgtgagagt gcattgtg gct aat gat  57
                                                Val Ala Asn Asp
                                                  1

ttt ata gaa cca aat gat gcc ccc gat gca cct gat aat ggt gac tcg  105
Phe Ile Glu Pro Asn Asp Ala Pro Asp Ala Pro Asp Asn Gly Asp Ser
  5                  10                  15                  20

gga agc tcg ggg ttt gtt gat gaa gca aaa gat aag acc cgc tca gct  153
Gly Ser Ser Gly Phe Val Asp Glu Ala Lys Asp Lys Thr Arg Ser Ala
                25                  30                  35

gca caa ggc tta ggt tat ggc gca cta cgt gta ggt ttt ggt act gca  201
Ala Gln Gly Leu Gly Tyr Gly Ala Leu Arg Val Gly Phe Gly Thr Ala
            40                  45                  50

gca ctt gca gcc aat ggt gct cgc tct atg ggt aat ttg gct aaa aac  249
Ala Leu Ala Ala Asn Gly Ala Arg Ser Met Gly Asn Leu Ala Lys Asn
        55                  60                  65

ctg tgg aca cga atg atg ggg ctt gcc ctg tct gcc ggt act ggt atc  297
Leu Trp Thr Arg Met Met Gly Leu Ala Leu Ser Ala Gly Thr Gly Ile
    70                  75                  80

tct gct gcc aca ggt ggc atg atc act gca cgt gta ggc gca atg ctg  345
Ser Ala Ala Thr Gly Gly Met Ile Thr Ala Arg Val Gly Ala Met Leu
 85                  90                  95                 100

gca ggt aca ggc tcg gtg ttg tcg tcg gtg acg act att gcg ttg att  393
Ala Gly Thr Gly Ser Val Leu Ser Ser Val Thr Thr Ile Ala Leu Ile
                105                 110                 115

gtg tcg atg att gtg gtg ccg gca ggt cga aaa gac ggc att atc gag  441
Val Ser Met Ile Val Val Pro Ala Gly Arg Lys Asp Gly Ile Ile Glu
            120                 125                 130
```

```
ttg tgt gag ccg cca gta acg gcc aac ccg ttt acc att gac gca ggt   489
Leu Cys Glu Pro Pro Val Thr Ala Asn Pro Phe Thr Ile Asp Ala Gly
        135                 140                 145

gat atg act gag aac gcg aag ttg gtg tac ggt gcg ctg tcg tat ctt   537
Asp Met Thr Glu Asn Ala Lys Leu Val Tyr Gly Ala Leu Ser Tyr Leu
    150                 155                 160

ggg atg aat gat caa aat atc gcc ggt gtc ttg ggc aac ttt gag aca   585
Gly Met Asn Asp Gln Asn Ile Ala Gly Val Leu Gly Asn Phe Glu Thr
165                 170                 175                 180

gaa tca ggt atc gac ccg act gcg gtg gag ggt att ttt gat gaa cca   633
Glu Ser Gly Ile Asp Pro Thr Ala Val Glu Gly Ile Phe Asp Glu Pro
                185                 190                 195

aat acc atc ggt cct cgg aag aga gct gcg tgg gat aag aac ttt gaa   681
Asn Thr Ile Gly Pro Arg Lys Arg Ala Ala Trp Asp Lys Asn Phe Glu
            200                 205                 210

cct cag ccg atg ggt att ggg ctt ggg cag tgg aca gca ggg cgc aca   729
Pro Gln Pro Met Gly Ile Gly Leu Gly Gln Trp Thr Ala Gly Arg Thr
        215                 220                 225

cag atg ttg cta gat ttt gcc gcc gat aga aac cga gac tgg cat tac   777
Gln Met Leu Leu Asp Phe Ala Ala Asp Arg Asn Arg Asp Trp His Tyr
    230                 235                 240

atc gac gtg cag ctt gca ttt gct att agt ggc gat aat gaa agc gat   825
Ile Asp Val Gln Leu Ala Phe Ala Ile Ser Gly Asp Asn Glu Ser Asp
245                 250                 255                 260

cgc aag gtt ttt ctg gaa atg gtt gat aat aaa aac tcc agt agc aat   873
Arg Lys Val Phe Leu Glu Met Val Asp Asn Lys Asn Ser Ser Ser Asn
                265                 270                 275

agc ccc acc gca gcg tcc gag tac ttc ctg cgt gag tgg gag cgc ccg   921
Ser Pro Thr Ala Ala Ser Glu Tyr Phe Leu Arg Glu Trp Glu Arg Pro
            280                 285                 290

gca gat gtc gca ggt aat gca ccc att cgt gca gag caa gca tct aag   969
Ala Asp Val Ala Gly Asn Ala Pro Ile Arg Ala Glu Gln Ala Ser Lys
        295                 300                 305

tgg tac gcg cag atg ggt ggt tgg caa aag aac tca acc ttg ggt gag   1017
Trp Tyr Ala Gln Met Gly Gly Trp Gln Lys Asn Ser Thr Leu Gly Glu
    310                 315                 320

tct gtg atc gct atg gct gat ggt gca gca gca aaa tcc acg gcg cgt   1065
Ser Val Ile Ala Met Ala Asp Gly Ala Ala Ala Lys Ser Thr Ala Arg
325                 330                 335                 340

gat gag cag gat gct ctt aat gat tgt cct gaa gag gac cgc acc tca   1113
Asp Glu Gln Asp Ala Leu Asn Asp Cys Pro Glu Glu Asp Arg Thr Ser
                345                 350                 355

ggt gga aat acg tcc gct gca gaa gca atg gtg act att tca cat cct   1161
Gly Gly Asn Thr Ser Ala Ala Glu Ala Met Val Thr Ile Ser His Pro
            360                 365                 370

tat ctg gct gat tct cgt ggc aat gac ggt act gat att tac cgc tat   1209
```

```
Tyr Leu Ala Asp Ser Arg Gly Asn Asp Gly Thr Asp Ile Tyr Arg Tyr
        375                 380                 385

atc cat gat gaa gtg ctc acc ggt gat ccg tat tac gca tcc tgt gac   1257
Ile His Asp Glu Val Leu Thr Gly Asp Pro Tyr Tyr Ala Ser Cys Asp
    390                 395                 400

cgt ggc gtt gct acc gct att cgc tgg tcg ggc acg gat gat acg ttc   1305
Arg Gly Val Ala Thr Ala Ile Arg Trp Ser Gly Thr Asp Asp Thr Phe
405                 410                 415                 420

cca gca ggt cca aca gca gca cag tat gaa tac gtt gtg ggc aca gga   1353
Pro Ala Gly Pro Thr Ala Ala Gln Tyr Glu Tyr Val Val Gly Thr Gly
                425                 430                 435

tcg ggc cgt tgg gag gaa atc ggc aat ctt gcc acc atg tca gag aac   1401
Ser Gly Arg Trp Glu Glu Ile Gly Asn Leu Ala Thr Met Ser Glu Asn
            440                 445                 450

gat ttg tta cct ggc gat gtg ctt ctt ggt gca ccg aat cac gtt gcg   1449
Asp Leu Leu Pro Gly Asp Val Leu Leu Gly Ala Pro Asn His Val Ala
        455                 460                 465

atg tat gtc agc aat gag gtt gtt gtg gac atg ttg ggc cct ggt aat   1497
Met Tyr Val Ser Asn Glu Val Val Val Asp Met Leu Gly Pro Gly Asn
    470                 475                 480

gca gag cct aat gca gct att ggt cat gca tcg ttg aat gac cgc tca   1545
Ala Glu Pro Asn Ala Ala Ile Gly His Ala Ser Leu Asn Asp Arg Ser
485                 490                 495                 500

cct ggt ctg gat acc ttg agt ctg gat gga tgg ggc gtg aac ttc aag   1593
Pro Gly Leu Asp Thr Leu Ser Leu Asp Gly Trp Gly Val Asn Phe Lys
                505                 510                 515

gtg ttc cgc aac acc cag gct gag aca aac tca gtg ttc tct ggt gta   1641
Val Phe Arg Asn Thr Gln Ala Glu Thr Asn Ser Val Phe Ser Gly Val
            520                 525                 530

cag att ccg gct ggt aaa gaa att ggc gaa atg act aac cca act cga   1689
Gln Ile Pro Ala Gly Lys Glu Ile Gly Glu Met Thr Asn Pro Thr Arg
        535                 540                 545

act act cct gca gga taagtttttt tcatcgctgg gtt                    1727
Thr Thr Pro Ala Gly
    550
```

<210> 666
<211> 553
<212> PRT
<213> Corynebacterium glutamicum

<400> 666

```
Val Ala Asn Asp Phe Ile Glu Pro Asn Asp Ala Pro Asp Ala Pro Asp
  1               5                  10                  15

Asn Gly Asp Ser Gly Ser Ser Gly Phe Val Asp Glu Ala Lys Asp Lys
             20                  25                  30

Thr Arg Ser Ala Ala Gln Gly Leu Gly Tyr Gly Ala Leu Arg Val Gly
```

```
         35                  40                  45

Phe Gly Thr Ala Ala Leu Ala Ala Asn Gly Ala Arg Ser Met Gly Asn
     50                  55                  60

Leu Ala Lys Asn Leu Trp Thr Arg Met Met Gly Leu Ala Leu Ser Ala
 65                  70                  75                  80

Gly Thr Gly Ile Ser Ala Ala Thr Gly Gly Met Ile Thr Ala Arg Val
                 85                  90                  95

Gly Ala Met Leu Ala Gly Thr Gly Ser Val Leu Ser Ser Val Thr Thr
            100                 105                 110

Ile Ala Leu Ile Val Ser Met Ile Val Val Pro Ala Gly Arg Lys Asp
        115                 120                 125

Gly Ile Ile Glu Leu Cys Glu Pro Pro Val Thr Ala Asn Pro Phe Thr
    130                 135                 140

Ile Asp Ala Gly Asp Met Thr Glu Asn Ala Lys Leu Val Tyr Gly Ala
145                 150                 155                 160

Leu Ser Tyr Leu Gly Met Asn Asp Gln Asn Ile Ala Gly Val Leu Gly
                165                 170                 175

Asn Phe Glu Thr Glu Ser Gly Ile Asp Pro Thr Ala Val Glu Gly Ile
            180                 185                 190

Phe Asp Glu Pro Asn Thr Ile Gly Pro Arg Lys Arg Ala Ala Trp Asp
        195                 200                 205

Lys Asn Phe Glu Pro Gln Pro Met Gly Ile Gly Leu Gly Gln Trp Thr
    210                 215                 220

Ala Gly Arg Thr Gln Met Leu Leu Asp Phe Ala Ala Asp Arg Asn Arg
225                 230                 235                 240

Asp Trp His Tyr Ile Asp Val Gln Leu Ala Phe Ala Ile Ser Gly Asp
                245                 250                 255

Asn Glu Ser Asp Arg Lys Val Phe Leu Glu Met Val Asp Asn Lys Asn
            260                 265                 270

Ser Ser Ser Asn Ser Pro Thr Ala Ala Ser Glu Tyr Phe Leu Arg Glu
        275                 280                 285

Trp Glu Arg Pro Ala Asp Val Ala Gly Asn Ala Pro Ile Arg Ala Glu
    290                 295                 300

Gln Ala Ser Lys Trp Tyr Ala Gln Met Gly Gly Trp Gln Lys Asn Ser
305                 310                 315                 320

Thr Leu Gly Glu Ser Val Ile Ala Met Ala Asp Gly Ala Ala Ala Lys
                325                 330                 335

Ser Thr Ala Arg Asp Glu Gln Asp Ala Leu Asn Asp Cys Pro Glu Glu
            340                 345                 350

Asp Arg Thr Ser Gly Gly Asn Thr Ser Ala Ala Glu Ala Met Val Thr
        355                 360                 365
```

```
Ile Ser His Pro Tyr Leu Ala Asp Ser Arg Gly Asn Asp Gly Thr Asp
    370                 375                 380

Ile Tyr Arg Tyr Ile His Asp Glu Val Leu Thr Gly Asp Pro Tyr Tyr
385                 390                 395                 400

Ala Ser Cys Asp Arg Gly Val Ala Thr Ala Ile Arg Trp Ser Gly Thr
                405                 410                 415

Asp Asp Thr Phe Pro Ala Gly Pro Thr Ala Ala Gln Tyr Glu Tyr Val
            420                 425                 430

Val Gly Thr Gly Ser Gly Arg Trp Glu Glu Ile Gly Asn Leu Ala Thr
        435                 440                 445

Met Ser Glu Asn Asp Leu Leu Pro Gly Asp Val Leu Leu Gly Ala Pro
    450                 455                 460

Asn His Val Ala Met Tyr Val Ser Asn Glu Val Val Val Asp Met Leu
465                 470                 475                 480

Gly Pro Gly Asn Ala Glu Pro Asn Ala Ala Ile Gly His Ala Ser Leu
                485                 490                 495

Asn Asp Arg Ser Pro Gly Leu Asp Thr Leu Ser Leu Asp Gly Trp Gly
            500                 505                 510

Val Asn Phe Lys Val Phe Arg Asn Thr Gln Ala Glu Thr Asn Ser Val
        515                 520                 525

Phe Ser Gly Val Gln Ile Pro Ala Gly Lys Glu Ile Gly Glu Met Thr
    530                 535                 540

Asn Pro Thr Arg Thr Thr Pro Ala Gly
545                 550
```

Sequence Listing - Page 814 of 1144

<210> 667
<211> 942
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (59)..(919)
<223> FRXA01549

<400> 667

```
cagcttgcat ttgctattag tggcgataat gaaagcgatc gcaaggtttt tctggaaaatg 61
                                                                 Met
                                                                   1

gtt gat aat aaa aac tcc agt agc aat agc ccc acc gca gcg tcc gag   109
Val Asp Asn Lys Asn Ser Ser Ser Asn Ser Pro Thr Ala Ala Ser Glu
  5                  10                  15

tac ttc ctg cgt gag tgg gag cgc ccg gca gat gtc gca ggt aat gca   157
Tyr Phe Leu Arg Glu Trp Glu Arg Pro Ala Asp Val Ala Gly Asn Ala
 20                  25                  30
```

```
ccc att cgt gca gag caa gca tct aag tgg tac gcg cag atg ggt ggt   205
Pro Ile Arg Ala Glu Gln Ala Ser Lys Trp Tyr Ala Gln Met Gly Gly
     35                  40                  45

tgg caa aag aac tca acc ttg ggt gag tct gtg atc gct atg gct gat   253
Trp Gln Lys Asn Ser Thr Leu Gly Glu Ser Val Ile Ala Met Ala Asp
 50                  55                  60                  65

ggt gca gca gca aaa tcc acg gcg cgt gat gag cag gat gct ctt aat   301
Gly Ala Ala Ala Lys Ser Thr Ala Arg Asp Glu Gln Asp Ala Leu Asn
                 70                  75                  80

gat tgt cct gaa gag gac cgc acc tca ggt gga aat acg tcc gct gca   349
Asp Cys Pro Glu Glu Asp Arg Thr Ser Gly Gly Asn Thr Ser Ala Ala
             85                  90                  95

gaa gca atg gtg act att tca cat cct tat ctg gct gat tct cgt ggc   397
Glu Ala Met Val Thr Ile Ser His Pro Tyr Leu Ala Asp Ser Arg Gly
        100                 105                 110

aat gac ggt act gat att tac cgc tat atc cat gat gaa gtg ctc acc   445
Asn Asp Gly Thr Asp Ile Tyr Arg Tyr Ile His Asp Glu Val Leu Thr
    115                 120                 125

ggt gat ccg tat tac gca tcc tgt gac cgt ggc gtt gct acc gct att   493
Gly Asp Pro Tyr Tyr Ala Ser Cys Asp Arg Gly Val Ala Thr Ala Ile
130                 135                 140                 145

cgc tgg tcg ggc acg gat gat acg ttc cca gca ggt cca aca gca gca   541
Arg Trp Ser Gly Thr Asp Asp Thr Phe Pro Ala Gly Pro Thr Ala Ala
                150                 155                 160

cag tat gaa tac gtt gtg ggc aca gga tcg ggc cgt tgg gag gaa atc   589
Gln Tyr Glu Tyr Val Val Gly Thr Gly Ser Gly Arg Trp Glu Glu Ile
            165                 170                 175

ggc aat ctt gcc acc atg tca gag aac gat ttg tta cct ggc gat gtg   637
Gly Asn Leu Ala Thr Met Ser Glu Asn Asp Leu Leu Pro Gly Asp Val
        180                 185                 190

ctt ctt ggt gca ccg aat cac gtt gcg atg tat gtc agc aat gag gtt   685
Leu Leu Gly Ala Pro Asn His Val Ala Met Tyr Val Ser Asn Glu Val
    195                 200                 205

gtt gtg gac atg ttg ggc cct ggt aat gca gag cct aat gca gct att   733
Val Val Asp Met Leu Gly Pro Gly Asn Ala Glu Pro Asn Ala Ala Ile
210                 215                 220                 225

ggt cat gca tcg ttg aat gac cgc tca cct ggt ctg gat acc ttg agt   781
Gly His Ala Ser Leu Asn Asp Arg Ser Pro Gly Leu Asp Thr Leu Ser
                230                 235                 240

ctg gat gga tgg ggc gtg aac ttc aag gtg ttc cgc aac acc cag gct   829
Leu Asp Gly Trp Gly Val Asn Phe Lys Val Phe Arg Asn Thr Gln Ala
            245                 250                 255

gag aca aac tca gtg ttc tct ggt gta cag att ccg gct ggt aaa gaa   877
Glu Thr Asn Ser Val Phe Ser Gly Val Gln Ile Pro Ala Gly Lys Glu
        260                 265                 270

att ggc gaa atg act aac cca act cga act act cct gca gga           919
```

```
Ile Gly Glu Met Thr Asn Pro Thr Arg Thr Thr Pro Ala Gly
    275                 280                 285

taagtttttt tcatcgctgg gtt                                          942


<210> 668
<211> 287
<212> PRT
<213> Corynebacterium glutamicum

<400> 668
Met Val Asp Asn Lys Asn Ser Ser Ser Asn Ser Pro Thr Ala Ala Ser
  1               5                  10                  15

Glu Tyr Phe Leu Arg Glu Trp Glu Arg Pro Ala Asp Val Ala Gly Asn
             20                  25                  30

Ala Pro Ile Arg Ala Glu Gln Ala Ser Lys Trp Tyr Ala Gln Met Gly
         35                  40                  45

Gly Trp Gln Lys Asn Ser Thr Leu Gly Glu Ser Val Ile Ala Met Ala
     50                  55                  60

Asp Gly Ala Ala Ala Lys Ser Thr Ala Arg Asp Glu Gln Asp Ala Leu
 65                  70                  75                  80

Asn Asp Cys Pro Glu Glu Asp Arg Thr Ser Gly Gly Asn Thr Ser Ala
                 85                  90                  95

Ala Glu Ala Met Val Thr Ile Ser His Pro Tyr Leu Ala Asp Ser Arg
            100                 105                 110

Gly Asn Asp Gly Thr Asp Ile Tyr Arg Tyr Ile His Asp Glu Val Leu
        115                 120                 125

Thr Gly Asp Pro Tyr Tyr Ala Ser Cys Asp Arg Gly Val Ala Thr Ala
    130                 135                 140

Ile Arg Trp Ser Gly Thr Asp Asp Thr Phe Pro Ala Gly Pro Thr Ala
145                 150                 155                 160

Ala Gln Tyr Glu Tyr Val Val Gly Thr Gly Ser Gly Arg Trp Glu Glu
                165                 170                 175

Ile Gly Asn Leu Ala Thr Met Ser Glu Asn Asp Leu Leu Pro Gly Asp
            180                 185                 190

Val Leu Leu Gly Ala Pro Asn His Val Ala Met Tyr Val Ser Asn Glu
        195                 200                 205

Val Val Val Asp Met Leu Gly Pro Gly Asn Ala Glu Pro Asn Ala Ala
    210                 215                 220

Ile Gly His Ala Ser Leu Asn Asp Arg Ser Pro Gly Leu Asp Thr Leu
225                 230                 235                 240

Ser Leu Asp Gly Trp Gly Val Asn Phe Lys Val Phe Arg Asn Thr Gln
                245                 250                 255

Ala Glu Thr Asn Ser Val Phe Ser Gly Val Gln Ile Pro Ala Gly Lys
```

```
            260                 265                 270

Glu Ile Gly Glu Met Thr Asn Pro Thr Arg Thr Thr Pro Ala Gly
        275                 280                 285


<210> 669
<211> 363
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (46)..(363)
<223> FRXA02011

<400> 669
tgaattccgt ttctagattt tttttattga ttgtgagagt gcattgtg gct aat gat  57
                                                 Val Ala Asn Asp
                                                   1

ttt ata gaa cca aat gat gcc ccc gat gca cct gat aat ggt gac tcg  105
Phe Ile Glu Pro Asn Asp Ala Pro Asp Ala Pro Asp Asn Gly Asp Ser
  5                  10                  15                  20

gga agc tcg ggg ttt gtt gat gaa gca aaa gat aag acc cgc tca gct  153
Gly Ser Ser Gly Phe Val Asp Glu Ala Lys Asp Lys Thr Arg Ser Ala
                 25                  30                  35

gca caa ggc tta ggt tat ggc gca cta cgt gta ggt ttt ggt act gca  201
Ala Gln Gly Leu Gly Tyr Gly Ala Leu Arg Val Gly Phe Gly Thr Ala
             40                  45                  50

gca ctt gca gcc aat ggt gct cgc tct atg ggt aat ttg gct aaa aac  249
Ala Leu Ala Ala Asn Gly Ala Arg Ser Met Gly Asn Leu Ala Lys Asn
         55                  60                  65

ctg tgg aca cca atg atg ggg ctt gcc ctg tct gcc ggt act ggt atc  297
Leu Trp Thr Pro Met Met Gly Leu Ala Leu Ser Ala Gly Thr Gly Ile
     70                  75                  80

tct gct gcc aca ggt ggc atg atc act gca cgt gta ggc gca atg ctg  345
Ser Ala Ala Thr Gly Gly Met Ile Thr Ala Arg Val Gly Ala Met Leu
 85                  90                  95                 100

gca ggt aca ggc tcg gcg                                         363
Ala Gly Thr Gly Ser Ala
                105


<210> 670
<211> 106
<212> PRT
<213> Corynebacterium glutamicum

<400> 670
Val Ala Asn Asp Phe Ile Glu Pro Asn Asp Ala Pro Asp Ala Pro Asp
  1               5                  10                  15

Asn Gly Asp Ser Gly Ser Ser Gly Phe Val Asp Glu Ala Lys Asp Lys
             20                  25                  30
```

```
Thr Arg Ser Ala Ala Gln Gly Leu Gly Tyr Gly Ala Leu Arg Val Gly
         35                  40                  45

Phe Gly Thr Ala Ala Leu Ala Ala Asn Gly Ala Arg Ser Met Gly Asn
     50                  55                  60

Leu Ala Lys Asn Leu Trp Thr Pro Met Met Gly Leu Ala Leu Ser Ala
 65                  70                  75                  80

Gly Thr Gly Ile Ser Ala Ala Thr Gly Gly Met Ile Thr Ala Arg Val
                 85                  90                  95

Gly Ala Met Leu Ala Gly Thr Gly Ser Ala
            100                 105


<210> 671
<211> 939
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(916)
<223> RXN01557

<400> 671
taaaggtgtg aaaatagttc ctcacgtggg gaactatact gatccttgat gcgttaactt 60

gattgacgac gaaaaatcaa ttgaaaggat cggggactcc gtg cga agc agc aat   115
                                              Val Arg Ser Ser Asn
                                                1               5

ccc gtt ttt agt tcc ctt aag gaa act caa cgt cca caa ggc cag aac   163
Pro Val Phe Ser Ser Leu Lys Glu Thr Gln Arg Pro Gln Gly Gln Asn
                10                  15                  20

cca tac ggt ggt tac gac aac ttc ggt ggt gtc tac cag caa aac gta   211
Pro Tyr Gly Gly Tyr Asp Asn Phe Gly Gly Val Tyr Gln Gln Asn Val
            25                  30                  35

gct cca cag aag gcg gag cgc cca atg act gtg gat gat gtg atc acc   259
Ala Pro Gln Lys Ala Glu Arg Pro Met Thr Val Asp Asp Val Ile Thr
        40                  45                  50

aag act ggt atc act ctc gcg gtt att atc gtt ttt gca ttg gtc acc   307
Lys Thr Gly Ile Thr Leu Ala Val Ile Ile Val Phe Ala Leu Val Thr
    55                  60                  65

ttt ggc gtg tgg ttg gtt agc ccc ggc ctc gga atg atc ttg acc ctt   355
Phe Gly Val Trp Leu Val Ser Pro Gly Leu Gly Met Ile Leu Thr Leu
70                  75                  80                  85

gtt ggt gcc atc ggt ggt ttc atc acc gtt ctg gtc agc acc ttc ggc   403
Val Gly Ala Ile Gly Gly Phe Ile Thr Val Leu Val Ser Thr Phe Gly
                90                  95                  100

aag aag tac gga tct gcg gca gtc act ttg att tac gca gta ttc gaa   451
Lys Lys Tyr Gly Ser Ala Ala Val Thr Leu Ile Tyr Ala Val Phe Glu
            105                 110                 115
```

```
ggc ctc ttc gtc ggc gga att tcc ctt ctg ctg tcc ggc ttc aca gtt   499
Gly Leu Phe Val Gly Gly Ile Ser Leu Leu Leu Ser Gly Phe Thr Val
        120                 125                 130

ggt aac gcc aac gca ggt ggc ctc att ggc cag gca gtc ctt ggc acc   547
Gly Asn Ala Asn Ala Gly Gly Leu Ile Gly Gln Ala Val Leu Gly Thr
    135                 140                 145

atc ggt gta ttc att ggc atg ctg ttt gta tac aag act ggc gct atc   595
Ile Gly Val Phe Ile Gly Met Leu Phe Val Tyr Lys Thr Gly Ala Ile
150                 155                 160                 165

aag gtc act cct aag ttc aac cgc atc ctc acc ggc atg atg gtt ggc   643
Lys Val Thr Pro Lys Phe Asn Arg Ile Leu Thr Gly Met Met Val Gly
                170                 175                 180

gtc ctg gtt ctt gtc ctg ggc aac gtt gta tgg gca ctg ttc act ggt   691
Val Leu Val Leu Val Leu Gly Asn Val Val Trp Ala Leu Phe Thr Gly
            185                 190                 195

ggc gca agc cca ctg cgt gac ggt gga atc atc gcg att atc ttc tcc   739
Gly Ala Ser Pro Leu Arg Asp Gly Gly Ile Ile Ala Ile Ile Phe Ser
        200                 205                 210

ctc ttc tgc atc ggc ctg gca gca ttc agc ttc ctc tcc gac ttc gat   787
Leu Phe Cys Ile Gly Leu Ala Ala Phe Ser Phe Leu Ser Asp Phe Asp
    215                 220                 225

gca gct gac cgc ctc gtc cgc gaa ggt gca cct tcc aag atg gca tgg   835
Ala Ala Asp Arg Leu Val Arg Glu Gly Ala Pro Ser Lys Met Ala Trp
230                 235                 240                 245

ggc gtt gcg ctt ggt ctt gca gtg acc ttg gtc tgg ctc tac acc gaa   883
Gly Val Ala Leu Gly Leu Ala Val Thr Leu Val Trp Leu Tyr Thr Glu
                250                 255                 260

atc cta cgt ctg ctt agc tac ttc caa aac cgc tagtttacgc agcacaagac 936
Ile Leu Arg Leu Leu Ser Tyr Phe Gln Asn Arg
            265                 270

ccc                                                               939
```

<210> 672
<211> 272
<212> PRT
<213> Corynebacterium glutamicum

<400> 672

```
Val Arg Ser Ser Asn Pro Val Phe Ser Ser Leu Lys Glu Thr Gln Arg
  1               5                  10                  15

Pro Gln Gly Gln Asn Pro Tyr Gly Gly Tyr Asp Asn Phe Gly Gly Val
             20                  25                  30

Tyr Gln Gln Asn Val Ala Pro Gln Lys Ala Glu Arg Pro Met Thr Val
         35                  40                  45

Asp Asp Val Ile Thr Lys Thr Gly Ile Thr Leu Ala Val Ile Ile Val
     50                  55                  60
```

```
Phe Ala Leu Val Thr Phe Gly Val Trp Leu Val Ser Pro Gly Leu Gly
 65                  70                  75                  80

Met Ile Leu Thr Leu Val Gly Ala Ile Gly Gly Phe Ile Thr Val Leu
                85                  90                  95

Val Ser Thr Phe Gly Lys Lys Tyr Gly Ser Ala Ala Val Thr Leu Ile
            100                 105                 110

Tyr Ala Val Phe Glu Gly Leu Phe Val Gly Gly Ile Ser Leu Leu Leu
        115                 120                 125

Ser Gly Phe Thr Val Gly Asn Ala Asn Ala Gly Gly Leu Ile Gly Gln
    130                 135                 140

Ala Val Leu Gly Thr Ile Gly Val Phe Ile Gly Met Leu Phe Val Tyr
145                 150                 155                 160

Lys Thr Gly Ala Ile Lys Val Thr Pro Lys Phe Asn Arg Ile Leu Thr
                165                 170                 175

Gly Met Met Val Gly Val Leu Val Leu Val Leu Gly Asn Val Val Trp
            180                 185                 190

Ala Leu Phe Thr Gly Gly Ala Ser Pro Leu Arg Asp Gly Gly Ile Ile
        195                 200                 205

Ala Ile Ile Phe Ser Leu Phe Cys Ile Gly Leu Ala Ala Phe Ser Phe
    210                 215                 220

Leu Ser Asp Phe Asp Ala Ala Asp Arg Leu Val Arg Glu Gly Ala Pro
225                 230                 235                 240

Ser Lys Met Ala Trp Gly Val Ala Leu Gly Leu Ala Val Thr Leu Val
                245                 250                 255

Trp Leu Tyr Thr Glu Ile Leu Arg Leu Leu Ser Tyr Phe Gln Asn Arg
            260                 265                 270
```

<210> 673
<211> 939
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(916)
<223> FRXA01557

<400> 673
taaaggtgtg aaaatagttc ctcacgtggg gaactatact gatccttgat gcgttaactt 60

gattgacgac gaaaaatcaa ttgaaaggat cggggactcc gtg cga agc agc aat 115
                                                Val Arg Ser Ser Asn
                                                  1   5

```
ccc gtt ttt agt tcc ctt aag gaa act caa cgt cca caa ggc cag aac   163
Pro Val Phe Ser Ser Leu Lys Glu Thr Gln Arg Pro Gln Gly Gln Asn
                10                  15                  20

cca tac ggt ggt tac gac aac ttc ggt ggt gtc tac cag caa aac gta   211
Pro Tyr Gly Gly Tyr Asp Asn Phe Gly Gly Val Tyr Gln Gln Asn Val
            25                  30                  35

gct cca cag aag gcg gag cgc cca atg act gtg gat gat gtg atc acc   259
Ala Pro Gln Lys Ala Glu Arg Pro Met Thr Val Asp Asp Val Ile Thr
        40                  45                  50

aag act ggt atc act ctc gcg gtt att atc gtt ttt gca ttg gtc acc   307
Lys Thr Gly Ile Thr Leu Ala Val Ile Ile Val Phe Ala Leu Val Thr
    55                  60                  65

ttt ggc gtg tgg ttg gtt agc ccc ggc ctc gga atg atc ttg acc ctt   355
Phe Gly Val Trp Leu Val Ser Pro Gly Leu Gly Met Ile Leu Thr Leu
70                  75                  80                  85

gtt ggt gcc atc ggt ggt ttc atc acc gtt ctg gtc agc acc ttc ggc   403
Val Gly Ala Ile Gly Gly Phe Ile Thr Val Leu Val Ser Thr Phe Gly
                90                  95                  100

aag aag tac gga tct gcg gca gtc act ttg att tac gca gta ttc gaa   451
Lys Lys Tyr Gly Ser Ala Ala Val Thr Leu Ile Tyr Ala Val Phe Glu
            105                 110                 115

ggc ctc ttc gtc ggc gga att tcc ctt ctg ctg tcc ggc ttc aca gtt   499
Gly Leu Phe Val Gly Gly Ile Ser Leu Leu Leu Ser Gly Phe Thr Val
        120                 125                 130

ggt aac gcc aac gca ggt ggc ctc att ggc cag gca gtc ctt ggc acc   547
Gly Asn Ala Asn Ala Gly Gly Leu Ile Gly Gln Ala Val Leu Gly Thr
    135                 140                 145

atc ggt gta ttc att ggc atg ctg ttt gta tac aag act ggc gct atc   595
Ile Gly Val Phe Ile Gly Met Leu Phe Val Tyr Lys Thr Gly Ala Ile
150                 155                 160                 165

aag gtc act cct aag ttc aac cgc atc ctc acc ggc atg atg gtt ggc   643
Lys Val Thr Pro Lys Phe Asn Arg Ile Leu Thr Gly Met Met Val Gly
                170                 175                 180

gtc ctg gtt ctt gtc ctg ggc aac gtt gta tgg gca ctg ttc act ggt   691
Val Leu Val Leu Val Leu Gly Asn Val Val Trp Ala Leu Phe Thr Gly
            185                 190                 195

ggc gca agc cca ctg cgt gac ggt gga atc atc gcg att atc ttc tcc   739
Gly Ala Ser Pro Leu Arg Asp Gly Gly Ile Ile Ala Ile Ile Phe Ser
        200                 205                 210

ctc ttc tgc atc ggc ctg gca gca ttc agc ttc ctc tcc gac ttc gat   787
Leu Phe Cys Ile Gly Leu Ala Ala Phe Ser Phe Leu Ser Asp Phe Asp
    215                 220                 225

gca gct gac cgc ctc gtc cgc gaa ggt gca cct tcc aag atg gca tgg   835
Ala Ala Asp Arg Leu Val Arg Glu Gly Ala Pro Ser Lys Met Ala Trp
230                 235                 240                 245

ggc gtt gcg ctt ggt ctt gca gtg acc ttg gtc tgg ctc tac acc gaa   883
```

Gly Val Ala Leu Gly Leu Ala Val Thr Leu Val Trp Leu Tyr Thr Glu
250 255 260

atc cta cgt ctg ctt agc tac ttc caa aac cgc tagtttacgc agcacaagac 936
Ile Leu Arg Leu Leu Ser Tyr Phe Gln Asn Arg
265 270

ccc 939

<210> 674
<211> 272
<212> PRT
<213> Corynebacterium glutamicum

<400> 674
Val Arg Ser Ser Asn Pro Val Phe Ser Ser Leu Lys Glu Thr Gln Arg
1 5 10 15

Pro Gln Gly Gln Asn Pro Tyr Gly Gly Tyr Asp Asn Phe Gly Gly Val
20 25 30

Tyr Gln Gln Asn Val Ala Pro Gln Lys Ala Glu Arg Pro Met Thr Val
35 40 45

Asp Asp Val Ile Thr Lys Thr Gly Ile Thr Leu Ala Val Ile Ile Val
50 55 60

Phe Ala Leu Val Thr Phe Gly Val Trp Leu Val Ser Pro Gly Leu Gly
65 70 75 80

Met Ile Leu Thr Leu Val Gly Ala Ile Gly Gly Phe Ile Thr Val Leu
85 90 95

Val Ser Thr Phe Gly Lys Lys Tyr Gly Ser Ala Ala Val Thr Leu Ile
100 105 110

Tyr Ala Val Phe Glu Gly Leu Phe Val Gly Gly Ile Ser Leu Leu Leu
115 120 125

Ser Gly Phe Thr Val Gly Asn Ala Asn Ala Gly Gly Leu Ile Gly Gln
130 135 140

Ala Val Leu Gly Thr Ile Gly Val Phe Ile Gly Met Leu Phe Val Tyr
145 150 155 160

Lys Thr Gly Ala Ile Lys Val Thr Pro Lys Phe Asn Arg Ile Leu Thr
165 170 175

Gly Met Met Val Gly Val Leu Val Leu Val Leu Gly Asn Val Val Trp
180 185 190

Ala Leu Phe Thr Gly Gly Ala Ser Pro Leu Arg Asp Gly Gly Ile Ile
195 200 205

Ala Ile Ile Phe Ser Leu Phe Cys Ile Gly Leu Ala Ala Phe Ser Phe
210 215 220

Leu Ser Asp Phe Asp Ala Ala Asp Arg Leu Val Arg Glu Gly Ala Pro
225 230 235 240

```
Ser Lys Met Ala Trp Gly Val Ala Leu Gly Leu Ala Val Thr Leu Val
               245                 250                 255

Trp Leu Tyr Thr Glu Ile Leu Arg Leu Leu Ser Tyr Phe Gln Asn Arg
            260                 265                 270
```

<210> 675
<211> 1158
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1135)
<223> RXN01574

<400> 675

```
aaaaatccgc acaccccaca ttgctcaaag gaattgacaa ggcgcttcgc aaggccgagt 60

aaggtgggca acgagtcggt gagagtatga ggaatatttg atg agc aac aaa cgc   115
                                            Met Ser Asn Lys Arg
                                              1               5

atc ggt gta gtg atc gtt tcc tac gga cac gaa caa gat gtt gcc aac   163
Ile Gly Val Val Ile Val Ser Tyr Gly His Glu Gln Asp Val Ala Asn
                10                  15                  20

ctg gta gac aca ttt gca gat cag ctg aaa act ggt gac cgc gta gtt   211
Leu Val Asp Thr Phe Ala Asp Gln Leu Lys Thr Gly Asp Arg Val Val
            25                  30                  35

gtc gtg gac aac cgc aaa cct tgg gtg tta aaa gac gcc gtg ggg gag   259
Val Val Asp Asn Arg Lys Pro Trp Val Leu Lys Asp Ala Val Gly Glu
        40                  45                  50

cgc ctg gaa aaa cac ggc gca gag atc atc aac cac gac aac ggt ggt   307
Arg Leu Glu Lys His Gly Ala Glu Ile Ile Asn His Asp Asn Gly Gly
    55                  60                  65

ttc gcc gct ggc tgc aac gtg ggc gca gcg cac atc gtg gat gac gtt   355
Phe Ala Ala Gly Cys Asn Val Gly Ala Ala His Ile Val Asp Asp Val
70                  75                  80                  85

gac ctg ctg ttc ttc ctc aac ccc gac aca gtg atc gac gat ccc acc   403
Asp Leu Leu Phe Phe Leu Asn Pro Asp Thr Val Ile Asp Asp Pro Thr
                90                  95                  100

ctg ttc aat tcg ctg aga cgc gtc gat gaa cag tgg gca gca ttc atg   451
Leu Phe Asn Ser Leu Arg Arg Val Asp Glu Gln Trp Ala Ala Phe Met
            105                 110                 115

ccg tac ctg ctg ctt cct gac agc acc att aac tcc gca ggc aac gcc   499
Pro Tyr Leu Leu Leu Pro Asp Ser Thr Ile Asn Ser Ala Gly Asn Ala
        120                 125                 130

ctg cat att tcc gga ctg tcg tgg gtg act ggt ctg gat gaa aaa cca   547
Leu His Ile Ser Gly Leu Ser Trp Val Thr Gly Leu Asp Glu Lys Pro
```

```
    135                 140                 145

gtt gaa ggc tca tct gaa gtt acc gat att tcc att gcc tct ggc gcc   595
Val Glu Gly Ser Ser Glu Val Thr Asp Ile Ser Ile Ala Ser Gly Ala
150                 155                 160                 165

tgc ctt gcc gtg cgc gtg gac tgg tgg aaa cgc ctc ggt ggc atg gaa   643
Cys Leu Ala Val Arg Val Asp Trp Trp Lys Arg Leu Gly Gly Met Glu
                170                 175                 180

gaa ctg tat ttc atg tac cac gaa gac act gac ttc tcc gcc cgc ttg   691
Glu Leu Tyr Phe Met Tyr His Glu Asp Thr Asp Phe Ser Ala Arg Leu
            185                 190                 195

ctg ctg gcc ggc ggt cga att ggt ctc ctg cat tcc gcg tat gtc acc   739
Leu Leu Ala Gly Gly Arg Ile Gly Leu Leu His Ser Ala Tyr Val Thr
        200                 205                 210

cac cat tac gac tac gcc aag ggt gac tac aag tgg att tac atc gaa   787
His His Tyr Asp Tyr Ala Lys Gly Asp Tyr Lys Trp Ile Tyr Ile Glu
    215                 220                 225

cga aac cga cac gtt ttg ctg ctc agc gtg ctg ccg ctt cca ttg ctg   835
Arg Asn Arg His Val Leu Leu Leu Ser Val Leu Pro Leu Pro Leu Leu
230                 235                 240                 245

ttc gtg ctg atc ccg cag atc ctc ggt gtg aac ctg gga ctg tgg gcg   883
Phe Val Leu Ile Pro Gln Ile Leu Gly Val Asn Leu Gly Leu Trp Ala
                250                 255                 260

att gcc gca aag gaa aag agg gtc gga ctc aag gtg aag tcc ctt cgc   931
Ile Ala Ala Lys Glu Lys Arg Val Gly Leu Lys Val Lys Ser Leu Arg
            265                 270                 275

ctc ctg atc cgc gat cta cca gcg att ttc aaa ctg cgt agg agc acg   979
Leu Leu Ile Arg Asp Leu Pro Ala Ile Phe Lys Leu Arg Arg Ser Thr
        280                 285                 290

cag gag ctt gcc gaa ctc aca cca tcg caa tat ctg gca aaa atg gaa   1027
Gln Glu Leu Ala Glu Leu Thr Pro Ser Gln Tyr Leu Ala Lys Met Glu
    295                 300                 305

tgg cgc cta gac aat ccc aac cta ggc aac att gga tcc aac aag att   1075
Trp Arg Leu Asp Asn Pro Asn Leu Gly Asn Ile Gly Ser Asn Lys Ile
310                 315                 320                 325

gtt gcg act gga tat aag acc tat tac aag ttg tgt atg agt atc ctg   1123
Val Ala Thr Gly Tyr Lys Thr Tyr Tyr Lys Leu Cys Met Ser Ile Leu
                330                 335                 340

aaa ttg ctc gct taacacccca taaagagggt gaa                        1158
Lys Leu Leu Ala
            345
```

<210> 676
<211> 345
<212> PRT
<213> Corynebacterium glutamicum

<400> 676

```
Met Ser Asn Lys Arg Ile Gly Val Val Ile Val Ser Tyr Gly His Glu
 1               5                  10                  15

Gln Asp Val Ala Asn Leu Val Asp Thr Phe Ala Asp Gln Leu Lys Thr
            20                  25                  30

Gly Asp Arg Val Val Val Val Asp Asn Arg Lys Pro Trp Val Leu Lys
        35                  40                  45

Asp Ala Val Gly Glu Arg Leu Glu Lys His Gly Ala Glu Ile Ile Asn
    50                  55                  60

His Asp Asn Gly Gly Phe Ala Ala Gly Cys Asn Val Gly Ala Ala His
65                  70                  75                  80

Ile Val Asp Asp Val Asp Leu Leu Phe Phe Leu Asn Pro Asp Thr Val
                85                  90                  95

Ile Asp Asp Pro Thr Leu Phe Asn Ser Leu Arg Arg Val Asp Glu Gln
            100                 105                 110

Trp Ala Ala Phe Met Pro Tyr Leu Leu Leu Pro Asp Ser Thr Ile Asn
        115                 120                 125

Ser Ala Gly Asn Ala Leu His Ile Ser Gly Leu Ser Trp Val Thr Gly
    130                 135                 140

Leu Asp Glu Lys Pro Val Glu Gly Ser Ser Glu Val Thr Asp Ile Ser
145                 150                 155                 160

Ile Ala Ser Gly Ala Cys Leu Ala Val Arg Val Asp Trp Trp Lys Arg
                165                 170                 175

Leu Gly Gly Met Glu Glu Leu Tyr Phe Met Tyr His Glu Asp Thr Asp
            180                 185                 190

Phe Ser Ala Arg Leu Leu Leu Ala Gly Gly Arg Ile Gly Leu Leu His
        195                 200                 205

Ser Ala Tyr Val Thr His His Tyr Asp Tyr Ala Lys Gly Asp Tyr Lys
    210                 215                 220

Trp Ile Tyr Ile Glu Arg Asn Arg His Val Leu Leu Leu Ser Val Leu
225                 230                 235                 240

Pro Leu Pro Leu Leu Phe Val Leu Ile Pro Gln Ile Leu Gly Val Asn
                245                 250                 255

Leu Gly Leu Trp Ala Ile Ala Ala Lys Glu Lys Arg Val Gly Leu Lys
            260                 265                 270

Val Lys Ser Leu Arg Leu Leu Ile Arg Asp Leu Pro Ala Ile Phe Lys
        275                 280                 285

Leu Arg Arg Ser Thr Gln Glu Leu Ala Glu Leu Thr Pro Ser Gln Tyr
    290                 295                 300

Leu Ala Lys Met Glu Trp Arg Leu Asp Asn Pro Asn Leu Gly Asn Ile
305                 310                 315                 320

Gly Ser Asn Lys Ile Val Ala Thr Gly Tyr Lys Thr Tyr Tyr Lys Leu
```

```
                325                 330                 335

Cys Met Ser Ile Leu Lys Leu Leu Ala
            340                 345


<210> 677
<211> 1158
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1135)
<223> FRXA01574

<400> 677
aaaaatccgc acaccccaca ttgctcaaag gaattgacaa ggcgcttcgc aaggccgagt 60

aaggtgggca acgagtcggt gagagtatga ggaatatttg atg agc aac aaa cgc   115
                                              Met Ser Asn Lys Arg
                                                1               5

atc ggt gta gtg atc gtt tcc tac gga cac gaa caa gat gtt gcc aac   163
Ile Gly Val Val Ile Val Ser Tyr Gly His Glu Gln Asp Val Ala Asn
                10                  15                  20

ctg gta gac aca ttt gca gat cag ctg aaa act ggt gac cgc gta gtt   211
Leu Val Asp Thr Phe Ala Asp Gln Leu Lys Thr Gly Asp Arg Val Val
            25                  30                  35

gtc gtg gac aac cgc aaa cct tgg gtg tta aaa gac gcc gtg ggg gag   259
Val Val Asp Asn Arg Lys Pro Trp Val Leu Lys Asp Ala Val Gly Glu
        40                  45                  50

cgc ctg gaa aaa cac ggc gca gag atc atc aac cac gac aac ggt ggt   307
Arg Leu Glu Lys His Gly Ala Glu Ile Ile Asn His Asp Asn Gly Gly
    55                  60                  65

ttc gcc gct ggc tgc aac gtg ggc gca gcg cac atc gtg gat gac gtt   355
Phe Ala Ala Gly Cys Asn Val Gly Ala Ala His Ile Val Asp Asp Val
70                  75                  80                  85

gac ctg ctg ttc ttc ctc aac ccc gac aca gtg atc gac gat ccc acc   403
Asp Leu Leu Phe Phe Leu Asn Pro Asp Thr Val Ile Asp Asp Pro Thr
                90                  95                  100

ctg ttc aat tcg ctg aga cgc gtc gat gaa cag tgg gca gca ttc atg   451
Leu Phe Asn Ser Leu Arg Arg Val Asp Glu Gln Trp Ala Ala Phe Met
            105                 110                 115

ccg tac ctg ctg ctt cct gac agc acc att aac tcc gca ggc aac gcc   499
Pro Tyr Leu Leu Leu Pro Asp Ser Thr Ile Asn Ser Ala Gly Asn Ala
        120                 125                 130

ctg cat att tcc gga ctg tcg tgg gtg act ggt ctg gat gaa aaa cca   547
Leu His Ile Ser Gly Leu Ser Trp Val Thr Gly Leu Asp Glu Lys Pro
    135                 140                 145

gtt gaa ggc tca tct gaa gtt acc gat att tcc att gcc tct ggc gcc   595
Val Glu Gly Ser Ser Glu Val Thr Asp Ile Ser Ile Ala Ser Gly Ala
```

```
150                 155                 160                 165

tgc ctt gcc gtg cgc gtg gac tgg tgg aaa cgc ctc ggt ggc atg gaa   643
Cys Leu Ala Val Arg Val Asp Trp Trp Lys Arg Leu Gly Gly Met Glu
                170                 175                 180

gaa ctg tat ttc atg tac cac gaa gac act gac ttc tcc gcc cgc ttg   691
Glu Leu Tyr Phe Met Tyr His Glu Asp Thr Asp Phe Ser Ala Arg Leu
            185                 190                 195

ctg ctg gcc ggc ggt cga att ggt ctc ctg cat tcc gcg tat gtc acc   739
Leu Leu Ala Gly Gly Arg Ile Gly Leu Leu His Ser Ala Tyr Val Thr
        200                 205                 210

cac cat tac gac tac gcc aag ggt gac tac aag tgg att tac atc gaa   787
His His Tyr Asp Tyr Ala Lys Gly Asp Tyr Lys Trp Ile Tyr Ile Glu
    215                 220                 225

cga aac cga cac gtt ttg ctg ctc agc gtg ctg ccg ctt cca ttg ctg   835
Arg Asn Arg His Val Leu Leu Leu Ser Val Leu Pro Leu Pro Leu Leu
230                 235                 240                 245

ttc gtg ctg atc ccg cag atc ctc ggt gtg aac ctg gga ctg tgg gcg   883
Phe Val Leu Ile Pro Gln Ile Leu Gly Val Asn Leu Gly Leu Trp Ala
                250                 255                 260

att gcc gca aag gaa aag agg gtc gga ctc aag gtg aag tcc ctt cgc   931
Ile Ala Ala Lys Glu Lys Arg Val Gly Leu Lys Val Lys Ser Leu Arg
            265                 270                 275

ctc ctg atc cgc gat cta cca gcg att ttc aaa ctg cgt agg agc acg   979
Leu Leu Ile Arg Asp Leu Pro Ala Ile Phe Lys Leu Arg Arg Ser Thr
        280                 285                 290

cag gag ctt gcc gaa ctc aca cca tcg caa tat ctg gca aaa atg gaa   1027
Gln Glu Leu Ala Glu Leu Thr Pro Ser Gln Tyr Leu Ala Lys Met Glu
    295                 300                 305

tgg cgc cta gac aat ccc aac cta ggc aac att gga tcc aac aag att   1075
Trp Arg Leu Asp Asn Pro Asn Leu Gly Asn Ile Gly Ser Asn Lys Ile
310                 315                 320                 325

gtt gcg act gga tat aag acc tat tac aag ttg tgt atg agt atc ctg   1123
Val Ala Thr Gly Tyr Lys Thr Tyr Tyr Lys Leu Cys Met Ser Ile Leu
                330                 335                 340

aaa ttg ctc gct taacacccca taaagagggt gaa                        1158
Lys Leu Leu Ala
            345
```

<210> 678
<211> 345
<212> PRT
<213> Corynebacterium glutamicum

<400> 678

```
Met Ser Asn Lys Arg Ile Gly Val Val Ile Val Ser Tyr Gly His Glu
  1               5                  10                  15

Gln Asp Val Ala Asn Leu Val Asp Thr Phe Ala Asp Gln Leu Lys Thr
```

```
            20                  25                  30

Gly Asp Arg Val Val Val Val Asp Asn Arg Lys Pro Trp Val Leu Lys
        35                  40                  45

Asp Ala Val Gly Glu Arg Leu Glu Lys His Gly Ala Glu Ile Ile Asn
    50                  55                  60

His Asp Asn Gly Gly Phe Ala Ala Gly Cys Asn Val Gly Ala Ala His
65                  70                  75                  80

Ile Val Asp Asp Val Asp Leu Leu Phe Phe Leu Asn Pro Asp Thr Val
                85                  90                  95

Ile Asp Asp Pro Thr Leu Phe Asn Ser Leu Arg Arg Val Asp Glu Gln
            100                 105                 110

Trp Ala Ala Phe Met Pro Tyr Leu Leu Leu Pro Asp Ser Thr Ile Asn
        115                 120                 125

Ser Ala Gly Asn Ala Leu His Ile Ser Gly Leu Ser Trp Val Thr Gly
    130                 135                 140

Leu Asp Glu Lys Pro Val Glu Gly Ser Ser Glu Val Thr Asp Ile Ser
145                 150                 155                 160

Ile Ala Ser Gly Ala Cys Leu Ala Val Arg Val Asp Trp Trp Lys Arg
                165                 170                 175

Leu Gly Gly Met Glu Glu Leu Tyr Phe Met Tyr His Glu Asp Thr Asp
            180                 185                 190

Phe Ser Ala Arg Leu Leu Leu Ala Gly Gly Arg Ile Gly Leu Leu His
        195                 200                 205

Ser Ala Tyr Val Thr His His Tyr Asp Tyr Ala Lys Gly Asp Tyr Lys
    210                 215                 220

Trp Ile Tyr Ile Glu Arg Asn Arg His Val Leu Leu Leu Ser Val Leu
225                 230                 235                 240

Pro Leu Pro Leu Leu Phe Val Leu Ile Pro Gln Ile Leu Gly Val Asn
                245                 250                 255

Leu Gly Leu Trp Ala Ile Ala Ala Lys Glu Lys Arg Val Gly Leu Lys
            260                 265                 270

Val Lys Ser Leu Arg Leu Leu Ile Arg Asp Leu Pro Ala Ile Phe Lys
        275                 280                 285

Leu Arg Arg Ser Thr Gln Glu Leu Ala Glu Leu Thr Pro Ser Gln Tyr
    290                 295                 300

Leu Ala Lys Met Glu Trp Arg Leu Asp Asn Pro Asn Leu Gly Asn Ile
305                 310                 315                 320

Gly Ser Asn Lys Ile Val Ala Thr Gly Tyr Lys Thr Tyr Tyr Lys Leu
                325                 330                 335

Cys Met Ser Ile Leu Lys Leu Leu Ala
            340                 345
```

<210> 679
<211> 1143
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1120)
<223> RXN01589

<400> 679
agggatgtag atgcgccctc atattggtac aaaaatataa attatcagca tgatttggac 60

gctttaattc aaaaattgta agctgttagg aggtccacaa atg gta gaa caa ata 115
Met Val Glu Gln Ile
1 5

aaa gat aaa cta gga cgt ccc atc cgt gac tta cgg tta tct gtg aca 163
Lys Asp Lys Leu Gly Arg Pro Ile Arg Asp Leu Arg Leu Ser Val Thr
10 15 20

gat cgg tgt aac ttt agg tgt gat tat tgc atg cct aaa gag gta ttt 211
Asp Arg Cys Asn Phe Arg Cys Asp Tyr Cys Met Pro Lys Glu Val Phe
25 30 35

gga gat gat ttc gta ttt tta cct aaa aat gaa ctg tta acg ttt gat 259
Gly Asp Asp Phe Val Phe Leu Pro Lys Asn Glu Leu Leu Thr Phe Asp
40 45 50

gaa atg gct aga atc gct aag gta tat gca gaa tta ggt gta aaa aaa 307
Glu Met Ala Arg Ile Ala Lys Val Tyr Ala Glu Leu Gly Val Lys Lys
55 60 65

ata cgc att aca ggt gga gaa cca ttg atg cga cgc gat tta gat gta 355
Ile Arg Ile Thr Gly Gly Glu Pro Leu Met Arg Arg Asp Leu Asp Val
70 75 80 85

ctt ata gct aaa tta aat caa atc gat ggt att gaa gat att ggt ttg 403
Leu Ile Ala Lys Leu Asn Gln Ile Asp Gly Ile Glu Asp Ile Gly Leu
90 95 100

act aca aat ggt ttg tta tta aaa aag cat gga caa aag tta tat gat 451
Thr Thr Asn Gly Leu Leu Leu Lys Lys His Gly Gln Lys Leu Tyr Asp
105 110 115

gct ggg cta cgc aga att aat gtc agt ttg gat gct att gat gat acg 499
Ala Gly Leu Arg Arg Ile Asn Val Ser Leu Asp Ala Ile Asp Asp Thr
120 125 130

cta ttt caa tca atc aat aat cgt aat att aaa gcg act acg att tta 547
Leu Phe Gln Ser Ile Asn Asn Arg Asn Ile Lys Ala Thr Thr Ile Leu
135 140 145

gaa caa att gat tac gcg acg tct att ggt ttg aat gta aaa gta aat 595
Glu Gln Ile Asp Tyr Ala Thr Ser Ile Gly Leu Asn Val Lys Val Asn
150 155 160 165

gtt gtt ata caa aaa ggt att aac gat gat caa atc ata cca atg ctt 643
Val Val Ile Gln Lys Gly Ile Asn Asp Asp Gln Ile Ile Pro Met Leu

```
                170                 175                 180

gaa tat ttt aaa gat aaa cat ata gag att cga ttt ata gaa ttt atg   691
Glu Tyr Phe Lys Asp Lys His Ile Glu Ile Arg Phe Ile Glu Phe Met
            185                 190                 195

gat gtt ggt aat gat aat gga tgg gat ttc agt aaa gtt gta act aaa   739
Asp Val Gly Asn Asp Asn Gly Trp Asp Phe Ser Lys Val Val Thr Lys
        200                 205                 210

gat gaa atg ctt aca atg ata gag cag cac ttt gaa atc gat cct gta   787
Asp Glu Met Leu Thr Met Ile Glu Gln His Phe Glu Ile Asp Pro Val
    215                 220                 225

gaa cca aaa tat ttt ggg gaa gta gca aaa tat tat cgc cat aag gat   835
Glu Pro Lys Tyr Phe Gly Glu Val Ala Lys Tyr Tyr Arg His Lys Asp
230                 235                 240                 245

aat ggt gtt caa ttt ggt ttg att aca agt gtt tca caa tca ttt tgt   883
Asn Gly Val Gln Phe Gly Leu Ile Thr Ser Val Ser Gln Ser Phe Cys
                250                 255                 260

tct aca tgt aca cgc gca agg ctg tca tca gat ggg aag ttt tac gga   931
Ser Thr Cys Thr Arg Ala Arg Leu Ser Ser Asp Gly Lys Phe Tyr Gly
            265                 270                 275

tgt tta ttt gca act gtc gat gga ttt aac gtt aaa gcg ttt att cgt   979
Cys Leu Phe Ala Thr Val Asp Gly Phe Asn Val Lys Ala Phe Ile Arg
        280                 285                 290

tct ggc gtg acc gac gaa gaa tta aaa gaa caa ttt aaa gct tta tgg   1027
Ser Gly Val Thr Asp Glu Glu Leu Lys Glu Gln Phe Lys Ala Leu Trp
    295                 300                 305

caa ata aga gat gat cga tat tca gat gag aga act gct caa aca gtt   1075
Gln Ile Arg Asp Asp Arg Tyr Ser Asp Glu Arg Thr Ala Gln Thr Val
310                 315                 320                 325

gcc aat cgt caa cgt aaa aag ata aac atg aat tat att ggt ggt       1120
Ala Asn Arg Gln Arg Lys Lys Ile Asn Met Asn Tyr Ile Gly Gly
                330                 335                 340

taatgtgtag ggaccactac ata                                        1143


<210> 680
<211> 340
<212> PRT
<213> Corynebacterium glutamicum

<400> 680
Met Val Glu Gln Ile Lys Asp Lys Leu Gly Arg Pro Ile Arg Asp Leu
  1               5                  10                  15

Arg Leu Ser Val Thr Asp Arg Cys Asn Phe Arg Cys Asp Tyr Cys Met
             20                  25                  30

Pro Lys Glu Val Phe Gly Asp Asp Phe Val Phe Leu Pro Lys Asn Glu
         35                  40                  45

Leu Leu Thr Phe Asp Glu Met Ala Arg Ile Ala Lys Val Tyr Ala Glu
```

```
     50                  55                  60

Leu Gly Val Lys Lys Ile Arg Ile Thr Gly Gly Glu Pro Leu Met Arg
 65                  70                  75                  80

Arg Asp Leu Asp Val Leu Ile Ala Lys Leu Asn Gln Ile Asp Gly Ile
                 85                  90                  95

Glu Asp Ile Gly Leu Thr Thr Asn Gly Leu Leu Leu Lys Lys His Gly
            100                 105                 110

Gln Lys Leu Tyr Asp Ala Gly Leu Arg Arg Ile Asn Val Ser Leu Asp
        115                 120                 125

Ala Ile Asp Asp Thr Leu Phe Gln Ser Ile Asn Asn Arg Asn Ile Lys
    130                 135                 140

Ala Thr Thr Ile Leu Glu Gln Ile Asp Tyr Ala Thr Ser Ile Gly Leu
145                 150                 155                 160

Asn Val Lys Val Asn Val Val Ile Gln Lys Gly Ile Asn Asp Asp Gln
                165                 170                 175

Ile Ile Pro Met Leu Glu Tyr Phe Lys Asp Lys His Ile Glu Ile Arg
            180                 185                 190

Phe Ile Glu Phe Met Asp Val Gly Asn Asp Asn Gly Trp Asp Phe Ser
        195                 200                 205

Lys Val Val Thr Lys Asp Glu Met Leu Thr Met Ile Glu Gln His Phe
    210                 215                 220

Glu Ile Asp Pro Val Glu Pro Lys Tyr Phe Gly Glu Val Ala Lys Tyr
225                 230                 235                 240

Tyr Arg His Lys Asp Asn Gly Val Gln Phe Gly Leu Ile Thr Ser Val
                245                 250                 255

Ser Gln Ser Phe Cys Ser Thr Cys Thr Arg Ala Arg Leu Ser Ser Asp
            260                 265                 270

Gly Lys Phe Tyr Gly Cys Leu Phe Ala Thr Val Asp Gly Phe Asn Val
        275                 280                 285

Lys Ala Phe Ile Arg Ser Gly Val Thr Asp Glu Glu Leu Lys Glu Gln
    290                 295                 300

Phe Lys Ala Leu Trp Gln Ile Arg Asp Asp Arg Tyr Ser Asp Glu Arg
305                 310                 315                 320

Thr Ala Gln Thr Val Ala Asn Arg Gln Arg Lys Lys Ile Asn Met Asn
                325                 330                 335

Tyr Ile Gly Gly
            340
```

<210> 681
<211> 1425
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1402)
<223> RXN01592

<400> 681
gattcaatgg tagaggtatt tcatttcctc ccattggatc acactctttt tgtcgttcta 60

taataaagtc tttacccggt tctcaacatc aaggaacaac atg gct gat aac ttc 115
Met Ala Asp Asn Phe
1 5

gac cgc tct cgt gac aac gat cgc tca agc gac cgc act cct cgt gga 163
Asp Arg Ser Arg Asp Asn Asp Arg Ser Ser Asp Arg Thr Pro Arg Gly
10 15 20

gac cgc ggc gat cgc ggt ggc tac cga aac tcc cgc ggc aac gat gac 211
Asp Arg Gly Asp Arg Gly Gly Tyr Arg Asn Ser Arg Gly Asn Asp Asp
25 30 35

cgc gga aac tac cgt caa aac cga gat ggt gaa tca cga gat cgc ggc 259
Arg Gly Asn Tyr Arg Gln Asn Arg Asp Gly Glu Ser Arg Asp Arg Gly
40 45 50

gga tac ctc ggt gac cgt cgc gac aac cgc tca ggt gaa tat cgt caa 307
Gly Tyr Leu Gly Asp Arg Arg Asp Asn Arg Ser Gly Glu Tyr Arg Gln
55 60 65

cgt gac gat agg cgt gac gat cgt agg gac aac cga agc gat gac cgc 355
Arg Asp Asp Arg Arg Asp Asp Arg Arg Asp Asn Arg Ser Asp Asp Arg
70 75 80 85

cgc ggt ggt tac cgc tcc gat cgc aac ttt gac gat cgc aac agc aac 403
Arg Gly Gly Tyr Arg Ser Asp Arg Asn Phe Asp Asp Arg Asn Ser Asn
90 95 100

atg cgt gat gat cgt cgc ggc ggc gac cgt tca tac agc cgt aat gat 451
Met Arg Asp Asp Arg Arg Gly Gly Asp Arg Ser Tyr Ser Arg Asn Asp
105 110 115

cgc tcc gat cgt ggc tat cgt agc aat gac cgc tac gac cgt aat gat 499
Arg Ser Asp Arg Gly Tyr Arg Ser Asn Asp Arg Tyr Asp Arg Asn Asp
120 125 130

cgt cgc gat gac aac agg gac acc agg ggt ggc gat cgc gga gac cgt 547
Arg Arg Asp Asp Asn Arg Asp Thr Arg Gly Gly Asp Arg Gly Asp Arg
135 140 145

cgc tac gac agg cgc gat gac cga cgt gat gat cgt cgc gat gat cgt 595
Arg Tyr Asp Arg Arg Asp Asp Arg Arg Asp Asp Arg Arg Asp Asp Arg
150 155 160 165

cgt ggc gga cag ggc cag ggg cgt cca ggt gga gat cgt cga cat gcg 643
Arg Gly Gly Gln Gly Gln Gly Arg Pro Gly Gly Asp Arg Arg His Ala
170 175 180

aac cgt gca ggt gca ggt cgc gat cag cag cgt gat tcg ctg cat cca 691
Asn Arg Ala Gly Ala Gly Arg Asp Gln Gln Arg Asp Ser Leu His Pro
185 190 195

```
cag cgc gct ggt ttc cgt gaa gag cgc ttg aac act cgt ctc aat gag   739
Gln Arg Ala Gly Phe Arg Glu Glu Arg Leu Asn Thr Arg Leu Asn Glu
        200                 205                 210

cct gat ttg ccg ggc gat att gat atc aag gac ttg gat cct ttg gtc   787
Pro Asp Leu Pro Gly Asp Ile Asp Ile Lys Asp Leu Asp Pro Leu Val
    215                 220                 225

ctg cag gat ttg aag gtt ttg tct aag gac aac gca gat gcc gtc gca   835
Leu Gln Asp Leu Lys Val Leu Ser Lys Asp Asn Ala Asp Ala Val Ala
230                 235                 240                 245

aag cat atg atc atg gct gcg acc tgg ctg gcc gac gat cct caa ttg   883
Lys His Met Ile Met Ala Ala Thr Trp Leu Ala Asp Asp Pro Gln Leu
                250                 255                 260

gca ctg cgc cac gcc cgt gct gcg aag gat cgc gcg gga cgc gtg tcc   931
Ala Leu Arg His Ala Arg Ala Ala Lys Asp Arg Ala Gly Arg Val Ser
            265                 270                 275

gtc gtg cgt gag acg aac ggc att gct gct tac cat gct ggt gag tgg   979
Val Val Arg Glu Thr Asn Gly Ile Ala Ala Tyr His Ala Gly Glu Trp
        280                 285                 290

aag gaa gct ctt tcg gag ctt cgt gct gcg cgc cgc atg tcg ggt ggt   1027
Lys Glu Ala Leu Ser Glu Leu Arg Ala Ala Arg Arg Met Ser Gly Gly
    295                 300                 305

cct ggt ttg att gct gtg atg gct gac tgt gag cgt ggc ttg ggt cgt   1075
Pro Gly Leu Ile Ala Val Met Ala Asp Cys Glu Arg Gly Leu Gly Arg
310                 315                 320                 325

cct gag aag gcg att gag ctg gct cga gaa gag gat ttg agc tct ttg   1123
Pro Glu Lys Ala Ile Glu Leu Ala Arg Glu Glu Asp Leu Ser Ser Leu
                330                 335                 340

gat cag gat aac ctg atc gag tta gcg att gtt gtt gct gga gca cgc   1171
Asp Gln Asp Asn Leu Ile Glu Leu Ala Ile Val Val Ala Gly Ala Arg
            345                 350                 355

cat gat ttg ggt cag cat gac tct gcg att gtg gaa ttg cag aag gtt   1219
His Asp Leu Gly Gln His Asp Ser Ala Ile Val Glu Leu Gln Lys Val
        360                 365                 370

aat cca agc ttg aag agc acc ggt ttc acc cat tct cgt ttg tct tac   1267
Asn Pro Ser Leu Lys Ser Thr Gly Phe Thr His Ser Arg Leu Ser Tyr
    375                 380                 385

gct tac gcc gat gcg ctt gtt ttg gct ggt cgt ggc gat gaa gca cgt   1315
Ala Tyr Ala Asp Ala Leu Val Leu Ala Gly Arg Gly Asp Glu Ala Arg
390                 395                 400                 405

gag tgg ttc cag cac gct gcc acc ttg gat gag gac ggc tac ctc gat   1363
Glu Trp Phe Gln His Ala Ala Thr Leu Asp Glu Asp Gly Tyr Leu Asp
                410                 415                 420

gca gag gag cgt atc gag cag ctc gat aat ggg aac aac tagactattg    1412
Ala Glu Glu Arg Ile Glu Gln Leu Asp Asn Gly Asn Asn
            425                 430

gtctagagtg taa                                                   1425
```

<210> 682
<211> 434
<212> PRT
<213> Corynebacterium glutamicum

<400> 682

```
Met Ala Asp Asn Phe Asp Arg Ser Arg Asp Asn Asp Arg Ser Ser Asp
 1               5                  10                  15

Arg Thr Pro Arg Gly Asp Arg Gly Asp Arg Gly Gly Tyr Arg Asn Ser
            20                  25                  30

Arg Gly Asn Asp Asp Arg Gly Asn Tyr Arg Gln Asn Arg Asp Gly Glu
        35                  40                  45

Ser Arg Asp Arg Gly Gly Tyr Leu Gly Asp Arg Arg Asp Asn Arg Ser
    50                  55                  60

Gly Glu Tyr Arg Gln Arg Asp Asp Arg Arg Asp Asp Arg Arg Asp Asn
65                  70                  75                  80

Arg Ser Asp Asp Arg Arg Gly Gly Tyr Arg Ser Asp Arg Asn Phe Asp
                85                  90                  95

Asp Arg Asn Ser Asn Met Arg Asp Asp Arg Arg Gly Gly Asp Arg Ser
            100                 105                 110

Tyr Ser Arg Asn Asp Arg Ser Asp Arg Gly Tyr Arg Ser Asn Asp Arg
        115                 120                 125

Tyr Asp Arg Asn Asp Arg Arg Asp Asp Asn Arg Asp Thr Arg Gly Gly
    130                 135                 140

Asp Arg Gly Asp Arg Arg Tyr Asp Arg Arg Asp Asp Arg Arg Asp Asp
145                 150                 155                 160

Arg Arg Asp Asp Arg Arg Gly Gly Gln Gly Gln Gly Arg Pro Gly Gly
                165                 170                 175

Asp Arg Arg His Ala Asn Arg Ala Gly Ala Gly Arg Asp Gln Gln Arg
            180                 185                 190

Asp Ser Leu His Pro Gln Arg Ala Gly Phe Arg Glu Glu Arg Leu Asn
        195                 200                 205

Thr Arg Leu Asn Glu Pro Asp Leu Pro Gly Asp Ile Asp Ile Lys Asp
    210                 215                 220

Leu Asp Pro Leu Val Leu Gln Asp Leu Lys Val Leu Ser Lys Asp Asn
225                 230                 235                 240

Ala Asp Ala Val Ala Lys His Met Ile Met Ala Ala Thr Trp Leu Ala
                245                 250                 255

Asp Asp Pro Gln Leu Ala Leu Arg His Ala Arg Ala Ala Lys Asp Arg
            260                 265                 270

Ala Gly Arg Val Ser Val Val Arg Glu Thr Asn Gly Ile Ala Ala Tyr
        275                 280                 285
```

```
His Ala Gly Glu Trp Lys Glu Ala Leu Ser Glu Leu Arg Ala Ala Arg
    290                 295                 300

Arg Met Ser Gly Gly Pro Gly Leu Ile Ala Val Met Ala Asp Cys Glu
305                 310                 315                 320

Arg Gly Leu Gly Arg Pro Glu Lys Ala Ile Glu Leu Ala Arg Glu Glu
                325                 330                 335

Asp Leu Ser Ser Leu Asp Gln Asp Asn Leu Ile Glu Leu Ala Ile Val
            340                 345                 350

Val Ala Gly Ala Arg His Asp Leu Gly Gln His Asp Ser Ala Ile Val
        355                 360                 365

Glu Leu Gln Lys Val Asn Pro Ser Leu Lys Ser Thr Gly Phe Thr His
    370                 375                 380

Ser Arg Leu Ser Tyr Ala Tyr Ala Asp Ala Leu Val Leu Ala Gly Arg
385                 390                 395                 400

Gly Asp Glu Ala Arg Glu Trp Phe Gln His Ala Ala Thr Leu Asp Glu
                405                 410                 415

Asp Gly Tyr Leu Asp Ala Glu Glu Arg Ile Glu Gln Leu Asp Asn Gly
            420                 425                 430

Asn Asn
```

<210> 683
<211> 1316
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1293)
<223> FRXA01592

<400> 683

```
aac ttc gac cgc tct cgt gac aac gat cgc tca agc gcc cgc act cct   48
Asn Phe Asp Arg Ser Arg Asp Asn Asp Arg Ser Ser Ala Arg Thr Pro
  1               5                  10                  15

cgt gga gac cgc ggc gat cgc ggt ggc tac cga aac tcc cgc ggc aac   96
Arg Gly Asp Arg Gly Asp Arg Gly Gly Tyr Arg Asn Ser Arg Gly Asn
             20                  25                  30

gat gac cgc gga aac tac cgt caa aac cga gat ggt gaa tca cga gat   144
Asp Asp Arg Gly Asn Tyr Arg Gln Asn Arg Asp Gly Glu Ser Arg Asp
         35                  40                  45

cgc ggc gga tac ctc ggt gac cgt cgc gac aac cgc tca ggt gaa tat   192
Arg Gly Gly Tyr Leu Gly Asp Arg Arg Asp Asn Arg Ser Gly Glu Tyr
     50                  55                  60

cgt caa cgt gac gat agg cgt gac gat cgt agg gac aac cga agc gat   240
Arg Gln Arg Asp Asp Arg Arg Asp Asp Arg Arg Asp Asn Arg Ser Asp
```

```
 65                  70                  75                  80

gac cgc cgc ggt ggt tac cgc tcc gat cgc aac ttt gac gat cgc aac   288
Asp Arg Arg Gly Gly Tyr Arg Ser Asp Arg Asn Phe Asp Asp Arg Asn
                 85                  90                  95

agc aac atg cgt gat gat cgt cgc ggc ggc gac cgt tca tac agc cgt   336
Ser Asn Met Arg Asp Asp Arg Arg Gly Gly Asp Arg Ser Tyr Ser Arg
            100                 105                 110

aat gat cgc tcc gat cgt ggc tat cgt agc aat gac cgc tac gac cgt   384
Asn Asp Arg Ser Asp Arg Gly Tyr Arg Ser Asn Asp Arg Tyr Asp Arg
        115                 120                 125

aat gat cgt cgc gat gac aac agg gac acc agg ggt ggc gat cgc gga   432
Asn Asp Arg Arg Asp Asp Asn Arg Asp Thr Arg Gly Gly Asp Arg Gly
    130                 135                 140

gac cgt cgc tac gac agg cgc gat gac cga cgt gat gat cgt cgc gat   480
Asp Arg Arg Tyr Asp Arg Arg Asp Asp Arg Arg Asp Asp Arg Arg Asp
145                 150                 155                 160

gat cgt cgt ggc gga cag ggc cag ggg cgt cca ggt gga gat cgt cga   528
Asp Arg Arg Gly Gly Gln Gly Gln Gly Arg Pro Gly Gly Asp Arg Arg
                165                 170                 175

cat gcg aac cgt gca ggt gca ggt cgc gat cag cag cgt gat tcg ctg   576
His Ala Asn Arg Ala Gly Ala Gly Arg Asp Gln Gln Arg Asp Ser Leu
            180                 185                 190

cat cca cag cgc gct ggt ttc cgt gaa gag cgc ttg aac act cgt ctc   624
His Pro Gln Arg Ala Gly Phe Arg Glu Glu Arg Leu Asn Thr Arg Leu
        195                 200                 205

aat gag cct gat ttg ccg ggc gat att gat atc aag gac ttg gat cct   672
Asn Glu Pro Asp Leu Pro Gly Asp Ile Asp Ile Lys Asp Leu Asp Pro
    210                 215                 220

ttg gtc ctg cag gat ttg aag gtt ttg tct aag gac aac gca gat gcc   720
Leu Val Leu Gln Asp Leu Lys Val Leu Ser Lys Asp Asn Ala Asp Ala
225                 230                 235                 240

gtc gca aag cat atg atc atg gct gcg acc tgg ctg gcc gac gat cct   768
Val Ala Lys His Met Ile Met Ala Ala Thr Trp Leu Ala Asp Asp Pro
                245                 250                 255

caa ttg gca ctg cgc cac gcc cgt gct gcg aag gat cgc gcg gga cgc   816
Gln Leu Ala Leu Arg His Ala Arg Ala Ala Lys Asp Arg Ala Gly Arg
            260                 265                 270

gtg tcc gtc gtg cgt gag acg aac ggc att gct gct tac cat gct ggt   864
Val Ser Val Val Arg Glu Thr Asn Gly Ile Ala Ala Tyr His Ala Gly
        275                 280                 285

gag tgg aag gaa gct ctt tcg gag ctt cgt gct gcg cgc cgc atg tcg   912
Glu Trp Lys Glu Ala Leu Ser Glu Leu Arg Ala Ala Arg Arg Met Ser
    290                 295                 300

ggt ggt cct ggt ttg att gct gtg atg gct gac tgt gag cgt ggc ttg   960
Gly Gly Pro Gly Leu Ile Ala Val Met Ala Asp Cys Glu Arg Gly Leu
305                 310                 315                 320
```

```
ggt cgt cct gag aag gcg att gag ctg gct cga gaa gag gat ttg agc   1008
Gly Arg Pro Glu Lys Ala Ile Glu Leu Ala Arg Glu Glu Asp Leu Ser
                325                 330                 335

tct ttg gat cag gat aac ctg atc gag tta gcg att gtt gtt gct gga   1056
Ser Leu Asp Gln Asp Asn Leu Ile Glu Leu Ala Ile Val Val Ala Gly
            340                 345                 350

gca cgc cat gat ttg ggt cag cat gac tct gcg att gtg gaa ttg cag   1104
Ala Arg His Asp Leu Gly Gln His Asp Ser Ala Ile Val Glu Leu Gln
        355                 360                 365

aag gtt aat cca agc ttg aag agc acc ggt ttc acc cat tct cgt ttg   1152
Lys Val Asn Pro Ser Leu Lys Ser Thr Gly Phe Thr His Ser Arg Leu
    370                 375                 380

tct tac gct tac gcc gat gcg ctt gtt ttg gct ggt cgt ggc gat gaa   1200
Ser Tyr Ala Tyr Ala Asp Ala Leu Val Leu Ala Gly Arg Gly Asp Glu
385                 390                 395                 400

gca cgt gag tgg ttc cag cac gct gcc acc ttg gat gag gac ggc tac   1248
Ala Arg Glu Trp Phe Gln His Ala Ala Thr Leu Asp Glu Asp Gly Tyr
                405                 410                 415

ctc gat gca gag gag cgt atc gag cag ctc gat aat ggg aac aac       1293
Leu Asp Ala Glu Glu Arg Ile Glu Gln Leu Asp Asn Gly Asn Asn
            420                 425                 430

tagactattg gtctagagtg taa                                        1316
```

<210> 684
<211> 431
<212> PRT
<213> Corynebacterium glutamicum

<400> 684

```
Asn Phe Asp Arg Ser Arg Asp Asn Asp Arg Ser Ser Ala Arg Thr Pro
  1               5                  10                  15

Arg Gly Asp Arg Gly Asp Arg Gly Gly Tyr Arg Asn Ser Arg Gly Asn
             20                  25                  30

Asp Asp Arg Gly Asn Tyr Arg Gln Asn Arg Asp Gly Glu Ser Arg Asp
         35                  40                  45

Arg Gly Gly Tyr Leu Gly Asp Arg Arg Asp Asn Arg Ser Gly Glu Tyr
     50                  55                  60

Arg Gln Arg Asp Asp Arg Arg Asp Asp Arg Arg Asp Asn Arg Ser Asp
 65                  70                  75                  80

Asp Arg Arg Gly Gly Tyr Arg Ser Asp Arg Asn Phe Asp Asp Arg Asn
                 85                  90                  95

Ser Asn Met Arg Asp Asp Arg Arg Gly Gly Asp Arg Ser Tyr Ser Arg
            100                 105                 110

Asn Asp Arg Ser Asp Arg Gly Tyr Arg Ser Asn Asp Arg Tyr Asp Arg
        115                 120                 125
```

```
Asn Asp Arg Arg Asp Asp Asn Arg Asp Thr Arg Gly Gly Asp Arg Gly
    130                 135                 140

Asp Arg Arg Tyr Asp Arg Arg Asp Asp Arg Arg Asp Asp Arg Arg Asp
145                 150                 155                 160

Asp Arg Arg Gly Gly Gln Gly Gln Gly Arg Pro Gly Gly Asp Arg Arg
                165                 170                 175

His Ala Asn Arg Ala Gly Ala Gly Arg Asp Gln Gln Arg Asp Ser Leu
            180                 185                 190

His Pro Gln Arg Ala Gly Phe Arg Glu Glu Arg Leu Asn Thr Arg Leu
        195                 200                 205

Asn Glu Pro Asp Leu Pro Gly Asp Ile Asp Ile Lys Asp Leu Asp Pro
    210                 215                 220

Leu Val Leu Gln Asp Leu Lys Val Leu Ser Lys Asp Asn Ala Asp Ala
225                 230                 235                 240

Val Ala Lys His Met Ile Met Ala Ala Thr Trp Leu Ala Asp Asp Pro
                245                 250                 255

Gln Leu Ala Leu Arg His Ala Arg Ala Ala Lys Asp Arg Ala Gly Arg
            260                 265                 270

Val Ser Val Val Arg Glu Thr Asn Gly Ile Ala Ala Tyr His Ala Gly
        275                 280                 285

Glu Trp Lys Glu Ala Leu Ser Glu Leu Arg Ala Ala Arg Arg Met Ser
    290                 295                 300

Gly Gly Pro Gly Leu Ile Ala Val Met Ala Asp Cys Glu Arg Gly Leu
305                 310                 315                 320

Gly Arg Pro Glu Lys Ala Ile Glu Leu Ala Arg Glu Glu Asp Leu Ser
                325                 330                 335

Ser Leu Asp Gln Asp Asn Leu Ile Glu Leu Ala Ile Val Val Ala Gly
            340                 345                 350

Ala Arg His Asp Leu Gly Gln His Asp Ser Ala Ile Val Glu Leu Gln
        355                 360                 365

Lys Val Asn Pro Ser Leu Lys Ser Thr Gly Phe Thr His Ser Arg Leu
    370                 375                 380

Ser Tyr Ala Tyr Ala Asp Ala Leu Val Leu Ala Gly Arg Gly Asp Glu
385                 390                 395                 400

Ala Arg Glu Trp Phe Gln His Ala Ala Thr Leu Asp Glu Asp Gly Tyr
                405                 410                 415

Leu Asp Ala Glu Glu Arg Ile Glu Gln Leu Asp Asn Gly Asn Asn
            420                 425                 430
```

<210> 685
<211> 1305

<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1282)
<223> RXN01597

<400> 685
gagtagaacc acttctcgcc gccagtgcat aagagttttc ttggaatttt ttaggcgcgc 60

ctccaccaaa ggttgagact ttggttccac aatgggctgc atg agt ctg ttc aac 115
Met Ser Leu Phe Asn
1 5

cgc aaa gcc gac ctg ccc ggc ctg caa ggt gcc acc cga atc tgc acc 163
Arg Lys Ala Asp Leu Pro Gly Leu Gln Gly Ala Thr Arg Ile Cys Thr
10 15 20

ccg cag ggc aaa ggg cta aag cgc ctg tcc gaa ggc gat ctc gca atc 211
Pro Gln Gly Lys Gly Leu Lys Arg Leu Ser Glu Gly Asp Leu Ala Ile
25 30 35

att gat gca cca gat cta tcc agg acc ttc gcc caa cga ttg cta gca 259
Ile Asp Ala Pro Asp Leu Ser Arg Thr Phe Ala Gln Arg Leu Leu Ala
40 45 50

gca aaa ccc gcc gca gtc ctc aac gtt tcc cgg ttc acc acc gga tcg 307
Ala Lys Pro Ala Ala Val Leu Asn Val Ser Arg Phe Thr Thr Gly Ser
55 60 65

gtg ccc aac ttt gga ccg caa atg ctt atc gac ggc ggc atc cag ctc 355
Val Pro Asn Phe Gly Pro Gln Met Leu Ile Asp Gly Gly Ile Gln Leu
70 75 80 85

gtg gaa ggc ttt ggc cag gag ctg ctc gac ggc acc aaa gac ggt aag 403
Val Glu Gly Phe Gly Gln Glu Leu Leu Asp Gly Thr Lys Asp Gly Lys
90 95 100

aaa ggt cgc ctg aca gaa gat gga cag ctc ttc tac ggc gaa cga ctg 451
Lys Gly Arg Leu Thr Glu Asp Gly Gln Leu Phe Tyr Gly Glu Arg Leu
105 110 115

atc tct aac ggc agt gtt ctc agt gga cct gcg gct gaa aat gca ttt 499
Ile Ser Asn Gly Ser Val Leu Ser Gly Pro Ala Ala Glu Asn Ala Phe
120 125 130

gca gac gcc cag caa tca ctg ctg gac cgc atg gaa gcc tat ttc ggc 547
Ala Asp Ala Gln Gln Ser Leu Leu Asp Arg Met Glu Ala Tyr Phe Gly
135 140 145

aac acc att cag ttc att cac tca gaa gca ccg ctc ctg atc gat ggc 595
Asn Thr Ile Gln Phe Ile His Ser Glu Ala Pro Leu Leu Ile Asp Gly
150 155 160 165

ctc ggc att ccc gat acc gga aat gcc att gaa ggc cgc aaa gtt ctc 643
Leu Gly Ile Pro Asp Thr Gly Asn Ala Ile Glu Gly Arg Lys Val Leu
170 175 180

att gcc tca cca ggg gat aac cac cgc agc agg ctc aaa gaa ctc cgc 691
Ile Ala Ser Pro Gly Asp Asn His Arg Ser Arg Leu Lys Glu Leu Arg

```
            185                 190                 195

agc ttc atc cgc gaa tac gat cca gta ctc atc ggt gtc gat ggg gca   739
Ser Phe Ile Arg Glu Tyr Asp Pro Val Leu Ile Gly Val Asp Gly Ala
        200                 205                 210

gca gac acc ttg gtg gaa ttg ggg tac aag ccc gcg ctg atc gtc ggc   787
Ala Asp Thr Leu Val Glu Leu Gly Tyr Lys Pro Ala Leu Ile Val Gly
    215                 220                 225

aat ccc act ggt atc ggc gca gat gcg ctg cgc agt ggc gcc aac gta   835
Asn Pro Thr Gly Ile Gly Ala Asp Ala Leu Arg Ser Gly Ala Asn Val
230                 235                 240                 245

att ttg cca gct gat cca gac ggc cac gct gtt ggt ctg gag cgc atc   883
Ile Leu Pro Ala Asp Pro Asp Gly His Ala Val Gly Leu Glu Arg Ile
                250                 255                 260

cag gat ctt ggc atc ggt gcg atg acc ttc cca tcc tca gta aat tcc   931
Gln Asp Leu Gly Ile Gly Ala Met Thr Phe Pro Ser Ser Val Asn Ser
            265                 270                 275

tcc acg gat ctg gcg ctc ctg ctt gcg gat ttc cac aac ccg cag atg   979
Ser Thr Asp Leu Ala Leu Leu Leu Ala Asp Phe His Asn Pro Gln Met
        280                 285                 290

atc gtc aac gtc ggc ggt cct gtc acc ctt gat ggt gtt ttt gaa aac  1027
Ile Val Asn Val Gly Gly Pro Val Thr Leu Asp Gly Val Phe Glu Asn
    295                 300                 305

cga gaa gat tcc gat ccc gcg gcg ctt ttg acg cgc gcc aag cta ggc  1075
Arg Glu Asp Ser Asp Pro Ala Ala Leu Leu Thr Arg Ala Lys Leu Gly
310                 315                 320                 325

acc aag ctt gtc gac gga tcc gtc atc gca agt ctt tac aca gtg cgc  1123
Thr Lys Leu Val Asp Gly Ser Val Ile Ala Ser Leu Tyr Thr Val Arg
                330                 335                 340

agc tcc agc aac ctt gga tgg atg tgg gca ctg tta gcc att ttg gtg  1171
Ser Ser Ser Asn Leu Gly Trp Met Trp Ala Leu Leu Ala Ile Leu Val
            345                 350                 355

gtt ctt gca gtc gtg att gtt atc gct ggc acc gca gga tca ggc tct  1219
Val Leu Ala Val Val Ile Val Ile Ala Gly Thr Ala Gly Ser Gly Ser
        360                 365                 370

ttt acc gac aac ctc att gac acc tgg aac agc ttc gcg ctg aca gtg  1267
Phe Thr Asp Asn Leu Ile Asp Thr Trp Asn Ser Phe Ala Leu Thr Val
    375                 380                 385

cag ggt tgg ttc aaa taggaaggca acatggctaa acg                   1305
Gln Gly Trp Phe Lys
390
```

<210> 686
<211> 394
<212> PRT
<213> Corynebacterium glutamicum

<400> 686

```
Met Ser Leu Phe Asn Arg Lys Ala Asp Leu Pro Gly Leu Gln Gly Ala
 1               5                  10                  15

Thr Arg Ile Cys Thr Pro Gln Gly Lys Gly Leu Lys Arg Leu Ser Glu
            20                  25                  30

Gly Asp Leu Ala Ile Ile Asp Ala Pro Asp Leu Ser Arg Thr Phe Ala
        35                  40                  45

Gln Arg Leu Leu Ala Ala Lys Pro Ala Ala Val Leu Asn Val Ser Arg
    50                  55                  60

Phe Thr Thr Gly Ser Val Pro Asn Phe Gly Pro Gln Met Leu Ile Asp
65                  70                  75                  80

Gly Gly Ile Gln Leu Val Glu Gly Phe Gly Gln Glu Leu Leu Asp Gly
                85                  90                  95

Thr Lys Asp Gly Lys Lys Gly Arg Leu Thr Glu Asp Gly Gln Leu Phe
            100                 105                 110

Tyr Gly Glu Arg Leu Ile Ser Asn Gly Ser Val Leu Ser Gly Pro Ala
        115                 120                 125

Ala Glu Asn Ala Phe Ala Asp Ala Gln Gln Ser Leu Leu Asp Arg Met
    130                 135                 140

Glu Ala Tyr Phe Gly Asn Thr Ile Gln Phe Ile His Ser Glu Ala Pro
145                 150                 155                 160

Leu Leu Ile Asp Gly Leu Gly Ile Pro Asp Thr Gly Asn Ala Ile Glu
                165                 170                 175

Gly Arg Lys Val Leu Ile Ala Ser Pro Gly Asp Asn His Arg Ser Arg
            180                 185                 190

Leu Lys Glu Leu Arg Ser Phe Ile Arg Glu Tyr Asp Pro Val Leu Ile
        195                 200                 205

Gly Val Asp Gly Ala Ala Asp Thr Leu Val Glu Leu Gly Tyr Lys Pro
    210                 215                 220

Ala Leu Ile Val Gly Asn Pro Thr Gly Ile Gly Ala Asp Ala Leu Arg
225                 230                 235                 240

Ser Gly Ala Asn Val Ile Leu Pro Ala Asp Pro Asp Gly His Ala Val
                245                 250                 255

Gly Leu Glu Arg Ile Gln Asp Leu Gly Ile Gly Ala Met Thr Phe Pro
            260                 265                 270

Ser Ser Val Asn Ser Ser Thr Asp Leu Ala Leu Leu Leu Ala Asp Phe
        275                 280                 285

His Asn Pro Gln Met Ile Val Asn Val Gly Gly Pro Val Thr Leu Asp
    290                 295                 300

Gly Val Phe Glu Asn Arg Glu Asp Ser Asp Pro Ala Ala Leu Leu Thr
305                 310                 315                 320

Arg Ala Lys Leu Gly Thr Lys Leu Val Asp Gly Ser Val Ile Ala Ser
```

```
                325                 330                 335

Leu Tyr Thr Val Arg Ser Ser Ser Asn Leu Gly Trp Met Trp Ala Leu
            340                 345                 350

Leu Ala Ile Leu Val Val Leu Ala Val Val Ile Val Ile Ala Gly Thr
        355                 360                 365

Ala Gly Ser Gly Ser Phe Thr Asp Asn Leu Ile Asp Thr Trp Asn Ser
    370                 375                 380

Phe Ala Leu Thr Val Gln Gly Trp Phe Lys
385                 390


<210> 687
<211> 1305
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1282)
<223> FRXA01597

<400> 687
gagtagaacc acttctcgcc gccagtgcat aagagttttc ttggaatttt ttaggcgcgc 60

ctccaccaaa ggttgagact ttggttccac aatgggctgc atg agt ctg ttc aac   115
                                            Met Ser Leu Phe Asn
                                              1               5

cgc aaa gcc gac ctg ccc ggc ctg caa ggt gcc acc cga atc tgc acc   163
Arg Lys Ala Asp Leu Pro Gly Leu Gln Gly Ala Thr Arg Ile Cys Thr
                10                  15                  20

ccg cag ggc aaa ggg cta aag cgc ctg tcc gaa ggc gat ctc gca atc   211
Pro Gln Gly Lys Gly Leu Lys Arg Leu Ser Glu Gly Asp Leu Ala Ile
            25                  30                  35

att gat gca cca gat cta tcc agg acc ttc gcc caa cga ttg cta gca   259
Ile Asp Ala Pro Asp Leu Ser Arg Thr Phe Ala Gln Arg Leu Leu Ala
        40                  45                  50

gca aaa ccc gcc gca gtc ctc aac gtt tcc cgg ttc acc acc gga tcg   307
Ala Lys Pro Ala Ala Val Leu Asn Val Ser Arg Phe Thr Thr Gly Ser
    55                  60                  65

gtg ccc aac ttt gga ccg caa atg ctt atc gac ggc ggc atc cag ctc   355
Val Pro Asn Phe Gly Pro Gln Met Leu Ile Asp Gly Gly Ile Gln Leu
70                  75                  80                  85

gtg gaa ggc ttt ggc cag gag ctg ctc gac ggc acc aaa gac ggt aag   403
Val Glu Gly Phe Gly Gln Glu Leu Leu Asp Gly Thr Lys Asp Gly Lys
                90                  95                  100

aaa ggt cgc ctg aca gaa gat gga cag ctc ttc tac ggc gaa cga ctg   451
Lys Gly Arg Leu Thr Glu Asp Gly Gln Leu Phe Tyr Gly Glu Arg Leu
            105                 110                 115

atc tct aac ggc agt gtt ctc agt gga cct gcg gct gaa aat gca ttt   499
```

```
Ile Ser Asn Gly Ser Val Leu Ser Gly Pro Ala Ala Glu Asn Ala Phe
        120                 125                 130

gca gac gcc cag caa tca ctg ctg gac cgc atg gaa gcc tat ttc ggc   547
Ala Asp Ala Gln Gln Ser Leu Leu Asp Arg Met Glu Ala Tyr Phe Gly
    135                 140                 145

aac acc att cag ttc att cac tca gaa gca ccg ctc ctg atc gat ggc   595
Asn Thr Ile Gln Phe Ile His Ser Glu Ala Pro Leu Leu Ile Asp Gly
150                 155                 160                 165

ctc ggc att ccc gat acc gga aat gcc att gaa ggc cgc aaa gtt ctc   643
Leu Gly Ile Pro Asp Thr Gly Asn Ala Ile Glu Gly Arg Lys Val Leu
                170                 175                 180

att gcc tca cca ggg gat aac cac cgc agc agg ctc aaa gaa ctc cgc   691
Ile Ala Ser Pro Gly Asp Asn His Arg Ser Arg Leu Lys Glu Leu Arg
            185                 190                 195

agc ttc atc cgc gaa tac gat cca gta ctc atc ggt gtc gat ggg gca   739
Ser Phe Ile Arg Glu Tyr Asp Pro Val Leu Ile Gly Val Asp Gly Ala
        200                 205                 210

gca gac acc ttg gtg gaa ttg ggg tac aag ccc gcg ctg atc gtc ggc   787
Ala Asp Thr Leu Val Glu Leu Gly Tyr Lys Pro Ala Leu Ile Val Gly
    215                 220                 225

aat ccc act ggt atc ggc gca gat gcg ctg cgc agt ggc gcc aac gta   835
Asn Pro Thr Gly Ile Gly Ala Asp Ala Leu Arg Ser Gly Ala Asn Val
230                 235                 240                 245

att ttg cca gct gat cca gac ggc cac gct gtt ggt ctg gag cgc atc   883
Ile Leu Pro Ala Asp Pro Asp Gly His Ala Val Gly Leu Glu Arg Ile
                250                 255                 260

cag gat ctt ggc atc ggt gcg atg acc ttc cca tcc tca gta aat tcc   931
Gln Asp Leu Gly Ile Gly Ala Met Thr Phe Pro Ser Ser Val Asn Ser
            265                 270                 275

tcc acg gat ctg gcg ctc ctg ctt gcg gat ttc cac aac ccg cag atg   979
Ser Thr Asp Leu Ala Leu Leu Leu Ala Asp Phe His Asn Pro Gln Met
        280                 285                 290

atc gtc aac gtc ggc ggt cct gtc acc ctt gat ggt gtt ttt gaa aac   1027
Ile Val Asn Val Gly Gly Pro Val Thr Leu Asp Gly Val Phe Glu Asn
    295                 300                 305

cga gaa gat tcc gat ccc gcg gcg ctt ttg acg cgc gcc aag cta ggc   1075
Arg Glu Asp Ser Asp Pro Ala Ala Leu Leu Thr Arg Ala Lys Leu Gly
310                 315                 320                 325

acc aag ctt gtc gac gga tcc gtc atc gca agt ctt tac aca gtg cgc   1123
Thr Lys Leu Val Asp Gly Ser Val Ile Ala Ser Leu Tyr Thr Val Arg
                330                 335                 340

agc tcc agc aac ctt gga tgg atg tgg gca ctg tta gcc att ttg gtg   1171
Ser Ser Ser Asn Leu Gly Trp Met Trp Ala Leu Leu Ala Ile Leu Val
            345                 350                 355

gtt ctt gca gtc gtg att gtt atc gct ggc acc gca gga tca ggc tct   1219
Val Leu Ala Val Val Ile Val Ile Ala Gly Thr Ala Gly Ser Gly Ser
```

```
        360                 365                 370

ttt acc gac aac ctc att gac acc tgg aac agc ttc gcg ctg aca gtg   1267
Phe Thr Asp Asn Leu Ile Asp Thr Trp Asn Ser Phe Ala Leu Thr Val
    375                 380                 385

cag ggt tgg ttc aaa taggaaggca acatggctaa acg                     1305
Gln Gly Trp Phe Lys
390
```

<210> 688
<211> 394
<212> PRT
<213> Corynebacterium glutamicum

<400> 688

```
Met Ser Leu Phe Asn Arg Lys Ala Asp Leu Pro Gly Leu Gln Gly Ala
  1               5                  10                  15

Thr Arg Ile Cys Thr Pro Gln Gly Lys Gly Leu Lys Arg Leu Ser Glu
             20                  25                  30

Gly Asp Leu Ala Ile Ile Asp Ala Pro Asp Leu Ser Arg Thr Phe Ala
         35                  40                  45

Gln Arg Leu Leu Ala Ala Lys Pro Ala Ala Val Leu Asn Val Ser Arg
     50                  55                  60

Phe Thr Thr Gly Ser Val Pro Asn Phe Gly Pro Gln Met Leu Ile Asp
 65                  70                  75                  80

Gly Gly Ile Gln Leu Val Glu Gly Phe Gly Gln Glu Leu Leu Asp Gly
                 85                  90                  95

Thr Lys Asp Gly Lys Lys Gly Arg Leu Thr Glu Asp Gly Gln Leu Phe
            100                 105                 110

Tyr Gly Glu Arg Leu Ile Ser Asn Gly Ser Val Leu Ser Gly Pro Ala
        115                 120                 125

Ala Glu Asn Ala Phe Ala Asp Ala Gln Gln Ser Leu Leu Asp Arg Met
    130                 135                 140

Glu Ala Tyr Phe Gly Asn Thr Ile Gln Phe Ile His Ser Glu Ala Pro
145                 150                 155                 160

Leu Leu Ile Asp Gly Leu Gly Ile Pro Asp Thr Gly Asn Ala Ile Glu
                165                 170                 175

Gly Arg Lys Val Leu Ile Ala Ser Pro Gly Asp Asn His Arg Ser Arg
            180                 185                 190

Leu Lys Glu Leu Arg Ser Phe Ile Arg Glu Tyr Asp Pro Val Leu Ile
        195                 200                 205

Gly Val Asp Gly Ala Ala Asp Thr Leu Val Glu Leu Gly Tyr Lys Pro
    210                 215                 220

Ala Leu Ile Val Gly Asn Pro Thr Gly Ile Gly Ala Asp Ala Leu Arg
225                 230                 235                 240
```

```
Ser Gly Ala Asn Val Ile Leu Pro Ala Asp Pro Asp Gly His Ala Val
                245                 250                 255

Gly Leu Glu Arg Ile Gln Asp Leu Gly Ile Gly Ala Met Thr Phe Pro
            260                 265                 270

Ser Ser Val Asn Ser Ser Thr Asp Leu Ala Leu Leu Leu Ala Asp Phe
        275                 280                 285

His Asn Pro Gln Met Ile Val Asn Val Gly Gly Pro Val Thr Leu Asp
    290                 295                 300

Gly Val Phe Glu Asn Arg Glu Asp Ser Asp Pro Ala Ala Leu Leu Thr
305                 310                 315                 320

Arg Ala Lys Leu Gly Thr Lys Leu Val Asp Gly Ser Val Ile Ala Ser
                325                 330                 335

Leu Tyr Thr Val Arg Ser Ser Ser Asn Leu Gly Trp Met Trp Ala Leu
            340                 345                 350

Leu Ala Ile Leu Val Val Leu Ala Val Val Ile Val Ile Ala Gly Thr
        355                 360                 365

Ala Gly Ser Gly Ser Phe Thr Asp Asn Leu Ile Asp Thr Trp Asn Ser
    370                 375                 380

Phe Ala Leu Thr Val Gln Gly Trp Phe Lys
385                 390


<210> 689
<211> 1086
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1063)
<223> RXN01598

<400> 689
cgctggcacc gcaggatcag gctcttttac cgacaacctc attgacacct ggaacagctt 60

cgcgctgaca gtgcagggtt ggttcaaata ggaaggcaac atg gct aaa cga cgt   115
                                            Met Ala Lys Arg Arg
                                              1               5

gga aga ggc gcc gca acc ttc gcc gca ctg gga ttt ggt gca gca gcc   163
Gly Arg Gly Ala Ala Thr Phe Ala Ala Leu Gly Phe Gly Ala Ala Ala
                 10                  15                  20

ggc att gcc ttt gga act tat gtg ctt gca ccc aac ctt cct gaa aac   211
Gly Ile Ala Phe Gly Thr Tyr Val Leu Ala Pro Asn Leu Pro Glu Asn
             25                  30                  35

att gac cca aat gca cca aca tca gct gaa tta gtc gag gca gag acc   259
Ile Asp Pro Asn Ala Pro Thr Ser Ala Glu Leu Val Glu Ala Glu Thr
         40                  45                  50
```

```
ttg gct gag gtt aat gcg gtg cag gcc gat caa gca gac agc atc att   307
Leu Ala Glu Val Asn Ala Val Gln Ala Asp Gln Ala Asp Ser Ile Ile
     55                  60                  65

gac cac atc gtg gaa gac gtg gtg gct ggc aca ctg acc gat cgc ccc   355
Asp His Ile Val Glu Asp Val Val Ala Gly Thr Leu Thr Asp Arg Pro
 70                  75                  80                  85

gta ctg gtg atg cgc acc gct gac gct gaa gaa tca gac gtt gcc gat   403
Val Leu Val Met Arg Thr Ala Asp Ala Glu Glu Ser Asp Val Ala Asp
                 90                  95                 100

gtg tca tgg ctg ttg cag caa gca gga gct att aat gct gga tcc att   451
Val Ser Trp Leu Leu Gln Gln Ala Gly Ala Ile Asn Ala Gly Ser Ile
            105                 110                 115

aca ctt gag gag aat ttc ttc tcc caa gac ggc gcg gac cag ctg aaa   499
Thr Leu Glu Glu Asn Phe Phe Ser Gln Asp Gly Ala Asp Gln Leu Lys
        120                 125                 130

tca atc gtg gca aat acg ttg cct gca ggc gct cag ctt tct gaa acc   547
Ser Ile Val Ala Asn Thr Leu Pro Ala Gly Ala Gln Leu Ser Glu Thr
    135                 140                 145

caa ctg gat cca gga act cac gct ggc gag gca ctt ggt gcc gct ttg   595
Gln Leu Asp Pro Gly Thr His Ala Gly Glu Ala Leu Gly Ala Ala Leu
150                 155                 160                 165

ctg ctc aac cct gaa act ggt gaa cca cta gcc agc act gca gag cgc   643
Leu Leu Asn Pro Glu Thr Gly Glu Pro Leu Ala Ser Thr Ala Glu Arg
                170                 175                 180

gga cta ttg ctc aac gtg ctg cgc gac aac ggt tac atc tcg tac gaa   691
Gly Leu Leu Leu Asn Val Leu Arg Asp Asn Gly Tyr Ile Ser Tyr Glu
            185                 190                 195

gac ggc acc att ttg cca ggc cag gtc atc gtg atg att act ggc gat   739
Asp Gly Thr Ile Leu Pro Gly Gln Val Ile Val Met Ile Thr Gly Asp
        200                 205                 210

agc gac ggc tca ggt gat ggt gcc ttc gct gca gaa aca caa tcg ctg   787
Ser Asp Gly Ser Gly Asp Gly Ala Phe Ala Ala Glu Thr Gln Ser Leu
    215                 220                 225

ttt gct cgc gca ctt gac gcc caa gga tca ggc gtg gtg gtt gca gga   835
Phe Ala Arg Ala Leu Asp Ala Gln Gly Ser Gly Val Val Val Ala Gly
230                 235                 240                 245

cgt att cac act gct gct gat act gga gtt att gga cgg ctt cgt gcc   883
Arg Ile His Thr Ala Ala Asp Thr Gly Val Ile Gly Arg Leu Arg Ala
                250                 255                 260

aac cct gat gct gca gaa aac gtc tct aca att gat tcc gtg aat cgt   931
Asn Pro Asp Ala Ala Glu Asn Val Ser Thr Ile Asp Ser Val Asn Arg
            265                 270                 275

act tgg ggc aag atg gct acc gtg cta tca gtt cgt gag gaa cta gcc   979
Thr Trp Gly Lys Met Ala Thr Val Leu Ser Val Arg Glu Glu Leu Ala
        280                 285                 290

ggt agg tct gga gcg ttt ggt tcc gct gcc tcc gca gac gcg gca agt   1027
```

```
Gly Arg Ser Gly Ala Phe Gly Ser Ala Ala Ser Ala Asp Ala Ala Ser
    295                 300                 305

ccg tct ctc gat gga act gca gca gcg cca gcg cag taggttttcc        1073
Pro Ser Leu Asp Gly Thr Ala Ala Ala Pro Ala Gln
310                 315                 320

aagcctttaa aac                                                    1086


<210> 690
<211> 321
<212> PRT
<213> Corynebacterium glutamicum

<400> 690
Met Ala Lys Arg Arg Gly Arg Gly Ala Ala Thr Phe Ala Ala Leu Gly
  1               5                  10                  15

Phe Gly Ala Ala Ala Gly Ile Ala Phe Gly Thr Tyr Val Leu Ala Pro
             20                  25                  30

Asn Leu Pro Glu Asn Ile Asp Pro Asn Ala Pro Thr Ser Ala Glu Leu
         35                  40                  45

Val Glu Ala Glu Thr Leu Ala Glu Val Asn Ala Val Gln Ala Asp Gln
     50                  55                  60

Ala Asp Ser Ile Ile Asp His Ile Val Glu Asp Val Val Ala Gly Thr
 65                  70                  75                  80

Leu Thr Asp Arg Pro Val Leu Val Met Arg Thr Ala Asp Ala Glu Glu
                 85                  90                  95

Ser Asp Val Ala Asp Val Ser Trp Leu Leu Gln Gln Ala Gly Ala Ile
            100                 105                 110

Asn Ala Gly Ser Ile Thr Leu Glu Glu Asn Phe Phe Ser Gln Asp Gly
        115                 120                 125

Ala Asp Gln Leu Lys Ser Ile Val Ala Asn Thr Leu Pro Ala Gly Ala
    130                 135                 140

Gln Leu Ser Glu Thr Gln Leu Asp Pro Gly Thr His Ala Gly Glu Ala
145                 150                 155                 160

Leu Gly Ala Ala Leu Leu Leu Asn Pro Glu Thr Gly Glu Pro Leu Ala
                165                 170                 175

Ser Thr Ala Glu Arg Gly Leu Leu Leu Asn Val Leu Arg Asp Asn Gly
            180                 185                 190

Tyr Ile Ser Tyr Glu Asp Gly Thr Ile Leu Pro Gly Gln Val Ile Val
        195                 200                 205

Met Ile Thr Gly Asp Ser Asp Gly Ser Gly Asp Gly Ala Phe Ala Ala
    210                 215                 220

Glu Thr Gln Ser Leu Phe Ala Arg Ala Leu Asp Ala Gln Gly Ser Gly
225                 230                 235                 240
```

```
Val Val Val Ala Gly Arg Ile His Thr Ala Ala Asp Thr Gly Val Ile
                245                 250                 255

Gly Arg Leu Arg Ala Asn Pro Asp Ala Ala Glu Asn Val Ser Thr Ile
            260                 265                 270

Asp Ser Val Asn Arg Thr Trp Gly Lys Met Ala Thr Val Leu Ser Val
        275                 280                 285

Arg Glu Glu Leu Ala Gly Arg Ser Gly Ala Phe Gly Ser Ala Ala Ser
    290                 295                 300

Ala Asp Ala Ala Ser Pro Ser Leu Asp Gly Thr Ala Ala Ala Pro Ala
305                 310                 315                 320

Gln
```

<210> 691
<211> 1086
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1063)
<223> FRXA01598

<400> 691
cgctggcacc gcaggatcag gctcttttac cgacaacctc attgacacct ggaacagctt 60

cgcgctgaca gtgcagggtt ggttcaaata ggaaggcaac atg gct aaa cga cgt 115
                                            Met Ala Lys Arg Arg
                                              1   5

gga aga ggc gcc gca acc ttc gcc gca ctg gga ttt ggt gca gca gcc 163
Gly Arg Gly Ala Ala Thr Phe Ala Ala Leu Gly Phe Gly Ala Ala Ala
                10   15   20

ggc att gcc ttt gga act tat gtg ctt gca ccc aac ctt cct gaa aac 211
Gly Ile Ala Phe Gly Thr Tyr Val Leu Ala Pro Asn Leu Pro Glu Asn
            25   30   35

att gac cca aat gca cca aca tca gct gaa tta gtc gag gca gag acc 259
Ile Asp Pro Asn Ala Pro Thr Ser Ala Glu Leu Val Glu Ala Glu Thr
        40   45   50

ttg gct gag gtt aat gcg gtg cag gcc gat caa gca gac agc atc att 307
Leu Ala Glu Val Asn Ala Val Gln Ala Asp Gln Ala Asp Ser Ile Ile
    55   60   65

gac cac atc gtg gaa gac gtg gtg gct ggc aca ctg acc gat cgc ccc 355
Asp His Ile Val Glu Asp Val Val Ala Gly Thr Leu Thr Asp Arg Pro
70   75   80   85

gta ctg gtg atg cgc acc gct gac gct gaa gaa tca gac gtt gcc gat 403
Val Leu Val Met Arg Thr Ala Asp Ala Glu Glu Ser Asp Val Ala Asp
                90   95   100

gtg tca tgg ctg ttg cag caa gca gga gct att aat gct gga tcc att 451
```
```

```
Val Ser Trp Leu Leu Gln Gln Ala Gly Ala Ile Asn Ala Gly Ser Ile
            105                 110                 115

aca ctt gag gag aat ttc ttc tcc caa gac ggc gcg gac cag ctg aaa   499
Thr Leu Glu Glu Asn Phe Phe Ser Gln Asp Gly Ala Asp Gln Leu Lys
        120                 125                 130

tca atc gtg gca aat acg ttg cct gca ggc gct cag ctt tct gaa acc   547
Ser Ile Val Ala Asn Thr Leu Pro Ala Gly Ala Gln Leu Ser Glu Thr
    135                 140                 145

caa ctg gat cca gga act cac gct ggc gag gca ctt ggt gcc gct ttg   595
Gln Leu Asp Pro Gly Thr His Ala Gly Glu Ala Leu Gly Ala Ala Leu
150                 155                 160                 165

ctg ctc aac cct gaa act ggt gaa cca cta gcc agc act gca gag cgc   643
Leu Leu Asn Pro Glu Thr Gly Glu Pro Leu Ala Ser Thr Ala Glu Arg
                170                 175                 180

gga cta ttg ctc aac gtg ctg cgc gac aac ggt tac atc tcg tac gaa   691
Gly Leu Leu Leu Asn Val Leu Arg Asp Asn Gly Tyr Ile Ser Tyr Glu
            185                 190                 195

gac ggc acc att ttg cca ggc cag gtc atc gtg atg att act ggc gat   739
Asp Gly Thr Ile Leu Pro Gly Gln Val Ile Val Met Ile Thr Gly Asp
        200                 205                 210

agc gac ggc tca ggt gat ggt gcc ttc gct gca gaa aca caa tcg ctg   787
Ser Asp Gly Ser Gly Asp Gly Ala Phe Ala Ala Glu Thr Gln Ser Leu
    215                 220                 225

ttt gct cgc gca ctt gac gcc caa gga tca ggc gtg gtg gtt gca gga   835
Phe Ala Arg Ala Leu Asp Ala Gln Gly Ser Gly Val Val Val Ala Gly
230                 235                 240                 245

cgt att cac act gct gct gat act gga gtt att gga cgg ctt cgt gcc   883
Arg Ile His Thr Ala Ala Asp Thr Gly Val Ile Gly Arg Leu Arg Ala
                250                 255                 260

aac cct gat gct gca gaa aac gtc tct aca att gat tcc gtg aat cgt   931
Asn Pro Asp Ala Ala Glu Asn Val Ser Thr Ile Asp Ser Val Asn Arg
            265                 270                 275

act tgg ggc aag atg gct acc gtg cta tca gtt cgt gag gaa cta gcc   979
Thr Trp Gly Lys Met Ala Thr Val Leu Ser Val Arg Glu Glu Leu Ala
        280                 285                 290

ggt agg tct gga gcg ttt ggt tcc gct gcc tcc gca gac gcg gca agt   1027
Gly Arg Ser Gly Ala Phe Gly Ser Ala Ala Ser Ala Asp Ala Ala Ser
    295                 300                 305

ccg tct ctc gat gga act gca gca gcg cca gcg cag taggttttcc        1073
Pro Ser Leu Asp Gly Thr Ala Ala Ala Pro Ala Gln
310                 315                 320

aagcctttaa aac                                                   1086
```

<210> 692
<211> 321
<212> PRT

<213> Corynebacterium glutamicum

<400> 692

```
Met Ala Lys Arg Arg Gly Arg Gly Ala Ala Thr Phe Ala Ala Leu Gly
  1               5                  10                  15

Phe Gly Ala Ala Ala Gly Ile Ala Phe Gly Thr Tyr Val Leu Ala Pro
             20                  25                  30

Asn Leu Pro Glu Asn Ile Asp Pro Asn Ala Pro Thr Ser Ala Glu Leu
         35                  40                  45

Val Glu Ala Glu Thr Leu Ala Glu Val Asn Ala Val Gln Ala Asp Gln
     50                  55                  60

Ala Asp Ser Ile Ile Asp His Ile Val Glu Asp Val Val Ala Gly Thr
 65                  70                  75                  80

Leu Thr Asp Arg Pro Val Leu Val Met Arg Thr Ala Asp Ala Glu Glu
                 85                  90                  95

Ser Asp Val Ala Asp Val Ser Trp Leu Leu Gln Gln Ala Gly Ala Ile
            100                 105                 110

Asn Ala Gly Ser Ile Thr Leu Glu Glu Asn Phe Phe Ser Gln Asp Gly
        115                 120                 125

Ala Asp Gln Leu Lys Ser Ile Val Ala Asn Thr Leu Pro Ala Gly Ala
    130                 135                 140

Gln Leu Ser Glu Thr Gln Leu Asp Pro Gly Thr His Ala Gly Glu Ala
145                 150                 155                 160

Leu Gly Ala Ala Leu Leu Leu Asn Pro Glu Thr Gly Glu Pro Leu Ala
                165                 170                 175

Ser Thr Ala Glu Arg Gly Leu Leu Leu Asn Val Leu Arg Asp Asn Gly
            180                 185                 190

Tyr Ile Ser Tyr Glu Asp Gly Thr Ile Leu Pro Gly Gln Val Ile Val
        195                 200                 205

Met Ile Thr Gly Asp Ser Asp Gly Ser Gly Asp Gly Ala Phe Ala Ala
    210                 215                 220

Glu Thr Gln Ser Leu Phe Ala Arg Ala Leu Asp Ala Gln Gly Ser Gly
225                 230                 235                 240

Val Val Val Ala Gly Arg Ile His Thr Ala Ala Asp Thr Gly Val Ile
                245                 250                 255

Gly Arg Leu Arg Ala Asn Pro Asp Ala Ala Glu Asn Val Ser Thr Ile
            260                 265                 270

Asp Ser Val Asn Arg Thr Trp Gly Lys Met Ala Thr Val Leu Ser Val
        275                 280                 285

Arg Glu Glu Leu Ala Gly Arg Ser Gly Ala Phe Gly Ser Ala Ala Ser
    290                 295                 300

Ala Asp Ala Ala Ser Pro Ser Leu Asp Gly Thr Ala Ala Ala Pro Ala
```

305 310 315 320

Gln

<210> 693
<211> 507
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(484)
<223> RXN01618

<400> 693
ggccgtgcgc gcctccagcg agcctggccg tgccggaaaa gtgctcattc gtttctaaac 60

gtttaaggcc cattagaccc ctgatttaaa aggatctcac atg atc att atc gga 115
Met Ile Ile Ile Gly
1 5

gca gtt ttc gcc atc ctc gca gtt cta ctg cat gtt ttc atc ttc tac 163
Ala Val Phe Ala Ile Leu Ala Val Leu Leu His Val Phe Ile Phe Tyr
10 15 20

atg gaa tca ttc gca tgg act agt gag aaa gca cgt gga gtt ttc ggc 211
Met Glu Ser Phe Ala Trp Thr Ser Glu Lys Ala Arg Gly Val Phe Gly
25 30 35

acc acc gaa atc gac gcc gaa aac acc aag gag atg gcc tac aac caa 259
Thr Thr Glu Ile Asp Ala Glu Asn Thr Lys Glu Met Ala Tyr Asn Gln
40 45 50

ggc ttc tac aac ttc ttc ctg gca gtc atc gcc ggc gtg ggt gtt gcg 307
Gly Phe Tyr Asn Phe Phe Leu Ala Val Ile Ala Gly Val Gly Val Ala
55 60 65

ttc ctc ttc gct ggt tca act ggc atc ggc gca gcc ctc gca ctc gct 355
Phe Leu Phe Ala Gly Ser Thr Gly Ile Gly Ala Ala Leu Ala Leu Ala
70 75 80 85

ggc acc ggt tcc atg ctg gca gcc gct gca gtg ttg gct ttg agc tca 403
Gly Thr Gly Ser Met Leu Ala Ala Ala Ala Val Leu Ala Leu Ser Ser
90 95 100

ccc gac aag cgt ggt gca gcc ttc aag caa ggc acg ttc ccg ctg ctc 451
Pro Asp Lys Arg Gly Ala Ala Phe Lys Gln Gly Thr Phe Pro Leu Leu
105 110 115

gca gtg gtg ttc ctt gtg att gga ttg ctg gtt taagcagttt tttaaaggaa 504
Ala Val Val Phe Leu Val Ile Gly Leu Leu Val
120 125

ctt 507

<210> 694
<211> 128
<212> PRT

<213> Corynebacterium glutamicum

<400> 694
Met Ile Ile Ile Gly Ala Val Phe Ala Ile Leu Ala Val Leu Leu His
1 5 10 15

Val Phe Ile Phe Tyr Met Glu Ser Phe Ala Trp Thr Ser Glu Lys Ala
20 25 30

Arg Gly Val Phe Gly Thr Thr Glu Ile Asp Ala Glu Asn Thr Lys Glu
35 40 45

Met Ala Tyr Asn Gln Gly Phe Tyr Asn Phe Phe Leu Ala Val Ile Ala
50 55 60

Gly Val Gly Val Ala Phe Leu Phe Ala Gly Ser Thr Gly Ile Gly Ala
65 70 75 80

Ala Leu Ala Leu Ala Gly Thr Gly Ser Met Leu Ala Ala Ala Ala Val
85 90 95

Leu Ala Leu Ser Ser Pro Asp Lys Arg Gly Ala Ala Phe Lys Gln Gly
100 105 110

Thr Phe Pro Leu Leu Ala Val Val Phe Leu Val Ile Gly Leu Leu Val
115 120 125

<210> 695
<211> 507
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(484)
<223> FRXA01618

<400> 695
ggccgtgcgc gcctccagcg agcctggccg tgccggaaaa gtgctcattc gtttctaaac 60

gtttaaggcc cattagaccc ctgatttaaa aggatctcac atg atc att atc gga 115
Met Ile Ile Ile Gly
1 5

gca gtt ttc gcc atc ctc gca gtt cta ctg cat gtt ttc atc ttc tac 163
Ala Val Phe Ala Ile Leu Ala Val Leu Leu His Val Phe Ile Phe Tyr
10 15 20

atg gaa tca ttc gca tgg act agt gag aaa gca cgt gga gtt ttc ggc 211
Met Glu Ser Phe Ala Trp Thr Ser Glu Lys Ala Arg Gly Val Phe Gly
25 30 35

acc acc gaa atc gac gcc gaa aac acc aag gag atg gcc tac aac caa 259
Thr Thr Glu Ile Asp Ala Glu Asn Thr Lys Glu Met Ala Tyr Asn Gln
40 45 50

ggc ttc tac aac ttc ttc ctg gca gtc atc gcc ggc gtg ggt gtt gcg 307

```
Gly Phe Tyr Asn Phe Phe Leu Ala Val Ile Ala Gly Val Gly Val Ala
     55                  60                  65

ttc ctc ttc gct ggt tca act ggc atc ggc gca gcc ctc gca ctc gct   355
Phe Leu Phe Ala Gly Ser Thr Gly Ile Gly Ala Ala Leu Ala Leu Ala
 70                  75                  80                  85

ggc acc ggt tcc atg ctg gca gcc gct gca gtg ttg gct ttg agc tca   403
Gly Thr Gly Ser Met Leu Ala Ala Ala Ala Val Leu Ala Leu Ser Ser
                 90                  95                 100

ccc gac aag cgt ggt gca gcc ttc aag caa ggc acg ttc ccg ctg ctc   451
Pro Asp Lys Arg Gly Ala Ala Phe Lys Gln Gly Thr Phe Pro Leu Leu
            105                 110                 115

gca gtg gtg ttc ctt gtg att gga ttg ctg gtt taagcagttt tttaaaggaa 504
Ala Val Val Phe Leu Val Ile Gly Leu Leu Val
        120                 125

ctt                                                               507
```

<210> 696
<211> 128
<212> PRT
<213> Corynebacterium glutamicum

<400> 696

```
Met Ile Ile Ile Gly Ala Val Phe Ala Ile Leu Ala Val Leu Leu His
  1               5                  10                  15

Val Phe Ile Phe Tyr Met Glu Ser Phe Ala Trp Thr Ser Glu Lys Ala
             20                  25                  30

Arg Gly Val Phe Gly Thr Thr Glu Ile Asp Ala Glu Asn Thr Lys Glu
         35                  40                  45

Met Ala Tyr Asn Gln Gly Phe Tyr Asn Phe Phe Leu Ala Val Ile Ala
     50                  55                  60

Gly Val Gly Val Ala Phe Leu Phe Ala Gly Ser Thr Gly Ile Gly Ala
 65                  70                  75                  80

Ala Leu Ala Leu Ala Gly Thr Gly Ser Met Leu Ala Ala Ala Ala Val
                 85                  90                  95

Leu Ala Leu Ser Ser Pro Asp Lys Arg Gly Ala Ala Phe Lys Gln Gly
            100                 105                 110

Thr Phe Pro Leu Leu Ala Val Val Phe Leu Val Ile Gly Leu Leu Val
        115                 120                 125
```

<210> 697
<211> 675
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(652)
<223> RXN01634

<400> 697
attggatcta ggaaaaatta tgaacatctc aaagctcgga ctgaggatcg cggtcacagc 60

aacggcgacc acaacggcgc ttgccctcgg tggcacgcac atg gca gtt ggt caa 115
Met Ala Val Gly Gln
1 5

gaa act gat ctg ctc aac gct atg gaa aca ctc gct ggg gtt ccc tca 163
Glu Thr Asp Leu Leu Asn Ala Met Glu Thr Leu Ala Gly Val Pro Ser
10 15 20

gac ttg gtg gtc act gaa atc ctc ccc gat acc acc agc tat gac aat 211
Asp Leu Val Val Thr Glu Ile Leu Pro Asp Thr Thr Ser Tyr Asp Asn
25 30 35

ttt gaa ttc ttt gaa gtt cac aac acc ggc agt gca ccc gtg acc att 259
Phe Glu Phe Phe Glu Val His Asn Thr Gly Ser Ala Pro Val Thr Ile
40 45 50

ggg gaa ggg gag tac acc ttc gcc tat tcc ttt gac gat tcc gcc gat 307
Gly Glu Gly Glu Tyr Thr Phe Ala Tyr Ser Phe Asp Asp Ser Ala Asp
55 60 65

acg tcc cgc gac aag gca ctg gat ctt ggc ggg gaa gtc acg gta gat 355
Thr Ser Arg Asp Lys Ala Leu Asp Leu Gly Gly Glu Val Thr Val Asp
70 75 80 85

gca ggc gaa acc att gtg gtg tgg att gag tac tcc agt tca act gtt 403
Ala Gly Glu Thr Ile Val Val Trp Ile Glu Tyr Ser Ser Ser Thr Val
90 95 100

gat acc gct gcg ttt agt gag caa gac ttc cgt gat ttc tac ggc atg 451
Asp Thr Ala Ala Phe Ser Glu Gln Asp Phe Arg Asp Phe Tyr Gly Met
105 110 115

gat tcc tca gcc cgc atc ttc cga gca act ggc cag gcg ggt ctc gct 499
Asp Ser Ser Ala Arg Ile Phe Arg Ala Thr Gly Gln Ala Gly Leu Ala
120 125 130

aac ggt ggt gat cgt ggc atc cga gtt ctg tac aat ggt gaa gtt tct 547
Asn Gly Gly Asp Arg Gly Ile Arg Val Leu Tyr Asn Gly Glu Val Ser
135 140 145

ggt tgg tcc cac tac cca tca gat agc gca gcg gtt caa aag gga att 595
Gly Trp Ser His Tyr Pro Ser Asp Ser Ala Ala Val Gln Lys Gly Ile
150 155 160 165

gac ttc gcg ctg cca aaa gta ggg gag cag gcc agc att gca agt gcg 643
Asp Phe Ala Leu Pro Lys Val Gly Glu Gln Ala Ser Ile Ala Ser Ala
170 175 180

cac caa aac tgatccaact ccaggatcaa tta 675
His Gln Asn

<210> 698
<211> 184
<212> PRT
<213> Corynebacterium glutamicum

<400> 698
Met Ala Val Gly Gln Glu Thr Asp Leu Leu Asn Ala Met Glu Thr Leu
1 5 10 15

Ala Gly Val Pro Ser Asp Leu Val Val Thr Glu Ile Leu Pro Asp Thr
20 25 30

Thr Ser Tyr Asp Asn Phe Glu Phe Phe Glu Val His Asn Thr Gly Ser
35 40 45

Ala Pro Val Thr Ile Gly Glu Gly Glu Tyr Thr Phe Ala Tyr Ser Phe
50 55 60

Asp Asp Ser Ala Asp Thr Ser Arg Asp Lys Ala Leu Asp Leu Gly Gly
65 70 75 80

Glu Val Thr Val Asp Ala Gly Glu Thr Ile Val Val Trp Ile Glu Tyr
85 90 95

Ser Ser Ser Thr Val Asp Thr Ala Ala Phe Ser Glu Gln Asp Phe Arg
100 105 110

Asp Phe Tyr Gly Met Asp Ser Ser Ala Arg Ile Phe Arg Ala Thr Gly
115 120 125

Gln Ala Gly Leu Ala Asn Gly Gly Asp Arg Gly Ile Arg Val Leu Tyr
130 135 140

Asn Gly Glu Val Ser Gly Trp Ser His Tyr Pro Ser Asp Ser Ala Ala
145 150 155 160

Val Gln Lys Gly Ile Asp Phe Ala Leu Pro Lys Val Gly Glu Gln Ala
165 170 175

Ser Ile Ala Ser Ala His Gln Asn
180

<210> 699
<211> 675
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(652)
<223> FRXA01634

<400> 699
attggatcta ggaaaaatta tgaacatctc aaagctcgga ctgaggatcg cggtcacagc 60

aacggcgacc acaacggcgc ttgccctcgg tggcacgcac atg gca gtt ggt caa 115
Met Ala Val Gly Gln
1 5

gaa act gat ctg ctc aac gct atg gaa aca ctc gct ggg gtt ccc tca 163

```
Glu Thr Asp Leu Leu Asn Ala Met Glu Thr Leu Ala Gly Val Pro Ser
                10                  15                  20

gac ttg gtg gtc act gaa atc ctc ccc gat acc acc agc tat gac aat   211
Asp Leu Val Val Thr Glu Ile Leu Pro Asp Thr Thr Ser Tyr Asp Asn
            25                  30                  35

ttt gaa ttc ttt gaa gtt cac aac acc ggc agt gca ccc gtg acc att   259
Phe Glu Phe Phe Glu Val His Asn Thr Gly Ser Ala Pro Val Thr Ile
        40                  45                  50

ggg gaa ggg gag tac acc ttc gcc tat tcc ttt gac gat tcc gcc gat   307
Gly Glu Gly Glu Tyr Thr Phe Ala Tyr Ser Phe Asp Asp Ser Ala Asp
    55                  60                  65

acg tcc cgc gac aag gca ctg gat ctt ggc ggg gaa gtc acg gta gat   355
Thr Ser Arg Asp Lys Ala Leu Asp Leu Gly Gly Glu Val Thr Val Asp
70                  75                  80                  85

gca ggc gaa acc att gtg gtg tgg att gag tac tcc agt tca act gtt   403
Ala Gly Glu Thr Ile Val Val Trp Ile Glu Tyr Ser Ser Ser Thr Val
                90                  95                  100

gat acc gct gcg ttt agt gag caa gac ttc cgt gat ttc tac ggc atg   451
Asp Thr Ala Ala Phe Ser Glu Gln Asp Phe Arg Asp Phe Tyr Gly Met
            105                 110                 115

gat tcc tca gcc cgc atc ttc cga gca act ggc cag gcg ggt ctc gct   499
Asp Ser Ser Ala Arg Ile Phe Arg Ala Thr Gly Gln Ala Gly Leu Ala
        120                 125                 130

aac ggt ggt gat cgt ggc atc cga gtt ctg tac aat ggt gaa gtt tct   547
Asn Gly Gly Asp Arg Gly Ile Arg Val Leu Tyr Asn Gly Glu Val Ser
    135                 140                 145

ggt tgg tcc cac tac cca tca gat agc gca gcg gtt caa aag gga att   595
Gly Trp Ser His Tyr Pro Ser Asp Ser Ala Ala Val Gln Lys Gly Ile
150                 155                 160                 165

gac ttc gcg ctg cca aaa gta ggg gag cag gcc agc att gca agt gcg   643
Asp Phe Ala Leu Pro Lys Val Gly Glu Gln Ala Ser Ile Ala Ser Ala
                170                 175                 180

cac caa aac tgatccaact ccaggatcaa tta                            675
His Gln Asn
```

<210> 700
<211> 184
<212> PRT
<213> Corynebacterium glutamicum

<400> 700

```
Met Ala Val Gly Gln Glu Thr Asp Leu Leu Asn Ala Met Glu Thr Leu
  1               5                  10                  15

Ala Gly Val Pro Ser Asp Leu Val Val Thr Glu Ile Leu Pro Asp Thr
            20                  25                  30

Thr Ser Tyr Asp Asn Phe Glu Phe Phe Glu Val His Asn Thr Gly Ser
```

```
         35                  40                  45

Ala Pro Val Thr Ile Gly Glu Gly Glu Tyr Thr Phe Ala Tyr Ser Phe
     50                  55                  60

Asp Asp Ser Ala Asp Thr Ser Arg Asp Lys Ala Leu Asp Leu Gly Gly
 65                  70                  75                  80

Glu Val Thr Val Asp Ala Gly Glu Thr Ile Val Val Trp Ile Glu Tyr
                 85                  90                  95

Ser Ser Ser Thr Val Asp Thr Ala Ala Phe Ser Glu Gln Asp Phe Arg
            100                 105                 110

Asp Phe Tyr Gly Met Asp Ser Ser Ala Arg Ile Phe Arg Ala Thr Gly
        115                 120                 125

Gln Ala Gly Leu Ala Asn Gly Gly Asp Arg Gly Ile Arg Val Leu Tyr
    130                 135                 140

Asn Gly Glu Val Ser Gly Trp Ser His Tyr Pro Ser Asp Ser Ala Ala
145                 150                 155                 160

Val Gln Lys Gly Ile Asp Phe Ala Leu Pro Lys Val Gly Glu Gln Ala
                165                 170                 175

Ser Ile Ala Ser Ala His Gln Asn
            180
```

<210> 701
<211> 864
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(841)
<223> RXN01635

<400> 701

```
agggaattga cttcgcgctg ccaaaagtag gggagcaggc cagcattgca agtgcgcacc 60

aaaactgatc caactccagg atcaattact tctgatcaag ttg att cct ggc gga   115
                                          Leu Ile Pro Gly Gly
                                            1               5

ttg gac act cca gaa gag cct gaa gcc cct gaa gac tct ctt ttt gaa   163
Leu Asp Thr Pro Glu Glu Pro Glu Ala Pro Glu Asp Ser Leu Phe Glu
                10                  15                  20

ggg cgc act ccc cct agg gat gca agc acc cgc ttg atc ctc act gaa   211
Gly Arg Thr Pro Pro Arg Asp Ala Ser Thr Arg Leu Ile Leu Thr Glu
            25                  30                  35

cta atg gtc aac tcc acc aac atg ggc agt tct gat ggt ttt gag tat   259
Leu Met Val Asn Ser Thr Asn Met Gly Ser Ser Asp Gly Phe Glu Tyr
        40                  45                  50

gtg gaa atc acc aac act act gcc gaa ccc atc gat ttt tcc gat tac   307
Val Glu Ile Thr Asn Thr Thr Ala Glu Pro Ile Asp Phe Ser Asp Tyr
```

```
     55                  60                  65

acc ttg aac tac ctg tac ccg cag gat gag ttc acc aac acc aac gaa   355
Thr Leu Asn Tyr Leu Tyr Pro Gln Asp Glu Phe Thr Asn Thr Asn Glu
 70                  75                  80                  85

gcc gtc tgg gct gcg gaa cct ggt gat gtc att att cag cct gga aaa   403
Ala Val Trp Ala Ala Glu Pro Gly Asp Val Ile Ile Gln Pro Gly Lys
                90                  95                 100

tct ctc gtg ttt tgg atc aaa aat ggc ccc aat gat gag gca acc gca   451
Ser Leu Val Phe Trp Ile Lys Asn Gly Pro Asn Asp Glu Ala Thr Ala
            105                 110                 115

gca gat ttc aat gca gaa tat ggc acc aac ctg gag gct gga aaa gac   499
Ala Asp Phe Asn Ala Glu Tyr Gly Thr Asn Leu Glu Ala Gly Lys Asp
        120                 125                 130

ctt gtt gaa atc tcc tca ggt ggg atg gcc aat ggt act gcc aga gga   547
Leu Val Glu Ile Ser Ser Gly Gly Met Ala Asn Gly Thr Ala Arg Gly
    135                 140                 145

atg cag att cag acc aac act ggc cac ata gtc aac cgt ggt ttc tac   595
Met Gln Ile Gln Thr Asn Thr Gly His Ile Val Asn Arg Gly Phe Tyr
150                 155                 160                 165

aac atg gct ggc gct tct gat gtg aaa gcc aac gag ggt ctt cat ttc   643
Asn Met Ala Gly Ala Ser Asp Val Lys Ala Asn Glu Gly Leu His Phe
                170                 175                 180

gca gtg gat gag tct gat ctt ctg aag caa acg ctt gtc ggc agc ggt   691
Ala Val Asp Glu Ser Asp Leu Leu Lys Gln Thr Leu Val Gly Ser Gly
            185                 190                 195

gcg cca acc ccg ggc act gtg tac act tcg cag att cct aat cca ctg   739
Ala Pro Thr Pro Gly Thr Val Tyr Thr Ser Gln Ile Pro Asn Pro Leu
        200                 205                 210

tct gcc gtt atc gct gat tct tct gta cca ctc atc aca gat aat acc   787
Ser Ala Val Ile Ala Asp Ser Ser Val Pro Leu Ile Thr Asp Asn Thr
    215                 220                 225

gca acc agt atc aac cct gcg gag ccg ttt acc ttc gcc ttc aaa tat   835
Ala Thr Ser Ile Asn Pro Ala Glu Pro Phe Thr Phe Ala Phe Lys Tyr
230                 235                 240                 245

cac cga tgatgtccag gtgcgcacgg caa                                 864
His Arg
```

<210> 702
<211> 247
<212> PRT
<213> Corynebacterium glutamicum

<400> 702

```
Leu Ile Pro Gly Gly Leu Asp Thr Pro Glu Glu Pro Glu Ala Pro Glu
  1               5                  10                  15

Asp Ser Leu Phe Glu Gly Arg Thr Pro Pro Arg Asp Ala Ser Thr Arg
```

```
            20                  25                  30

Leu Ile Leu Thr Glu Leu Met Val Asn Ser Thr Asn Met Gly Ser Ser
        35                  40                  45

Asp Gly Phe Glu Tyr Val Glu Ile Thr Asn Thr Thr Ala Glu Pro Ile
    50                  55                  60

Asp Phe Ser Asp Tyr Thr Leu Asn Tyr Leu Tyr Pro Gln Asp Glu Phe
65                  70                  75                  80

Thr Asn Thr Asn Glu Ala Val Trp Ala Ala Glu Pro Gly Asp Val Ile
                85                  90                  95

Ile Gln Pro Gly Lys Ser Leu Val Phe Trp Ile Lys Asn Gly Pro Asn
            100                 105                 110

Asp Glu Ala Thr Ala Ala Asp Phe Asn Ala Glu Tyr Gly Thr Asn Leu
        115                 120                 125

Glu Ala Gly Lys Asp Leu Val Glu Ile Ser Ser Gly Gly Met Ala Asn
    130                 135                 140

Gly Thr Ala Arg Gly Met Gln Ile Gln Thr Asn Thr Gly His Ile Val
145                 150                 155                 160

Asn Arg Gly Phe Tyr Asn Met Ala Gly Ala Ser Asp Val Lys Ala Asn
                165                 170                 175

Glu Gly Leu His Phe Ala Val Asp Glu Ser Asp Leu Leu Lys Gln Thr
            180                 185                 190

Leu Val Gly Ser Gly Ala Pro Thr Pro Gly Thr Val Tyr Thr Ser Gln
        195                 200                 205

Ile Pro Asn Pro Leu Ser Ala Val Ile Ala Asp Ser Ser Val Pro Leu
    210                 215                 220

Ile Thr Asp Asn Thr Ala Thr Ser Ile Asn Pro Ala Glu Pro Phe Thr
225                 230                 235                 240

Phe Ala Phe Lys Tyr His Arg
                245
```

<210> 703
<211> 864
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(841)
<223> FRXA01635

<400> 703
agggaattga cttcgcgctg ccaaaagtag gggagcaggc cagcattgca agtgcgcacc 60

aaaactgatc caactccagg atcaattact tctgatcaag ttg att cct ggc gga 115
                                    Leu Ile Pro Gly Gly
                                      1   5

```
ttg gac act cca gaa gag cct gaa gcc cct gaa gac tct ctt ttt gaa   163
Leu Asp Thr Pro Glu Glu Pro Glu Ala Pro Glu Asp Ser Leu Phe Glu
                10                  15                  20

ggg cgc act ccc cct agg gat gca agc acc cgc ttg atc ctc act gaa   211
Gly Arg Thr Pro Pro Arg Asp Ala Ser Thr Arg Leu Ile Leu Thr Glu
            25                  30                  35

cta atg gtc aac tcc acc aac atg ggc agt tct gat ggt ttt gag tat   259
Leu Met Val Asn Ser Thr Asn Met Gly Ser Ser Asp Gly Phe Glu Tyr
        40                  45                  50

gtg gaa atc acc aac act act gcc gaa ccc atc gat ttt tcc gat tac   307
Val Glu Ile Thr Asn Thr Thr Ala Glu Pro Ile Asp Phe Ser Asp Tyr
    55                  60                  65

acc ttg aac tac ctg tac ccg cag gat gag ttc acc aac acc aac gaa   355
Thr Leu Asn Tyr Leu Tyr Pro Gln Asp Glu Phe Thr Asn Thr Asn Glu
70                  75                  80                  85

gcc gtc tgg gct gcg gaa cct ggt gat gtc att att cag cct gga aaa   403
Ala Val Trp Ala Ala Glu Pro Gly Asp Val Ile Ile Gln Pro Gly Lys
                90                  95                  100

tct ctc gtg ttt tgg atc aaa aat ggc ccc aat gat gag gca acc gca   451
Ser Leu Val Phe Trp Ile Lys Asn Gly Pro Asn Asp Glu Ala Thr Ala
            105                 110                 115

gca gat ttc aat gca gaa tat ggc acc aac ctg gag gct gga aaa gac   499
Ala Asp Phe Asn Ala Glu Tyr Gly Thr Asn Leu Glu Ala Gly Lys Asp
        120                 125                 130

ctt gtt gaa atc tcc tca ggt ggg atg gcc aat ggt act gcc aga gga   547
Leu Val Glu Ile Ser Ser Gly Gly Met Ala Asn Gly Thr Ala Arg Gly
    135                 140                 145

atg cag att cag acc aac act ggc cac ata gtc aac cgt ggt ttc tac   595
Met Gln Ile Gln Thr Asn Thr Gly His Ile Val Asn Arg Gly Phe Tyr
150                 155                 160                 165

aac atg gct ggc gct tct gat gtg aaa gcc aac gag ggt ctt cat ttc   643
Asn Met Ala Gly Ala Ser Asp Val Lys Ala Asn Glu Gly Leu His Phe
                170                 175                 180

gca gtg gat gag tct gat ctt ctg aag caa acg ctt gtc ggc agc ggt   691
Ala Val Asp Glu Ser Asp Leu Leu Lys Gln Thr Leu Val Gly Ser Gly
            185                 190                 195

gcg cca acc ccg ggc act gtg tac act tcg cag att cct aat cca ctg   739
Ala Pro Thr Pro Gly Thr Val Tyr Thr Ser Gln Ile Pro Asn Pro Leu
        200                 205                 210

tct gcc gtt atc gct gat tct tct gta cca ctc atc aca gat aat acc   787
Ser Ala Val Ile Ala Asp Ser Ser Val Pro Leu Ile Thr Asp Asn Thr
    215                 220                 225

gca acc agt atc aac cct gcg gag ccg ttt acc ttc gcc ttc aaa tat   835
Ala Thr Ser Ile Asn Pro Ala Glu Pro Phe Thr Phe Ala Phe Lys Tyr
230                 235                 240                 245
```

cac cga tgatgtccag gtgcgcacgg caa 864
His Arg

<210> 704
<211> 247
<212> PRT
<213> Corynebacterium glutamicum

<400> 704
Leu Ile Pro Gly Gly Leu Asp Thr Pro Glu Glu Pro Glu Ala Pro Glu
1 5 10 15

Asp Ser Leu Phe Glu Gly Arg Thr Pro Pro Arg Asp Ala Ser Thr Arg
20 25 30

Leu Ile Leu Thr Glu Leu Met Val Asn Ser Thr Asn Met Gly Ser Ser
35 40 45

Asp Gly Phe Glu Tyr Val Glu Ile Thr Asn Thr Thr Ala Glu Pro Ile
50 55 60

Asp Phe Ser Asp Tyr Thr Leu Asn Tyr Leu Tyr Pro Gln Asp Glu Phe
65 70 75 80

Thr Asn Thr Asn Glu Ala Val Trp Ala Ala Glu Pro Gly Asp Val Ile
85 90 95

Ile Gln Pro Gly Lys Ser Leu Val Phe Trp Ile Lys Asn Gly Pro Asn
100 105 110

Asp Glu Ala Thr Ala Ala Asp Phe Asn Ala Glu Tyr Gly Thr Asn Leu
115 120 125

Glu Ala Gly Lys Asp Leu Val Glu Ile Ser Ser Gly Gly Met Ala Asn
130 135 140

Gly Thr Ala Arg Gly Met Gln Ile Gln Thr Asn Thr Gly His Ile Val
145 150 155 160

Asn Arg Gly Phe Tyr Asn Met Ala Gly Ala Ser Asp Val Lys Ala Asn
165 170 175

Glu Gly Leu His Phe Ala Val Asp Glu Ser Asp Leu Leu Lys Gln Thr
180 185 190

Leu Val Gly Ser Gly Ala Pro Thr Pro Gly Thr Val Tyr Thr Ser Gln
195 200 205

Ile Pro Asn Pro Leu Ser Ala Val Ile Ala Asp Ser Ser Val Pro Leu
210 215 220

Ile Thr Asp Asn Thr Ala Thr Ser Ile Asn Pro Ala Glu Pro Phe Thr
225 230 235 240

Phe Ala Phe Lys Tyr His Arg
245

<210> 705

<211> 1293
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1270)
<223> RXN01647

<400> 705
gctgggggaa tacatggctg aaggcatgtt gatgcccacg acatcggcgc aggtgtcggg 60

```
gcataaattt ctggtgcggc gcatcgaaca tgggttggtg atg ggc gat gtg cgc   115
                                              Met Gly Asp Val Arg
                                                1               5

atg att cat gat cca ctt ggt agg cgc cgg cgg gcg ttg gtg ttt ggg   163
Met Ile His Asp Pro Leu Gly Arg Arg Arg Arg Ala Leu Val Phe Gly
                10                  15                  20

gtg gtg gcg tgc gtg atg ttg gcg gtg gga tca ttg gcg ttg gct att   211
Val Val Ala Cys Val Met Leu Ala Val Gly Ser Leu Ala Leu Ala Ile
            25                  30                  35

ttt cga ccc gcg aag gat ccg gcc gat gcg ccg ttg atc cgc tct gaa   259
Phe Arg Pro Ala Lys Asp Pro Ala Asp Ala Pro Leu Ile Arg Ser Glu
        40                  45                  50

tcc ggc gcg ctc ttt gtg cag ctg gat ggg tcg gtg cat ccg gtg gct   307
Ser Gly Ala Leu Phe Val Gln Leu Asp Gly Ser Val His Pro Val Ala
    55                  60                  65

aat gtg gcc tcg gct cgg ttg att gtg ggg gag ccg gtg gat ccg gtg   355
Asn Val Ala Ser Ala Arg Leu Ile Val Gly Glu Pro Val Asp Pro Val
70                  75                  80                  85

aac gcc agc gat gcg atc atc gcg ggc atg ccg cgc gga gtg ccg gtg   403
Asn Ala Ser Asp Ala Ile Ile Ala Gly Met Pro Arg Gly Val Pro Val
                90                  95                  100

ggg gtt cct gat gcg ccg ggg ctt ttc agc agc acc gaa gaa ccc gag   451
Gly Val Pro Asp Ala Pro Gly Leu Phe Ser Ser Thr Glu Glu Pro Glu
            105                 110                 115

caa gat tgg ttt gtg tgc cag gat gtc ggc act ggg gat cta cac att   499
Gln Asp Trp Phe Val Cys Gln Asp Val Gly Thr Gly Asp Leu His Ile
        120                 125                 130

acg gtt cct agg ggc gga cta ggg ccc acc ctg att gcg gaa gga aat   547
Thr Val Pro Arg Gly Gly Leu Gly Pro Thr Leu Ile Ala Glu Gly Asn
    135                 140                 145

ggg tgg ctg ggg gcg tcg aaa agc gaa acc ggc gag gtc acc tgg aac   595
Gly Trp Leu Gly Ala Ser Lys Ser Glu Thr Gly Glu Val Thr Trp Asn
150                 155                 160                 165

ctg att acc gcg gac ggg cgc cgc gaa ctg ccg gcg tgg ggc agc gaa   643
Leu Ile Thr Ala Asp Gly Arg Arg Glu Leu Pro Ala Trp Gly Ser Glu
                170                 175                 180

cat ggg cgc att atg cgc cgc cac ctg ggg att tcc gag gac acc ccg   691
```

```
His Gly Arg Ile Met Arg Arg His Leu Gly Ile Ser Glu Asp Thr Pro
            185                 190                 195

cgc gta tac ctg acc act gag ctg ctc aac gcg atc ccc gag cac gac   739
Arg Val Tyr Leu Thr Thr Glu Leu Leu Asn Ala Ile Pro Glu His Asp
        200                 205                 210

gcg gtc cgc ttc cca gcc ccg ctg ccc gag ctt gtc gac gcc tcc acc   787
Ala Val Arg Phe Pro Ala Pro Leu Pro Glu Leu Val Asp Ala Ser Thr
    215                 220                 225

cgc aac tgg tta cgg ctc gac ggg gcg ctc gcc gaa atc acg ccg cta   835
Arg Asn Trp Leu Arg Leu Asp Gly Ala Leu Ala Glu Ile Thr Pro Leu
230                 235                 240                 245

cag cgc ggg ttg ctt atc gac gcc ggt tcc ggt gtt ttc ccc gac ccc   883
Gln Arg Gly Leu Leu Ile Asp Ala Gly Ser Gly Val Phe Pro Asp Pro
                250                 255                 260

acc gcg ctt ctt ggt gtg cat gaa gaa aca gcc aac acc ttg acg ctg   931
Thr Ala Leu Leu Gly Val His Glu Glu Thr Ala Asn Thr Leu Thr Leu
            265                 270                 275

ccc gag caa aca gtt tct tgg caa gat ctg gac ggt ggt ttt gcc tgc   979
Pro Glu Gln Thr Val Ser Trp Gln Asp Leu Asp Gly Gly Phe Ala Cys
        280                 285                 290

gcg gat ggt gaa ggc cag atc ggt ttc ctg gaa act ctg gaa tcg ggg   1027
Ala Asp Gly Glu Gly Gln Ile Gly Phe Leu Glu Thr Leu Glu Ser Gly
    295                 300                 305

gtg gcg cta tct ggt gat tcc agg gcg aaa agt ttc agc aca aac gct   1075
Val Ala Leu Ser Gly Asp Ser Arg Ala Lys Ser Phe Ser Thr Asn Ala
310                 315                 320                 325

ggt ggg gca gtg ggc gtg gac agt ggc ttt ggc tac tat gtg gtc tct   1123
Gly Gly Ala Val Gly Val Asp Ser Gly Phe Gly Tyr Tyr Val Val Ser
                330                 335                 340

gat ttt ggg ctg atg cac cct gtt tct act ggt gaa tcg atg gtt gcc   1171
Asp Phe Gly Leu Met His Pro Val Ser Thr Gly Glu Ser Met Val Ala
            345                 350                 355

cta gga atc act gac gtg cag gtc gtg ccg tgg agc gtg ctg cga ttg   1219
Leu Gly Ile Thr Asp Val Gln Val Val Pro Trp Ser Val Leu Arg Leu
        360                 365                 370

ttg ccg cag gga agt gaa tta gca aaa gag aca gcg ctc gcg ccc acc   1267
Leu Pro Gln Gly Ser Glu Leu Ala Lys Glu Thr Ala Leu Ala Pro Thr
    375                 380                 385

tat taaggagtat ggtggcctta cat                                    1293
Tyr
390
```

<210> 706
<211> 390
<212> PRT
<213> Corynebacterium glutamicum

<400> 706

```
Met Gly Asp Val Arg Met Ile His Asp Pro Leu Gly Arg Arg Arg Arg
 1               5                  10                  15

Ala Leu Val Phe Gly Val Val Ala Cys Val Met Leu Ala Val Gly Ser
            20                  25                  30

Leu Ala Leu Ala Ile Phe Arg Pro Ala Lys Asp Pro Ala Asp Ala Pro
        35                  40                  45

Leu Ile Arg Ser Glu Ser Gly Ala Leu Phe Val Gln Leu Asp Gly Ser
    50                  55                  60

Val His Pro Val Ala Asn Val Ala Ser Ala Arg Leu Ile Val Gly Glu
65                  70                  75                  80

Pro Val Asp Pro Val Asn Ala Ser Asp Ala Ile Ile Ala Gly Met Pro
                85                  90                  95

Arg Gly Val Pro Val Gly Val Pro Asp Ala Pro Gly Leu Phe Ser Ser
            100                 105                 110

Thr Glu Glu Pro Glu Gln Asp Trp Phe Val Cys Gln Asp Val Gly Thr
        115                 120                 125

Gly Asp Leu His Ile Thr Val Pro Arg Gly Gly Leu Gly Pro Thr Leu
    130                 135                 140

Ile Ala Glu Gly Asn Gly Trp Leu Gly Ala Ser Lys Ser Glu Thr Gly
145                 150                 155                 160

Glu Val Thr Trp Asn Leu Ile Thr Ala Asp Gly Arg Arg Glu Leu Pro
                165                 170                 175

Ala Trp Gly Ser Glu His Gly Arg Ile Met Arg Arg His Leu Gly Ile
            180                 185                 190

Ser Glu Asp Thr Pro Arg Val Tyr Leu Thr Thr Glu Leu Leu Asn Ala
        195                 200                 205

Ile Pro Glu His Asp Ala Val Arg Phe Pro Ala Pro Leu Pro Glu Leu
    210                 215                 220

Val Asp Ala Ser Thr Arg Asn Trp Leu Arg Leu Asp Gly Ala Leu Ala
225                 230                 235                 240

Glu Ile Thr Pro Leu Gln Arg Gly Leu Leu Ile Asp Ala Gly Ser Gly
                245                 250                 255

Val Phe Pro Asp Pro Thr Ala Leu Leu Gly Val His Glu Glu Thr Ala
            260                 265                 270

Asn Thr Leu Thr Leu Pro Glu Gln Thr Val Ser Trp Gln Asp Leu Asp
        275                 280                 285

Gly Gly Phe Ala Cys Ala Asp Gly Glu Gly Gln Ile Gly Phe Leu Glu
    290                 295                 300

Thr Leu Glu Ser Gly Val Ala Leu Ser Gly Asp Ser Arg Ala Lys Ser
305                 310                 315                 320
```

```
Phe Ser Thr Asn Ala Gly Gly Ala Val Gly Val Asp Ser Gly Phe Gly
                325                 330                 335

Tyr Tyr Val Val Ser Asp Phe Gly Leu Met His Pro Val Ser Thr Gly
            340                 345                 350

Glu Ser Met Val Ala Leu Gly Ile Thr Asp Val Gln Val Val Pro Trp
        355                 360                 365

Ser Val Leu Arg Leu Leu Pro Gln Gly Ser Glu Leu Ala Lys Glu Thr
    370                 375                 380

Ala Leu Ala Pro Thr Tyr
385                 390


<210> 707
<211> 911
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(888)
<223> FRXA01647

<400> 707
atg ccg cgc gga gtg ccg gtg ggg gtt cct gat gcg ccg ggg ctt ttc   48
Met Pro Arg Gly Val Pro Val Gly Val Pro Asp Ala Pro Gly Leu Phe
  1               5                  10                  15

agc agc acc gaa gaa ccc gag caa gat tgg ttt gtg tgc cag gat gtc   96
Ser Ser Thr Glu Glu Pro Glu Gln Asp Trp Phe Val Cys Gln Asp Val
             20                  25                  30

ggc act ggg gat cta cac att acg gtt cct agg ggc gga cta ggg ccc   144
Gly Thr Gly Asp Leu His Ile Thr Val Pro Arg Gly Gly Leu Gly Pro
         35                  40                  45

acc ctg att gcg gaa gga aat ggg tgg ctg ggg gcg tcg aaa agc gaa   192
Thr Leu Ile Ala Glu Gly Asn Gly Trp Leu Gly Ala Ser Lys Ser Glu
     50                  55                  60

acc ggc gag gtc acc tgg aac ctg att acc gcg gac ggg cgc cgc gaa   240
Thr Gly Glu Val Thr Trp Asn Leu Ile Thr Ala Asp Gly Arg Arg Glu
 65                  70                  75                  80

ctg ccg gcg tgg ggc agc gaa cat ggg cgc att atg cgc cgc cac ctg   288
Leu Pro Ala Trp Gly Ser Glu His Gly Arg Ile Met Arg Arg His Leu
                 85                  90                  95

ggg att tcc gag gac acc ccg cgc gta tac ctg acc act gag ctg ctc   336
Gly Ile Ser Glu Asp Thr Pro Arg Val Tyr Leu Thr Thr Glu Leu Leu
            100                 105                 110

aac gcg atc ccc gag cac gac gcg gtc cgc ttc cca gcc ccg ctg ccc   384
Asn Ala Ile Pro Glu His Asp Ala Val Arg Phe Pro Ala Pro Leu Pro
        115                 120                 125

gag ctt gtc gac gcc tcc acc cgc aac tgg tta cgg ctc gac ggg gcg   432
Glu Leu Val Asp Ala Ser Thr Arg Asn Trp Leu Arg Leu Asp Gly Ala
```

```
    130                 135                 140

ctc gcc gaa atc acg ccg cta cag cgc ggg ttg ctt atc gac gcc ggt   480
Leu Ala Glu Ile Thr Pro Leu Gln Arg Gly Leu Leu Ile Asp Ala Gly
145                 150                 155                 160

tcc ggt gtt ttc ccc gac ccc acc gcg ctt ctt ggt gtg cat gaa gaa   528
Ser Gly Val Phe Pro Asp Pro Thr Ala Leu Leu Gly Val His Glu Glu
                165                 170                 175

aca gcc aac acc ttg acg ctg ccc gag caa aca gtt tct tgg caa gat   576
Thr Ala Asn Thr Leu Thr Leu Pro Glu Gln Thr Val Ser Trp Gln Asp
            180                 185                 190

ctg gac ggt ggt ttt gcc tgc gcg gat ggt gaa ggc cag atc ggt ttc   624
Leu Asp Gly Gly Phe Ala Cys Ala Asp Gly Glu Gly Gln Ile Gly Phe
        195                 200                 205

ctg gaa act ctg gaa tcg ggg gtg gcg cta tct ggt gat tcc agg gcg   672
Leu Glu Thr Leu Glu Ser Gly Val Ala Leu Ser Gly Asp Ser Arg Ala
    210                 215                 220

aaa agt ttc agc aca aac gct ggt ggg gca gtg ggc gtg gac agt ggc   720
Lys Ser Phe Ser Thr Asn Ala Gly Gly Ala Val Gly Val Asp Ser Gly
225                 230                 235                 240

ttt ggc tac tat gtg gtc tct gat ttt ggg ctg atg cac cct gtt tct   768
Phe Gly Tyr Tyr Val Val Ser Asp Phe Gly Leu Met His Pro Val Ser
                245                 250                 255

act ggt gaa tcg atg gtt gcc cta gga atc act gac gtg cag gtc gtg   816
Thr Gly Glu Ser Met Val Ala Leu Gly Ile Thr Asp Val Gln Val Val
            260                 265                 270

ccg tgg agc gtg ctg cga ttg ttg ccg cag gga agt gaa tta gca aaa   864
Pro Trp Ser Val Leu Arg Leu Leu Pro Gln Gly Ser Glu Leu Ala Lys
        275                 280                 285

gag aca gcg ctc gcg ccc acc tat taaggagtat ggtggcctta cat         911
Glu Thr Ala Leu Ala Pro Thr Tyr
    290                 295
```

<210> 708
<211> 296
<212> PRT
<213> Corynebacterium glutamicum

<400> 708

```
Met Pro Arg Gly Val Pro Val Gly Val Pro Asp Ala Pro Gly Leu Phe
  1               5                  10                  15

Ser Ser Thr Glu Glu Pro Glu Gln Asp Trp Phe Val Cys Gln Asp Val
             20                  25                  30

Gly Thr Gly Asp Leu His Ile Thr Val Pro Arg Gly Gly Leu Gly Pro
         35                  40                  45

Thr Leu Ile Ala Glu Gly Asn Gly Trp Leu Gly Ala Ser Lys Ser Glu
     50                  55                  60
```

```
Thr Gly Glu Val Thr Trp Asn Leu Ile Thr Ala Asp Gly Arg Arg Glu
 65                  70                  75                  80

Leu Pro Ala Trp Gly Ser Glu His Gly Arg Ile Met Arg Arg His Leu
                85                  90                  95

Gly Ile Ser Glu Asp Thr Pro Arg Val Tyr Leu Thr Thr Glu Leu Leu
            100                 105                 110

Asn Ala Ile Pro Glu His Asp Ala Val Arg Phe Pro Ala Pro Leu Pro
        115                 120                 125

Glu Leu Val Asp Ala Ser Thr Arg Asn Trp Leu Arg Leu Asp Gly Ala
    130                 135                 140

Leu Ala Glu Ile Thr Pro Leu Gln Arg Gly Leu Leu Ile Asp Ala Gly
145                 150                 155                 160

Ser Gly Val Phe Pro Asp Pro Thr Ala Leu Leu Gly Val His Glu Glu
                165                 170                 175

Thr Ala Asn Thr Leu Thr Leu Pro Glu Gln Thr Val Ser Trp Gln Asp
            180                 185                 190

Leu Asp Gly Gly Phe Ala Cys Ala Asp Gly Glu Gly Gln Ile Gly Phe
        195                 200                 205

Leu Glu Thr Leu Glu Ser Gly Val Ala Leu Ser Gly Asp Ser Arg Ala
    210                 215                 220

Lys Ser Phe Ser Thr Asn Ala Gly Gly Ala Val Gly Val Asp Ser Gly
225                 230                 235                 240

Phe Gly Tyr Tyr Val Val Ser Asp Phe Gly Leu Met His Pro Val Ser
                245                 250                 255

Thr Gly Glu Ser Met Val Ala Leu Gly Ile Thr Asp Val Gln Val Val
            260                 265                 270

Pro Trp Ser Val Leu Arg Leu Leu Pro Gln Gly Ser Glu Leu Ala Lys
        275                 280                 285

Glu Thr Ala Leu Ala Pro Thr Tyr
    290                 295
```

<210> 709
<211> 1856
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1833)
<223> RXN01658

<400> 709

```
gat cca cag atc ctg tca cca acc ttc acc cag caa cag cag ctg cga   48
Asp Pro Gln Ile Leu Ser Pro Thr Phe Thr Gln Gln Gln Gln Leu Arg
  1               5                  10                  15
```

```
aac ttc tac ggt ttc cca gac cag ctg gcg atg gac cgc ttt gaa gta   96
Asn Phe Tyr Gly Phe Pro Asp Gln Leu Ala Met Asp Arg Phe Glu Val
             20                  25                  30

gat ggc aaa ctc cgc gac ttt gtt gtg gca gca cgt gag ctc gat cca   144
Asp Gly Lys Leu Arg Asp Phe Val Val Ala Ala Arg Glu Leu Asp Pro
         35                  40                  45

aac gcc ctg cag caa aac cag cag gac tgg att aac cgt cac act gtt   192
Asn Ala Leu Gln Gln Asn Gln Gln Asp Trp Ile Asn Arg His Thr Val
     50                  55                  60

tat acc cac ggc aac ggc ttc att gca gct caa gca aac cag gtg gat   240
Tyr Thr His Gly Asn Gly Phe Ile Ala Ala Gln Ala Asn Gln Val Asp
 65                  70                  75                  80

gag gtc gcc cgc gac gtc gga tcc act cgt ggt ggt tac cct gtc tac   288
Glu Val Ala Arg Asp Val Gly Ser Thr Arg Gly Gly Tyr Pro Val Tyr
                 85                  90                  95

acc gtc tct gat ttg cag tcg aat gct cgt gct gca gaa agc gaa gat   336
Thr Val Ser Asp Leu Gln Ser Asn Ala Arg Ala Ala Glu Ser Glu Asp
            100                 105                 110

gct gag gag ctt ggc atc aag gtt gat gag cct cgt gtg tac tac gga   384
Ala Glu Glu Leu Gly Ile Lys Val Asp Glu Pro Arg Val Tyr Tyr Gly
        115                 120                 125

cca ctg att gct tct gcg act gat ggt gct gac tac gca att gtc ggt   432
Pro Leu Ile Ala Ser Ala Thr Asp Gly Ala Asp Tyr Ala Ile Val Gly
    130                 135                 140

gac acc ggc gat ggc cca gtc gag tac gac act gac acc tcc agc tac   480
Asp Thr Gly Asp Gly Pro Val Glu Tyr Asp Thr Asp Thr Ser Ser Tyr
145                 150                 155                 160

acc tac gaa ggt gct ggc ggc gtg gac att gga aac atg gtc aac cgt   528
Thr Tyr Glu Gly Ala Gly Gly Val Asp Ile Gly Asn Met Val Asn Arg
                165                 170                 175

gcg atg ttt gca ttg cgc tac cag gaa atg aac atg ctc ctg tct gat   576
Ala Met Phe Ala Leu Arg Tyr Gln Glu Met Asn Met Leu Leu Ser Asp
            180                 185                 190

cgt gtt ggt tcc gaa tcc aag atc cta ttt gag cgc gat cct cgt tcc   624
Arg Val Gly Ser Glu Ser Lys Ile Leu Phe Glu Arg Asp Pro Arg Ser
        195                 200                 205

cgt gtg gaa aag gtt gca cct tgg ttg acc act gac tcc aag acc tac   672
Arg Val Glu Lys Val Ala Pro Trp Leu Thr Thr Asp Ser Lys Thr Tyr
    210                 215                 220

cca act gtg att gat ggt cgc atc aag tgg atc gtc gat ggc tac acc   720
Pro Thr Val Ile Asp Gly Arg Ile Lys Trp Ile Val Asp Gly Tyr Thr
225                 230                 235                 240

acc ttg gat agt ctt ccg tac tcc acg cgc acc tca ctg acg gaa gcg   768
Thr Leu Asp Ser Leu Pro Tyr Ser Thr Arg Thr Ser Leu Thr Glu Ala
                245                 250                 255

act cag gat gct gtc atg cct gac ggc acc cca cag cca ctg atc aca   816
```

```
Thr Gln Asp Ala Val Met Pro Asp Gly Thr Pro Gln Pro Leu Ile Thr
            260                 265                 270

gat agg gtc ggt tac atc cgc aac tcc gtg aag gct gtt gtt gat gcg   864
Asp Arg Val Gly Tyr Ile Arg Asn Ser Val Lys Ala Val Val Asp Ala
        275                 280                 285

tac gac gga act gtt gaa ctc tac gaa ttc gac acc gaa gat cct gtt   912
Tyr Asp Gly Thr Val Glu Leu Tyr Glu Phe Asp Thr Glu Asp Pro Val
    290                 295                 300

ctg aag gca tgg cgt ggc gtg ttc cca gac acc gtg aag gac ggg tcg   960
Leu Lys Ala Trp Arg Gly Val Phe Pro Asp Thr Val Lys Asp Gly Ser
305                 310                 315                 320

gag att tcc gat gag ctt cgc gca cac ctg cgt tac cca gaa gat ttg   1008
Glu Ile Ser Asp Glu Leu Arg Ala His Leu Arg Tyr Pro Glu Asp Leu
                325                 330                 335

ttc aag gtc cag cgt gac atg ctg gcc aag tac aac gtt gat gat tct   1056
Phe Lys Val Gln Arg Asp Met Leu Ala Lys Tyr Asn Val Asp Asp Ser
            340                 345                 350

gga aca ttc ttc acc aac gat gcg ttc tgg tct gtc cca ggt gac cca   1104
Gly Thr Phe Phe Thr Asn Asp Ala Phe Trp Ser Val Pro Gly Asp Pro
        355                 360                 365

act gca gcg gag ggc cgc cag gaa ctt aag cag cct cct tac tac gtg   1152
Thr Ala Ala Glu Gly Arg Gln Glu Leu Lys Gln Pro Pro Tyr Tyr Val
    370                 375                 380

gtg gca gca gac cca gag acc ggt gag tcc agc ttc cag ctg atc acc   1200
Val Ala Ala Asp Pro Glu Thr Gly Glu Ser Ser Phe Gln Leu Ile Thr
385                 390                 395                 400

ccg ttc cgt gga ctt cag cgc gag tac ctc tct gca cac atg tct gcg   1248
Pro Phe Arg Gly Leu Gln Arg Glu Tyr Leu Ser Ala His Met Ser Ala
                405                 410                 415

tcg tct gat cca gtt acc tac ggt gaa atc act gtt cgt gtg ctg cct   1296
Ser Ser Asp Pro Val Thr Tyr Gly Glu Ile Thr Val Arg Val Leu Pro
            420                 425                 430

acc gat tct gtg acc cag ggt cca aag cag gcc cag gat gcg atg atg   1344
Thr Asp Ser Val Thr Gln Gly Pro Lys Gln Ala Gln Asp Ala Met Met
        435                 440                 445

tca tct gac cag gtt gct cag gac caa aca ctg tgg cgt gga tcg aac   1392
Ser Ser Asp Gln Val Ala Gln Asp Gln Thr Leu Trp Arg Gly Ser Asn
    450                 455                 460

gat ctg cac aac gga aac ctg ttg acc ttg cca gtt ggt ggc gga gag   1440
Asp Leu His Asn Gly Asn Leu Leu Thr Leu Pro Val Gly Gly Gly Glu
465                 470                 475                 480

atc ctc tac gtt gag ccg att tac tcg cag cgc aag gat cag gca tcg   1488
Ile Leu Tyr Val Glu Pro Ile Tyr Ser Gln Arg Lys Asp Gln Ala Ser
                485                 490                 495

gcc ttc ccg aag ctt ctg cgc gtg ctg gtc ttc tac aag ggt cag gtt   1536
Ala Phe Pro Lys Leu Leu Arg Val Leu Val Phe Tyr Lys Gly Gln Val
```

```
            500                 505                 510

ggt tac gca cca acg atc gct gaa gcc cta tcg cag gtc ggc att gat   1584
Gly Tyr Ala Pro Thr Ile Ala Glu Ala Leu Ser Gln Val Gly Ile Asp
        515                 520                 525

ccg aag gaa gcg cag gac atc gaa gag gta gat ggc acc gct acg acg   1632
Pro Lys Glu Ala Gln Asp Ile Glu Glu Val Asp Gly Thr Ala Thr Thr
    530                 535                 540

cca tcg act gat gag act gac act gac act gat cag cct gca acc gaa   1680
Pro Ser Thr Asp Glu Thr Asp Thr Asp Thr Asp Gln Pro Ala Thr Glu
545                 550                 555                 560

acc cca act gca cca gtg agt gag gcg gaa gga atc gcg gcc atc aac   1728
Thr Pro Thr Ala Pro Val Ser Glu Ala Glu Gly Ile Ala Ala Ile Asn
                565                 570                 575

gat gcg ttg agc aac ctt gaa gct gct cgc gat agc tct ttc gaa gag   1776
Asp Ala Leu Ser Asn Leu Glu Ala Ala Arg Asp Ser Ser Phe Glu Glu
            580                 585                 590

tat ggt cgt gca ctc gat gcg ctt gat cgt gcc gtc gat agc tac cag   1824
Tyr Gly Arg Ala Leu Asp Ala Leu Asp Arg Ala Val Asp Ser Tyr Gln
        595                 600                 605

tcc gca cag tagcgtttga gtaaacagcc cga                            1856
Ser Ala Gln
    610


<210> 710
<211> 611
<212> PRT
<213> Corynebacterium glutamicum

<400> 710
Asp Pro Gln Ile Leu Ser Pro Thr Phe Thr Gln Gln Gln Gln Leu Arg
  1               5                  10                  15

Asn Phe Tyr Gly Phe Pro Asp Gln Leu Ala Met Asp Arg Phe Glu Val
             20                  25                  30

Asp Gly Lys Leu Arg Asp Phe Val Val Ala Ala Arg Glu Leu Asp Pro
         35                  40                  45

Asn Ala Leu Gln Gln Asn Gln Gln Asp Trp Ile Asn Arg His Thr Val
     50                  55                  60

Tyr Thr His Gly Asn Gly Phe Ile Ala Ala Gln Ala Asn Gln Val Asp
 65                  70                  75                  80

Glu Val Ala Arg Asp Val Gly Ser Thr Arg Gly Gly Tyr Pro Val Tyr
                 85                  90                  95

Thr Val Ser Asp Leu Gln Ser Asn Ala Arg Ala Ala Glu Ser Glu Asp
            100                 105                 110

Ala Glu Glu Leu Gly Ile Lys Val Asp Glu Pro Arg Val Tyr Tyr Gly
        115                 120                 125
```

```
Pro Leu Ile Ala Ser Ala Thr Asp Gly Ala Asp Tyr Ala Ile Val Gly
    130                 135                 140

Asp Thr Gly Asp Gly Pro Val Glu Tyr Asp Thr Asp Thr Ser Ser Tyr
145                 150                 155                 160

Thr Tyr Glu Gly Ala Gly Gly Val Asp Ile Gly Asn Met Val Asn Arg
                165                 170                 175

Ala Met Phe Ala Leu Arg Tyr Gln Glu Met Asn Met Leu Leu Ser Asp
            180                 185                 190

Arg Val Gly Ser Glu Ser Lys Ile Leu Phe Glu Arg Asp Pro Arg Ser
        195                 200                 205

Arg Val Glu Lys Val Ala Pro Trp Leu Thr Thr Asp Ser Lys Thr Tyr
    210                 215                 220

Pro Thr Val Ile Asp Gly Arg Ile Lys Trp Ile Val Asp Gly Tyr Thr
225                 230                 235                 240

Thr Leu Asp Ser Leu Pro Tyr Ser Thr Arg Thr Ser Leu Thr Glu Ala
                245                 250                 255

Thr Gln Asp Ala Val Met Pro Asp Gly Thr Pro Gln Pro Leu Ile Thr
            260                 265                 270

Asp Arg Val Gly Tyr Ile Arg Asn Ser Val Lys Ala Val Val Asp Ala
        275                 280                 285

Tyr Asp Gly Thr Val Glu Leu Tyr Glu Phe Asp Thr Glu Asp Pro Val
    290                 295                 300

Leu Lys Ala Trp Arg Gly Val Phe Pro Asp Thr Val Lys Asp Gly Ser
305                 310                 315                 320

Glu Ile Ser Asp Glu Leu Arg Ala His Leu Arg Tyr Pro Glu Asp Leu
                325                 330                 335

Phe Lys Val Gln Arg Asp Met Leu Ala Lys Tyr Asn Val Asp Asp Ser
            340                 345                 350

Gly Thr Phe Phe Thr Asn Asp Ala Phe Trp Ser Val Pro Gly Asp Pro
        355                 360                 365

Thr Ala Ala Glu Gly Arg Gln Glu Leu Lys Gln Pro Pro Tyr Tyr Val
    370                 375                 380

Val Ala Ala Asp Pro Glu Thr Gly Glu Ser Ser Phe Gln Leu Ile Thr
385                 390                 395                 400

Pro Phe Arg Gly Leu Gln Arg Glu Tyr Leu Ser Ala His Met Ser Ala
                405                 410                 415

Ser Ser Asp Pro Val Thr Tyr Gly Glu Ile Thr Val Arg Val Leu Pro
            420                 425                 430

Thr Asp Ser Val Thr Gln Gly Pro Lys Gln Ala Gln Asp Ala Met Met
        435                 440                 445

Ser Ser Asp Gln Val Ala Gln Asp Gln Thr Leu Trp Arg Gly Ser Asn
```

```
    450                 455                 460

Asp Leu His Asn Gly Asn Leu Leu Thr Leu Pro Val Gly Gly Gly Glu
465                 470                 475                 480

Ile Leu Tyr Val Glu Pro Ile Tyr Ser Gln Arg Lys Asp Gln Ala Ser
                485                 490                 495

Ala Phe Pro Lys Leu Leu Arg Val Leu Val Phe Tyr Lys Gly Gln Val
            500                 505                 510

Gly Tyr Ala Pro Thr Ile Ala Glu Ala Leu Ser Gln Val Gly Ile Asp
        515                 520                 525

Pro Lys Glu Ala Gln Asp Ile Glu Glu Val Asp Gly Thr Ala Thr Thr
    530                 535                 540

Pro Ser Thr Asp Glu Thr Asp Thr Asp Thr Asp Gln Pro Ala Thr Glu
545                 550                 555                 560

Thr Pro Thr Ala Pro Val Ser Glu Ala Glu Gly Ile Ala Ala Ile Asn
                565                 570                 575

Asp Ala Leu Ser Asn Leu Glu Ala Ala Arg Asp Ser Ser Phe Glu Glu
            580                 585                 590

Tyr Gly Arg Ala Leu Asp Ala Leu Asp Arg Ala Val Asp Ser Tyr Gln
        595                 600                 605

Ser Ala Gln
    610


<210> 711
<211> 1485
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1485)
<223> FRXA01658

<400> 711
gat cca cag atc ctg tca cca acc ttc acc cag caa cag cag ctg cga   48
Asp Pro Gln Ile Leu Ser Pro Thr Phe Thr Gln Gln Gln Leu Arg
  1               5                  10                  15

aac ttc tac ggt ttc cca gac cag ctg gcg atg gac cgc ttt gaa gta   96
Asn Phe Tyr Gly Phe Pro Asp Gln Leu Ala Met Asp Arg Phe Glu Val
             20                  25                  30

gat ggc aaa ctc cgc gac ttt gtt gtg gca gca cgt gag ctc gat cca   144
Asp Gly Lys Leu Arg Asp Phe Val Val Ala Ala Arg Glu Leu Asp Pro
         35                  40                  45

aac gcc ctg cag caa aac cag cag gac tgg att aac cgt cac act gtt   192
Asn Ala Leu Gln Gln Asn Gln Gln Asp Trp Ile Asn Arg His Thr Val
     50                  55                  60

tat acc cac ggc aac ggc ttc att gca gct caa gca aac cag gtg gat   240
```

```
Tyr Thr His Gly Asn Gly Phe Ile Ala Ala Gln Ala Asn Gln Val Asp
 65                  70                  75                  80

gag gtc gcc cgc gac gtc gga tcc act cgt ggt ggt tac cct gtc tac   288
Glu Val Ala Arg Asp Val Gly Ser Thr Arg Gly Gly Tyr Pro Val Tyr
                85                  90                  95

acc gtc tct gat ttg cag tcg aat gct cgt gct gca gaa agc gaa gat   336
Thr Val Ser Asp Leu Gln Ser Asn Ala Arg Ala Ala Glu Ser Glu Asp
            100                 105                 110

gct gag gag ctt ggc atc aag gtt gat gag cct cgt gtg tac tac gga   384
Ala Glu Glu Leu Gly Ile Lys Val Asp Glu Pro Arg Val Tyr Tyr Gly
        115                 120                 125

cca ctg att gct tct gcg act gat ggt gct gac tac gca att gtc ggt   432
Pro Leu Ile Ala Ser Ala Thr Asp Gly Ala Asp Tyr Ala Ile Val Gly
    130                 135                 140

gac acc ggc gat ggc cca gtc gag tac gac act gac acc tcc agc tac   480
Asp Thr Gly Asp Gly Pro Val Glu Tyr Asp Thr Asp Thr Ser Ser Tyr
145                 150                 155                 160

acc tac gaa ggt gct ggc ggc gtg gac att gga aac atg gtc aac cgt   528
Thr Tyr Glu Gly Ala Gly Gly Val Asp Ile Gly Asn Met Val Asn Arg
                165                 170                 175

gcg atg ttt gca ttg cgc tac cag gaa atg aac atg ctc ctg tct gat   576
Ala Met Phe Ala Leu Arg Tyr Gln Glu Met Asn Met Leu Leu Ser Asp
            180                 185                 190

cgt gtt ggt tcc gaa tcc aag atc cta ttt gag cgc gat cct cgt tcc   624
Arg Val Gly Ser Glu Ser Lys Ile Leu Phe Glu Arg Asp Pro Arg Ser
        195                 200                 205

cgt gtg gaa aag gtt gca cct tgg ttg acc act gac tcc aag acc tac   672
Arg Val Glu Lys Val Ala Pro Trp Leu Thr Thr Asp Ser Lys Thr Tyr
    210                 215                 220

cca act gtg att gat ggt cgc atc aag tgg atc gtc gat ggc tac acc   720
Pro Thr Val Ile Asp Gly Arg Ile Lys Trp Ile Val Asp Gly Tyr Thr
225                 230                 235                 240

acc ttg gat agt ctt ccg tac tcc acg cgc acc tca ctg acg gaa gcg   768
Thr Leu Asp Ser Leu Pro Tyr Ser Thr Arg Thr Ser Leu Thr Glu Ala
                245                 250                 255

act cag gat gct gtc atg cct gac ggc acc cca cag cca ctg atc aca   816
Thr Gln Asp Ala Val Met Pro Asp Gly Thr Pro Gln Pro Leu Ile Thr
            260                 265                 270

gat agg gtc ggt tac atc cgc aac tcc gtg aag gct gtt gtt gat gcg   864
Asp Arg Val Gly Tyr Ile Arg Asn Ser Val Lys Ala Val Val Asp Ala
        275                 280                 285

tac gac gga act gtt gaa ctc tac gaa ttc gac acc gaa gat cct gtt   912
Tyr Asp Gly Thr Val Glu Leu Tyr Glu Phe Asp Thr Glu Asp Pro Val
    290                 295                 300

ctg aag gca tgg cgt ggc gtg ttc cca gac acc gtg aag gac ggg tcg   960
Leu Lys Ala Trp Arg Gly Val Phe Pro Asp Thr Val Lys Asp Gly Ser
```

```
305                 310                 315                 320

gag att tcc gat gag ctt cgc gca cac ctg cgt tac cca gaa gat ttg   1008
Glu Ile Ser Asp Glu Leu Arg Ala His Leu Arg Tyr Pro Glu Asp Leu
                325                 330                 335

ttc aag gtc cag cgt gac atg ctg gcc aag tac aac gtt gat gat tct   1056
Phe Lys Val Gln Arg Asp Met Leu Ala Lys Tyr Asn Val Asp Asp Ser
            340                 345                 350

gga aca ttc ttc acc aac gat gcg ttc tgg tct gtc cca ggt gac cca   1104
Gly Thr Phe Phe Thr Asn Asp Ala Phe Trp Ser Val Pro Gly Asp Pro
        355                 360                 365

act gca gcg gag ggc cgc cag gaa ctt aag cag cct cct tac tac gtg   1152
Thr Ala Ala Glu Gly Arg Gln Glu Leu Lys Gln Pro Pro Tyr Tyr Val
    370                 375                 380

gtg gca gca gac cca gag acc ggt gag tcc agc ttc cag ctg atc acc   1200
Val Ala Ala Asp Pro Glu Thr Gly Glu Ser Ser Phe Gln Leu Ile Thr
385                 390                 395                 400

ccg ttc cgt gga ctt cag cgc gag tac ctc tct gca cac atg tct gcg   1248
Pro Phe Arg Gly Leu Gln Arg Glu Tyr Leu Ser Ala His Met Ser Ala
                405                 410                 415

tcg tct gat cca gtt acc tac ggt gaa atc act gtt cgt gtg ctg cct   1296
Ser Ser Asp Pro Val Thr Tyr Gly Glu Ile Thr Val Arg Val Leu Pro
            420                 425                 430

acc gat tct gtg acc cag ggt cca aag cag gcc cag gat gcg atg atg   1344
Thr Asp Ser Val Thr Gln Gly Pro Lys Gln Ala Gln Asp Ala Met Met
        435                 440                 445

tca tct gac cag gtt gct cag gac caa aca ctg tgg cgt gga tcg aac   1392
Ser Ser Asp Gln Val Ala Gln Asp Gln Thr Leu Trp Arg Gly Ser Asn
    450                 455                 460

gat ctg cac aac gga aac ctg ttg acc ttg cca gtt ggt ggc gga gag   1440
Asp Leu His Asn Gly Asn Leu Leu Thr Leu Pro Val Gly Gly Gly Glu
465                 470                 475                 480

atc ctc tac gtt gag ccg att tac tcg cag cgc aag gat cag gca       1485
Ile Leu Tyr Val Glu Pro Ile Tyr Ser Gln Arg Lys Asp Gln Ala
                485                 490                 495
```

<210> 712
<211> 495
<212> PRT
<213> Corynebacterium glutamicum

<400> 712

```
Asp Pro Gln Ile Leu Ser Pro Thr Phe Thr Gln Gln Gln Gln Leu Arg
  1               5                  10                  15

Asn Phe Tyr Gly Phe Pro Asp Gln Leu Ala Met Asp Arg Phe Glu Val
             20                  25                  30

Asp Gly Lys Leu Arg Asp Phe Val Val Ala Ala Arg Glu Leu Asp Pro
         35                  40                  45
```

```
Asn Ala Leu Gln Gln Asn Gln Gln Asp Trp Ile Asn Arg His Thr Val
     50                  55                  60

Tyr Thr His Gly Asn Gly Phe Ile Ala Ala Gln Ala Asn Gln Val Asp
 65                  70                  75                  80

Glu Val Ala Arg Asp Val Gly Ser Thr Arg Gly Gly Tyr Pro Val Tyr
                 85                  90                  95

Thr Val Ser Asp Leu Gln Ser Asn Ala Arg Ala Ala Glu Ser Glu Asp
            100                 105                 110

Ala Glu Glu Leu Gly Ile Lys Val Asp Glu Pro Arg Val Tyr Tyr Gly
        115                 120                 125

Pro Leu Ile Ala Ser Ala Thr Asp Gly Ala Asp Tyr Ala Ile Val Gly
    130                 135                 140

Asp Thr Gly Asp Gly Pro Val Glu Tyr Asp Thr Asp Thr Ser Ser Tyr
145                 150                 155                 160

Thr Tyr Glu Gly Ala Gly Gly Val Asp Ile Gly Asn Met Val Asn Arg
                165                 170                 175

Ala Met Phe Ala Leu Arg Tyr Gln Glu Met Asn Met Leu Leu Ser Asp
            180                 185                 190

Arg Val Gly Ser Glu Ser Lys Ile Leu Phe Glu Arg Asp Pro Arg Ser
        195                 200                 205

Arg Val Glu Lys Val Ala Pro Trp Leu Thr Thr Asp Ser Lys Thr Tyr
    210                 215                 220

Pro Thr Val Ile Asp Gly Arg Ile Lys Trp Ile Val Asp Gly Tyr Thr
225                 230                 235                 240

Thr Leu Asp Ser Leu Pro Tyr Ser Thr Arg Thr Ser Leu Thr Glu Ala
                245                 250                 255

Thr Gln Asp Ala Val Met Pro Asp Gly Thr Pro Gln Pro Leu Ile Thr
            260                 265                 270

Asp Arg Val Gly Tyr Ile Arg Asn Ser Val Lys Ala Val Val Asp Ala
        275                 280                 285

Tyr Asp Gly Thr Val Glu Leu Tyr Glu Phe Asp Thr Glu Asp Pro Val
    290                 295                 300

Leu Lys Ala Trp Arg Gly Val Phe Pro Asp Thr Val Lys Asp Gly Ser
305                 310                 315                 320

Glu Ile Ser Asp Glu Leu Arg Ala His Leu Arg Tyr Pro Glu Asp Leu
                325                 330                 335

Phe Lys Val Gln Arg Asp Met Leu Ala Lys Tyr Asn Val Asp Asp Ser
            340                 345                 350

Gly Thr Phe Phe Thr Asn Asp Ala Phe Trp Ser Val Pro Gly Asp Pro
        355                 360                 365
```

```
Thr Ala Ala Glu Gly Arg Gln Glu Leu Lys Gln Pro Pro Tyr Tyr Val
    370                 375                 380

Val Ala Ala Asp Pro Glu Thr Gly Glu Ser Ser Phe Gln Leu Ile Thr
385                 390                 395                 400

Pro Phe Arg Gly Leu Gln Arg Glu Tyr Leu Ser Ala His Met Ser Ala
                405                 410                 415

Ser Ser Asp Pro Val Thr Tyr Gly Glu Ile Thr Val Arg Val Leu Pro
            420                 425                 430

Thr Asp Ser Val Thr Gln Gly Pro Lys Gln Ala Gln Asp Ala Met Met
        435                 440                 445

Ser Ser Asp Gln Val Ala Gln Asp Gln Thr Leu Trp Arg Gly Ser Asn
    450                 455                 460

Asp Leu His Asn Gly Asn Leu Leu Thr Leu Pro Val Gly Gly Gly Glu
465                 470                 475                 480

Ile Leu Tyr Val Glu Pro Ile Tyr Ser Gln Arg Lys Asp Gln Ala
                485                 490                 495
```

Application Filed

<210> 713
<211> 669
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(646)
<223> RXN01659

<400> 713

```
ttgatgcgcg ccgcggtgag cagcctgccg atccagagcg tgaagaatct gatgatttag 60

tcgagattga taccgtctct ggattccgcc tgctcagtac gtg gcg ggg gtt gcg   115
                                              Val Ala Gly Val Ala
                                                1               5

cag cgt ttt gtc gac gag cgc att cac gtc ggt ttg gat tcc atg cca   163
Gln Arg Phe Val Asp Glu Arg Ile His Val Gly Leu Asp Ser Met Pro
               10                  15                  20

gaa gct gtg act gct gtg tgg atg gaa tct gat tgg gtg ttg gcg gaa   211
Glu Ala Val Thr Ala Val Trp Met Glu Ser Asp Trp Val Leu Ala Glu
           25                  30                  35

acc atc aag ggt tcc acg cct tcc gat tgg gaa gag att ttg cgg ccg   259
Thr Ile Lys Gly Ser Thr Pro Ser Asp Trp Glu Glu Ile Leu Arg Pro
       40                  45                  50

ttg gcg ctg ctc acg gac gcg tct ttc acg ttg cca cct cgt tcc acg   307
Leu Ala Leu Leu Thr Asp Ala Ser Phe Thr Leu Pro Pro Arg Ser Thr
   55                  60                  65

cgt gcg caa acc ttg gat ttg aag cat ttg gaa cca agc cgt ctg aag   355
Arg Ala Gln Thr Leu Asp Leu Lys His Leu Glu Pro Ser Arg Leu Lys
70                  75                  80                  85
```

```
ccg gag cag cca gaa aag cca gcg ttt act ccc aat gct tcg gaa gaa   403
Pro Glu Gln Pro Glu Lys Pro Ala Phe Thr Pro Asn Ala Ser Glu Glu
                 90                  95                 100

gat ttg tct cag ccg ttg gtg atc cgc ccc gag gag ccg ttg cag atg   451
Asp Leu Ser Gln Pro Leu Val Ile Arg Pro Glu Glu Pro Leu Gln Met
            105                 110                 115

ccg gtt cgc ggt gtg cag gaa agc cgc gga gtg gtc gag cca cgg tca   499
Pro Val Arg Gly Val Gln Glu Ser Arg Gly Val Val Glu Pro Arg Ser
        120                 125                 130

ttg ggt gcg gat gat gtg gag tcg att gcg gag ggc gat cca gag cgt   547
Leu Gly Ala Asp Asp Val Glu Ser Ile Ala Glu Gly Asp Pro Glu Arg
    135                 140                 145

ccg agc gat ctt tat ggc acg cgt gtg ctg cgt gat ctc aat ggt cag   595
Pro Ser Asp Leu Tyr Gly Thr Arg Val Leu Arg Asp Leu Asn Gly Gln
150                 155                 160                 165

tcc agt att ttc caa gat tcc acc gac gcg gat gag cca cca aaa aag   643
Ser Ser Ile Phe Gln Asp Ser Thr Asp Ala Asp Glu Pro Pro Lys Lys
                170                 175                 180

tgg tagaaaactg gtgtttttcg gcc                                    669
Trp
```

<210> 714
<211> 182
<212> PRT
<213> Corynebacterium glutamicum

<400> 714

```
Val Ala Gly Val Ala Gln Arg Phe Val Asp Glu Arg Ile His Val Gly
  1               5                  10                  15

Leu Asp Ser Met Pro Glu Ala Val Thr Ala Val Trp Met Glu Ser Asp
             20                  25                  30

Trp Val Leu Ala Glu Thr Ile Lys Gly Ser Thr Pro Ser Asp Trp Glu
         35                  40                  45

Glu Ile Leu Arg Pro Leu Ala Leu Leu Thr Asp Ala Ser Phe Thr Leu
     50                  55                  60

Pro Pro Arg Ser Thr Arg Ala Gln Thr Leu Asp Leu Lys His Leu Glu
 65                  70                  75                  80

Pro Ser Arg Leu Lys Pro Glu Gln Pro Glu Lys Pro Ala Phe Thr Pro
                85                  90                  95

Asn Ala Ser Glu Glu Asp Leu Ser Gln Pro Leu Val Ile Arg Pro Glu
            100                 105                 110

Glu Pro Leu Gln Met Pro Val Arg Gly Val Gln Glu Ser Arg Gly Val
        115                 120                 125

Val Glu Pro Arg Ser Leu Gly Ala Asp Asp Val Glu Ser Ile Ala Glu
```

```
    130                 135                 140

Gly Asp Pro Glu Arg Pro Ser Asp Leu Tyr Gly Thr Arg Val Leu Arg
145                 150                 155                 160

Asp Leu Asn Gly Gln Ser Ser Ile Phe Gln Asp Ser Thr Asp Ala Asp
                165                 170                 175

Glu Pro Pro Lys Lys Trp
            180


<210> 715
<211> 509
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(486)
<223> FRXA01659

<400> 715
cca gaa gct gtg act gct gtg tgg atg gaa tct gat tgg gtg ttg gcg   48
Pro Glu Ala Val Thr Ala Val Trp Met Glu Ser Asp Trp Val Leu Ala
  1               5                  10                  15

gaa acc atc aag ggt tcc acg cct tcc gat tgg gaa gag att ttg cgg   96
Glu Thr Ile Lys Gly Ser Thr Pro Ser Asp Trp Glu Glu Ile Leu Arg
             20                  25                  30

ccg ttg gcg ctg ctc acg gac gcg tct ttc acg ttg cca cct cgt tcc   144
Pro Leu Ala Leu Leu Thr Asp Ala Ser Phe Thr Leu Pro Pro Arg Ser
         35                  40                  45

acg cgt gcg caa acc ttg gat ttg aag cat ttg gaa cca agc cgt ctg   192
Thr Arg Ala Gln Thr Leu Asp Leu Lys His Leu Glu Pro Ser Arg Leu
     50                  55                  60

aag ccg gag cag cca gaa aag cca gcg ttt act ccc aat gct tcg gaa   240
Lys Pro Glu Gln Pro Glu Lys Pro Ala Phe Thr Pro Asn Ala Ser Glu
 65                  70                  75                  80

gaa gat ttg tct cag ccg ttg gtg atc cgc ccc gag gag ccg ttg cag   288
Glu Asp Leu Ser Gln Pro Leu Val Ile Arg Pro Glu Glu Pro Leu Gln
                 85                  90                  95

atg ccg gtt cgc ggt gtg cag gaa agc cgc gga gtg gtc gag cca cgg   336
Met Pro Val Arg Gly Val Gln Glu Ser Arg Gly Val Val Glu Pro Arg
            100                 105                 110

tca ttg ggt gcg gat gat gtg gag tcg att gcg gag ggc gat cca gag   384
Ser Leu Gly Ala Asp Asp Val Glu Ser Ile Ala Glu Gly Asp Pro Glu
        115                 120                 125

cgt ccg agc gat ctt tat ggc acg cgt gtg ctg cgt gat ctc aat ggt   432
Arg Pro Ser Asp Leu Tyr Gly Thr Arg Val Leu Arg Asp Leu Asn Gly
    130                 135                 140

cag tcc agt att ttc caa gat tcc acc gac gcg gat gag cca cca aaa   480
Gln Ser Ser Ile Phe Gln Asp Ser Thr Asp Ala Asp Glu Pro Pro Lys
```

145 150 155 160

aag tgg tagaaaactg gtgtttttcg gcc 509
Lys Trp

<210> 716
<211> 162
<212> PRT
<213> Corynebacterium glutamicum

<400> 716
Pro Glu Ala Val Thr Ala Val Trp Met Glu Ser Asp Trp Val Leu Ala
1 5 10 15

Glu Thr Ile Lys Gly Ser Thr Pro Ser Asp Trp Glu Glu Ile Leu Arg
20 25 30

Pro Leu Ala Leu Leu Thr Asp Ala Ser Phe Thr Leu Pro Pro Arg Ser
35 40 45

Thr Arg Ala Gln Thr Leu Asp Leu Lys His Leu Glu Pro Ser Arg Leu
50 55 60

Lys Pro Glu Gln Pro Glu Lys Pro Ala Phe Thr Pro Asn Ala Ser Glu
65 70 75 80

Glu Asp Leu Ser Gln Pro Leu Val Ile Arg Pro Glu Glu Pro Leu Gln
85 90 95

Met Pro Val Arg Gly Val Gln Glu Ser Arg Gly Val Val Glu Pro Arg
100 105 110

Ser Leu Gly Ala Asp Asp Val Glu Ser Ile Ala Glu Gly Asp Pro Glu
115 120 125

Arg Pro Ser Asp Leu Tyr Gly Thr Arg Val Leu Arg Asp Leu Asn Gly
130 135 140

Gln Ser Ser Ile Phe Gln Asp Ser Thr Asp Ala Asp Glu Pro Pro Lys
145 150 155 160

Lys Trp

<210> 717
<211> 981
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(958)
<223> RXN01663

<400> 717
tattttgctg gttggtcaca gtggagcgct aaccccgaga atcctatcga ggcctaaaat 60

cgtggcttga gtacgcactg ccagtaaggt gtgtgatgtg atg gaa ata agt gtc 115

```
                                                  Met Glu Ile Ser Val
                                                    1               5

ttg atc atc gcc gca ctg atc ttg gtg gca ggc atc gta ctg tgg cgc   163
Leu Ile Ile Ala Ala Leu Ile Leu Val Ala Gly Ile Val Leu Trp Arg
                10                  15                  20

gcg gac tcg tct aaa cag gca gct aaa aag gct gaa tca cct gtg ggc   211
Ala Asp Ser Ser Lys Gln Ala Ala Lys Lys Ala Glu Ser Pro Val Gly
            25                  30                  35

tca gtc gca cct gcg ccc gtg ctg gtt gaa gaa gag ccg gac cct gag   259
Ser Val Ala Pro Ala Pro Val Leu Val Glu Glu Glu Pro Asp Pro Glu
        40                  45                  50

ttt gag cca gaa ctg gac cct gaa cca gaa gcg caa cca gaa cca gag   307
Phe Glu Pro Glu Leu Asp Pro Glu Pro Glu Ala Gln Pro Glu Pro Glu
    55                  60                  65

ctg gaa gtt gcg cct aga ttt gcg cca gaa cca gtt caa gat ctt gag   355
Leu Glu Val Ala Pro Arg Phe Ala Pro Glu Pro Val Gln Asp Leu Glu
70                  75                  80                  85

ccg gat cag gct gag gac att tat ttt gat gat tcc cct gaa ctc gat   403
Pro Asp Gln Ala Glu Asp Ile Tyr Phe Asp Asp Ser Pro Glu Leu Asp
                90                  95                  100

gct gat gtt gaa aat gcc ttg gct gag ctt act gag gta gaa gac tac   451
Ala Asp Val Glu Asn Ala Leu Ala Glu Leu Thr Glu Val Glu Asp Tyr
            105                 110                 115

ccg gaa gag cca gtg cag tct gag caa cct caa gcc cct gcc acg gcg   499
Pro Glu Glu Pro Val Gln Ser Glu Gln Pro Gln Ala Pro Ala Thr Ala
        120                 125                 130

gag gta gct gcg gac gag gag caa cgg ggc gtc gat aag cat tcg ttt   547
Glu Val Ala Ala Asp Glu Glu Gln Arg Gly Val Asp Lys His Ser Phe
    135                 140                 145

ttg agc tct ttg cct ggt tcg cag cgc cgg gag cgc cga aac tgg gcg   595
Leu Ser Ser Leu Pro Gly Ser Gln Arg Arg Glu Arg Arg Asn Trp Ala
150                 155                 160                 165

gcg aag cac cac ttc gat ttc atc aag gaa gat gcc ttt ttg acc gat   643
Ala Lys His His Phe Asp Phe Ile Lys Glu Asp Ala Phe Leu Thr Asp
                170                 175                 180

gaa tgg tca agg ggt gcg gca tcg act ggt gcc gtt gca cgt gat gtg   691
Glu Trp Ser Arg Gly Ala Ala Ser Thr Gly Ala Val Ala Arg Asp Val
            185                 190                 195

gtc agt ggc atg gct gaa gga tat gaa acg cat ctg gtg gat ttg gcg   739
Val Ser Gly Met Ala Glu Gly Tyr Glu Thr His Leu Val Asp Leu Ala
        200                 205                 210

ggc gtg ccc gtg atg gcg atg cgc cgt gga att acc tct gac gtg gtc   787
Gly Val Pro Val Met Ala Met Arg Arg Gly Ile Thr Ser Asp Val Val
    215                 220                 225

att gat gcg cgc cgc ggt gag cag cct gcc gat cca gag cgt gaa gaa   835
Ile Asp Ala Arg Arg Gly Glu Gln Pro Ala Asp Pro Glu Arg Glu Glu
```

```
230                 235                 240                 245

tct gat gat tta gtc gag att gat acc gtc tct gga ttc cgc ctg ctc   883
Ser Asp Asp Leu Val Glu Ile Asp Thr Val Ser Gly Phe Arg Leu Leu
                250                 255                 260

agt acg tgg cgg ggg ttg cgc agc gtt ttg tcg acg agc gca ttc acg   931
Ser Thr Trp Arg Gly Leu Arg Ser Val Leu Ser Thr Ser Ala Phe Thr
            265                 270                 275

tcg gtt tgg att cca tgc cag aag ctg tgactgctgt gtggatggaa         978
Ser Val Trp Ile Pro Cys Gln Lys Leu
        280                 285

tct                                                               981


<210> 718
<211> 286
<212> PRT
<213> Corynebacterium glutamicum

<400> 718
Met Glu Ile Ser Val Leu Ile Ile Ala Ala Leu Ile Leu Val Ala Gly
  1               5                  10                  15

Ile Val Leu Trp Arg Ala Asp Ser Ser Lys Gln Ala Ala Lys Lys Ala
             20                  25                  30

Glu Ser Pro Val Gly Ser Val Ala Pro Ala Pro Val Leu Val Glu Glu
         35                  40                  45

Glu Pro Asp Pro Glu Phe Glu Pro Glu Leu Asp Pro Glu Pro Glu Ala
     50                  55                  60

Gln Pro Glu Pro Glu Leu Glu Val Ala Pro Arg Phe Ala Pro Glu Pro
 65                  70                  75                  80

Val Gln Asp Leu Glu Pro Asp Gln Ala Glu Asp Ile Tyr Phe Asp Asp
                 85                  90                  95

Ser Pro Glu Leu Asp Ala Asp Val Glu Asn Ala Leu Ala Glu Leu Thr
            100                 105                 110

Glu Val Glu Asp Tyr Pro Glu Glu Pro Val Gln Ser Glu Gln Pro Gln
        115                 120                 125

Ala Pro Ala Thr Ala Glu Val Ala Ala Asp Glu Glu Gln Arg Gly Val
    130                 135                 140

Asp Lys His Ser Phe Leu Ser Ser Leu Pro Gly Ser Gln Arg Arg Glu
145                 150                 155                 160

Arg Arg Asn Trp Ala Ala Lys His His Phe Asp Phe Ile Lys Glu Asp
                165                 170                 175

Ala Phe Leu Thr Asp Glu Trp Ser Arg Gly Ala Ala Ser Thr Gly Ala
            180                 185                 190

Val Ala Arg Asp Val Val Ser Gly Met Ala Glu Gly Tyr Glu Thr His
        195                 200                 205
```

```
Leu Val Asp Leu Ala Gly Val Pro Val Met Ala Met Arg Arg Gly Ile
    210                 215                 220

Thr Ser Asp Val Val Ile Asp Ala Arg Arg Gly Glu Gln Pro Ala Asp
225                 230                 235                 240

Pro Glu Arg Glu Glu Ser Asp Asp Leu Val Glu Ile Asp Thr Val Ser
                245                 250                 255

Gly Phe Arg Leu Leu Ser Thr Trp Arg Gly Leu Arg Ser Val Leu Ser
            260                 265                 270

Thr Ser Ala Phe Thr Ser Val Trp Ile Pro Cys Gln Lys Leu
        275                 280                 285


<210> 719
<211> 535
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(535)
<223> FRXA01663

<400> 719
tattttgctg gttggtcaca gtggagcgct aaccccgaga atcctatcga ggcctaaaat 60

cgtggcttga gtacgcactg ccagtaaggt gtgtgatgtg atg gaa ata agt gtc   115
                                            Met Glu Ile Ser Val
                                              1               5


ttg atc atc gcc gca ctg atc ttg gtg gca ggc atc gta ctg tgg cgc   163
Leu Ile Ile Ala Ala Leu Ile Leu Val Ala Gly Ile Val Leu Trp Arg
                 10                  15                  20

gcg gac tcg tct aaa cag gca gct aaa aag gct gaa tca cct gtg ggc   211
Ala Asp Ser Ser Lys Gln Ala Ala Lys Lys Ala Glu Ser Pro Val Gly
             25                  30                  35

tca gtc gca cct gcg ccc gtg ctg gtt gaa gaa gag ccg gac cct gag   259
Ser Val Ala Pro Ala Pro Val Leu Val Glu Glu Glu Pro Asp Pro Glu
         40                  45                  50

ttt gag cca gaa ctg gac cct gaa cca gaa gcg caa cca gaa cca gag   307
Phe Glu Pro Glu Leu Asp Pro Glu Pro Glu Ala Gln Pro Glu Pro Glu
     55                  60                  65

ctg gaa gtt gcg cct aga ttt gcg cca gaa cca gtt caa gat ctt gag   355
Leu Glu Val Ala Pro Arg Phe Ala Pro Glu Pro Val Gln Asp Leu Glu
 70                  75                  80                  85

ccg gat cag gct gag gac att tat ttt gat gat tcc cct gaa ctc gat   403
Pro Asp Gln Ala Glu Asp Ile Tyr Phe Asp Asp Ser Pro Glu Leu Asp
                 90                  95                 100

gct gat gtt gaa aat gcc ttg gct gag ctt act gag gta gaa gac tac   451
Ala Asp Val Glu Asn Ala Leu Ala Glu Leu Thr Glu Val Glu Asp Tyr
             105                 110                 115
```

ccg gaa gag cca gtg cag tct gag caa cct caa gcc cct gcc acg gcg 499
Pro Glu Glu Pro Val Gln Ser Glu Gln Pro Gln Ala Pro Ala Thr Ala
120 125 130

gag gta gct gcg gac gag gag caa cgg ggc gtc gat 535
Glu Val Ala Ala Asp Glu Glu Gln Arg Gly Val Asp
135 140 145

<210> 720
<211> 145
<212> PRT
<213> Corynebacterium glutamicum

<400> 720
Met Glu Ile Ser Val Leu Ile Ile Ala Ala Leu Ile Leu Val Ala Gly
1 5 10 15

Ile Val Leu Trp Arg Ala Asp Ser Ser Lys Gln Ala Ala Lys Lys Ala
20 25 30

Glu Ser Pro Val Gly Ser Val Ala Pro Ala Pro Val Leu Val Glu Glu
35 40 45

Glu Pro Asp Pro Glu Phe Glu Pro Glu Leu Asp Pro Glu Pro Glu Ala
50 55 60

Gln Pro Glu Pro Glu Leu Glu Val Ala Pro Arg Phe Ala Pro Glu Pro
65 70 75 80

Val Gln Asp Leu Glu Pro Asp Gln Ala Glu Asp Ile Tyr Phe Asp Asp
85 90 95

Ser Pro Glu Leu Asp Ala Asp Val Glu Asn Ala Leu Ala Glu Leu Thr
100 105 110

Glu Val Glu Asp Tyr Pro Glu Glu Pro Val Gln Ser Glu Gln Pro Gln
115 120 125

Ala Pro Ala Thr Ala Glu Val Ala Ala Asp Glu Glu Gln Arg Gly Val
130 135 140

Asp
145

<210> 721
<211> 1038
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1015)
<223> RXN01669

<400> 721
cacccacagt caccaagaac atagccactc cacacacaac cactccacac acaaccacga 60

gggtcacgac caccatcacc ccaccggatt caaaggattt ttg tac gag att ttc 115

```
                                                  Leu Tyr Glu Ile Phe
                                                    1               5

gtt cca cac tcc cat gac acc gcc gac tcg att gat gat gct atg gag   163
Val Pro His Ser His Asp Thr Ala Asp Ser Ile Asp Asp Ala Met Glu
                10                  15                  20

gcg aac tca gag ggt att cga gcg ctg aag ttt agc ctt gta ttg atg   211
Ala Asn Ser Glu Gly Ile Arg Ala Leu Lys Phe Ser Leu Val Leu Met
            25                  30                  35

ctg ctc acg acg gtt ttg cag gct atc att gtg tct ttt tct gga tct   259
Leu Leu Thr Thr Val Leu Gln Ala Ile Ile Val Ser Phe Ser Gly Ser
        40                  45                  50

gtt gca ctg ttg gcg gat acg gtt cac aac ctt tcc gac gca ttg act   307
Val Ala Leu Leu Ala Asp Thr Val His Asn Leu Ser Asp Ala Leu Thr
    55                  60                  65

gcg att cct ctt tgg att gct ttc ata ctt tcc cgg cgc gca gcg act   355
Ala Ile Pro Leu Trp Ile Ala Phe Ile Leu Ser Arg Arg Ala Ala Thr
70                  75                  80                  85

caa aaa tat acg tat gga ttc aat cgt gca gag gat tta gcg ggg ttg   403
Gln Lys Tyr Thr Tyr Gly Phe Asn Arg Ala Glu Asp Leu Ala Gly Leu
                90                  95                  100

ttt att gtc gcg atg att gct ctt tcg gcg att gtt gct gca tgg cag   451
Phe Ile Val Ala Met Ile Ala Leu Ser Ala Ile Val Ala Ala Trp Gln
            105                 110                 115

gcg atc gac cgg atg att aat cct cgc ccg atg gag aat att gaa tgg   499
Ala Ile Asp Arg Met Ile Asn Pro Arg Pro Met Glu Asn Ile Glu Trp
        120                 125                 130

gtg att gcg gca ggt gtt att ggt ttc tta gga aat gag gct gtg gca   547
Val Ile Ala Ala Gly Val Ile Gly Phe Leu Gly Asn Glu Ala Val Ala
    135                 140                 145

atg tat cgc att cgg gtt ggt aag agg att ggc tcg gct gct ttg gtt   595
Met Tyr Arg Ile Arg Val Gly Lys Arg Ile Gly Ser Ala Ala Leu Val
150                 155                 160                 165

gca gat ggc gtt cat gct cgc acg gat ggt ttt act tca ctt gca gtt   643
Ala Asp Gly Val His Ala Arg Thr Asp Gly Phe Thr Ser Leu Ala Val
                170                 175                 180

gtc gca ggt ggt gtt gga gtt ttt ctg gga ttc ccc ctg gct gac cca   691
Val Ala Gly Gly Val Gly Val Phe Leu Gly Phe Pro Leu Ala Asp Pro
            185                 190                 195

att atc gga ttg atc att tct gcg atg att gcc acc ctt ctt gtt ggt   739
Ile Ile Gly Leu Ile Ile Ser Ala Met Ile Ala Thr Leu Leu Val Gly
        200                 205                 210

acg atc cgt tcg gtt ggc aga cgc ctc atg gat gga att gag ccg gag   787
Thr Ile Arg Ser Val Gly Arg Arg Leu Met Asp Gly Ile Glu Pro Glu
    215                 220                 225

ttg gta gag aag gct acg cac gcg atc tgg cat gtg aag gaa att gag   835
Leu Val Glu Lys Ala Thr His Ala Ile Trp His Val Lys Glu Ile Glu
```

```
230                 235                 240                 245

tcg att gat cga ctg agg ttg agg tgg gtt gga cac cgt ctt cac ggc   883
Ser Ile Asp Arg Leu Arg Leu Arg Trp Val Gly His Arg Leu His Gly
                250                 255                 260

gat gcc acg gtc agc act tct aca tca tcg cta tcg gaa gcc acc gca   931
Asp Ala Thr Val Ser Thr Ser Thr Ser Ser Leu Ser Glu Ala Thr Ala
            265                 270                 275

atc gcc ctt gag gct gag ctt tcc gtc aaa caa cat ctt ccc aat gtg   979
Ile Ala Leu Glu Ala Glu Leu Ser Val Lys Gln His Leu Pro Asn Val
        280                 285                 290

gat gaa atg act gtg acc atc acc cct tcc aaa cct tgagtcccgt       1025
Asp Glu Met Thr Val Thr Ile Thr Pro Ser Lys Pro
    295                 300                 305

gatacaattg ttg                                                  1038


<210> 722
<211> 305
<212> PRT
<213> Corynebacterium glutamicum

<400> 722
Leu Tyr Glu Ile Phe Val Pro His Ser His Asp Thr Ala Asp Ser Ile
  1               5                  10                  15

Asp Asp Ala Met Glu Ala Asn Ser Glu Gly Ile Arg Ala Leu Lys Phe
            20                  25                  30

Ser Leu Val Leu Met Leu Leu Thr Thr Val Leu Gln Ala Ile Ile Val
        35                  40                  45

Ser Phe Ser Gly Ser Val Ala Leu Leu Ala Asp Thr Val His Asn Leu
    50                  55                  60

Ser Asp Ala Leu Thr Ala Ile Pro Leu Trp Ile Ala Phe Ile Leu Ser
65                  70                  75                  80

Arg Arg Ala Ala Thr Gln Lys Tyr Thr Tyr Gly Phe Asn Arg Ala Glu
                85                  90                  95

Asp Leu Ala Gly Leu Phe Ile Val Ala Met Ile Ala Leu Ser Ala Ile
            100                 105                 110

Val Ala Ala Trp Gln Ala Ile Asp Arg Met Ile Asn Pro Arg Pro Met
        115                 120                 125

Glu Asn Ile Glu Trp Val Ile Ala Ala Gly Val Ile Gly Phe Leu Gly
    130                 135                 140

Asn Glu Ala Val Ala Met Tyr Arg Ile Arg Val Gly Lys Arg Ile Gly
145                 150                 155                 160

Ser Ala Ala Leu Val Ala Asp Gly Val His Ala Arg Thr Asp Gly Phe
                165                 170                 175

Thr Ser Leu Ala Val Val Ala Gly Gly Val Gly Val Phe Leu Gly Phe
```

```
            180                 185                 190

Pro Leu Ala Asp Pro Ile Ile Gly Leu Ile Ile Ser Ala Met Ile Ala
        195                 200                 205

Thr Leu Leu Val Gly Thr Ile Arg Ser Val Gly Arg Arg Leu Met Asp
    210                 215                 220

Gly Ile Glu Pro Glu Leu Val Glu Lys Ala Thr His Ala Ile Trp His
225                 230                 235                 240

Val Lys Glu Ile Glu Ser Ile Asp Arg Leu Arg Leu Arg Trp Val Gly
                245                 250                 255

His Arg Leu His Gly Asp Ala Thr Val Ser Thr Ser Thr Ser Ser Leu
            260                 265                 270

Ser Glu Ala Thr Ala Ile Ala Leu Glu Ala Glu Leu Ser Val Lys Gln
        275                 280                 285

His Leu Pro Asn Val Asp Glu Met Thr Val Thr Ile Thr Pro Ser Lys
    290                 295                 300

Pro
305


<210> 723
<211> 755
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(732)
<223> FRXA01669

<400> 723
cac aac ctt tcc gac gca ttg act gcg att cct ctt tgg att gct ttc   48
His Asn Leu Ser Asp Ala Leu Thr Ala Ile Pro Leu Trp Ile Ala Phe
  1               5                  10                  15

ata ctt tcc cgg cgc gca gcg act caa aaa tat acg tat gga ttc aat   96
Ile Leu Ser Arg Arg Ala Ala Thr Gln Lys Tyr Thr Tyr Gly Phe Asn
             20                  25                  30

cgt gca gag gat tta gcg ggg ttg ttt att gtc gcg atg att gct ctt   144
Arg Ala Glu Asp Leu Ala Gly Leu Phe Ile Val Ala Met Ile Ala Leu
         35                  40                  45

tcg gcg att gtt gct gca tgg cag gcg atc gac cgg atg att aat cct   192
Ser Ala Ile Val Ala Ala Trp Gln Ala Ile Asp Arg Met Ile Asn Pro
     50                  55                  60

cgc ccg atg gag aat att gaa tgg gtg att gcg gca ggt gtt att ggt   240
Arg Pro Met Glu Asn Ile Glu Trp Val Ile Ala Ala Gly Val Ile Gly
 65                  70                  75                  80

ttc tta gga aat gag gct gtg gca atg tat cgc att cgg gtt ggt aag   288
Phe Leu Gly Asn Glu Ala Val Ala Met Tyr Arg Ile Arg Val Gly Lys
                85                  90                  95
```

```
agg att ggc tcg gct gct ttg gtt gca gat ggc gtt cat gct cgc acg   336
Arg Ile Gly Ser Ala Ala Leu Val Ala Asp Gly Val His Ala Arg Thr
            100                 105                 110

gat ggt ttt act tca ctt gca gtt gtc gca ggt ggt gtt gga gtt ttt   384
Asp Gly Phe Thr Ser Leu Ala Val Val Ala Gly Gly Val Gly Val Phe
        115                 120                 125

ctg gga ttc ccc ctg gct gac cca att atc gga ttg atc att tct gcg   432
Leu Gly Phe Pro Leu Ala Asp Pro Ile Ile Gly Leu Ile Ile Ser Ala
    130                 135                 140

atg att gcc acc ctt ctt gtt ggt acg atc cgt tcg gtt ggc aga cgc   480
Met Ile Ala Thr Leu Leu Val Gly Thr Ile Arg Ser Val Gly Arg Arg
145                 150                 155                 160

ctc atg gat gga att gag ccg gag ttg gta gag aag gct acg cac gcg   528
Leu Met Asp Gly Ile Glu Pro Glu Leu Val Glu Lys Ala Thr His Ala
                165                 170                 175

atc tgg cat gtg aag gaa att gag tcg att gat cga ctg agg ttg agg   576
Ile Trp His Val Lys Glu Ile Glu Ser Ile Asp Arg Leu Arg Leu Arg
            180                 185                 190

tgg gtt gga cac cgt ctt cac ggc gat gcc acg gtc agc act tct aca   624
Trp Val Gly His Arg Leu His Gly Asp Ala Thr Val Ser Thr Ser Thr
        195                 200                 205

tca tcg cta tcg gaa gcc acc gca atc gcc ctt gag gct gag ctt tcc   672
Ser Ser Leu Ser Glu Ala Thr Ala Ile Ala Leu Glu Ala Glu Leu Ser
    210                 215                 220

gtc aaa caa cat ctt ccc aat gtg gat gaa atg act gtg acc atc acc   720
Val Lys Gln His Leu Pro Asn Val Asp Glu Met Thr Val Thr Ile Thr
225                 230                 235                 240

cct tcc aaa cct tgagtcccgt gatacaattg ttg                        755
Pro Ser Lys Pro
```

<210> 724
<211> 244
<212> PRT
<213> Corynebacterium glutamicum

<400> 724

```
His Asn Leu Ser Asp Ala Leu Thr Ala Ile Pro Leu Trp Ile Ala Phe
  1               5                  10                  15

Ile Leu Ser Arg Arg Ala Ala Thr Gln Lys Tyr Thr Tyr Gly Phe Asn
             20                  25                  30

Arg Ala Glu Asp Leu Ala Gly Leu Phe Ile Val Ala Met Ile Ala Leu
         35                  40                  45

Ser Ala Ile Val Ala Ala Trp Gln Ala Ile Asp Arg Met Ile Asn Pro
     50                  55                  60

Arg Pro Met Glu Asn Ile Glu Trp Val Ile Ala Ala Gly Val Ile Gly
```

```
65                  70                  75                  80

Phe Leu Gly Asn Glu Ala Val Ala Met Tyr Arg Ile Arg Val Gly Lys
                85                  90                  95

Arg Ile Gly Ser Ala Ala Leu Val Ala Asp Gly Val His Ala Arg Thr
            100                 105                 110

Asp Gly Phe Thr Ser Leu Ala Val Val Ala Gly Gly Val Gly Val Phe
        115                 120                 125

Leu Gly Phe Pro Leu Ala Asp Pro Ile Ile Gly Leu Ile Ile Ser Ala
    130                 135                 140

Met Ile Ala Thr Leu Leu Val Gly Thr Ile Arg Ser Val Gly Arg Arg
145                 150                 155                 160

Leu Met Asp Gly Ile Glu Pro Glu Leu Val Glu Lys Ala Thr His Ala
                165                 170                 175

Ile Trp His Val Lys Glu Ile Glu Ser Ile Asp Arg Leu Arg Leu Arg
            180                 185                 190

Trp Val Gly His Arg Leu His Gly Asp Ala Thr Val Ser Thr Ser Thr
        195                 200                 205

Ser Ser Leu Ser Glu Ala Thr Ala Ile Ala Leu Glu Ala Glu Leu Ser
    210                 215                 220

Val Lys Gln His Leu Pro Asn Val Asp Glu Met Thr Val Thr Ile Thr
225                 230                 235                 240

Pro Ser Lys Pro
```

<210> 725
<211> 465
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(442)
<223> RXN01672

<400> 725
agtagcaaag ggtgcagtcg aaggaccagc atccaagact gctgccgaag aaaccgactc 60

cgttgacaac ggatccgacg aaaacggcga ggaataattt atg gca tcc cga gaa 115
Met Ala Ser Arg Glu
1 5

gta tcc atc acc cga atc tca cca cta gca acc ttc cga gtt gca ctg 163
Val Ser Ile Thr Arg Ile Ser Pro Leu Ala Thr Phe Arg Val Ala Leu
10 15 20

gca atg tcc atc atc gga ctc gtg gcg tgg atc atc tgc gta acc gtc 211
Ala Met Ser Ile Ile Gly Leu Val Ala Trp Ile Ile Cys Val Thr Val
25 30 35

```
ctc tat ttc gga ctt aac gtg gct ggc gtc tgg cag aac ttc aac gat   259
Leu Tyr Phe Gly Leu Asn Val Ala Gly Val Trp Gln Asn Phe Asn Asp
         40                  45                  50

gtc atc ggc ggt gtt ggt gca gaa caa acc atc acc ttc ggg ctc gtc   307
Val Ile Gly Gly Val Gly Ala Glu Gln Thr Ile Thr Phe Gly Leu Val
     55                  60                  65

ctg agc att tcc gca ctt ctg gga gct atc gga gcg att acc gtc gct   355
Leu Ser Ile Ser Ala Leu Leu Gly Ala Ile Gly Ala Ile Thr Val Ala
 70                  75                  80                  85

gtg ctt gca cca ttg tgt gca atc atc tac aac tcg att gtt gac ctc   403
Val Leu Ala Pro Leu Cys Ala Ile Ile Tyr Asn Ser Ile Val Asp Leu
                90                  95                 100

ttc ggt gga ctg cag att caa ctg caa gaa gaa gta gac taacctctga   452
Phe Gly Gly Leu Gln Ile Gln Leu Gln Glu Glu Val Asp
            105                 110

aacacaaacc cct                                                  465
```

<210> 726
<211> 114
<212> PRT
<213> Corynebacterium glutamicum

<400> 726

```
Met Ala Ser Arg Glu Val Ser Ile Thr Arg Ile Ser Pro Leu Ala Thr
  1               5                  10                  15

Phe Arg Val Ala Leu Ala Met Ser Ile Ile Gly Leu Val Ala Trp Ile
             20                  25                  30

Ile Cys Val Thr Val Leu Tyr Phe Gly Leu Asn Val Ala Gly Val Trp
         35                  40                  45

Gln Asn Phe Asn Asp Val Ile Gly Gly Val Gly Ala Glu Gln Thr Ile
     50                  55                  60

Thr Phe Gly Leu Val Leu Ser Ile Ser Ala Leu Leu Gly Ala Ile Gly
 65                  70                  75                  80

Ala Ile Thr Val Ala Val Leu Ala Pro Leu Cys Ala Ile Ile Tyr Asn
                 85                  90                  95

Ser Ile Val Asp Leu Phe Gly Gly Leu Gln Ile Gln Leu Gln Glu Glu
            100                 105                 110

Val Asp
```

<210> 727
<211> 332
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS

<222> (1)..(309)
<223> FRXA01672

<400> 727
```
tca cca cta gca acc ttc cga gtt gca ctg gca atg tcc atc atc gga   48
Ser Pro Leu Ala Thr Phe Arg Val Ala Leu Ala Met Ser Ile Ile Gly
  1               5                  10                  15

ctc gtg gcg tgg atc atc tgc gta acc gtc ctc tat ttc gga ctt aac   96
Leu Val Ala Trp Ile Ile Cys Val Thr Val Leu Tyr Phe Gly Leu Asn
             20                  25                  30

gtg gct ggc gtc tgg cag aac ttc aac gat gtc atc ggc ggt gtt ggt   144
Val Ala Gly Val Trp Gln Asn Phe Asn Asp Val Ile Gly Gly Val Gly
         35                  40                  45

gca gaa caa acc atc acc ttc ggg ctc gtc ctg agc att tcc gca ctt   192
Ala Glu Gln Thr Ile Thr Phe Gly Leu Val Leu Ser Ile Ser Ala Leu
     50                  55                  60

ctg gga gct atc gga gcg att acc gtc gct gtg ctt gca cca ttg tgt   240
Leu Gly Ala Ile Gly Ala Ile Thr Val Ala Val Leu Ala Pro Leu Cys
 65                  70                  75                  80

gca atc atc tac aac tcg att gtt gac ctc ttc ggt gga ctg cag att   288
Ala Ile Ile Tyr Asn Ser Ile Val Asp Leu Phe Gly Gly Leu Gln Ile
                 85                  90                  95

caa ctg caa gaa gaa gta gac taacctctga aacacaaacc cct            332
Gln Leu Gln Glu Glu Val Asp
            100
```

<210> 728
<211> 103
<212> PRT
<213> Corynebacterium glutamicum

<400> 728
```
Ser Pro Leu Ala Thr Phe Arg Val Ala Leu Ala Met Ser Ile Ile Gly
  1               5                  10                  15

Leu Val Ala Trp Ile Ile Cys Val Thr Val Leu Tyr Phe Gly Leu Asn
             20                  25                  30

Val Ala Gly Val Trp Gln Asn Phe Asn Asp Val Ile Gly Gly Val Gly
         35                  40                  45

Ala Glu Gln Thr Ile Thr Phe Gly Leu Val Leu Ser Ile Ser Ala Leu
     50                  55                  60

Leu Gly Ala Ile Gly Ala Ile Thr Val Ala Val Leu Ala Pro Leu Cys
 65                  70                  75                  80

Ala Ile Ile Tyr Asn Ser Ile Val Asp Leu Phe Gly Gly Leu Gln Ile
                 85                  90                  95

Gln Leu Gln Glu Glu Val Asp
            100
```

<210> 729
<211> 1023
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1000)
<223> RXN01694

<400> 729
cgacaccaat aatttattgg gtatccacca attaccgctg tgagcactgc aaattacgta 60

ttcgaaaagc catgtccacc acgtgttcta tcctggcggc atg caa aaa atc acc 115
Met Gln Lys Ile Thr
1 5

cca aac atc tgg tgc caa ggc acc gca gac gaa gca gcc gaa ttc tac 163
Pro Asn Ile Trp Cys Gln Gly Thr Ala Asp Glu Ala Ala Glu Phe Tyr
10 15 20

gtc aat gcg ttt tct gag ttt ccg ggt ggc gca gaa gta ctc acc aca 211
Val Asn Ala Phe Ser Glu Phe Pro Gly Gly Ala Glu Val Leu Thr Thr
25 30 35

gtt aag tat ccc gaa gct ggc ttg ctg gac ttc cag gag cct ttc gca 259
Val Lys Tyr Pro Glu Ala Gly Leu Leu Asp Phe Gln Glu Pro Phe Ala
40 45 50

gga aaa acc ttg acg gtg gaa ctc gct atc tca ggc ttt aag atc atc 307
Gly Lys Thr Leu Thr Val Glu Leu Ala Ile Ser Gly Phe Lys Ile Ile
55 60 65

ttg atc aat gct ggt gaa gag ttc act ccc aac cca tcg atc agc ttc 355
Leu Ile Asn Ala Gly Glu Glu Phe Thr Pro Asn Pro Ser Ile Ser Phe
70 75 80 85

atg gtg aat ttt gat gcg gtg cgt gat gaa aat gcc aaa gag cac ctt 403
Met Val Asn Phe Asp Ala Val Arg Asp Glu Asn Ala Lys Glu His Leu
90 95 100

gat gcg gtg tgg gaa aaa ctc cat gaa ggc ggc agc aca ctg atg cca 451
Asp Ala Val Trp Glu Lys Leu His Glu Gly Gly Ser Thr Leu Met Pro
105 110 115

gtc gat act tac cca ttt tcg gaa tac tac ggg tgg gta caa gac aaa 499
Val Asp Thr Tyr Pro Phe Ser Glu Tyr Tyr Gly Trp Val Gln Asp Lys
120 125 130

tat ggt gtg agc tgg caa ttg atg ctc agc cgc cca gaa gaa aag cca 547
Tyr Gly Val Ser Trp Gln Leu Met Leu Ser Arg Pro Glu Glu Lys Pro
135 140 145

ggt ccc gca gta atc cca acg ctc tta ttt ggt ggg gca gct caa aat 595
Gly Pro Ala Val Ile Pro Thr Leu Leu Phe Gly Gly Ala Ala Gln Asn
150 155 160 165

cag gca ggc cca gct caa gaa aac tac gtt gag gtg ttc ccg aac tcc 643
Gln Ala Gly Pro Ala Gln Glu Asn Tyr Val Glu Val Phe Pro Asn Ser
170 175 180

```
caa ctt ggt gat cgt gca cct tat gga cag caa aca ggt cct gcc act   691
Gln Leu Gly Asp Arg Ala Pro Tyr Gly Gln Gln Thr Gly Pro Ala Thr
            185                 190                 195

cct gag gcc ctc atg ttt tcc cag ttc caa ctc gac ggt cag tgg att   739
Pro Glu Ala Leu Met Phe Ser Gln Phe Gln Leu Asp Gly Gln Trp Ile
        200                 205                 210

ttc gcg atg gat tcc gga gtt gag caa gat ttc acc ttc agt gag ggt   787
Phe Ala Met Asp Ser Gly Val Glu Gln Asp Phe Thr Phe Ser Glu Gly
    215                 220                 225

gtc tca ttg atg tat gaa gct cat ggt caa gaa gaa ctc gat gcc atc   835
Val Ser Leu Met Tyr Glu Ala His Gly Gln Glu Glu Leu Asp Ala Ile
230                 235                 240                 245

tgg aat gca ctc tcg gca gtt cca gaa gct gag gct tgt ggt tgg ttg   883
Trp Asn Ala Leu Ser Ala Val Pro Glu Ala Glu Ala Cys Gly Trp Leu
                250                 255                 260

aag gac aag ttc ggc gtg agc tgg cag att gtt ccc gac aac atg gag   931
Lys Asp Lys Phe Gly Val Ser Trp Gln Ile Val Pro Asp Asn Met Glu
            265                 270                 275

gag ctc atg gct aaa ccc ggc gcg tat gaa aag ctt ctt gcg atg aag   979
Glu Leu Met Ala Lys Pro Gly Ala Tyr Glu Lys Leu Leu Ala Met Lys
        280                 285                 290

aag atc aat atc gcg gag ttc tagcagttct aagcgctcca cgc            1023
Lys Ile Asn Ile Ala Glu Phe
    295                 300
```

Patent Application Publication

<210> 730
<211> 300
<212> PRT
<213> Corynebacterium glutamicum

<400> 730

```
Met Gln Lys Ile Thr Pro Asn Ile Trp Cys Gln Gly Thr Ala Asp Glu
  1               5                  10                  15

Ala Ala Glu Phe Tyr Val Asn Ala Phe Ser Glu Phe Pro Gly Gly Ala
             20                  25                  30

Glu Val Leu Thr Thr Val Lys Tyr Pro Glu Ala Gly Leu Leu Asp Phe
         35                  40                  45

Gln Glu Pro Phe Ala Gly Lys Thr Leu Thr Val Glu Leu Ala Ile Ser
     50                  55                  60

Gly Phe Lys Ile Ile Leu Ile Asn Ala Gly Glu Glu Phe Thr Pro Asn
 65                  70                  75                  80

Pro Ser Ile Ser Phe Met Val Asn Phe Asp Ala Val Arg Asp Glu Asn
                 85                  90                  95

Ala Lys Glu His Leu Asp Ala Val Trp Glu Lys Leu His Glu Gly Gly
            100                 105                 110

Ser Thr Leu Met Pro Val Asp Thr Tyr Pro Phe Ser Glu Tyr Tyr Gly
```

```
        115                 120                 125

Trp Val Gln Asp Lys Tyr Gly Val Ser Trp Gln Leu Met Leu Ser Arg
    130                 135                 140

Pro Glu Glu Lys Pro Gly Pro Ala Val Ile Pro Thr Leu Leu Phe Gly
145                 150                 155                 160

Gly Ala Ala Gln Asn Gln Ala Gly Pro Ala Gln Glu Asn Tyr Val Glu
                165                 170                 175

Val Phe Pro Asn Ser Gln Leu Gly Asp Arg Ala Pro Tyr Gly Gln Gln
            180                 185                 190

Thr Gly Pro Ala Thr Pro Glu Ala Leu Met Phe Ser Gln Phe Gln Leu
        195                 200                 205

Asp Gly Gln Trp Ile Phe Ala Met Asp Ser Gly Val Glu Gln Asp Phe
    210                 215                 220

Thr Phe Ser Glu Gly Val Ser Leu Met Tyr Glu Ala His Gly Gln Glu
225                 230                 235                 240

Glu Leu Asp Ala Ile Trp Asn Ala Leu Ser Ala Val Pro Glu Ala Glu
                245                 250                 255

Ala Cys Gly Trp Leu Lys Asp Lys Phe Gly Val Ser Trp Gln Ile Val
            260                 265                 270

Pro Asp Asn Met Glu Glu Leu Met Ala Lys Pro Gly Ala Tyr Glu Lys
        275                 280                 285

Leu Leu Ala Met Lys Lys Ile Asn Ile Ala Glu Phe
    290                 295                 300


<210> 731
<211> 1023
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1000)
<223> FRXA01694

<400> 731
cgacaccaat aatttattgg gtatccacca attaccgctg tgagcactgc aaattacgta 60

ttcgaaaagc catgtccacc acgtgttcta tcctggcggc atg caa aaa atc acc   115
                                              Met Gln Lys Ile Thr
                                                1               5

cca aac atc tgg tgc caa ggc acc gca gac gaa gca gcc gaa ttc tac   163
Pro Asn Ile Trp Cys Gln Gly Thr Ala Asp Glu Ala Ala Glu Phe Tyr
                10                  15                  20

gtc aat gcg ttt tct gag ttt ccg ggt ggc gca gaa gta ctc acc aca   211
Val Asn Ala Phe Ser Glu Phe Pro Gly Gly Ala Glu Val Leu Thr Thr
            25                  30                  35
```

```
gtt aag tat ccc gaa gct ggc ttg ctg gac ttc cag gag cct ttc gca   259
Val Lys Tyr Pro Glu Ala Gly Leu Leu Asp Phe Gln Glu Pro Phe Ala
         40                  45                  50

gga aaa acc ttg acg gtg gaa ctc gct atc tca ggc ttt aag atc atc   307
Gly Lys Thr Leu Thr Val Glu Leu Ala Ile Ser Gly Phe Lys Ile Ile
     55                  60                  65

ttg atc aat gct ggt gaa gag ttc act ccc aac cca tcg atc agc ttc   355
Leu Ile Asn Ala Gly Glu Glu Phe Thr Pro Asn Pro Ser Ile Ser Phe
 70                  75                  80                  85

atg gtg aat ttt gat gcg gtg cgt gat gaa aat gcc aaa gag cac ctt   403
Met Val Asn Phe Asp Ala Val Arg Asp Glu Asn Ala Lys Glu His Leu
                 90                  95                 100

gat gcg gtg tgg gaa aaa ctc cat gaa ggc ggc agc aca ctg atg cca   451
Asp Ala Val Trp Glu Lys Leu His Glu Gly Gly Ser Thr Leu Met Pro
            105                 110                 115

gtc gat act tac cca ttt tcg gaa tac tac ggg tgg gta caa gac aaa   499
Val Asp Thr Tyr Pro Phe Ser Glu Tyr Tyr Gly Trp Val Gln Asp Lys
        120                 125                 130

tat ggt gtg agc tgg caa ttg atg ctc agc cgc cca gaa gaa aag cca   547
Tyr Gly Val Ser Trp Gln Leu Met Leu Ser Arg Pro Glu Glu Lys Pro
    135                 140                 145

ggt ccc gca gta atc cca acg ctc tta ttt ggt ggg gca gct caa aat   595
Gly Pro Ala Val Ile Pro Thr Leu Leu Phe Gly Gly Ala Ala Gln Asn
150                 155                 160                 165

cag gca ggc cca gct caa gaa aac tac gtt gag gtg ttc ccg aac tcc   643
Gln Ala Gly Pro Ala Gln Glu Asn Tyr Val Glu Val Phe Pro Asn Ser
                170                 175                 180

caa ctt ggt gat cgt gca cct tat gga cag caa aca ggt cct gcc act   691
Gln Leu Gly Asp Arg Ala Pro Tyr Gly Gln Gln Thr Gly Pro Ala Thr
            185                 190                 195

cct gag gcc ctc atg ttt tcc cag ttc caa ctc gac ggt cag tgg att   739
Pro Glu Ala Leu Met Phe Ser Gln Phe Gln Leu Asp Gly Gln Trp Ile
        200                 205                 210

ttc gcg atg gat tcc gga gtt gag caa gat ttc acc ttc agt gag ggt   787
Phe Ala Met Asp Ser Gly Val Glu Gln Asp Phe Thr Phe Ser Glu Gly
    215                 220                 225

gtc tca ttg atg tat gaa gct cat ggt caa gaa gaa ctc gat gcc atc   835
Val Ser Leu Met Tyr Glu Ala His Gly Gln Glu Glu Leu Asp Ala Ile
230                 235                 240                 245

tgg aat gca ctc tcg gca gtt cca gaa gct gag gct tgt ggt tgg ttg   883
Trp Asn Ala Leu Ser Ala Val Pro Glu Ala Glu Ala Cys Gly Trp Leu
                250                 255                 260

aag gac aag ttc ggc gtg agc tgg cag att gtt ccc gac aac atg gag   931
Lys Asp Lys Phe Gly Val Ser Trp Gln Ile Val Pro Asp Asn Met Glu
            265                 270                 275

gag ctc atg gct aaa ccc ggc gcg tat gaa aag ctt ctt gcg atg aag   979
```

```
Glu Leu Met Ala Lys Pro Gly Ala Tyr Glu Lys Leu Leu Ala Met Lys
        280                 285                 290

aag atc aat atc gcg gag ttc tagcagttct aagcgctcca cgc            1023
Lys Ile Asn Ile Ala Glu Phe
    295                 300


<210> 732
<211> 300
<212> PRT
<213> Corynebacterium glutamicum

<400> 732
Met Gln Lys Ile Thr Pro Asn Ile Trp Cys Gln Gly Thr Ala Asp Glu
  1               5                  10                  15

Ala Ala Glu Phe Tyr Val Asn Ala Phe Ser Glu Phe Pro Gly Gly Ala
             20                  25                  30

Glu Val Leu Thr Thr Val Lys Tyr Pro Glu Ala Gly Leu Leu Asp Phe
         35                  40                  45

Gln Glu Pro Phe Ala Gly Lys Thr Leu Thr Val Glu Leu Ala Ile Ser
     50                  55                  60

Gly Phe Lys Ile Ile Leu Ile Asn Ala Gly Glu Glu Phe Thr Pro Asn
 65                  70                  75                  80

Pro Ser Ile Ser Phe Met Val Asn Phe Asp Ala Val Arg Asp Glu Asn
                 85                  90                  95

Ala Lys Glu His Leu Asp Ala Val Trp Glu Lys Leu His Glu Gly Gly
            100                 105                 110

Ser Thr Leu Met Pro Val Asp Thr Tyr Pro Phe Ser Glu Tyr Tyr Gly
        115                 120                 125

Trp Val Gln Asp Lys Tyr Gly Val Ser Trp Gln Leu Met Leu Ser Arg
    130                 135                 140

Pro Glu Glu Lys Pro Gly Pro Ala Val Ile Pro Thr Leu Leu Phe Gly
145                 150                 155                 160

Gly Ala Ala Gln Asn Gln Ala Gly Pro Ala Gln Glu Asn Tyr Val Glu
                165                 170                 175

Val Phe Pro Asn Ser Gln Leu Gly Asp Arg Ala Pro Tyr Gly Gln Gln
            180                 185                 190

Thr Gly Pro Ala Thr Pro Glu Ala Leu Met Phe Ser Gln Phe Gln Leu
        195                 200                 205

Asp Gly Gln Trp Ile Phe Ala Met Asp Ser Gly Val Glu Gln Asp Phe
    210                 215                 220

Thr Phe Ser Glu Gly Val Ser Leu Met Tyr Glu Ala His Gly Gln Glu
225                 230                 235                 240

Glu Leu Asp Ala Ile Trp Asn Ala Leu Ser Ala Val Pro Glu Ala Glu
                245                 250                 255
```

```
Ala Cys Gly Trp Leu Lys Asp Lys Phe Gly Val Ser Trp Gln Ile Val
            260                 265                 270

Pro Asp Asn Met Glu Glu Leu Met Ala Lys Pro Gly Ala Tyr Glu Lys
        275                 280                 285

Leu Leu Ala Met Lys Lys Ile Asn Ile Ala Glu Phe
    290                 295                 300


<210> 733
<211> 1302
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1279)
<223> RXN01696

<400> 733
aggtgacggt gatacaattt tgccataact gacttaaccc agaacgttgt ccggaagcac 60

acagaccttt gtgcggcttc cttttctagg agcatgtaac ttg tct acc cca atc   115
                                              Leu Ser Thr Pro Ile
                                                1               5

ggc ctt ggc ctt cct ccg acc cca cct cca gtg ttg gcg cca cgt cgt   163
Gly Leu Gly Leu Pro Pro Thr Pro Pro Val Leu Ala Pro Arg Arg
                10                  15                  20

aaa aca cgc caa ctc atg gtc ggc aaa gtg ggc gtt ggt tcg gat cac   211
Lys Thr Arg Gln Leu Met Val Gly Lys Val Gly Val Gly Ser Asp His
            25                  30                  35

ccg att tcc gtc cag tcg atg acc acc acc aaa acc cac gac atc aac   259
Pro Ile Ser Val Gln Ser Met Thr Thr Thr Lys Thr His Asp Ile Asn
        40                  45                  50

ggc acc ctg caa cag atc gca cag ttg aca gcc acc ggt tgt gac atc   307
Gly Thr Leu Gln Gln Ile Ala Gln Leu Thr Ala Thr Gly Cys Asp Ile
    55                  60                  65

gtc cgc gtt gcc tgc cca aag act gtt gat gcg gaa gca ctg ccg atc   355
Val Arg Val Ala Cys Pro Lys Thr Val Asp Ala Glu Ala Leu Pro Ile
70                  75                  80                  85

atc gca aag aag tct ccg atc cca gtg atc gca gat atc cac ttc cag   403
Ile Ala Lys Lys Ser Pro Ile Pro Val Ile Ala Asp Ile His Phe Gln
                90                  95                  100

ccc aag tac atc ttc gcg gca atc gat gca ggt tgc gcc gcc gtt cgt   451
Pro Lys Tyr Ile Phe Ala Ala Ile Asp Ala Gly Cys Ala Ala Val Arg
            105                 110                 115

gtg aac cca ggc aac atc aag gaa ttc gat ggt cgc gtt aaa gaa gta   499
Val Asn Pro Gly Asn Ile Lys Glu Phe Asp Gly Arg Val Lys Glu Val
        120                 125                 130

gca aaa gct gca ggc gat gcc gga att cca att cgt att ggt gtc aac   547
```

```
Ala Lys Ala Ala Gly Asp Ala Gly Ile Pro Ile Arg Ile Gly Val Asn
    135                 140                 145

ggc gga tcc ctg gat aag cgc atc ctg gac aaa tac cac ggc aaa gcc   595
Gly Gly Ser Leu Asp Lys Arg Ile Leu Asp Lys Tyr His Gly Lys Ala
150                 155                 160                 165

acc cca gaa gct ctc gtg gaa tcc gca atg tgg gaa gcc ggc ctg ttt   643
Thr Pro Glu Ala Leu Val Glu Ser Ala Met Trp Glu Ala Gly Leu Phe
                170                 175                 180

gaa gag cac ggc ttc ggc gac atc gca atc tct gtg aag cac tcc gac   691
Glu Glu His Gly Phe Gly Asp Ile Ala Ile Ser Val Lys His Ser Asp
            185                 190                 195

cca gta ctc atg gtg gag gcc tac cgc cag ctc gct gaa caa agc gac   739
Pro Val Leu Met Val Glu Ala Tyr Arg Gln Leu Ala Glu Gln Ser Asp
        200                 205                 210

tac cca ctg cac ctc ggt gtt act gaa gct ggt ccc aag ttc atg gga   787
Tyr Pro Leu His Leu Gly Val Thr Glu Ala Gly Pro Lys Phe Met Gly
    215                 220                 225

aca atc aag tct tcc gta gca ttc ggc gct ctg ctg tcc cag ggc atc   835
Thr Ile Lys Ser Ser Val Ala Phe Gly Ala Leu Leu Ser Gln Gly Ile
230                 235                 240                 245

ggc gac act atc cgt gtg tct ctt tct gct gac cca gtg gaa gaa atc   883
Gly Asp Thr Ile Arg Val Ser Leu Ser Ala Asp Pro Val Glu Glu Ile
                250                 255                 260

aag gtt ggc gac cag att ctg cag tcc ctc aac ctg cgc cca cgc aag   931
Lys Val Gly Asp Gln Ile Leu Gln Ser Leu Asn Leu Arg Pro Arg Lys
            265                 270                 275

ctg gaa atc gtg tcc tgc cca tca tgt ggc cgc gca cag gtc gat gtg   979
Leu Glu Ile Val Ser Cys Pro Ser Cys Gly Arg Ala Gln Val Asp Val
        280                 285                 290

tac tca ctt gct gaa gaa gtc acc gaa gca ctc gac ggc atg gaa gtt   1027
Tyr Ser Leu Ala Glu Glu Val Thr Glu Ala Leu Asp Gly Met Glu Val
    295                 300                 305

cca ctg cgc gtc gct gtc atg ggt tgc gtt gtt aac ggc cca ggt gag   1075
Pro Leu Arg Val Ala Val Met Gly Cys Val Val Asn Gly Pro Gly Glu
310                 315                 320                 325

gct cgc gac gct gac ctc ggt gtt gca tcc ggt aac ggc aag ggc cag   1123
Ala Arg Asp Ala Asp Leu Gly Val Ala Ser Gly Asn Gly Lys Gly Gln
                330                 335                 340

atc ttt gtc aag ggc gaa gtc atc aag act gtc cca gaa tcc cag atc   1171
Ile Phe Val Lys Gly Glu Val Ile Lys Thr Val Pro Glu Ser Gln Ile
            345                 350                 355

gtg gaa acc ctc atc gaa gaa gca atg cgt atc gca gag gaa atg gac   1219
Val Glu Thr Leu Ile Glu Glu Ala Met Arg Ile Ala Glu Glu Met Asp
        360                 365                 370

cca gaa gtc ctc gct gca gca agt gct tcc ggt atg aag gct gaa gtg   1267
Pro Glu Val Leu Ala Ala Ala Ser Ala Ser Gly Met Lys Ala Glu Val
```

375 380 385

aag gta acc aag taagttttgg ttaattaagg cac 1302
Lys Val Thr Lys
390

<210> 734
<211> 393
<212> PRT
<213> Corynebacterium glutamicum

<400> 734
Leu Ser Thr Pro Ile Gly Leu Gly Leu Pro Pro Thr Pro Pro Pro Val
1 5 10 15

Leu Ala Pro Arg Arg Lys Thr Arg Gln Leu Met Val Gly Lys Val Gly
20 25 30

Val Gly Ser Asp His Pro Ile Ser Val Gln Ser Met Thr Thr Thr Lys
35 40 45

Thr His Asp Ile Asn Gly Thr Leu Gln Gln Ile Ala Gln Leu Thr Ala
50 55 60

Thr Gly Cys Asp Ile Val Arg Val Ala Cys Pro Lys Thr Val Asp Ala
65 70 75 80

Glu Ala Leu Pro Ile Ile Ala Lys Lys Ser Pro Ile Pro Val Ile Ala
85 90 95

Asp Ile His Phe Gln Pro Lys Tyr Ile Phe Ala Ala Ile Asp Ala Gly
100 105 110

Cys Ala Ala Val Arg Val Asn Pro Gly Asn Ile Lys Glu Phe Asp Gly
115 120 125

Arg Val Lys Glu Val Ala Lys Ala Ala Gly Asp Ala Gly Ile Pro Ile
130 135 140

Arg Ile Gly Val Asn Gly Gly Ser Leu Asp Lys Arg Ile Leu Asp Lys
145 150 155 160

Tyr His Gly Lys Ala Thr Pro Glu Ala Leu Val Glu Ser Ala Met Trp
165 170 175

Glu Ala Gly Leu Phe Glu Glu His Gly Phe Gly Asp Ile Ala Ile Ser
180 185 190

Val Lys His Ser Asp Pro Val Leu Met Val Glu Ala Tyr Arg Gln Leu
195 200 205

Ala Glu Gln Ser Asp Tyr Pro Leu His Leu Gly Val Thr Glu Ala Gly
210 215 220

Pro Lys Phe Met Gly Thr Ile Lys Ser Ser Val Ala Phe Gly Ala Leu
225 230 235 240

Leu Ser Gln Gly Ile Gly Asp Thr Ile Arg Val Ser Leu Ser Ala Asp
245 250 255

```
Pro Val Glu Glu Ile Lys Val Gly Asp Gln Ile Leu Gln Ser Leu Asn
            260                 265                 270

Leu Arg Pro Arg Lys Leu Glu Ile Val Ser Cys Pro Ser Cys Gly Arg
        275                 280                 285

Ala Gln Val Asp Val Tyr Ser Leu Ala Glu Glu Val Thr Glu Ala Leu
    290                 295                 300

Asp Gly Met Glu Val Pro Leu Arg Val Ala Val Met Gly Cys Val Val
305                 310                 315                 320

Asn Gly Pro Gly Glu Ala Arg Asp Ala Asp Leu Gly Val Ala Ser Gly
                325                 330                 335

Asn Gly Lys Gly Gln Ile Phe Val Lys Gly Glu Val Ile Lys Thr Val
            340                 345                 350

Pro Glu Ser Gln Ile Val Glu Thr Leu Ile Glu Glu Ala Met Arg Ile
        355                 360                 365

Ala Glu Glu Met Asp Pro Glu Val Leu Ala Ala Ala Ser Ala Ser Gly
    370                 375                 380

Met Lys Ala Glu Val Lys Val Thr Lys
385                 390


<210> 735
<211> 620
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(597)
<223> FRXA01696

<400> 735
cac tcc gac cca gta ctc atg gtg gag gcc tac cgc cag ctc gct gaa   48
His Ser Asp Pro Val Leu Met Val Glu Ala Tyr Arg Gln Leu Ala Glu
  1               5                  10                  15

caa agc gac tac cca ctg cac ctc ggt gtt act gaa gct ggt ccc aag   96
Gln Ser Asp Tyr Pro Leu His Leu Gly Val Thr Glu Ala Gly Pro Lys
             20                  25                  30

ttc atg gga aca atc aag tct tcc gta gca ttc ggc gct ctg ctg tcc   144
Phe Met Gly Thr Ile Lys Ser Ser Val Ala Phe Gly Ala Leu Leu Ser
         35                  40                  45

cag ggc atc ggc gac act atc cgt gtg tct ctt tct gct gac cca gtg   192
Gln Gly Ile Gly Asp Thr Ile Arg Val Ser Leu Ser Ala Asp Pro Val
     50                  55                  60

gaa gaa atc aag gtt ggc gac cag att ctg cag tcc ctc aac ctg cgc   240
Glu Glu Ile Lys Val Gly Asp Gln Ile Leu Gln Ser Leu Asn Leu Arg
 65                  70                  75                  80

cca cgc aag ctg gaa atc gtg tcc tgc cca tca tgt ggc cgc gca cag   288
Pro Arg Lys Leu Glu Ile Val Ser Cys Pro Ser Cys Gly Arg Ala Gln
```

```
                85                  90                  95

gtc gat gtg tac tca ctt gct gaa gaa gtc acc gaa gca ctc gac ggc   336
Val Asp Val Tyr Ser Leu Ala Glu Glu Val Thr Glu Ala Leu Asp Gly
            100                 105                 110

atg gaa gtt cca ctg cgc gtc gct gtc atg ggt tgc gtt gtt aac ggc   384
Met Glu Val Pro Leu Arg Val Ala Val Met Gly Cys Val Val Asn Gly
        115                 120                 125

cca ggt gag gct cgc gac gct gac ctc ggt gtt gca tcc ggt aac ggc   432
Pro Gly Glu Ala Arg Asp Ala Asp Leu Gly Val Ala Ser Gly Asn Gly
    130                 135                 140

aag ggc cag atc ttt gtc aag ggc gaa gtc atc aag act gtc cca gaa   480
Lys Gly Gln Ile Phe Val Lys Gly Glu Val Ile Lys Thr Val Pro Glu
145                 150                 155                 160

tcc cag atc gtg gaa acc ctc atc gaa gaa gca atg cgt atc gca gag   528
Ser Gln Ile Val Glu Thr Leu Ile Glu Glu Ala Met Arg Ile Ala Glu
                165                 170                 175

gaa atg gac cca gaa gtc ctc gct gca gca agt gct tcc ggt atg aag   576
Glu Met Asp Pro Glu Val Leu Ala Ala Ala Ser Ala Ser Gly Met Lys
            180                 185                 190

gct gaa gtg aag gta acc aag taagttttgg ttaattaagg cac            620
Ala Glu Val Lys Val Thr Lys
        195
```

Sequence Listing - 2006-05-25 - 15:05:05

<210> 736
<211> 199
<212> PRT
<213> Corynebacterium glutamicum

<400> 736

```
His Ser Asp Pro Val Leu Met Val Glu Ala Tyr Arg Gln Leu Ala Glu
  1               5                  10                  15

Gln Ser Asp Tyr Pro Leu His Leu Gly Val Thr Glu Ala Gly Pro Lys
             20                  25                  30

Phe Met Gly Thr Ile Lys Ser Ser Val Ala Phe Gly Ala Leu Leu Ser
         35                  40                  45

Gln Gly Ile Gly Asp Thr Ile Arg Val Ser Leu Ser Ala Asp Pro Val
     50                  55                  60

Glu Glu Ile Lys Val Gly Asp Gln Ile Leu Gln Ser Leu Asn Leu Arg
 65                  70                  75                  80

Pro Arg Lys Leu Glu Ile Val Ser Cys Pro Ser Cys Gly Arg Ala Gln
                 85                  90                  95

Val Asp Val Tyr Ser Leu Ala Glu Glu Val Thr Glu Ala Leu Asp Gly
            100                 105                 110

Met Glu Val Pro Leu Arg Val Ala Val Met Gly Cys Val Val Asn Gly
        115                 120                 125
```

```
Pro Gly Glu Ala Arg Asp Ala Asp Leu Gly Val Ala Ser Gly Asn Gly
    130                 135                 140

Lys Gly Gln Ile Phe Val Lys Gly Glu Val Ile Lys Thr Val Pro Glu
145                 150                 155                 160

Ser Gln Ile Val Glu Thr Leu Ile Glu Glu Ala Met Arg Ile Ala Glu
                165                 170                 175

Glu Met Asp Pro Glu Val Leu Ala Ala Ala Ser Ala Ser Gly Met Lys
            180                 185                 190

Ala Glu Val Lys Val Thr Lys
        195


<210> 737
<211> 1080
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1057)
<223> RXN01697

<400> 737
tagatcaact aagtatgaac gcgaatccga ctttggtcgt actgcaagaa tcgaccagag 60

cccgattaaa aaatgccccc gcgcaacgaa actagtaatc atg ttt caa gga cta   115
                                            Met Phe Gln Gly Leu
                                              1               5

aaa gaa ctc acc gca gca aaa ggc cgc acg ctg ctg atc acc gtc acc   163
Lys Glu Leu Thr Ala Ala Lys Gly Arg Thr Leu Leu Ile Thr Val Thr
                10                  15                  20

gtc ggg ctg atc gcc gtg ctg gtt act ttc ctc tct gcc ctc acc gcc   211
Val Gly Leu Ile Ala Val Leu Val Thr Phe Leu Ser Ala Leu Thr Ala
            25                  30                  35

ggg ctt ggc cac caa tca gta tcc gca ctg aaa tac cta gcg ggt gat   259
Gly Leu Gly His Gln Ser Val Ser Ala Leu Lys Tyr Leu Ala Gly Asp
        40                  45                  50

aat gaa ctt atc ctc gcc gat tcc gga tcc acc acg ctt tcc gcg tcc   307
Asn Glu Leu Ile Leu Ala Asp Ser Gly Ser Thr Thr Leu Ser Ala Ser
    55                  60                  65

acg ctt tct gat caa gca gtt gcc caa ctc gaa gac gaa ggc gca cag   355
Thr Leu Ser Asp Gln Ala Val Ala Gln Leu Glu Asp Glu Gly Ala Gln
70                  75                  80                  85

atg ctg tgg cag gtc cgc gac cga gta gca gac acc ccc acc atg ctc   403
Met Leu Trp Gln Val Arg Asp Arg Val Ala Asp Thr Pro Thr Met Leu
                90                  95                  100

ctc aac tcc cct gac ctt gcg cct ggt gaa gta tcc ctt cct gcc gaa   451
Leu Asn Ser Pro Asp Leu Ala Pro Gly Glu Val Ser Leu Pro Ala Glu
            105                 110                 115
```

```
ctc gct gat tcg gaa ctc gct act gcg cat gat gta gtg gat tct tcc   499
Leu Ala Asp Ser Glu Leu Ala Thr Ala His Asp Val Val Asp Ser Ser
        120                 125                 130

aac gat ctg tac ctc gat cac ctg ccc gtg gta ttg atg aac acc tcc   547
Asn Asp Leu Tyr Leu Asp His Leu Pro Val Val Leu Met Asn Thr Ser
    135                 140                 145

gat tta gcc tca ctc gcg caa gtc cga ggc gtg aca gga cca gca ggc   595
Asp Leu Ala Ser Leu Ala Gln Val Arg Gly Val Thr Gly Pro Ala Gly
150                 155                 160                 165

gca ttc gcc tct gac gtt gcg ctc ccc tcc gac acc gtt gcg ctc tct   643
Ala Phe Ala Ser Asp Val Ala Leu Pro Ser Asp Thr Val Ala Leu Ser
                170                 175                 180

gga tcc gaa cgg tgg aac gca tcc gcc tcc tac cag ggc gaa cag atg   691
Gly Ser Glu Arg Trp Asn Ala Ser Ala Ser Tyr Gln Gly Glu Gln Met
            185                 190                 195

tca ctc aac ctc atg atc gtc atg ctg tat gtt atc tcc gca ctc gtg   739
Ser Leu Asn Leu Met Ile Val Met Leu Tyr Val Ile Ser Ala Leu Val
        200                 205                 210

ctc ggc gca ttc ttc acc gtc tgg acc atc caa cgc ctc cgc ggc atc   787
Leu Gly Ala Phe Phe Thr Val Trp Thr Ile Gln Arg Leu Arg Gly Ile
    215                 220                 225

gcc atc tct agt gct ttg gga gca gcc cgc cga gta ctt atc gcc gac   835
Ala Ile Ser Ser Ala Leu Gly Ala Ala Arg Arg Val Leu Ile Ala Asp
230                 235                 240                 245

gct ctc ggc caa gcc atc atc gtc tta gga atc ggc atc acc gca ggc   883
Ala Leu Gly Gln Ala Ile Ile Val Leu Gly Ile Gly Ile Thr Ala Gly
                250                 255                 260

aca ttg atc aca gtc atc tcc gca ttc ggc atg gga gac gca atg ccc   931
Thr Leu Ile Thr Val Ile Ser Ala Phe Gly Met Gly Asp Ala Met Pro
            265                 270                 275

gtg gtc atc tcc tcc tcc acc acg ctc ttc ccc gca ctt atc ctc gcc   979
Val Val Ile Ser Ser Ser Thr Thr Leu Phe Pro Ala Leu Ile Leu Ala
        280                 285                 290

gca gca gga ctc atc ggt gcc gcc att tca ctc ggc ccc atc ctt cgc   1027
Ala Ala Gly Leu Ile Gly Ala Ala Ile Ser Leu Gly Pro Ile Leu Arg
    295                 300                 305

gtc gaa cca cgc tcc gca ctc atg aac gca taagaaaagg aacctcacat     1077
Val Glu Pro Arg Ser Ala Leu Met Asn Ala
310                 315

gac                                                               1080
```

<210> 738
<211> 319
<212> PRT
<213> Corynebacterium glutamicum

<400> 738

```
Met Phe Gln Gly Leu Lys Glu Leu Thr Ala Ala Lys Gly Arg Thr Leu
 1               5                  10                  15

Leu Ile Thr Val Thr Val Gly Leu Ile Ala Val Leu Val Thr Phe Leu
            20                  25                  30

Ser Ala Leu Thr Ala Gly Leu Gly His Gln Ser Val Ser Ala Leu Lys
        35                  40                  45

Tyr Leu Ala Gly Asp Asn Glu Leu Ile Leu Ala Asp Ser Gly Ser Thr
    50                  55                  60

Thr Leu Ser Ala Ser Thr Leu Ser Asp Gln Ala Val Ala Gln Leu Glu
65                  70                  75                  80

Asp Glu Gly Ala Gln Met Leu Trp Gln Val Arg Asp Arg Val Ala Asp
                85                  90                  95

Thr Pro Thr Met Leu Leu Asn Ser Pro Asp Leu Ala Pro Gly Glu Val
            100                 105                 110

Ser Leu Pro Ala Glu Leu Ala Asp Ser Glu Leu Ala Thr Ala His Asp
        115                 120                 125

Val Val Asp Ser Ser Asn Asp Leu Tyr Leu Asp His Leu Pro Val Val
    130                 135                 140

Leu Met Asn Thr Ser Asp Leu Ala Ser Leu Ala Gln Val Arg Gly Val
145                 150                 155                 160

Thr Gly Pro Ala Gly Ala Phe Ala Ser Asp Val Ala Leu Pro Ser Asp
                165                 170                 175

Thr Val Ala Leu Ser Gly Ser Glu Arg Trp Asn Ala Ser Ala Ser Tyr
            180                 185                 190

Gln Gly Glu Gln Met Ser Leu Asn Leu Met Ile Val Met Leu Tyr Val
        195                 200                 205

Ile Ser Ala Leu Val Leu Gly Ala Phe Phe Thr Val Trp Thr Ile Gln
    210                 215                 220

Arg Leu Arg Gly Ile Ala Ile Ser Ser Ala Leu Gly Ala Ala Arg Arg
225                 230                 235                 240

Val Leu Ile Ala Asp Ala Leu Gly Gln Ala Ile Ile Val Leu Gly Ile
                245                 250                 255

Gly Ile Thr Ala Gly Thr Leu Ile Thr Val Ile Ser Ala Phe Gly Met
            260                 265                 270

Gly Asp Ala Met Pro Val Val Ile Ser Ser Ser Thr Thr Leu Phe Pro
        275                 280                 285

Ala Leu Ile Leu Ala Ala Ala Gly Leu Ile Gly Ala Ala Ile Ser Leu
    290                 295                 300

Gly Pro Ile Leu Arg Val Glu Pro Arg Ser Ala Leu Met Asn Ala
305                 310                 315
```

<210> 739
<211> 826
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(826)
<223> FRXA01697

<400> 739
tagatcaact aagtatgaac gcgaatccga ctttggtcgt actgcaagaa tcgaccagag 60

cccgattaaa aaatgccccc gcgcaacgaa actagtaatc atg ttt caa gga cta 115
Met Phe Gln Gly Leu
1 5

aaa gaa ctc acc gca gca aaa ggc cgc acg ctg ctg atc acc gtc acc 163
Lys Glu Leu Thr Ala Ala Lys Gly Arg Thr Leu Leu Ile Thr Val Thr
10 15 20

gtc ggg ctg atc gcc gtg ctg gtt act ttc ctc tct gcc ctc acc gcc 211
Val Gly Leu Ile Ala Val Leu Val Thr Phe Leu Ser Ala Leu Thr Ala
25 30 35

ggg ctt ggc cac caa tca gta tcc gca ctg aaa tac cta gcg ggt gat 259
Gly Leu Gly His Gln Ser Val Ser Ala Leu Lys Tyr Leu Ala Gly Asp
40 45 50

aat gaa ctt atc ctc gcc gat tcc gga tcc acc acg ctt tcc gcg tcc 307
Asn Glu Leu Ile Leu Ala Asp Ser Gly Ser Thr Thr Leu Ser Ala Ser
55 60 65

acg ctt tct gat caa gca gtt gcc caa ctc gaa gac gaa ggc gca cag 355
Thr Leu Ser Asp Gln Ala Val Ala Gln Leu Glu Asp Glu Gly Ala Gln
70 75 80 85

atg ctg tgg cag gtc cgc gac cga gta gca gac acc ccc acc atg ctc 403
Met Leu Trp Gln Val Arg Asp Arg Val Ala Asp Thr Pro Thr Met Leu
90 95 100

ctc aac tcc cct gac ctt gcg cct ggt gaa gta tcc ctt cct gcc gaa 451
Leu Asn Ser Pro Asp Leu Ala Pro Gly Glu Val Ser Leu Pro Ala Glu
105 110 115

ctc gct gat tcg gaa ctc gct act gcg cat gat gta gtg gat tct tcc 499
Leu Ala Asp Ser Glu Leu Ala Thr Ala His Asp Val Val Asp Ser Ser
120 125 130

aac gat ctg tac ctc gat cac ctg ccc gtg gta ttg atg aac acc tcc 547
Asn Asp Leu Tyr Leu Asp His Leu Pro Val Val Leu Met Asn Thr Ser
135 140 145

gat tta gcc tca ctc gcg caa gtc cga ggc gtg aca gga cca gca ggc 595
Asp Leu Ala Ser Leu Ala Gln Val Arg Gly Val Thr Gly Pro Ala Gly
150 155 160 165

gca ttc gcc tct gac gtt gcg ctc ccc tcc gac acc gtt gcg ctc tct 643
Ala Phe Ala Ser Asp Val Ala Leu Pro Ser Asp Thr Val Ala Leu Ser
170 175 180

```
gga tcc gaa cgg tgg aac gca tcc gcc tcc tac cag ggc gaa cag atg   691
Gly Ser Glu Arg Trp Asn Ala Ser Ala Ser Tyr Gln Gly Glu Gln Met
            185                 190                 195

tca ctc aac ctc atg atc gtc atg ctg tat gtc atc tcc gca ctc gtg   739
Ser Leu Asn Leu Met Ile Val Met Leu Tyr Val Ile Ser Ala Leu Val
        200                 205                 210

ctc ggc gca ttc ttc acc gtc tgg acc atc caa cgc ctc cgc ggc atc   787
Leu Gly Ala Phe Phe Thr Val Trp Thr Ile Gln Arg Leu Arg Gly Ile
    215                 220                 225

gcc atc tct agt gct ttg gga gca gcc cgc cga gta ctt               826
Ala Ile Ser Ser Ala Leu Gly Ala Ala Arg Arg Val Leu
230                 235                 240
```

<210> 740
<211> 242
<212> PRT
<213> Corynebacterium glutamicum

<400> 740

```
Met Phe Gln Gly Leu Lys Glu Leu Thr Ala Ala Lys Gly Arg Thr Leu
  1               5                  10                  15

Leu Ile Thr Val Thr Val Gly Leu Ile Ala Val Leu Val Thr Phe Leu
             20                  25                  30

Ser Ala Leu Thr Ala Gly Leu Gly His Gln Ser Val Ser Ala Leu Lys
         35                  40                  45

Tyr Leu Ala Gly Asp Asn Glu Leu Ile Leu Ala Asp Ser Gly Ser Thr
     50                  55                  60

Thr Leu Ser Ala Ser Thr Leu Ser Asp Gln Ala Val Ala Gln Leu Glu
 65                  70                  75                  80

Asp Glu Gly Ala Gln Met Leu Trp Gln Val Arg Asp Arg Val Ala Asp
                 85                  90                  95

Thr Pro Thr Met Leu Leu Asn Ser Pro Asp Leu Ala Pro Gly Glu Val
            100                 105                 110

Ser Leu Pro Ala Glu Leu Ala Asp Ser Glu Leu Ala Thr Ala His Asp
        115                 120                 125

Val Val Asp Ser Ser Asn Asp Leu Tyr Leu Asp His Leu Pro Val Val
    130                 135                 140

Leu Met Asn Thr Ser Asp Leu Ala Ser Leu Ala Gln Val Arg Gly Val
145                 150                 155                 160

Thr Gly Pro Ala Gly Ala Phe Ala Ser Asp Val Ala Leu Pro Ser Asp
                165                 170                 175

Thr Val Ala Leu Ser Gly Ser Glu Arg Trp Asn Ala Ser Ala Ser Tyr
            180                 185                 190

Gln Gly Glu Gln Met Ser Leu Asn Leu Met Ile Val Met Leu Tyr Val
        195                 200                 205
```

```
Ile Ser Ala Leu Val Leu Gly Ala Phe Phe Thr Val Trp Thr Ile Gln
    210                 215                 220

Arg Leu Arg Gly Ile Ala Ile Ser Ser Ala Leu Gly Ala Ala Arg Arg
225                 230                 235                 240

Val Leu
```

<210> 741
<211> 472
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(472)
<223> RXN01701

<400> 741

```
gccgatcaaa ttcattgatt gttaatcgga agtttttga acaggtaaag ctaggggacc 60

tgttcagtgc ctgttggcgg atgtattaag gagaatgccc atg ctg agc cac gaa   115
                                            Met Leu Ser His Glu
                                              1               5

gaa att gtt gcg atc gca gaa gat ttg ctg tct aaa cgc tac ggc ggt   163
Glu Ile Val Ala Ile Ala Glu Asp Leu Leu Ser Lys Arg Tyr Gly Gly
                 10                  15                  20

gta caa act ctt tct gac gtg gag cag ctc aac ggt tcc ggc acc tcc   211
Val Gln Thr Leu Ser Asp Val Glu Gln Leu Asn Gly Ser Gly Thr Ser
             25                  30                  35

gcg gtg ctg cgt gcc agg gtg gct aac tcc cca ttc ctc caa cag cgc   259
Ala Val Leu Arg Ala Arg Val Ala Asn Ser Pro Phe Leu Gln Gln Arg
         40                  45                  50

tcc gtg gtg ctg aag tac gtg ccc agc acc gga gac gtc ttt gat gat   307
Ser Val Val Leu Lys Tyr Val Pro Ser Thr Gly Asp Val Phe Asp Asp
     55                  60                  65

tct gcg ctg gtg cgt gaa atc gtc tcc tac cag ttc acc acc tcc ttg   355
Ser Ala Leu Val Arg Glu Ile Val Ser Tyr Gln Phe Thr Thr Ser Leu
 70                  75                  80                  85

tcg gaa gat gtc cgc cca ggg cca gtc att ttg gcc tat gac att gac   403
Ser Glu Asp Val Arg Pro Gly Pro Val Ile Leu Ala Tyr Asp Ile Asp
                 90                  95                 100

aag cgc atc ctg gtc att tca gat tcc ggc aac ggc gac acc ttt gcg   451
Lys Arg Ile Leu Val Ile Ser Asp Ser Gly Asn Gly Asp Thr Phe Ala
            105                 110                 115

gat ctg atc gat cag cgt ccg                                      472
Asp Leu Ile Asp Gln Arg Pro
        120
```

<210> 742
<211> 124
<212> PRT
<213> Corynebacterium glutamicum

<400> 742
Met Leu Ser His Glu Glu Ile Val Ala Ile Ala Glu Asp Leu Leu Ser
1 5 10 15

Lys Arg Tyr Gly Gly Val Gln Thr Leu Ser Asp Val Glu Gln Leu Asn
20 25 30

Gly Ser Gly Thr Ser Ala Val Leu Arg Ala Arg Val Ala Asn Ser Pro
35 40 45

Phe Leu Gln Gln Arg Ser Val Val Leu Lys Tyr Val Pro Ser Thr Gly
50 55 60

Asp Val Phe Asp Asp Ser Ala Leu Val Arg Glu Ile Val Ser Tyr Gln
65 70 75 80

Phe Thr Thr Ser Leu Ser Glu Asp Val Arg Pro Gly Pro Val Ile Leu
85 90 95

Ala Tyr Asp Ile Asp Lys Arg Ile Leu Val Ile Ser Asp Ser Gly Asn
100 105 110

Gly Asp Thr Phe Ala Asp Leu Ile Asp Gln Arg Pro
115 120

<210> 743
<211> 433
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(433)
<223> FRXA01701

<400> 743
gccgatcaaa ttcattgatt gttaatcgga agtttttga acaggtaaag ctaggggacc 60

tgttcagtgc ctgttggcgg atgtattaag gagaatgccc atg ctg agc cac gaa 115
Met Leu Ser His Glu
1 5

gaa att gtt gcg atc gca gaa gat ttg ctg tct aaa cgc tac ggc ggt 163
Glu Ile Val Ala Ile Ala Glu Asp Leu Leu Ser Lys Arg Tyr Gly Gly
10 15 20

gta caa act ctt tct gac gtg gag cag ctc aac ggt tcc ggc acc tcc 211
Val Gln Thr Leu Ser Asp Val Glu Gln Leu Asn Gly Ser Gly Thr Ser
25 30 35

gcg gtg ctg cgt gcc agg gtg gct aac tcc cca ttc ctc caa cag cgc 259
Ala Val Leu Arg Ala Arg Val Ala Asn Ser Pro Phe Leu Gln Gln Arg
40 45 50

tcc gtg gtg ctg aag tac gtg ccc agc acc gga gac gtc ttt gat gat 307

```
Ser Val Val Leu Lys Tyr Val Pro Ser Thr Gly Asp Val Phe Asp Asp
     55                  60                  65

tct gcg ctg gtg cgt gaa atc gtc tcc tac cag ttc acc acc tcc ttg   355
Ser Ala Leu Val Arg Glu Ile Val Ser Tyr Gln Phe Thr Thr Ser Leu
 70                  75                  80                  85

tcg gaa gat gtc cgc cca ggg cca gtc att ttg gcc tat gac att gac   403
Ser Glu Asp Val Arg Pro Gly Pro Val Ile Leu Ala Tyr Asp Ile Asp
                 90                  95                 100

aag cgc atc ctg gtc att tca gat tcc ggc                          433
Lys Arg Ile Leu Val Ile Ser Asp Ser Gly
            105                 110


<210> 744
<211> 111
<212> PRT
<213> Corynebacterium glutamicum

<400> 744
Met Leu Ser His Glu Glu Ile Val Ala Ile Ala Glu Asp Leu Leu Ser
  1               5                  10                  15

Lys Arg Tyr Gly Gly Val Gln Thr Leu Ser Asp Val Glu Gln Leu Asn
             20                  25                  30

Gly Ser Gly Thr Ser Ala Val Leu Arg Ala Arg Val Ala Asn Ser Pro
         35                  40                  45

Phe Leu Gln Gln Arg Ser Val Val Leu Lys Tyr Val Pro Ser Thr Gly
     50                  55                  60

Asp Val Phe Asp Asp Ser Ala Leu Val Arg Glu Ile Val Ser Tyr Gln
 65                  70                  75                  80

Phe Thr Thr Ser Leu Ser Glu Asp Val Arg Pro Gly Pro Val Ile Leu
                 85                  90                  95

Ala Tyr Asp Ile Asp Lys Arg Ile Leu Val Ile Ser Asp Ser Gly
            100                 105                 110


<210> 745
<211> 1236
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1213)
<223> RXN01703

<400> 745
gttagacaaa tgggtaaaca gagctgacct agcggaatcc gccatcaacg aaaggcattc 60

cgcgagggtt tggggtctgc ctcgaacaaa tcttgggttt gtg gca tgg cca tcc   115
                                               Val Ala Trp Pro Ser
                                                 1               5
```

```
aac gcc aaa gaa aaa ctg ttt atc cac tgg cac tac tgg tgg caa gcg   163
Asn Ala Lys Glu Lys Leu Phe Ile His Trp His Tyr Trp Trp Gln Ala
                10                  15                  20

cat tat cta gac tgc ctg gtg gat gct gct cgt cga cgc acc aca aag   211
His Tyr Leu Asp Cys Leu Val Asp Ala Ala Arg Arg Arg Thr Thr Lys
            25                  30                  35

gcc cgt cgc gac cgc atc agg gac acc atc cgc ggc att tcg gtg cgc   259
Ala Arg Arg Asp Arg Ile Arg Asp Thr Ile Arg Gly Ile Ser Val Arg
        40                  45                  50

aat gtg ggc aag ctg acc tcg aat cgt tat tac gac gac aaa gct tgg   307
Asn Val Gly Lys Leu Thr Ser Asn Arg Tyr Tyr Asp Asp Lys Ala Trp
    55                  60                  65

ctg gcc ctt gct ctt ggg cgt gcc gga aaa gtg cga aag gtg cgc aca   355
Leu Ala Leu Ala Leu Gly Arg Ala Gly Lys Val Arg Lys Val Arg Thr
70                  75                  80                  85

cca aaa tca ttg ccc tcg ttg gaa caa aac atc gtc gat ggc att gat   403
Pro Lys Ser Leu Pro Ser Leu Glu Gln Asn Ile Val Asp Gly Ile Asp
                90                  95                  100

tcc ctt act ggt gtg ctg ccg tgg cgt tcc ggc gaa acc ttc tac aac   451
Ser Leu Thr Gly Val Leu Pro Trp Arg Ser Gly Glu Thr Phe Tyr Asn
            105                 110                 115

gtt ccc tcc aac ggt cct gct gcg atc atg atg gcc cgc acc gac cgt   499
Val Pro Ser Asn Gly Pro Ala Ala Ile Met Met Ala Arg Thr Asp Arg
        120                 125                 130

ttg gac gag gct atg aaa atc acc gat tgg att ttt gac aac ctg atc   547
Leu Asp Glu Ala Met Lys Ile Thr Asp Trp Ile Phe Asp Asn Leu Ile
    135                 140                 145

gat ggc gac ggc ctt gtg atg gac gga ttg cgc atg cgc atg cac gga   595
Asp Gly Asp Gly Leu Val Met Asp Gly Leu Arg Met Arg Met His Gly
150                 155                 160                 165

cct gag ctt gtc cgt tcc atc cac ccg tat tgc caa ggt gtc gcc att   643
Pro Glu Leu Val Arg Ser Ile His Pro Tyr Cys Gln Gly Val Ala Ile
                170                 175                 180

ggt gcg tgt ttg gaa att gct ctc aaa ctg cgt gag cgc gca ggc ttg   691
Gly Ala Cys Leu Glu Ile Ala Leu Lys Leu Arg Glu Arg Ala Gly Leu
            185                 190                 195

acc act act gtg gtg gat cac tgg tcg gat gcc gat aag gca gaa gac   739
Thr Thr Thr Val Val Asp His Trp Ser Asp Ala Asp Lys Ala Glu Asp
        200                 205                 210

tcc ctc aaa tac ttt gca cac atc cac gct gtg gtt cag gct gtg tcg   787
Ser Leu Lys Tyr Phe Ala His Ile His Ala Val Val Gln Ala Val Ser
    215                 220                 225

cgg aag atg acc aac ttc cac ggc gtt att gat tgg gac acc ggt gac   835
Arg Lys Met Thr Asn Phe His Gly Val Ile Asp Trp Asp Thr Gly Asp
230                 235                 240                 245

ggc gac ggc ggt ttg ttc aag ggc att ttg gtc cgc tat tta gct gat   883
```

```
Gly Asp Gly Gly Leu Phe Lys Gly Ile Leu Val Arg Tyr Leu Ala Asp
                250                 255                 260

gtg gcc atc cgc ctg cct gac gat tca cca acc aac cgg gaa acc aaa   931
Val Ala Ile Arg Leu Pro Asp Asp Ser Pro Thr Asn Arg Glu Thr Lys
            265                 270                 275

aag att gca gca cgc ctg gta ctg gaa tcg gcg gaa agc gta tgg aac   979
Lys Ile Ala Ala Arg Leu Val Leu Glu Ser Ala Glu Ser Val Trp Asn
        280                 285                 290

cac cga ttg gaa gtt gat ggc ctt ccg gta ttc gcc aca gac tgg aca   1027
His Arg Leu Glu Val Asp Gly Leu Pro Val Phe Ala Thr Asp Trp Thr
    295                 300                 305

acg gat gca cgc ctg cca caa aac ttt ggt ttg agt tcc tct agt ttg   1075
Thr Asp Ala Arg Leu Pro Gln Asn Phe Gly Leu Ser Ser Ser Ser Leu
310                 315                 320                 325

agc gat ctg gtg agt gtt gtg cgc gtg gat gaa cgt gat ctg tcc gtg   1123
Ser Asp Leu Val Ser Val Val Arg Val Asp Glu Arg Asp Leu Ser Val
                330                 335                 340

caa ttg tcc ggt tgg atg ctc atg gaa gca gca gcg aaa gtg gcc gaa   1171
Gln Leu Ser Gly Trp Met Leu Met Glu Ala Ala Ala Lys Val Ala Glu
            345                 350                 355

gaa ctg gaa aac aac ggc aat agt tac acc ggt cgc tcc cga           1213
Glu Leu Glu Asn Asn Gly Asn Ser Tyr Thr Gly Arg Ser Arg
        360                 365                 370

tagccccgat agtgtatgtg ctg                                        1236


<210> 746
<211> 371
<212> PRT
<213> Corynebacterium glutamicum

<400> 746
Val Ala Trp Pro Ser Asn Ala Lys Glu Lys Leu Phe Ile His Trp His
  1               5                  10                  15

Tyr Trp Trp Gln Ala His Tyr Leu Asp Cys Leu Val Asp Ala Ala Arg
             20                  25                  30

Arg Arg Thr Thr Lys Ala Arg Arg Asp Arg Ile Arg Asp Thr Ile Arg
         35                  40                  45

Gly Ile Ser Val Arg Asn Val Gly Lys Leu Thr Ser Asn Arg Tyr Tyr
     50                  55                  60

Asp Asp Lys Ala Trp Leu Ala Leu Ala Leu Gly Arg Ala Gly Lys Val
 65                  70                  75                  80

Arg Lys Val Arg Thr Pro Lys Ser Leu Pro Ser Leu Glu Gln Asn Ile
                 85                  90                  95

Val Asp Gly Ile Asp Ser Leu Thr Gly Val Leu Pro Trp Arg Ser Gly
            100                 105                 110
```

```
Glu Thr Phe Tyr Asn Val Pro Ser Asn Gly Pro Ala Ala Ile Met Met
        115                 120                 125

Ala Arg Thr Asp Arg Leu Asp Glu Ala Met Lys Ile Thr Asp Trp Ile
    130                 135                 140

Phe Asp Asn Leu Ile Asp Gly Asp Gly Leu Val Met Asp Gly Leu Arg
145                 150                 155                 160

Met Arg Met His Gly Pro Glu Leu Val Arg Ser Ile His Pro Tyr Cys
                165                 170                 175

Gln Gly Val Ala Ile Gly Ala Cys Leu Glu Ile Ala Leu Lys Leu Arg
            180                 185                 190

Glu Arg Ala Gly Leu Thr Thr Thr Val Val Asp His Trp Ser Asp Ala
        195                 200                 205

Asp Lys Ala Glu Asp Ser Leu Lys Tyr Phe Ala His Ile His Ala Val
    210                 215                 220

Val Gln Ala Val Ser Arg Lys Met Thr Asn Phe His Gly Val Ile Asp
225                 230                 235                 240

Trp Asp Thr Gly Asp Gly Asp Gly Gly Leu Phe Lys Gly Ile Leu Val
                245                 250                 255

Arg Tyr Leu Ala Asp Val Ala Ile Arg Leu Pro Asp Asp Ser Pro Thr
            260                 265                 270

Asn Arg Glu Thr Lys Lys Ile Ala Ala Arg Leu Val Leu Glu Ser Ala
        275                 280                 285

Glu Ser Val Trp Asn His Arg Leu Glu Val Asp Gly Leu Pro Val Phe
    290                 295                 300

Ala Thr Asp Trp Thr Thr Asp Ala Arg Leu Pro Gln Asn Phe Gly Leu
305                 310                 315                 320

Ser Ser Ser Ser Leu Ser Asp Leu Val Ser Val Val Arg Val Asp Glu
                325                 330                 335

Arg Asp Leu Ser Val Gln Leu Ser Gly Trp Met Leu Met Glu Ala Ala
            340                 345                 350

Ala Lys Val Ala Glu Glu Leu Glu Asn Asn Gly Asn Ser Tyr Thr Gly
        355                 360                 365

Arg Ser Arg
    370
```

<210> 747
<211> 494
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(471)
<223> FRXA01703

<400> 747
ctc aaa tac ttt gca cac atc cac gct gtg gtt cag gct gtg tcg cgg 48
Leu Lys Tyr Phe Ala His Ile His Ala Val Val Gln Ala Val Ser Arg
1 5 10 15

aag atg acc aac ttc cac ggc gtt att gat tgg gac acc ggt gac ggc 96
Lys Met Thr Asn Phe His Gly Val Ile Asp Trp Asp Thr Gly Asp Gly
20 25 30

gac ggc ggt ttg ttc aag ggc att ttg gtc cgc tat tta gct gat gtg 144
Asp Gly Gly Leu Phe Lys Gly Ile Leu Val Arg Tyr Leu Ala Asp Val
35 40 45

gcc atc cgc ctg cct gac gat tca cca acc aac cgg gaa acc aaa aag 192
Ala Ile Arg Leu Pro Asp Asp Ser Pro Thr Asn Arg Glu Thr Lys Lys
50 55 60

att gca gca cgc ctg gta ctg gaa tcg gcg gaa agc gta tgg aac cac 240
Ile Ala Ala Arg Leu Val Leu Glu Ser Ala Glu Ser Val Trp Asn His
65 70 75 80

cga ttg gaa gtt gat ggc ctt ccg gta ttc gcc aca gac tgg aca acg 288
Arg Leu Glu Val Asp Gly Leu Pro Val Phe Ala Thr Asp Trp Thr Thr
85 90 95

gat gca cgc ctg cca caa aac ttt ggt ttg agt tcc tct agt ttg agc 336
Asp Ala Arg Leu Pro Gln Asn Phe Gly Leu Ser Ser Ser Ser Leu Ser
100 105 110

gat ctg gtg agt gtt gtg cgc gtg gat gaa cgt gat ctg tcc gtg caa 384
Asp Leu Val Ser Val Val Arg Val Asp Glu Arg Asp Leu Ser Val Gln
115 120 125

ttg tcc ggt tgg atg ctc atg gaa gca gca gcg aaa gtg gcc gaa gaa 432
Leu Ser Gly Trp Met Leu Met Glu Ala Ala Ala Lys Val Ala Glu Glu
130 135 140

ctg gaa aac aac ggc aat agt tac acc ggt cgc tcc cga tagccccgat 481
Leu Glu Asn Asn Gly Asn Ser Tyr Thr Gly Arg Ser Arg
145 150 155

agtgtatgtg ctg 494

<210> 748
<211> 157
<212> PRT
<213> Corynebacterium glutamicum

<400> 748
Leu Lys Tyr Phe Ala His Ile His Ala Val Val Gln Ala Val Ser Arg
1 5 10 15

Lys Met Thr Asn Phe His Gly Val Ile Asp Trp Asp Thr Gly Asp Gly
20 25 30

Asp Gly Gly Leu Phe Lys Gly Ile Leu Val Arg Tyr Leu Ala Asp Val
35 40 45

Ala Ile Arg Leu Pro Asp Asp Ser Pro Thr Asn Arg Glu Thr Lys Lys

```
     50                  55                  60

Ile Ala Ala Arg Leu Val Leu Glu Ser Ala Glu Ser Val Trp Asn His
 65                  70                  75                  80

Arg Leu Glu Val Asp Gly Leu Pro Val Phe Ala Thr Asp Trp Thr Thr
                 85                  90                  95

Asp Ala Arg Leu Pro Gln Asn Phe Gly Leu Ser Ser Ser Ser Leu Ser
            100                 105                 110

Asp Leu Val Ser Val Val Arg Val Asp Glu Arg Asp Leu Ser Val Gln
        115                 120                 125

Leu Ser Gly Trp Met Leu Met Glu Ala Ala Ala Lys Val Ala Glu Glu
    130                 135                 140

Leu Glu Asn Asn Gly Asn Ser Tyr Thr Gly Arg Ser Arg
145                 150                 155


<210> 749
<211> 555
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(532)
<223> RXN01709

<400> 749
gcaagtggaa ccacgatggg aacggtaact gctgccgctg cggtattact cgtagtttca 60

gaaattaggt gtcgatgcag caatacggaa ctttgccaat gtg ttt gaa caa gct   115
                                            Val Phe Glu Gln Ala
                                              1               5

ctc ggg ctc acc acc ctt gca caa aca gct gga gcg ggc gca gcg ggg   163
Leu Gly Leu Thr Thr Leu Ala Gln Thr Ala Gly Ala Gly Ala Ala Gly
                 10                  15                  20

ggc ttg ggt ttc atg gca atg gcg ttg ttg tct gca ggg atg cgc tcc   211
Gly Leu Gly Phe Met Ala Met Ala Leu Leu Ser Ala Gly Met Arg Ser
             25                  30                  35

ggc gtg gac atg att ctt aat gaa acc ggg ggt gaa aag atg ctt gca   259
Gly Val Asp Met Ile Leu Asn Glu Thr Gly Gly Glu Lys Met Leu Ala
         40                  45                  50

cag gca gat tta gtc atc act gga gaa gga cgc att gat gca cag acc   307
Gln Ala Asp Leu Val Ile Thr Gly Glu Gly Arg Ile Asp Ala Gln Thr
     55                  60                  65

ctc agc ggg aaa gct cct act gga atc gcc aaa cgg gca cgt gcg aaa   355
Leu Ser Gly Lys Ala Pro Thr Gly Ile Ala Lys Arg Ala Arg Ala Lys
 70                  75                  80                  85

gga att cca gta ctg gcg gtt tgt ggg cag agc cta ttg ggt cca gca   403
Gly Ile Pro Val Leu Ala Val Cys Gly Gln Ser Leu Leu Gly Pro Ala
                 90                  95                 100
```

```
atc tca aat gag cta ttt gaa gac atc tac agc ttt acc gat ttc gaa   451
Ile Ser Asn Glu Leu Phe Glu Asp Ile Tyr Ser Phe Thr Asp Phe Glu
            105                 110                 115

tct gac atc aat gaa tgc att cga aac ccg ctc cca att ttg gaa ggt   499
Ser Asp Ile Asn Glu Cys Ile Arg Asn Pro Leu Pro Ile Leu Glu Gly
        120                 125                 130

atc ggt ttt aac atc gcc aaa cat cat ctg agt tagcgatatt tcagcaaacc 552
Ile Gly Phe Asn Ile Ala Lys His His Leu Ser
    135                 140

gat                                                               555
```

<210> 750
<211> 144
<212> PRT
<213> Corynebacterium glutamicum

<400> 750

```
Val Phe Glu Gln Ala Leu Gly Leu Thr Thr Leu Ala Gln Thr Ala Gly
  1               5                  10                  15

Ala Gly Ala Ala Gly Gly Leu Gly Phe Met Ala Met Ala Leu Leu Ser
             20                  25                  30

Ala Gly Met Arg Ser Gly Val Asp Met Ile Leu Asn Glu Thr Gly Gly
         35                  40                  45

Glu Lys Met Leu Ala Gln Ala Asp Leu Val Ile Thr Gly Glu Gly Arg
     50                  55                  60

Ile Asp Ala Gln Thr Leu Ser Gly Lys Ala Pro Thr Gly Ile Ala Lys
 65                  70                  75                  80

Arg Ala Arg Ala Lys Gly Ile Pro Val Leu Ala Val Cys Gly Gln Ser
                 85                  90                  95

Leu Leu Gly Pro Ala Ile Ser Asn Glu Leu Phe Glu Asp Ile Tyr Ser
            100                 105                 110

Phe Thr Asp Phe Glu Ser Asp Ile Asn Glu Cys Ile Arg Asn Pro Leu
        115                 120                 125

Pro Ile Leu Glu Gly Ile Gly Phe Asn Ile Ala Lys His His Leu Ser
    130                 135                 140
```

<210> 751
<211> 368
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (16)..(345)

<223> FRXA01709

<400> 751
```
ttgttgtctg cagggatg cgc tcc ggc gtg gac atg att ctt aat gaa acc   51
                Met Arg Ser Gly Val Asp Met Ile Leu Asn Glu Thr
                  1               5                  10

ggg ggt gaa aag atg ctt gca cag gca gat tta gtc atc act gga gaa   99
Gly Gly Glu Lys Met Leu Ala Gln Ala Asp Leu Val Ile Thr Gly Glu
         15                  20                  25

gga cgc att gat gca cag acc ctc agc ggg aaa gct cct act gga atc   147
Gly Arg Ile Asp Ala Gln Thr Leu Ser Gly Lys Ala Pro Thr Gly Ile
     30                  35                  40

gcc aaa cgg gca cgt gcg aaa gga att cca gta ctg gcg gtt tgt ggg   195
Ala Lys Arg Ala Arg Ala Lys Gly Ile Pro Val Leu Ala Val Cys Gly
 45                  50                  55                  60

cag agc cta ttg ggt cca gca atc tca aat gag cta ttt gaa gac atc   243
Gln Ser Leu Leu Gly Pro Ala Ile Ser Asn Glu Leu Phe Glu Asp Ile
                65                  70                  75

tac agc ttt acc gat ttc gaa tct gac atc aat gaa tgc att cga aac   291
Tyr Ser Phe Thr Asp Phe Glu Ser Asp Ile Asn Glu Cys Ile Arg Asn
            80                  85                  90

ccg ctc cca att ttg gaa ggt atc ggt ttt aac atc gcc aaa cat cat   339
Pro Leu Pro Ile Leu Glu Gly Ile Gly Phe Asn Ile Ala Lys His His
         95                  100                 105

ctg agt tagcgatatt tcagcaaacc gat                                 368
Leu Ser
    110
```

<210> 752
<211> 110
<212> PRT
<213> Corynebacterium glutamicum

<400> 752
```
Met Arg Ser Gly Val Asp Met Ile Leu Asn Glu Thr Gly Gly Glu Lys
  1               5                  10                  15

Met Leu Ala Gln Ala Asp Leu Val Ile Thr Gly Glu Gly Arg Ile Asp
            20                  25                  30

Ala Gln Thr Leu Ser Gly Lys Ala Pro Thr Gly Ile Ala Lys Arg Ala
         35                  40                  45

Arg Ala Lys Gly Ile Pro Val Leu Ala Val Cys Gly Gln Ser Leu Leu
     50                  55                  60

Gly Pro Ala Ile Ser Asn Glu Leu Phe Glu Asp Ile Tyr Ser Phe Thr
 65                  70                  75                  80

Asp Phe Glu Ser Asp Ile Asn Glu Cys Ile Arg Asn Pro Leu Pro Ile
                85                  90                  95

Leu Glu Gly Ile Gly Phe Asn Ile Ala Lys His His Leu Ser
```

```
            100                 105                 110

<210> 753
<211> 1281
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1258)
<223> RXN01711

<400> 753
tctcgtgagt ttctccccgg tagcaccttc tatatcagcc cccacgccgc gtcggagcag 60

gtgggatagc atcggcaacg cggttgcatg gccgttggcc atg ttg ttg atg gcg   115
                                            Met Leu Leu Met Ala
                                              1               5

cat cgc ttc ttc gtg ctt gcg att aac ggc gca gtc acc gac gat ttc   163
His Arg Phe Phe Val Leu Ala Ile Asn Gly Ala Val Thr Asp Asp Phe
                 10                  15                  20

acg acg gtt tat agt gct tta cga cgt ttc gtt gaa ggt att ccg gtc   211
Thr Thr Val Tyr Ser Ala Leu Arg Arg Phe Val Glu Gly Ile Pro Val
             25                  30                  35

tac aac gag gtc tac cac ttc gtc gat ccg cac tac ctc tat aac ccg   259
Tyr Asn Glu Val Tyr His Phe Val Asp Pro His Tyr Leu Tyr Asn Pro
         40                  45                  50

ggc gcc acc ctc cta ttg gca cca ttg gga tat atc acc cat ttc acg   307
Gly Ala Thr Leu Leu Leu Ala Pro Leu Gly Tyr Ile Thr His Phe Thr
     55                  60                  65

ttg gct cgg tgg atg ttc atc gcg gtg aac ctc ctt gcc att gtt tta   355
Leu Ala Arg Trp Met Phe Ile Ala Val Asn Leu Leu Ala Ile Val Leu
 70                  75                  80                  85

gcg ttc ggg ctg ctg acc aga ctc tcc ggt tgg gcg ctg cgc agc atg   403
Ala Phe Gly Leu Leu Thr Arg Leu Ser Gly Trp Ala Leu Arg Ser Met
                 90                  95                 100

gtg tgg ccg att gcg atc gcc ttg gcg atg ctg aca gaa acc gtg caa   451
Val Trp Pro Ile Ala Ile Ala Leu Ala Met Leu Thr Glu Thr Val Gln
             105                 110                 115

aac acc ctc att ttc tcc aac atc aac ggc atc ctg ctg ctc atg ttg   499
Asn Thr Leu Ile Phe Ser Asn Ile Asn Gly Ile Leu Leu Leu Met Leu
         120                 125                 130

gcg att ttc ctg tgg tgc gtg gtg cac aaa aaa tcc tgg ttg ggc gga   547
Ala Ile Phe Leu Trp Cys Val Val His Lys Lys Ser Trp Leu Gly Gly
     135                 140                 145

cta gtc att ggt ttg gcc att ttg atc aaa ccc atg ttc ctg cca ctt   595
Leu Val Ile Gly Leu Ala Ile Leu Ile Lys Pro Met Phe Leu Pro Leu
150                 155                 160                 165

ctc ttc cta cct ttg gtg aaa aag caa tgg gga tcg ctc atc ctc ggc   643
```

```
Leu Phe Leu Pro Leu Val Lys Lys Gln Trp Gly Ser Leu Ile Leu Gly
                170                 175                 180

att tta acc cca gtg att ttc aat gca gtg gcc tgg ttc tta gtt ccg   691
Ile Leu Thr Pro Val Ile Phe Asn Ala Val Ala Trp Phe Leu Val Pro
            185                 190                 195

gga gca tct gaa tac gtc acc cgc acg atg ccc tac ctt ggt gaa act   739
Gly Ala Ser Glu Tyr Val Thr Arg Thr Met Pro Tyr Leu Gly Glu Thr
        200                 205                 210

cga gat ttt gcc aac agc tca ctc cca ggc ttg gcc atc tat ttc gga   787
Arg Asp Phe Ala Asn Ser Ser Leu Pro Gly Leu Ala Ile Tyr Phe Gly
    215                 220                 225

atg ccc acc tgg atg gaa atc acc tgg ttc ctc atc ttc ggc gca atg   835
Met Pro Thr Trp Met Glu Ile Thr Trp Phe Leu Ile Phe Gly Ala Met
230                 235                 240                 245

gtc ggc ctc gca gtg ctg gca ctc ctg aga ttc cgt aac acc gag cca   883
Val Gly Leu Ala Val Leu Ala Leu Leu Arg Phe Arg Asn Thr Glu Pro
                250                 255                 260

tac ttc tgg gca gca acc acc acc ggt gta ctc ctg act ggc gta ttc   931
Tyr Phe Trp Ala Ala Thr Thr Thr Gly Val Leu Leu Thr Gly Val Phe
            265                 270                 275

ttc ctg tcc tca ctg gga cag atg tac tac tcc atg atg atc ttc cct   979
Phe Leu Ser Ser Leu Gly Gln Met Tyr Tyr Ser Met Met Ile Phe Pro
        280                 285                 290

atg atc ttc acc ctg ctc gga agc cga tcc gta ttc cac aac tgg gtt   1027
Met Ile Phe Thr Leu Leu Gly Ser Arg Ser Val Phe His Asn Trp Val
    295                 300                 305

gcc tgg gtc gcc gcc tac ttc tta cta tcc cct gac act ttc acc tcc   1075
Ala Trp Val Ala Ala Tyr Phe Leu Leu Ser Pro Asp Thr Phe Thr Ser
310                 315                 320                 325

cag cga cta ccc gat gta gcc cgc tgg atg gaa ttt ttc agc gcg acc   1123
Gln Arg Leu Pro Asp Val Ala Arg Trp Met Glu Phe Phe Ser Ala Thr
                330                 335                 340

gtt ggt tgg gga cta ttg ata gtg gtt aca ttt gtc tcg gcg cta atc   1171
Val Gly Trp Gly Leu Leu Ile Val Val Thr Phe Val Ser Ala Leu Ile
            345                 350                 355

tgg ttt att ggt gat atc cga gcc aag gga act ccg agc tca ccc att   1219
Trp Phe Ile Gly Asp Ile Arg Ala Lys Gly Thr Pro Ser Ser Pro Ile
        360                 365                 370

acc act gat cca acg cac gac cat ctt gag agg aca gca tgacagactt    1268
Thr Thr Asp Pro Thr His Asp His Leu Glu Arg Thr Ala
    375                 380                 385

caaactcatc agc                                                   1281
```

<210> 754
<211> 386
<212> PRT

<213> Corynebacterium glutamicum

<400> 754

```
Met Leu Leu Met Ala His Arg Phe Phe Val Leu Ala Ile Asn Gly Ala
 1               5                  10                  15

Val Thr Asp Asp Phe Thr Thr Val Tyr Ser Ala Leu Arg Arg Phe Val
            20                  25                  30

Glu Gly Ile Pro Val Tyr Asn Glu Val Tyr His Phe Val Asp Pro His
        35                  40                  45

Tyr Leu Tyr Asn Pro Gly Ala Thr Leu Leu Leu Ala Pro Leu Gly Tyr
    50                  55                  60

Ile Thr His Phe Thr Leu Ala Arg Trp Met Phe Ile Ala Val Asn Leu
65                  70                  75                  80

Leu Ala Ile Val Leu Ala Phe Gly Leu Leu Thr Arg Leu Ser Gly Trp
                85                  90                  95

Ala Leu Arg Ser Met Val Trp Pro Ile Ala Ile Ala Leu Ala Met Leu
            100                 105                 110

Thr Glu Thr Val Gln Asn Thr Leu Ile Phe Ser Asn Ile Asn Gly Ile
        115                 120                 125

Leu Leu Leu Met Leu Ala Ile Phe Leu Trp Cys Val Val His Lys Lys
    130                 135                 140

Ser Trp Leu Gly Gly Leu Val Ile Gly Leu Ala Ile Leu Ile Lys Pro
145                 150                 155                 160

Met Phe Leu Pro Leu Leu Phe Leu Pro Leu Val Lys Lys Gln Trp Gly
                165                 170                 175

Ser Leu Ile Leu Gly Ile Leu Thr Pro Val Ile Phe Asn Ala Val Ala
            180                 185                 190

Trp Phe Leu Val Pro Gly Ala Ser Glu Tyr Val Thr Arg Thr Met Pro
        195                 200                 205

Tyr Leu Gly Glu Thr Arg Asp Phe Ala Asn Ser Ser Leu Pro Gly Leu
    210                 215                 220

Ala Ile Tyr Phe Gly Met Pro Thr Trp Met Glu Ile Thr Trp Phe Leu
225                 230                 235                 240

Ile Phe Gly Ala Met Val Gly Leu Ala Val Leu Ala Leu Leu Arg Phe
                245                 250                 255

Arg Asn Thr Glu Pro Tyr Phe Trp Ala Ala Thr Thr Thr Gly Val Leu
            260                 265                 270

Leu Thr Gly Val Phe Phe Leu Ser Ser Leu Gly Gln Met Tyr Tyr Ser
        275                 280                 285

Met Met Ile Phe Pro Met Ile Phe Thr Leu Leu Gly Ser Arg Ser Val
    290                 295                 300

Phe His Asn Trp Val Ala Trp Val Ala Ala Tyr Phe Leu Leu Ser Pro
```

```
305                 310                 315                 320

Asp Thr Phe Thr Ser Gln Arg Leu Pro Asp Val Ala Arg Trp Met Glu
                325                 330                 335

Phe Phe Ser Ala Thr Val Gly Trp Gly Leu Leu Ile Val Val Thr Phe
            340                 345                 350

Val Ser Ala Leu Ile Trp Phe Ile Gly Asp Ile Arg Ala Lys Gly Thr
        355                 360                 365

Pro Ser Ser Pro Ile Thr Thr Asp Pro Thr His Asp His Leu Glu Arg
    370                 375                 380

Thr Ala
385
```

<210> 755
<211> 1281
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1258)
<223> FRXA01711

<400> 755

```
tctcgtgagt ttctccccgg tagcaccttc tatatcagcc cccacgccgc gtcggagcag 60

gtgggatagc atcggcaacg cggttgcatg gccgttggcc atg ttg ttg atg gcg   115
                                            Met Leu Leu Met Ala
                                              1               5

cat cgc ttc ttc gtg ctt gcg att aac ggc gca gtc acc gac gat ttc   163
His Arg Phe Phe Val Leu Ala Ile Asn Gly Ala Val Thr Asp Asp Phe
                 10                  15                  20

acg acg gtt tat agt gct tta cga cgt ttc gtt gaa ggt att ccg gtc   211
Thr Thr Val Tyr Ser Ala Leu Arg Arg Phe Val Glu Gly Ile Pro Val
             25                  30                  35

tac aac gag gtc tac cac ttc gtc gat ccg cac tac ctc tat aac ccg   259
Tyr Asn Glu Val Tyr His Phe Val Asp Pro His Tyr Leu Tyr Asn Pro
         40                  45                  50

ggc gcc acc ctc cta ttg gca cca ttg gga tat atc acc cat ttc acg   307
Gly Ala Thr Leu Leu Leu Ala Pro Leu Gly Tyr Ile Thr His Phe Thr
     55                  60                  65

ttg gct cgg tgg atg ttc atc gcg gtg aac ctc ctt gcc att gtt tta   355
Leu Ala Arg Trp Met Phe Ile Ala Val Asn Leu Leu Ala Ile Val Leu
 70                  75                  80                  85

gcg ttc ggg ctg ctg acc aga ctc tcc ggt tgg gcg ctg cgc agc atg   403
Ala Phe Gly Leu Leu Thr Arg Leu Ser Gly Trp Ala Leu Arg Ser Met
                 90                  95                 100

gtg tgg ccg att gcg atc gcc ttg gcg atg ctg aca gaa acc gtg caa   451
Val Trp Pro Ile Ala Ile Ala Leu Ala Met Leu Thr Glu Thr Val Gln
```

```
            105                 110                 115

aac acc ctc att ttc tcc aac atc aac ggc atc ctg ctg ctc atg ttg   499
Asn Thr Leu Ile Phe Ser Asn Ile Asn Gly Ile Leu Leu Leu Met Leu
        120                 125                 130

gcg att ttc ctg tgg tgc gtg gtg cac aaa aaa tcc tgg ttg ggc gga   547
Ala Ile Phe Leu Trp Cys Val Val His Lys Lys Ser Trp Leu Gly Gly
    135                 140                 145

cta gtc att ggt ttg gcc att ttg atc aaa ccc atg ttc ctg cca ctt   595
Leu Val Ile Gly Leu Ala Ile Leu Ile Lys Pro Met Phe Leu Pro Leu
150                 155                 160                 165

ctc ttc cta cct ttg gtg aaa aag caa tgg gga tcg ctc atc ctc ggc   643
Leu Phe Leu Pro Leu Val Lys Lys Gln Trp Gly Ser Leu Ile Leu Gly
                170                 175                 180

att tta acc cca gtg att ttc aat gca gtg gcc tgg ttc tta gtt ccg   691
Ile Leu Thr Pro Val Ile Phe Asn Ala Val Ala Trp Phe Leu Val Pro
            185                 190                 195

gga gca tct gaa tac gtc acc cgc acg atg ccc tac ctt ggt gaa act   739
Gly Ala Ser Glu Tyr Val Thr Arg Thr Met Pro Tyr Leu Gly Glu Thr
        200                 205                 210

cga gat ttt gcc aac agc tca ctc cca ggc ttg gcc atc tat ttc gga   787
Arg Asp Phe Ala Asn Ser Ser Leu Pro Gly Leu Ala Ile Tyr Phe Gly
    215                 220                 225

atg ccc acc tgg atg gaa atc acc tgg ttc ctc atc ttc ggc gca atg   835
Met Pro Thr Trp Met Glu Ile Thr Trp Phe Leu Ile Phe Gly Ala Met
230                 235                 240                 245

gtc ggc ctc gca gtg ctg gca ctc ctg aga ttc cgt aac acc gag cca   883
Val Gly Leu Ala Val Leu Ala Leu Leu Arg Phe Arg Asn Thr Glu Pro
                250                 255                 260

tac ttc tgg gca gca acc acc acc ggt gta ctc ctg act ggc gta ttc   931
Tyr Phe Trp Ala Ala Thr Thr Thr Gly Val Leu Leu Thr Gly Val Phe
            265                 270                 275

ttc ctg tcc tca ctg gga cag atg tac tac tcc atg atg atc ttc cct   979
Phe Leu Ser Ser Leu Gly Gln Met Tyr Tyr Ser Met Met Ile Phe Pro
        280                 285                 290

atg atc ttc acc ctg ctc gga agc cga tcc gta ttc cac aac tgg gtt   1027
Met Ile Phe Thr Leu Leu Gly Ser Arg Ser Val Phe His Asn Trp Val
    295                 300                 305

gcc tgg gtc gcc gcc tac ttc tta cta tcc cct gac act ttc acc tcc   1075
Ala Trp Val Ala Ala Tyr Phe Leu Leu Ser Pro Asp Thr Phe Thr Ser
310                 315                 320                 325

cag cga cta ccc gat gta gcc cgc tgg atg gaa ttt ttc agc gcg acc   1123
Gln Arg Leu Pro Asp Val Ala Arg Trp Met Glu Phe Phe Ser Ala Thr
                330                 335                 340

gtt ggt tgg gga cta ttg ata gtg gtt aca ttt gtc tcg gcg cta atc   1171
Val Gly Trp Gly Leu Leu Ile Val Val Thr Phe Val Ser Ala Leu Ile
            345                 350                 355
```

```
tgg ttt att ggt gat atc cga gcc aag gga act ccg agc tca ccc att   1219
Trp Phe Ile Gly Asp Ile Arg Ala Lys Gly Thr Pro Ser Ser Pro Ile
        360                 365                 370

acc act gat cca acg cac gac cat ctt gag agg aca gca tgacagactt   1268
Thr Thr Asp Pro Thr His Asp His Leu Glu Arg Thr Ala
    375                 380                 385

caaactcatc agc                                                   1281
```

<210> 756
<211> 386
<212> PRT
<213> Corynebacterium glutamicum

<400> 756

```
Met Leu Leu Met Ala His Arg Phe Phe Val Leu Ala Ile Asn Gly Ala
  1               5                  10                  15

Val Thr Asp Asp Phe Thr Thr Val Tyr Ser Ala Leu Arg Arg Phe Val
             20                  25                  30

Glu Gly Ile Pro Val Tyr Asn Glu Val Tyr His Phe Val Asp Pro His
         35                  40                  45

Tyr Leu Tyr Asn Pro Gly Ala Thr Leu Leu Leu Ala Pro Leu Gly Tyr
     50                  55                  60

Ile Thr His Phe Thr Leu Ala Arg Trp Met Phe Ile Ala Val Asn Leu
 65                  70                  75                  80

Leu Ala Ile Val Leu Ala Phe Gly Leu Leu Thr Arg Leu Ser Gly Trp
                 85                  90                  95

Ala Leu Arg Ser Met Val Trp Pro Ile Ala Ile Ala Leu Ala Met Leu
            100                 105                 110

Thr Glu Thr Val Gln Asn Thr Leu Ile Phe Ser Asn Ile Asn Gly Ile
        115                 120                 125

Leu Leu Leu Met Leu Ala Ile Phe Leu Trp Cys Val Val His Lys Lys
    130                 135                 140

Ser Trp Leu Gly Gly Leu Val Ile Gly Leu Ala Ile Leu Ile Lys Pro
145                 150                 155                 160

Met Phe Leu Pro Leu Leu Phe Leu Pro Leu Val Lys Lys Gln Trp Gly
                165                 170                 175

Ser Leu Ile Leu Gly Ile Leu Thr Pro Val Ile Phe Asn Ala Val Ala
            180                 185                 190

Trp Phe Leu Val Pro Gly Ala Ser Glu Tyr Val Thr Arg Thr Met Pro
        195                 200                 205

Tyr Leu Gly Glu Thr Arg Asp Phe Ala Asn Ser Ser Leu Pro Gly Leu
    210                 215                 220

Ala Ile Tyr Phe Gly Met Pro Thr Trp Met Glu Ile Thr Trp Phe Leu
```

```
225                 230                 235                 240

Ile Phe Gly Ala Met Val Gly Leu Ala Val Leu Ala Leu Leu Arg Phe
                245                 250                 255

Arg Asn Thr Glu Pro Tyr Phe Trp Ala Ala Thr Thr Thr Gly Val Leu
            260                 265                 270

Leu Thr Gly Val Phe Phe Leu Ser Ser Leu Gly Gln Met Tyr Tyr Ser
        275                 280                 285

Met Met Ile Phe Pro Met Ile Phe Thr Leu Leu Gly Ser Arg Ser Val
    290                 295                 300

Phe His Asn Trp Val Ala Trp Val Ala Ala Tyr Phe Leu Leu Ser Pro
305                 310                 315                 320

Asp Thr Phe Thr Ser Gln Arg Leu Pro Asp Val Ala Arg Trp Met Glu
                325                 330                 335

Phe Phe Ser Ala Thr Val Gly Trp Gly Leu Leu Ile Val Val Thr Phe
            340                 345                 350

Val Ser Ala Leu Ile Trp Phe Ile Gly Asp Ile Arg Ala Lys Gly Thr
        355                 360                 365

Pro Ser Ser Pro Ile Thr Thr Asp Pro Thr His Asp His Leu Glu Arg
    370                 375                 380

Thr Ala
385
```

US 2005-0196848 A1 Sep. 8, 2005

<210> 757
<211> 1123
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1123)
<223> RXN01721

<400> 757
ttcgccaacg ccgccccgaa atgatcggga gggggcgtcg aaaagcactt ctgcgagcat 60

caaacatgat gcgtacctgc cacccgcaga cggcaatcgc gtg ctt gtg gac aga 115
                                        Val Leu Val Asp Arg
                                          1   5

ttc gga cgc atc gcg cgt gac ctg cgg gtg tca ctg acc gac cga tgc 163
Phe Gly Arg Ile Ala Arg Asp Leu Arg Val Ser Leu Thr Asp Arg Cys
                 10   15   20

aac ctc cgc tgc acc tat tgc atg ccc gcg gag ggt tta gag tgg ctg 211
Asn Leu Arg Cys Thr Tyr Cys Met Pro Ala Glu Gly Leu Glu Trp Leu
             25   30   35

ccc acc gag cag acg ctt aac gac gcc gag gtg ctg cga ctc atc cgc 259
Pro Thr Glu Gln Thr Leu Asn Asp Ala Glu Val Leu Arg Leu Ile Arg
         40   45   50
```
```

```
att gcg gtg gtt aag ctg ggc att cgt caa att cga ttc acc ggc ggc   307
Ile Ala Val Val Lys Leu Gly Ile Arg Gln Ile Arg Phe Thr Gly Gly
     55                  60                  65

gag cct tta ctg cgg aaa aat ttg gaa gac atc atc gcc ggc acc gca   355
Glu Pro Leu Leu Arg Lys Asn Leu Glu Asp Ile Ile Ala Gly Thr Ala
 70                  75                  80                  85

gcc ctg cgc acc gac gaa ggc gaa aaa gtt cac atc gct ctc acc acc   403
Ala Leu Arg Thr Asp Glu Gly Glu Lys Val His Ile Ala Leu Thr Thr
                 90                  95                 100

aac ggc ctt ggc cta gac aaa cgc atc gca gga ctg aaa gaa gct ggt   451
Asn Gly Leu Gly Leu Asp Lys Arg Ile Ala Gly Leu Lys Glu Ala Gly
            105                 110                 115

ctt gac cgg gtc aat att tca ctc gac acc atc gac gcc gaa cgc tac   499
Leu Asp Arg Val Asn Ile Ser Leu Asp Thr Ile Asp Ala Glu Arg Tyr
        120                 125                 130

gtc tcg cta acc aag cgt gat cga ttg tcc ggt gtg ttg gcg tcc atc   547
Val Ser Leu Thr Lys Arg Asp Arg Leu Ser Gly Val Leu Ala Ser Ile
    135                 140                 145

gat gcc gct gtt gcc gct ggc ctt cac cca gtg aag atc aac gcc gtg   595
Asp Ala Ala Val Ala Ala Gly Leu His Pro Val Lys Ile Asn Ala Val
150                 155                 160                 165

gtc atg cct ggg gtc aat gaa gta gat atc gtc ccc ctt gcg gaa tac   643
Val Met Pro Gly Val Asn Glu Val Asp Ile Val Pro Leu Ala Glu Tyr
                170                 175                 180

tgc att tcc aaa ggc tcc caa ctg cga ttc atc gaa caa atg cca ctt   691
Cys Ile Ser Lys Gly Ser Gln Leu Arg Phe Ile Glu Gln Met Pro Leu
            185                 190                 195

ggc ccg cgc gag cag tgg aaa cgc ggc gat atg gtc aca gcc gaa gaa   739
Gly Pro Arg Glu Gln Trp Lys Arg Gly Asp Met Val Thr Ala Glu Glu
        200                 205                 210

atc ctg gcg cgc ctg gaa gaa aaa ttc acc tta tcc ccc gcc aag gaa   787
Ile Leu Ala Arg Leu Glu Glu Lys Phe Thr Leu Ser Pro Ala Lys Glu
    215                 220                 225

ccc cga gga gct gca cct gct gcg ctg tgg aat gtg gta gat aaa tcc   835
Pro Arg Gly Ala Ala Pro Ala Ala Leu Trp Asn Val Val Asp Lys Ser
230                 235                 240                 245

aac cct gat atc act gga caa atc ggc atc atc gcc tcg gtg acg cac   883
Asn Pro Asp Ile Thr Gly Gln Ile Gly Ile Ile Ala Ser Val Thr His
                250                 255                 260

cca ttt tgc gga gat tgc gat cgc tcc cgc ctc acc acc gac ggc acc   931
Pro Phe Cys Gly Asp Cys Asp Arg Ser Arg Leu Thr Thr Asp Gly Thr
            265                 270                 275

atc cga aac tgc ctt ttc tcc cgc act gaa act ccc cta cgt gac gcg   979
Ile Arg Asn Cys Leu Phe Ser Arg Thr Glu Thr Pro Leu Arg Asp Ala
        280                 285                 290
```

```
ctt cgc gac ggc gcc tcc gac gat gag ctc gcg caa ctg tgg gca ggc   1027
Leu Arg Asp Gly Ala Ser Asp Asp Glu Leu Ala Gln Leu Trp Ala Gly
    295                 300                 305

gcc atg tgg gag aag aaa ccc ggc cat ggc atc gac gat gaa ggc ttc   1075
Ala Met Trp Glu Lys Lys Pro Gly His Gly Ile Asp Asp Glu Gly Phe
310                 315                 320                 325

ctc caa cca gat cgc ccc atg tct gcc atc ggg gct agc cca tac cag   1123
Leu Gln Pro Asp Arg Pro Met Ser Ala Ile Gly Ala Ser Pro Tyr Gln
                330                 335                 340


<210> 758
<211> 341
<212> PRT
<213> Corynebacterium glutamicum

<400> 758
Val Leu Val Asp Arg Phe Gly Arg Ile Ala Arg Asp Leu Arg Val Ser
  1               5                  10                  15

Leu Thr Asp Arg Cys Asn Leu Arg Cys Thr Tyr Cys Met Pro Ala Glu
             20                  25                  30

Gly Leu Glu Trp Leu Pro Thr Glu Gln Thr Leu Asn Asp Ala Glu Val
         35                  40                  45

Leu Arg Leu Ile Arg Ile Ala Val Val Lys Leu Gly Ile Arg Gln Ile
     50                  55                  60

Arg Phe Thr Gly Gly Glu Pro Leu Leu Arg Lys Asn Leu Glu Asp Ile
 65                  70                  75                  80

Ile Ala Gly Thr Ala Ala Leu Arg Thr Asp Glu Gly Glu Lys Val His
                 85                  90                  95

Ile Ala Leu Thr Thr Asn Gly Leu Gly Leu Asp Lys Arg Ile Ala Gly
            100                 105                 110

Leu Lys Glu Ala Gly Leu Asp Arg Val Asn Ile Ser Leu Asp Thr Ile
        115                 120                 125

Asp Ala Glu Arg Tyr Val Ser Leu Thr Lys Arg Asp Arg Leu Ser Gly
    130                 135                 140

Val Leu Ala Ser Ile Asp Ala Ala Val Ala Ala Gly Leu His Pro Val
145                 150                 155                 160

Lys Ile Asn Ala Val Val Met Pro Gly Val Asn Glu Val Asp Ile Val
                165                 170                 175

Pro Leu Ala Glu Tyr Cys Ile Ser Lys Gly Ser Gln Leu Arg Phe Ile
            180                 185                 190

Glu Gln Met Pro Leu Gly Pro Arg Glu Gln Trp Lys Arg Gly Asp Met
        195                 200                 205

Val Thr Ala Glu Glu Ile Leu Ala Arg Leu Glu Glu Lys Phe Thr Leu
    210                 215                 220
```

```
Ser Pro Ala Lys Glu Pro Arg Gly Ala Ala Pro Ala Ala Leu Trp Asn
225                 230                 235                 240

Val Val Asp Lys Ser Asn Pro Asp Ile Thr Gly Gln Ile Gly Ile Ile
                245                 250                 255

Ala Ser Val Thr His Pro Phe Cys Gly Asp Cys Asp Arg Ser Arg Leu
            260                 265                 270

Thr Thr Asp Gly Thr Ile Arg Asn Cys Leu Phe Ser Arg Thr Glu Thr
        275                 280                 285

Pro Leu Arg Asp Ala Leu Arg Asp Gly Ala Ser Asp Asp Glu Leu Ala
    290                 295                 300

Gln Leu Trp Ala Gly Ala Met Trp Glu Lys Lys Pro Gly His Gly Ile
305                 310                 315                 320

Asp Asp Glu Gly Phe Leu Gln Pro Asp Arg Pro Met Ser Ala Ile Gly
                325                 330                 335

Ala Ser Pro Tyr Gln
            340
```

<210> 759
<211> 657
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(634)
<223> RXN01734

<400> 759

```
acgatctgcc ggagaatctc aagaaagtgc tcactgcgca gcacaccgtc accgtccaag 60

acaccggcac cgggcggatt tcactcctgg atgtgcaacc atg aca gat cca att   115
                                              Met Thr Asp Pro Ile
                                                1               5

gag cag gca ttt gaa cgc atc cgc gcc gaa gcc atg cgc aga aat gga   163
Glu Gln Ala Phe Glu Arg Ile Arg Ala Glu Ala Met Arg Arg Asn Gly
                10                  15                  20

tcc gtt ccc gac ctc aat aaa aac gat gct ttt cga cgc cca cct gcg   211
Ser Val Pro Asp Leu Asn Lys Asn Asp Ala Phe Arg Arg Pro Pro Ala
            25                  30                  35

ccg aaa ggg ggc gtc gaa aag cgc aaa aaa ggc cgt gca agc ggc cta   259
Pro Lys Gly Gly Val Glu Lys Arg Lys Lys Gly Arg Ala Ser Gly Leu
        40                  45                  50

gac ggc cgc cag aaa cga tat gtg cgc ggc gcg gag tcg ctg gga tcg   307
Asp Gly Arg Gln Lys Arg Tyr Val Arg Gly Ala Glu Ser Leu Gly Ser
    55                  60                  65

gtg ctg aac aag gaa att cag cgt cgt ggc tgg ggc aaa gac att gcc   355
Val Leu Asn Lys Glu Ile Gln Arg Arg Gly Trp Gly Lys Asp Ile Ala
70                  75                  80                  85
```

```
ggc ggt tgg gtg acg tcc aac tgg gaa gag ctt gtt ggc gcg aag att   403
Gly Gly Trp Val Thr Ser Asn Trp Glu Glu Leu Val Gly Ala Lys Ile
                 90                  95                  100

gcg cag cat acg cgc gtg gaa atg atc aaa gat aag aag ctt ttt atc   451
Ala Gln His Thr Arg Val Glu Met Ile Lys Asp Lys Lys Leu Phe Ile
            105                 110                 115

act tgt gat tcc aca gcg tgg gcc acc aat ctg cgc atg atg cag cgg   499
Thr Cys Asp Ser Thr Ala Trp Ala Thr Asn Leu Arg Met Met Gln Arg
        120                 125                 130

caa atc ctg cag gta atc gct gaa aaa gtg ggt cca aat att att aca   547
Gln Ile Leu Gln Val Ile Ala Glu Lys Val Gly Pro Asn Ile Ile Thr
    135                 140                 145

gag ctg cgt att ttt ggg cct cag gcc cca agc tgg cgc aag ggg ccg   595
Glu Leu Arg Ile Phe Gly Pro Gln Ala Pro Ser Trp Arg Lys Gly Pro
150                 155                 160                 165

ttg cac gta aaa gga cgc ggt ccg aga gac aca tac gga tagtttggtg    644
Leu His Val Lys Gly Arg Gly Pro Arg Asp Thr Tyr Gly
                170                 175

ataaaaaccg tcg                                                   657


<210> 760
<211> 178
<212> PRT
<213> Corynebacterium glutamicum

<400> 760
Met Thr Asp Pro Ile Glu Gln Ala Phe Glu Arg Ile Arg Ala Glu Ala
  1               5                  10                  15

Met Arg Arg Asn Gly Ser Val Pro Asp Leu Asn Lys Asn Asp Ala Phe
             20                  25                  30

Arg Arg Pro Pro Ala Pro Lys Gly Gly Val Glu Lys Arg Lys Lys Gly
         35                  40                  45

Arg Ala Ser Gly Leu Asp Gly Arg Gln Lys Arg Tyr Val Arg Gly Ala
     50                  55                  60

Glu Ser Leu Gly Ser Val Leu Asn Lys Glu Ile Gln Arg Arg Gly Trp
 65                  70                  75                  80

Gly Lys Asp Ile Ala Gly Gly Trp Val Thr Ser Asn Trp Glu Glu Leu
                 85                  90                  95

Val Gly Ala Lys Ile Ala Gln His Thr Arg Val Glu Met Ile Lys Asp
            100                 105                 110

Lys Lys Leu Phe Ile Thr Cys Asp Ser Thr Ala Trp Ala Thr Asn Leu
        115                 120                 125

Arg Met Met Gln Arg Gln Ile Leu Gln Val Ile Ala Glu Lys Val Gly
    130                 135                 140
```

```
Pro Asn Ile Ile Thr Glu Leu Arg Ile Phe Gly Pro Gln Ala Pro Ser
145                 150                 155                 160

Trp Arg Lys Gly Pro Leu His Val Lys Gly Arg Gly Pro Arg Asp Thr
                165                 170                 175

Tyr Gly
```

<210> 761
<211> 657
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(634)
<223> FRXA01734

<400> 761

```
acgatctgcc ggagaatctc aagaaagtgc tcactgcgca gcacaccgtc accgtccaag 60

acaccggcac cgggcggatt tcactcctgg atgtgcaacc atg aca gat cca att   115
                                            Met Thr Asp Pro Ile
                                              1               5

gag cag gca ttt gaa cgc atc cgc gcc gaa gcc atg cgc aga aat gga   163
Glu Gln Ala Phe Glu Arg Ile Arg Ala Glu Ala Met Arg Arg Asn Gly
                10                  15                  20

tcc gtt ccc gac ctc aat aaa aac gat gct ttt cga cgc cca cct gcg   211
Ser Val Pro Asp Leu Asn Lys Asn Asp Ala Phe Arg Arg Pro Pro Ala
            25                  30                  35

ccg aaa ggg ggc gtc gaa aag cgc aaa aaa ggc cgt gca agc ggc cta   259
Pro Lys Gly Gly Val Glu Lys Arg Lys Lys Gly Arg Ala Ser Gly Leu
        40                  45                  50

gac ggc cgc cag aaa cga tat gtg cgc ggc gcg gag tcg ctg gga tcg   307
Asp Gly Arg Gln Lys Arg Tyr Val Arg Gly Ala Glu Ser Leu Gly Ser
    55                  60                  65

gtg ctg aac aag gaa att cag cgt cgt ggc tgg ggc aaa gac att gcc   355
Val Leu Asn Lys Glu Ile Gln Arg Arg Gly Trp Gly Lys Asp Ile Ala
70                  75                  80                  85

ggc ggt tgg gtg acg tcc aac tgg gaa gag ctt gtt ggc gcg aag att   403
Gly Gly Trp Val Thr Ser Asn Trp Glu Glu Leu Val Gly Ala Lys Ile
                90                  95                  100

gcg cag cat acg cgc gtg gaa atg atc aaa gat aag aag ctt ttt atc   451
Ala Gln His Thr Arg Val Glu Met Ile Lys Asp Lys Lys Leu Phe Ile
            105                 110                 115

act tgt gat tcc aca gcg tgg gcc acc aat ctg cgc atg atg cag cgg   499
Thr Cys Asp Ser Thr Ala Trp Ala Thr Asn Leu Arg Met Met Gln Arg
        120                 125                 130

caa atc ctg cag gta atc gct gaa aaa gtg ggt cca aat att att aca   547
Gln Ile Leu Gln Val Ile Ala Glu Lys Val Gly Pro Asn Ile Ile Thr
```

```
    135                 140                 145

gag ctg cgt att ttt ggg cct cag gcc cca agc tgg cgc aag ggg ccg   595
Glu Leu Arg Ile Phe Gly Pro Gln Ala Pro Ser Trp Arg Lys Gly Pro
150                 155                 160                 165

ttg cac gta aaa gga cgc ggt ccg aga gac aca tac gga tagtttggtg    644
Leu His Val Lys Gly Arg Gly Pro Arg Asp Thr Tyr Gly
                170                 175

ataaaaaccg tcg                                                   657


<210> 762
<211> 178
<212> PRT
<213> Corynebacterium glutamicum

<400> 762
Met Thr Asp Pro Ile Glu Gln Ala Phe Glu Arg Ile Arg Ala Glu Ala
  1               5                  10                  15

Met Arg Arg Asn Gly Ser Val Pro Asp Leu Asn Lys Asn Asp Ala Phe
             20                  25                  30

Arg Arg Pro Pro Ala Pro Lys Gly Gly Val Glu Lys Arg Lys Lys Gly
         35                  40                  45

Arg Ala Ser Gly Leu Asp Gly Arg Gln Lys Arg Tyr Val Arg Gly Ala
     50                  55                  60

Glu Ser Leu Gly Ser Val Leu Asn Lys Glu Ile Gln Arg Arg Gly Trp
 65                  70                  75                  80

Gly Lys Asp Ile Ala Gly Gly Trp Val Thr Ser Asn Trp Glu Glu Leu
                 85                  90                  95

Val Gly Ala Lys Ile Ala Gln His Thr Arg Val Glu Met Ile Lys Asp
            100                 105                 110

Lys Lys Leu Phe Ile Thr Cys Asp Ser Thr Ala Trp Ala Thr Asn Leu
        115                 120                 125

Arg Met Met Gln Arg Gln Ile Leu Gln Val Ile Ala Glu Lys Val Gly
    130                 135                 140

Pro Asn Ile Ile Thr Glu Leu Arg Ile Phe Gly Pro Gln Ala Pro Ser
145                 150                 155                 160

Trp Arg Lys Gly Pro Leu His Val Lys Gly Arg Gly Pro Arg Asp Thr
                165                 170                 175

Tyr Gly


<210> 763
<211> 627
<212> DNA
<213> Corynebacterium glutamicum
```

<220>
<221> CDS
<222> (101)..(604)
<223> RXN01742

<400> 763
tggctaaagc gatgtgtgtc atctgaaaaa tttcccccaa aacttaatcg acacagttac 60

ttcatctggc cttatttcat cacagttaca atcatctgtc atg cag gaa aag cca 115
Met Gln Glu Lys Pro
1 5

gag atg cca gcg att gag gtc atc cgt tca gcg aaa cgc acc aaa act 163
Glu Met Pro Ala Ile Glu Val Ile Arg Ser Ala Lys Arg Thr Lys Thr
10 15 20

gtt caa gct cga att gtg gac ggg caa atc cag gtg cgc atc cct gcg 211
Val Gln Ala Arg Ile Val Asp Gly Gln Ile Gln Val Arg Ile Pro Ala
25 30 35

agg atg tct aaa gcg gag gaa gaa aaa gcg gtg ggg gag atc gtc gca 259
Arg Met Ser Lys Ala Glu Glu Glu Lys Ala Val Gly Glu Ile Val Ala
40 45 50

aag cta aag cga cgc acc caa tcg gcc gtc tca agc gac gct gac ctg 307
Lys Leu Lys Arg Arg Thr Gln Ser Ala Val Ser Ser Asp Ala Asp Leu
55 60 65

att gag cgc gcc cat aag ttg aac aag act gtg ttg gag ggg cgg gcg 355
Ile Glu Arg Ala His Lys Leu Asn Lys Thr Val Leu Glu Gly Arg Ala
70 75 80 85

cgg gtg gaa agt att cgg tgg gtg agt aat cag aag ggg cgg tgg ggg 403
Arg Val Glu Ser Ile Arg Trp Val Ser Asn Gln Lys Gly Arg Trp Gly
90 95 100

tcg tgc acg gtg gcg act gcg gag att cgg att tcg gat cgt tta aag 451
Ser Cys Thr Val Ala Thr Ala Glu Ile Arg Ile Ser Asp Arg Leu Lys
105 110 115

cac gtg ccg gat tat gtg ttg gat gcg gtg ttg gtg cat gag ctg acg 499
His Val Pro Asp Tyr Val Leu Asp Ala Val Leu Val His Glu Leu Thr
120 125 130

cat acg ttt att gcg ggg cat tcg gcg gag ttt tgg gag tgg gca gac 547
His Thr Phe Ile Ala Gly His Ser Ala Glu Phe Trp Glu Trp Ala Asp
135 140 145

aaa acg ccc ctg gca gag agg gcc aag ggc tat ttg gag gcg tat cag 595
Lys Thr Pro Leu Ala Glu Arg Ala Lys Gly Tyr Leu Glu Ala Tyr Gln
150 155 160 165

cgg tgg ggc tgaaggttta gttcttgtcg gag 627
Arg Trp Gly

<210> 764
<211> 168
<212> PRT
<213> Corynebacterium glutamicum

<400> 764
Met Gln Glu Lys Pro Glu Met Pro Ala Ile Glu Val Ile Arg Ser Ala
1 5 10 15

Lys Arg Thr Lys Thr Val Gln Ala Arg Ile Val Asp Gly Gln Ile Gln
20 25 30

Val Arg Ile Pro Ala Arg Met Ser Lys Ala Glu Glu Glu Lys Ala Val
35 40 45

Gly Glu Ile Val Ala Lys Leu Lys Arg Arg Thr Gln Ser Ala Val Ser
50 55 60

Ser Asp Ala Asp Leu Ile Glu Arg Ala His Lys Leu Asn Lys Thr Val
65 70 75 80

Leu Glu Gly Arg Ala Arg Val Glu Ser Ile Arg Trp Val Ser Asn Gln
85 90 95

Lys Gly Arg Trp Gly Ser Cys Thr Val Ala Thr Ala Glu Ile Arg Ile
100 105 110

Ser Asp Arg Leu Lys His Val Pro Asp Tyr Val Leu Asp Ala Val Leu
115 120 125

Val His Glu Leu Thr His Thr Phe Ile Ala Gly His Ser Ala Glu Phe
130 135 140

Trp Glu Trp Ala Asp Lys Thr Pro Leu Ala Glu Arg Ala Lys Gly Tyr
145 150 155 160

Leu Glu Ala Tyr Gln Arg Trp Gly
165

<210> 765
<211> 627
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(604)
<223> FRXA01742

<400> 765
tggctaaagc gatgtgtgtc atctgaaaaa tttcccccaa aacttaatcg acacagttac 60

ttcatctggc cttatttcat cacagttaca atcatctgtc atg cag gaa aag cca 115
Met Gln Glu Lys Pro
1 5

gag atg cca gcg att gag gtc atc cgt tca gcg aaa cgc acc aaa act 163
Glu Met Pro Ala Ile Glu Val Ile Arg Ser Ala Lys Arg Thr Lys Thr
10 15 20

gtt caa gct cga att gtg gac ggg caa atc cag gtg cgc atc cct gcg 211
Val Gln Ala Arg Ile Val Asp Gly Gln Ile Gln Val Arg Ile Pro Ala
25 30 35

```
agg atg tct aaa gcg gag gaa gaa aaa gcg gtg ggg gag atc gtc gca   259
Arg Met Ser Lys Ala Glu Glu Glu Lys Ala Val Gly Glu Ile Val Ala
         40                  45                  50

aag cta aag cga cgc acc caa tcg gcc gtc tca agc gac gct gac ctg   307
Lys Leu Lys Arg Arg Thr Gln Ser Ala Val Ser Ser Asp Ala Asp Leu
     55                  60                  65

att gag cgc gcc cat aag ttg aac aag act gtg ttg gag ggg cgg gcg   355
Ile Glu Arg Ala His Lys Leu Asn Lys Thr Val Leu Glu Gly Arg Ala
 70                  75                  80                  85

cgg gtg gaa agt att cgg tgg gtg agt aat cag aag ggg cgg tgg ggg   403
Arg Val Glu Ser Ile Arg Trp Val Ser Asn Gln Lys Gly Arg Trp Gly
                 90                  95                 100

tcg tgc acg gtg gcg act gcg gag att cgg att tcg gat cgt tta aag   451
Ser Cys Thr Val Ala Thr Ala Glu Ile Arg Ile Ser Asp Arg Leu Lys
            105                 110                 115

cac gtg ccg gat tat gtg ttg gat gcg gtg ttg gtg cat gag ctg acg   499
His Val Pro Asp Tyr Val Leu Asp Ala Val Leu Val His Glu Leu Thr
        120                 125                 130

cat acg ttt att gcg ggg cat tcg gcg gag ttt tgg gag tgg gca gac   547
His Thr Phe Ile Ala Gly His Ser Ala Glu Phe Trp Glu Trp Ala Asp
    135                 140                 145

aaa acg ccc ctg gca gag agg gcc aag ggc tat ttg gag gcg tat cag   595
Lys Thr Pro Leu Ala Glu Arg Ala Lys Gly Tyr Leu Glu Ala Tyr Gln
150                 155                 160                 165

cgg tgg ggc tgaaggttta gttcttgtcg gag                            627
Arg Trp Gly
```

<210> 766
<211> 168
<212> PRT
<213> Corynebacterium glutamicum

<400> 766

```
Met Gln Glu Lys Pro Glu Met Pro Ala Ile Glu Val Ile Arg Ser Ala
  1               5                  10                  15

Lys Arg Thr Lys Thr Val Gln Ala Arg Ile Val Asp Gly Gln Ile Gln
             20                  25                  30

Val Arg Ile Pro Ala Arg Met Ser Lys Ala Glu Glu Glu Lys Ala Val
         35                  40                  45

Gly Glu Ile Val Ala Lys Leu Lys Arg Arg Thr Gln Ser Ala Val Ser
     50                  55                  60

Ser Asp Ala Asp Leu Ile Glu Arg Ala His Lys Leu Asn Lys Thr Val
 65                  70                  75                  80

Leu Glu Gly Arg Ala Arg Val Glu Ser Ile Arg Trp Val Ser Asn Gln
                 85                  90                  95
```

```
Lys Gly Arg Trp Gly Ser Cys Thr Val Ala Thr Ala Glu Ile Arg Ile
            100                 105                 110

Ser Asp Arg Leu Lys His Val Pro Asp Tyr Val Leu Asp Ala Val Leu
        115                 120                 125

Val His Glu Leu Thr His Thr Phe Ile Ala Gly His Ser Ala Glu Phe
    130                 135                 140

Trp Glu Trp Ala Asp Lys Thr Pro Leu Ala Glu Arg Ala Lys Gly Tyr
145                 150                 155                 160

Leu Glu Ala Tyr Gln Arg Trp Gly
                165
```

<210> 767
<211> 2064
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2041)
<223> RXN01754

<400> 767

```
tgtggctgaa gacaagaatg aatagcattc atctcgtcga atttcatgta gaaatttgtc 60

ccccttttt ttgatgtgaa agttgaatcg gtaagctcct gtg aaa att aaa tcc   115
                                            Val Lys Ile Lys Ser
                                              1               5

gta ttt ttg agc acc gct tta agc gct tcc tta ctg ctc gga atc acc   163
Val Phe Leu Ser Thr Ala Leu Ser Ala Ser Leu Leu Leu Gly Ile Thr
                10                  15                  20

cca ccc gtg ctg gga gca acg atc aac ccc agt ttg cct ctt tct gcg   211
Pro Pro Val Leu Gly Ala Thr Ile Asn Pro Ser Leu Pro Leu Ser Ala
            25                  30                  35

ttg agc tcc tcg gac gat atc gcc gta ccc aac ttc gcc aaa gaa tta   259
Leu Ser Ser Ser Asp Asp Ile Ala Val Pro Asn Phe Ala Lys Glu Leu
        40                  45                  50

ccg tta gct ttt gat gta cca gca ggc act gtt ccc caa agc ttg agt   307
Pro Leu Ala Phe Asp Val Pro Ala Gly Thr Val Pro Gln Ser Leu Ser
    55                  60                  65

gga acg ctg cag att cct gcc gag ttt tct ggc ggc gtc gtg gag ttt   355
Gly Thr Leu Gln Ile Pro Ala Glu Phe Ser Gly Gly Val Val Glu Phe
70                  75                  80                  85

tat gac ggt gac cgg ctc ttt cac acc ctg cgc cta gaa gtt aat gat   403
Tyr Asp Gly Asp Arg Leu Phe His Thr Leu Arg Leu Glu Val Asn Asp
                90                  95                  100

tcc cga gca cac att gag gtt ccg ctg caa agc gtt cct gtc gaa gac   451
Ser Arg Ala His Ile Glu Val Pro Leu Gln Ser Val Pro Val Glu Asp
            105                 110                 115
```

```
ggc cgc gcc acc ttt tgg ttg cgc gcc atg ttg gat cct gta aac aac   499
Gly Arg Ala Thr Phe Trp Leu Arg Ala Met Leu Asp Pro Val Asn Asn
        120                 125                 130

cag tgg tgc tac gag gag cag gaa gtc cgc ttc tta gac gga aac gtc   547
Gln Trp Cys Tyr Glu Glu Gln Glu Val Arg Phe Leu Asp Gly Asn Val
    135                 140                 145

acc ttt gaa ggg gcg acg att aac cca gct gtg gtg gct gat tac ttc   595
Thr Phe Glu Gly Ala Thr Ile Asn Pro Ala Val Val Ala Asp Tyr Phe
150                 155                 160                 165

ccg tca gtg ctg cgc gcg ttg aca att tac gtc ccg gaa aac ccc tct   643
Pro Ser Val Leu Arg Ala Leu Thr Ile Tyr Val Pro Glu Asn Pro Ser
                170                 175                 180

gag gca gta caa gaa gcc acg tta gag gtt gcg acc tcc ctg gat tcg   691
Glu Ala Val Gln Glu Ala Thr Leu Glu Val Ala Thr Ser Leu Asp Ser
            185                 190                 195

gtg tac cga aga tca ggt ctg gat gtc aac gta gaa acg ctt cca acc   739
Val Tyr Arg Arg Ser Gly Leu Asp Val Asn Val Glu Thr Leu Pro Thr
        200                 205                 210

ggc acc gat gct cct cct aca cgt cct caa gat ttt gaa cgc cag att   787
Gly Thr Asp Ala Pro Pro Thr Arg Pro Gln Asp Phe Glu Arg Gln Ile
    215                 220                 225

gtg ctg gtt gac gag gca aca gaa agt aac acg caa aaa acc gaa ttg   835
Val Leu Val Asp Glu Ala Thr Glu Ser Asn Thr Gln Lys Thr Glu Leu
230                 235                 240                 245

gtc aat ccc ggc caa gac aat gca ttc ttg cgc ctg aac ggc aac gcc   883
Val Asn Pro Gly Gln Asp Asn Ala Phe Leu Arg Leu Asn Gly Asn Ala
                250                 255                 260

gac gag ctt tac gat caa gcg cgc ttg ctt acc gac gca acc ctg cca   931
Asp Glu Leu Tyr Asp Gln Ala Arg Leu Leu Thr Asp Ala Thr Leu Pro
            265                 270                 275

ctt gcc gta gac acc gaa gta acg gcc tca ggt ttt ggt gat gtg ccc   979
Leu Ala Val Asp Thr Glu Val Thr Ala Ser Gly Phe Gly Asp Val Pro
        280                 285                 290

aac ctt tct aca gat gtg gcc acc ctc caa gaa ctg ggt atc acg cag  1027
Asn Leu Ser Thr Asp Val Ala Thr Leu Gln Glu Leu Gly Ile Thr Gln
    295                 300                 305

ctc acc tct gaa tca gtt gcg cgc aca agc gtc acc ttg ggc att gaa  1075
Leu Thr Ser Glu Ser Val Ala Arg Thr Ser Val Thr Leu Gly Ile Glu
310                 315                 320                 325

cgc tcc cgc ctg cgg acc tac tcg cag tcc atg gac ctg cac ata acg  1123
Arg Ser Arg Leu Arg Thr Tyr Ser Gln Ser Met Asp Leu His Ile Thr
                330                 335                 340

gga acc tac acc cca ttg cca ccc caa aat gca gga cag atc acg ttc  1171
Gly Thr Tyr Thr Pro Leu Pro Pro Gln Asn Ala Gly Gln Ile Thr Phe
            345                 350                 355

tcc att ggt gac acc gtg ttg gac tcc ttg acc acc gat gac act ggc  1219
```

```
Ser Ile Gly Asp Thr Val Leu Asp Ser Leu Thr Thr Asp Asp Thr Gly
        360                 365                 370

atc att gac cgt gag ttc aac gtt cct gga gac ttg gtc aac cgc tac   1267
Ile Ile Asp Arg Glu Phe Asn Val Pro Gly Asp Leu Val Asn Arg Tyr
    375                 380                 385

acg gcg atc gtc gtg gaa ttc acc agc acc ggc gac gtt aat tgt ggg   1315
Thr Ala Ile Val Val Glu Phe Thr Ser Thr Gly Asp Val Asn Cys Gly
390                 395                 400                 405

gtc acc cag ccc gta ggc ctc aac att gat tcc gac agc ctt gtc acc   1363
Val Thr Gln Pro Val Gly Leu Asn Ile Asp Ser Asp Ser Leu Val Thr
                410                 415                 420

tcc caa cat tca gat gtt cct gta ctc aac ggc ttc cgg tcc cta ccg   1411
Ser Gln His Ser Asp Val Pro Val Leu Asn Gly Phe Arg Ser Leu Pro
            425                 430                 435

cag tcc ttc caa cct cgt gtg gac gtg gcg ttt gct gat ccc agc gtg   1459
Gln Ser Phe Gln Pro Arg Val Asp Val Ala Phe Ala Asp Pro Ser Val
        440                 445                 450

cag gaa ctc tcc cgc gct gtc agc gta gtg ttg gga att caa tct atg   1507
Gln Glu Leu Ser Arg Ala Val Ser Val Val Leu Gly Ile Gln Ser Met
    455                 460                 465

agc tcc cag cgc atc cgc cca cac ctg gtt aac tgg gat gaa gcc gta   1555
Ser Ser Gln Arg Ile Arg Pro His Leu Val Asn Trp Asp Glu Ala Val
470                 475                 480                 485

gcc agc gag cgc cca aca att ttc att gat gct gcg ggc gca aag act   1603
Ala Ser Glu Arg Pro Thr Ile Phe Ile Asp Ala Ala Gly Ala Lys Thr
                490                 495                 500

gat caa gtg cca agc tac ctc gcc caa caa ggc caa acc cta gag atc   1651
Asp Gln Val Pro Ser Tyr Leu Ala Gln Gln Gly Gln Thr Leu Glu Ile
            505                 510                 515

acc agc aag aac gac caa aat gcg gac ggc gaa caa ctc acc cga tcc   1699
Thr Ser Lys Asn Asp Gln Asn Ala Asp Gly Glu Gln Leu Thr Arg Ser
        520                 525                 530

ctg caa acc aac gct gcg ctt gtt gtc ggt tcc att cag gcc gtg tgg   1747
Leu Gln Thr Asn Ala Ala Leu Val Val Gly Ser Ile Gln Ala Val Trp
    535                 540                 545

gat gcc gat aag aag cgc acg gtg att gtg gca agt tcc cag gac aac   1795
Asp Ala Asp Lys Lys Arg Thr Val Ile Val Ala Ser Ser Gln Asp Asn
550                 555                 560                 565

ccc ccc gat ttg gat gcc ttg att tcg tgg atg gga gaa gac cgc gaa   1843
Pro Pro Asp Leu Asp Ala Leu Ile Ser Trp Met Gly Glu Asp Arg Glu
                570                 575                 580

cgc tgg agt gat ctc aac ggc gac ctg att gtc aaa gtc cga gac cgc   1891
Arg Trp Ser Asp Leu Asn Gly Asp Leu Ile Val Lys Val Arg Asp Arg
            585                 590                 595

gaa cct gtg caa ttg acc acc gtg gaa gcc cca gat cag cct ggt cga   1939
Glu Pro Val Gln Leu Thr Thr Val Glu Ala Pro Asp Gln Pro Gly Arg
```

```
        600                 605                 610

tcg gcc aca gcc ttt att gcg atc ggc gtc agc ctt gtg gtc att gcc   1987
Ser Ala Thr Ala Phe Ile Ala Ile Gly Val Ser Leu Val Val Ile Ala
    615                 620                 625

ctg att gtc gca gcc gtg gtg tca gtg tcc agg cgt tcg caa aaa gga   2035
Leu Ile Val Ala Ala Val Val Ser Val Ser Arg Arg Ser Gln Lys Gly
630                 635                 640                 645

tac aaa tgatttcttc tttacccagt aga                                 2064
Tyr Lys
```

<210> 768
<211> 647
<212> PRT
<213> Corynebacterium glutamicum

<400> 768

```
Val Lys Ile Lys Ser Val Phe Leu Ser Thr Ala Leu Ser Ala Ser Leu
  1               5                  10                  15

Leu Leu Gly Ile Thr Pro Pro Val Leu Gly Ala Thr Ile Asn Pro Ser
             20                  25                  30

Leu Pro Leu Ser Ala Leu Ser Ser Ser Asp Asp Ile Ala Val Pro Asn
         35                  40                  45

Phe Ala Lys Glu Leu Pro Leu Ala Phe Asp Val Pro Ala Gly Thr Val
     50                  55                  60

Pro Gln Ser Leu Ser Gly Thr Leu Gln Ile Pro Ala Glu Phe Ser Gly
 65                  70                  75                  80

Gly Val Val Glu Phe Tyr Asp Gly Asp Arg Leu Phe His Thr Leu Arg
                 85                  90                  95

Leu Glu Val Asn Asp Ser Arg Ala His Ile Glu Val Pro Leu Gln Ser
            100                 105                 110

Val Pro Val Glu Asp Gly Arg Ala Thr Phe Trp Leu Arg Ala Met Leu
        115                 120                 125

Asp Pro Val Asn Asn Gln Trp Cys Tyr Glu Glu Gln Glu Val Arg Phe
    130                 135                 140

Leu Asp Gly Asn Val Thr Phe Glu Gly Ala Thr Ile Asn Pro Ala Val
145                 150                 155                 160

Val Ala Asp Tyr Phe Pro Ser Val Leu Arg Ala Leu Thr Ile Tyr Val
                165                 170                 175

Pro Glu Asn Pro Ser Glu Ala Val Gln Glu Ala Thr Leu Glu Val Ala
            180                 185                 190

Thr Ser Leu Asp Ser Val Tyr Arg Arg Ser Gly Leu Asp Val Asn Val
        195                 200                 205

Glu Thr Leu Pro Thr Gly Thr Asp Ala Pro Pro Thr Arg Pro Gln Asp
```

```
    210                 215                 220

Phe Glu Arg Gln Ile Val Leu Val Asp Glu Ala Thr Glu Ser Asn Thr
225                 230                 235                 240

Gln Lys Thr Glu Leu Val Asn Pro Gly Gln Asp Asn Ala Phe Leu Arg
                245                 250                 255

Leu Asn Gly Asn Ala Asp Glu Leu Tyr Asp Gln Ala Arg Leu Leu Thr
            260                 265                 270

Asp Ala Thr Leu Pro Leu Ala Val Asp Thr Glu Val Thr Ala Ser Gly
        275                 280                 285

Phe Gly Asp Val Pro Asn Leu Ser Thr Asp Val Ala Thr Leu Gln Glu
    290                 295                 300

Leu Gly Ile Thr Gln Leu Thr Ser Glu Ser Val Ala Arg Thr Ser Val
305                 310                 315                 320

Thr Leu Gly Ile Glu Arg Ser Arg Leu Arg Thr Tyr Ser Gln Ser Met
                325                 330                 335

Asp Leu His Ile Thr Gly Thr Tyr Thr Pro Leu Pro Pro Gln Asn Ala
            340                 345                 350

Gly Gln Ile Thr Phe Ser Ile Gly Asp Thr Val Leu Asp Ser Leu Thr
        355                 360                 365

Thr Asp Asp Thr Gly Ile Ile Asp Arg Glu Phe Asn Val Pro Gly Asp
    370                 375                 380

Leu Val Asn Arg Tyr Thr Ala Ile Val Val Glu Phe Thr Ser Thr Gly
385                 390                 395                 400

Asp Val Asn Cys Gly Val Thr Gln Pro Val Gly Leu Asn Ile Asp Ser
                405                 410                 415

Asp Ser Leu Val Thr Ser Gln His Ser Asp Val Pro Val Leu Asn Gly
            420                 425                 430

Phe Arg Ser Leu Pro Gln Ser Phe Gln Pro Arg Val Asp Val Ala Phe
        435                 440                 445

Ala Asp Pro Ser Val Gln Glu Leu Ser Arg Ala Val Ser Val Val Leu
    450                 455                 460

Gly Ile Gln Ser Met Ser Ser Gln Arg Ile Arg Pro His Leu Val Asn
465                 470                 475                 480

Trp Asp Glu Ala Val Ala Ser Glu Arg Pro Thr Ile Phe Ile Asp Ala
                485                 490                 495

Ala Gly Ala Lys Thr Asp Gln Val Pro Ser Tyr Leu Ala Gln Gln Gly
            500                 505                 510

Gln Thr Leu Glu Ile Thr Ser Lys Asn Asp Gln Asn Ala Asp Gly Glu
        515                 520                 525

Gln Leu Thr Arg Ser Leu Gln Thr Asn Ala Ala Leu Val Val Gly Ser
    530                 535                 540
```

```
Ile Gln Ala Val Trp Asp Ala Asp Lys Lys Arg Thr Val Ile Val Ala
545                 550                 555                 560

Ser Ser Gln Asp Asn Pro Pro Asp Leu Asp Ala Leu Ile Ser Trp Met
                565                 570                 575

Gly Glu Asp Arg Glu Arg Trp Ser Asp Leu Asn Gly Asp Leu Ile Val
            580                 585                 590

Lys Val Arg Asp Arg Glu Pro Val Gln Leu Thr Thr Val Glu Ala Pro
        595                 600                 605

Asp Gln Pro Gly Arg Ser Ala Thr Ala Phe Ile Ala Ile Gly Val Ser
    610                 615                 620

Leu Val Val Ile Ala Leu Ile Val Ala Ala Val Val Ser Val Ser Arg
625                 630                 635                 640

Arg Ser Gln Lys Gly Tyr Lys
                645
```

20040229 09:00:00 PM

<210> 769
<211> 2064
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2041)
<223> FRXA01754

<400> 769

```
tgtggctgaa gacaagaatg aatagcattc atctcgtcga atttcatgta gaaatttgtc 60

ccccttttt ttgatgtgaa agttgaatcg gtaagctcct gtg aaa att aaa tcc   115
                                              Val Lys Ile Lys Ser
                                                1               5

gta ttt ttg agc acc gct tta agc gct tcc tta ctg ctc gga atc acc   163
Val Phe Leu Ser Thr Ala Leu Ser Ala Ser Leu Leu Leu Gly Ile Thr
                  10                  15                  20

cca ccc gtg ctg gga gca acg atc aac ccc agt ttg cct ctt tct gcg   211
Pro Pro Val Leu Gly Ala Thr Ile Asn Pro Ser Leu Pro Leu Ser Ala
             25                  30                  35

ttg agc tcc tcg gac gat atc gcc gta ccc aac ttc gcc aaa gaa tta   259
Leu Ser Ser Ser Asp Asp Ile Ala Val Pro Asn Phe Ala Lys Glu Leu
         40                  45                  50

ccg tta gct ttt gat gta cca gca ggc act gtt ccc caa agc ttg agt   307
Pro Leu Ala Phe Asp Val Pro Ala Gly Thr Val Pro Gln Ser Leu Ser
     55                  60                  65

gga acg ctg cag att cct gcc gag ttt tct ggc ggc gtc gtg gag ttt   355
Gly Thr Leu Gln Ile Pro Ala Glu Phe Ser Gly Gly Val Val Glu Phe
 70                  75                  80                  85

tat gac ggt gac cgg ctc ttt cac acc ctg cgc cta gaa gtt aat gat   403
```

```
Tyr Asp Gly Asp Arg Leu Phe His Thr Leu Arg Leu Glu Val Asn Asp
                 90                  95                 100

tcc cga gca cac att gag gtt ccg ctg caa agc gtt cct gtc gaa gac   451
Ser Arg Ala His Ile Glu Val Pro Leu Gln Ser Val Pro Val Glu Asp
            105                 110                 115

ggc cgc gcc acc ttt tgg ttg cgc gcc atg ttg gat cct gta aac aac   499
Gly Arg Ala Thr Phe Trp Leu Arg Ala Met Leu Asp Pro Val Asn Asn
        120                 125                 130

cag tgg tgc tac gag gag cag gaa gtc cgc ttc tta gac gga aac gtc   547
Gln Trp Cys Tyr Glu Glu Gln Glu Val Arg Phe Leu Asp Gly Asn Val
    135                 140                 145

acc ttt gaa ggg gcg acg att aac cca gct gtg gtg gct gat tac ttc   595
Thr Phe Glu Gly Ala Thr Ile Asn Pro Ala Val Val Ala Asp Tyr Phe
150                 155                 160                 165

ccg tca gtg ctg cgc gcg ttg aca att tac gtc ccg gaa aac ccc tct   643
Pro Ser Val Leu Arg Ala Leu Thr Ile Tyr Val Pro Glu Asn Pro Ser
                170                 175                 180

gag gca gta caa gaa gcc acg tta gag gtt gcg acc tcc ctg gat tcg   691
Glu Ala Val Gln Glu Ala Thr Leu Glu Val Ala Thr Ser Leu Asp Ser
            185                 190                 195

gtg tac cga aga tca ggt ctg gat gtc aac gta gaa acg ctt cca acc   739
Val Tyr Arg Arg Ser Gly Leu Asp Val Asn Val Glu Thr Leu Pro Thr
        200                 205                 210

ggc acc gat gct cct cct aca cgt cct caa gat ttt gaa cgc cag att   787
Gly Thr Asp Ala Pro Pro Thr Arg Pro Gln Asp Phe Glu Arg Gln Ile
    215                 220                 225

gtg ctg gtt gac gag gca aca gaa agt aac acg caa aaa acc gaa ttg   835
Val Leu Val Asp Glu Ala Thr Glu Ser Asn Thr Gln Lys Thr Glu Leu
230                 235                 240                 245

gtc aat ccc ggc caa gac aat gca ttc ttg cgc ctg aac ggc aac gcc   883
Val Asn Pro Gly Gln Asp Asn Ala Phe Leu Arg Leu Asn Gly Asn Ala
                250                 255                 260

gac gag ctt tac gat caa gcg cgc ttg ctt acc gac gca acc ctg cca   931
Asp Glu Leu Tyr Asp Gln Ala Arg Leu Leu Thr Asp Ala Thr Leu Pro
            265                 270                 275

ctt gcc gta gac acc gaa gta acg gcc tca ggt ttt ggt gat gtg ccc   979
Leu Ala Val Asp Thr Glu Val Thr Ala Ser Gly Phe Gly Asp Val Pro
        280                 285                 290

aac ctt tct aca gat gtg gcc acc ctc caa gaa ctg ggt atc acg cag   1027
Asn Leu Ser Thr Asp Val Ala Thr Leu Gln Glu Leu Gly Ile Thr Gln
    295                 300                 305

ctc acc tct gaa tca gtt gcg cgc aca agc gtc acc ttg ggc att gaa   1075
Leu Thr Ser Glu Ser Val Ala Arg Thr Ser Val Thr Leu Gly Ile Glu
310                 315                 320                 325

cgc tcc cgc ctg cgg acc tac tcg cag tcc atg gac ctg cac ata acg   1123
Arg Ser Arg Leu Arg Thr Tyr Ser Gln Ser Met Asp Leu His Ile Thr
```

```
                330                 335                 340

gga acc tac acc cca ttg cca ccc caa aat gca gga cag atc acg ttc   1171
Gly Thr Tyr Thr Pro Leu Pro Pro Gln Asn Ala Gly Gln Ile Thr Phe
            345                 350                 355

tcc att ggt gac acc gtg ttg gac tcc ttg acc acc gat gac act ggc   1219
Ser Ile Gly Asp Thr Val Leu Asp Ser Leu Thr Thr Asp Asp Thr Gly
        360                 365                 370

atc att gac cgt gag ttc aac gtt cct gga gac ttg gtc aac cgc tac   1267
Ile Ile Asp Arg Glu Phe Asn Val Pro Gly Asp Leu Val Asn Arg Tyr
    375                 380                 385

acg gcg atc gtc gtg gaa ttc acc agc acc ggc gac gtt aat tgt ggg   1315
Thr Ala Ile Val Val Glu Phe Thr Ser Thr Gly Asp Val Asn Cys Gly
390                 395                 400                 405

gtc acc cag ccc gta ggc ctc aac att gat tcc gac agc ctt gtc acc   1363
Val Thr Gln Pro Val Gly Leu Asn Ile Asp Ser Asp Ser Leu Val Thr
                410                 415                 420

tcc caa cat tca gat gtt cct gta ctc aac ggc ttc cgg tcc cta ccg   1411
Ser Gln His Ser Asp Val Pro Val Leu Asn Gly Phe Arg Ser Leu Pro
            425                 430                 435

cag tcc ttc caa cct cgt gtg gac gtg gcg ttt gct gat ccc agc gtg   1459
Gln Ser Phe Gln Pro Arg Val Asp Val Ala Phe Ala Asp Pro Ser Val
        440                 445                 450

cag gaa ctc tcc cgc gct gtc agc gta gtg ttg gga att caa tct atg   1507
Gln Glu Leu Ser Arg Ala Val Ser Val Val Leu Gly Ile Gln Ser Met
    455                 460                 465

agc tcc cag cgc atc cgc cca cac ctg gtt aac tgg gat gaa gcc gta   1555
Ser Ser Gln Arg Ile Arg Pro His Leu Val Asn Trp Asp Glu Ala Val
470                 475                 480                 485

gcc agc gag cgc cca aca att ttc att gat gct gcg ggc gca aag act   1603
Ala Ser Glu Arg Pro Thr Ile Phe Ile Asp Ala Ala Gly Ala Lys Thr
                490                 495                 500

gat caa gtg cca agc tac ctc gcc caa caa ggc caa acc cta gag atc   1651
Asp Gln Val Pro Ser Tyr Leu Ala Gln Gln Gly Gln Thr Leu Glu Ile
            505                 510                 515

acc agc aag aac gac caa aat gcg gac ggc gaa caa ctc acc cga tcc   1699
Thr Ser Lys Asn Asp Gln Asn Ala Asp Gly Glu Gln Leu Thr Arg Ser
        520                 525                 530

ctg caa acc aac gct gcg ctt gtt gtc ggt tcc att cag gcc gtg tgg   1747
Leu Gln Thr Asn Ala Ala Leu Val Val Gly Ser Ile Gln Ala Val Trp
    535                 540                 545

gat gcc gat aag aag cgc acg gtg att gtg gca agt tcc cag gac aac   1795
Asp Ala Asp Lys Lys Arg Thr Val Ile Val Ala Ser Ser Gln Asp Asn
550                 555                 560                 565

ccc ccc gat ttg gat gcc ttg att tcg tgg atg gga gaa gac cgc gaa   1843
Pro Pro Asp Leu Asp Ala Leu Ile Ser Trp Met Gly Glu Asp Arg Glu
                570                 575                 580
```

```
cgc tgg agt gat ctc aac ggc gac ctg att gtc aaa gtc cga gac cgc   1891
Arg Trp Ser Asp Leu Asn Gly Asp Leu Ile Val Lys Val Arg Asp Arg
            585                 590                 595

gaa cct gtg caa ttg acc acc gtg gaa gcc cca gat cag cct ggt cga   1939
Glu Pro Val Gln Leu Thr Thr Val Glu Ala Pro Asp Gln Pro Gly Arg
        600                 605                 610

tcg gcc aca gcc ttt att gcg atc ggc gtc agc ctt gtg gtc att gcc   1987
Ser Ala Thr Ala Phe Ile Ala Ile Gly Val Ser Leu Val Val Ile Ala
    615                 620                 625

ctg att gtc gca gcc gtg gtg tca gtg tcc agg cgt tcg caa aaa gga   2035
Leu Ile Val Ala Ala Val Val Ser Val Ser Arg Arg Ser Gln Lys Gly
630                 635                 640                 645

tac aaa tgatttcttc tttacccagt aga                                 2064
Tyr Lys
```

<210> 770
<211> 647
<212> PRT
<213> Corynebacterium glutamicum

<400> 770

```
Val Lys Ile Lys Ser Val Phe Leu Ser Thr Ala Leu Ser Ala Ser Leu
  1               5                  10                  15

Leu Leu Gly Ile Thr Pro Pro Val Leu Gly Ala Thr Ile Asn Pro Ser
             20                  25                  30

Leu Pro Leu Ser Ala Leu Ser Ser Ser Asp Asp Ile Ala Val Pro Asn
         35                  40                  45

Phe Ala Lys Glu Leu Pro Leu Ala Phe Asp Val Pro Ala Gly Thr Val
     50                  55                  60

Pro Gln Ser Leu Ser Gly Thr Leu Gln Ile Pro Ala Glu Phe Ser Gly
 65                  70                  75                  80

Gly Val Val Glu Phe Tyr Asp Gly Asp Arg Leu Phe His Thr Leu Arg
                 85                  90                  95

Leu Glu Val Asn Asp Ser Arg Ala His Ile Glu Val Pro Leu Gln Ser
            100                 105                 110

Val Pro Val Glu Asp Gly Arg Ala Thr Phe Trp Leu Arg Ala Met Leu
        115                 120                 125

Asp Pro Val Asn Asn Gln Trp Cys Tyr Glu Glu Gln Glu Val Arg Phe
    130                 135                 140

Leu Asp Gly Asn Val Thr Phe Glu Gly Ala Thr Ile Asn Pro Ala Val
145                 150                 155                 160

Val Ala Asp Tyr Phe Pro Ser Val Leu Arg Ala Leu Thr Ile Tyr Val
                165                 170                 175
```

Pro Glu Asn Pro Ser Glu Ala Val Gln Glu Ala Thr Leu Glu Val Ala
180 185 190

Thr Ser Leu Asp Ser Val Tyr Arg Arg Ser Gly Leu Asp Val Asn Val
195 200 205

Glu Thr Leu Pro Thr Gly Thr Asp Ala Pro Pro Thr Arg Pro Gln Asp
210 215 220

Phe Glu Arg Gln Ile Val Leu Val Asp Glu Ala Thr Glu Ser Asn Thr
225 230 235 240

Gln Lys Thr Glu Leu Val Asn Pro Gly Gln Asp Asn Ala Phe Leu Arg
245 250 255

Leu Asn Gly Asn Ala Asp Glu Leu Tyr Asp Gln Ala Arg Leu Leu Thr
260 265 270

Asp Ala Thr Leu Pro Leu Ala Val Asp Thr Glu Val Thr Ala Ser Gly
275 280 285

Phe Gly Asp Val Pro Asn Leu Ser Thr Asp Val Ala Thr Leu Gln Glu
290 295 300

Leu Gly Ile Thr Gln Leu Thr Ser Glu Ser Val Ala Arg Thr Ser Val
305 310 315 320

Thr Leu Gly Ile Glu Arg Ser Arg Leu Arg Thr Tyr Ser Gln Ser Met
325 330 335

Asp Leu His Ile Thr Gly Thr Tyr Tnr Pro Leu Pro Pro Gln Asn Ala
340 345 350

Gly Gln Ile Thr Phe Ser Ile Gly Asp Thr Val Leu Asp Ser Leu Thr
355 360 365

Thr Asp Asp Thr Gly Ile Ile Asp Arg Glu Phe Asn Val Pro Gly Asp
370 375 380

Leu Val Asn Arg Tyr Thr Ala Ile Val Val Glu Phe Thr Ser Thr Gly
385 390 395 400

Asp Val Asn Cys Gly Val Thr Gln Pro Val Gly Leu Asn Ile Asp Ser
405 410 415

Asp Ser Leu Val Thr Ser Gln His Ser Asp Val Pro Val Leu Asn Gly
420 425 430

Phe Arg Ser Leu Pro Gln Ser Phe Gln Pro Arg Val Asp Val Ala Phe
435 440 445

Ala Asp Pro Ser Val Gln Glu Leu Ser Arg Ala Val Ser Val Val Leu
450 455 460

Gly Ile Gln Ser Met Ser Ser Gln Arg Ile Arg Pro His Leu Val Asn
465 470 475 480

Trp Asp Glu Ala Val Ala Ser Glu Arg Pro Thr Ile Phe Ile Asp Ala
485 490 495

Ala Gly Ala Lys Thr Asp Gln Val Pro Ser Tyr Leu Ala Gln Gln Gly

```
            500                 505                 510

Gln Thr Leu Glu Ile Thr Ser Lys Asn Asp Gln Asn Ala Asp Gly Glu
        515                 520                 525

Gln Leu Thr Arg Ser Leu Gln Thr Asn Ala Ala Leu Val Val Gly Ser
    530                 535                 540

Ile Gln Ala Val Trp Asp Ala Asp Lys Lys Arg Thr Val Ile Val Ala
545                 550                 555                 560

Ser Ser Gln Asp Asn Pro Pro Asp Leu Asp Ala Leu Ile Ser Trp Met
                565                 570                 575

Gly Glu Asp Arg Glu Arg Trp Ser Asp Leu Asn Gly Asp Leu Ile Val
            580                 585                 590

Lys Val Arg Asp Arg Glu Pro Val Gln Leu Thr Thr Val Glu Ala Pro
        595                 600                 605

Asp Gln Pro Gly Arg Ser Ala Thr Ala Phe Ile Ala Ile Gly Val Ser
    610                 615                 620

Leu Val Val Ile Ala Leu Ile Val Ala Ala Val Val Ser Val Ser Arg
625                 630                 635                 640

Arg Ser Gln Lys Gly Tyr Lys
                645
```

<210> 771
<211> 4587
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(4564)
<223> RXN01761

<400> 771

```
ttaaagtttc tatattccat tctaaaataa ctttgaattg gggattaatg aaacttttta 60

agcaattgtt taaaacgaat attgaggggg tggcgggcaa gtg act gcg aca gtt   115
                                            Val Thr Ala Thr Val
                                              1               5

tta gaa ccg caa cct gta cag ctt agt gag cag gac gta gat gct gag   163
Leu Glu Pro Gln Pro Val Gln Leu Ser Glu Gln Asp Val Asp Ala Glu
                10                  15                  20

att gcg cgc atg gag ctt aaa cac aac cga cac aag acg tgg cga cgc   211
Ile Ala Arg Met Glu Leu Lys His Asn Arg His Lys Thr Trp Arg Arg
            25                  30                  35

cga acg atg gct gtt gtc atg acg ctc ttg atc tca gtg ggt ttg agc   259
Arg Thr Met Ala Val Val Met Thr Leu Leu Ile Ser Val Gly Leu Ser
        40                  45                  50

ttt ggt gcg ttt ggt aac aag gaa cgt gaa gct aat gct ttc gcc agc   307
Phe Gly Ala Phe Gly Asn Lys Glu Arg Glu Ala Asn Ala Phe Ala Ser
```

```
     55                  60                  65

gct att att gcc cag gtt gtc ggt gct atg ggc gag gtt gcc ttt gaa   355
Ala Ile Ile Ala Gln Val Val Gly Ala Met Gly Glu Val Ala Phe Glu
 70                  75                  80                  85

gcg att tgt ccc agt gat ggt gac acc gag atg ctt ctt aag tgc atc   403
Ala Ile Cys Pro Ser Asp Gly Asp Thr Glu Met Leu Leu Lys Cys Ile
                90                  95                 100

acc gag aac tta ggt gaa atg cac att atc gag aag tgt ctc gaa gca   451
Thr Glu Asn Leu Gly Glu Met His Ile Ile Glu Lys Cys Leu Glu Ala
            105                 110                 115

gaa gat gtc ttg aag tgc ttc tac gat gcg aaa aac gaa gag caa cgt   499
Glu Asp Val Leu Lys Cys Phe Tyr Asp Ala Lys Asn Glu Glu Gln Arg
        120                 125                 130

aaa gaa cag aac ctt gat aaa gcc cct gat tac tcc atg tac cgt atg   547
Lys Glu Gln Asn Leu Asp Lys Ala Pro Asp Tyr Ser Met Tyr Arg Met
    135                 140                 145

gcc tct gcg atg gca tcg ttc tat ggc aat ggt cgg gca gct act gcc   595
Ala Ser Ala Met Ala Ser Phe Tyr Gly Asn Gly Arg Ala Ala Thr Ala
150                 155                 160                 165

ggt gta gag gaa ggc gga ccg aac gag ttc ctc gat tct gag gac gcc   643
Gly Val Glu Glu Gly Gly Pro Asn Glu Phe Leu Asp Ser Glu Asp Ala
                170                 175                 180

ggt ctt aag gtg tgg gag ggc att ctc agt aag gcc gcc aac gga ggc   691
Gly Leu Lys Val Trp Glu Gly Ile Leu Ser Lys Ala Ala Asn Gly Gly
            185                 190                 195

aat gtc ctt ggt tat gct gac gcg aaa cac aac gag gac tct ggt tgg   739
Asn Val Leu Gly Tyr Ala Asp Ala Lys His Asn Glu Asp Ser Gly Trp
        200                 205                 210

ttc ttt ggt aat ggt gtt gcc aac aac gag aaa acg tac tcc tat gat   787
Phe Phe Gly Asn Gly Val Ala Asn Asn Glu Lys Thr Tyr Ser Tyr Asp
    215                 220                 225

tct cta gct gat cat gcc ttt caa ggg cct tat cac ttt gca tta ttt   835
Ser Leu Ala Asp His Ala Phe Gln Gly Pro Tyr His Phe Ala Leu Phe
230                 235                 240                 245

ggc gcg aca ctg agt ggc tta ggc ttt gat agc tca aag gcg gag gat   883
Gly Ala Thr Leu Ser Gly Leu Gly Phe Asp Ser Ser Lys Ala Glu Asp
                250                 255                 260

tcg cag act gat ttt gct cag cgt aag ggc atg ggg tac gcg atg atg   931
Ser Gln Thr Asp Phe Ala Gln Arg Lys Gly Met Gly Tyr Ala Met Met
            265                 270                 275

atc gcg tac atc atc tcc gga ggc att gat ctg gtt ttt aac act gtg   979
Ile Ala Tyr Ile Ile Ser Gly Gly Ile Asp Leu Val Phe Asn Thr Val
        280                 285                 290

ctg aat atc ttg agc acc ata aac cca ttt aga ctg ctc gtt gga cca  1027
Leu Asn Ile Leu Ser Thr Ile Asn Pro Phe Arg Leu Leu Val Gly Pro
    295                 300                 305
```

```
gta tct cag aat act aac aag aca ttc act gag aat atg gct ggt ggg   1075
Val Ser Gln Asn Thr Asn Lys Thr Phe Thr Glu Asn Met Ala Gly Gly
310                 315                 320                 325

cag acc aca gaa gga aca ccg ttt gaa gga atg act gat ttc ttc ggg   1123
Gln Thr Thr Glu Gly Thr Pro Phe Glu Gly Met Thr Asp Phe Phe Gly
                330                 335                 340

ttg atc tat aac tgg tca gtg act gtg ggc tgg ctc atc ggt att cct   1171
Leu Ile Tyr Asn Trp Ser Val Thr Val Gly Trp Leu Ile Gly Ile Pro
            345                 350                 355

gtc tcc att ggt ctg ttt atg atg ggt gcg ttg atg ttt cga cgc atg   1219
Val Ser Ile Gly Leu Phe Met Met Gly Ala Leu Met Phe Arg Arg Met
        360                 365                 370

gac aag gga tca gcg ttt aaa aag gtt gtt atc cgc gtc gtg tac ggt   1267
Asp Lys Gly Ser Ala Phe Lys Lys Val Val Ile Arg Val Val Tyr Gly
    375                 380                 385

gtc gtt ggc ctg cca ctg ctt ggt gtc tct tat acc ggt gcg ctg gat   1315
Val Val Gly Leu Pro Leu Leu Gly Val Ser Tyr Thr Gly Ala Leu Asp
390                 395                 400                 405

tcc ttc ctc gac agc ggt agt tcc aca agt gct gga tca aat gcg aca   1363
Ser Phe Leu Asp Ser Gly Ser Ser Thr Ser Ala Gly Ser Asn Ala Thr
                410                 415                 420

aag att gtg ttg tcc acc tac gtg gat ttc caa tca tgg gca gaa aac   1411
Lys Ile Val Leu Ser Thr Tyr Val Asp Phe Gln Ser Trp Ala Glu Asn
            425                 430                 435

acc cgt atg cgt gtt cct gac aaa gta aca ctg gcg tgg agt ctg gag   1459
Thr Arg Met Arg Val Pro Asp Lys Val Thr Leu Ala Trp Ser Leu Glu
        440                 445                 450

gat cag gcg cca aca ggg cag tcc atg cgg atg gta cgc aat tcg gcg   1507
Asp Gln Ala Pro Thr Gly Gln Ser Met Arg Met Val Arg Asn Ser Ala
    455                 460                 465

ttg gaa att aat gct caa tca aat gag agt ttt act act ttt aag aat   1555
Leu Glu Ile Asn Ala Gln Ser Asn Glu Ser Phe Thr Thr Phe Lys Asn
470                 475                 480                 485

cca ggt tcc atg gat cta ggc tat agc atg gac tgg atg gaa aag atg   1603
Pro Gly Ser Met Asp Leu Gly Tyr Ser Met Asp Trp Met Glu Lys Met
                490                 495                 500

gcg gat cca gcc aat tct ggc acc gat ggg acc tca tca agt tcg gcg   1651
Ala Asp Pro Ala Asn Ser Gly Thr Asp Gly Thr Ser Ser Ser Ser Ala
            505                 510                 515

acg act att ttc cag gga acc atc gcg cta ctg agt cgt tat atc gac   1699
Thr Thr Ile Phe Gln Gly Thr Ile Ala Leu Leu Ser Arg Tyr Ile Asp
        520                 525                 530

aac gac agt atc tcc tct ggc agt ttc gaa acc tct att cga agt gcg   1747
Asn Asp Ser Ile Ser Ser Gly Ser Phe Glu Thr Ser Ile Arg Ser Ala
    535                 540                 545
```

```
atg gaa tct ttg acc tcg aaa gag gga agt ggc gaa gct gtt gcc ggt   1795
Met Glu Ser Leu Thr Ser Lys Glu Gly Ser Gly Glu Ala Val Ala Gly
550                 555                 560                 565

ggt gat gta atg gcc tgg gtt act ggt tac aac aca gcc tct ggt ctt   1843
Gly Asp Val Met Ala Trp Val Thr Gly Tyr Asn Thr Ala Ser Gly Leu
                570                 575                 580

aat gag atc act gct gct gaa tta gct gat gcg aac aat cca ttg ctt   1891
Asn Glu Ile Thr Ala Ala Glu Leu Ala Asp Ala Asn Asn Pro Leu Leu
            585                 590                 595

gag gtc agc gac tca gct ggt ctg cag gga cga cct att gac cgc aat   1939
Glu Val Ser Asp Ser Ala Gly Leu Gln Gly Arg Pro Ile Asp Arg Asn
        600                 605                 610

gcg gtg tca ttt aaa tct ggt gat gcg aca gcg tca tgc aac aac tca   1987
Ala Val Ser Phe Lys Ser Gly Asp Ala Thr Ala Ser Cys Asn Asn Ser
    615                 620                 625

gtc gtg aca ggt tct cgt gct gtg gtc ggg gac tac cga agt gac tgc   2035
Val Val Thr Gly Ser Arg Ala Val Val Gly Asp Tyr Arg Ser Asp Cys
630                 635                 640                 645

aat atg tcg ccc ttg acg atg tac aac ttc ctc aac acc tca ttc cat   2083
Asn Met Ser Pro Leu Thr Met Tyr Asn Phe Leu Asn Thr Ser Phe His
                650                 655                 660

cca gct gat gca agt gtc ttt tct acg tcc act tct gcg tca agc tac   2131
Pro Ala Asp Ala Ser Val Phe Ser Thr Ser Thr Ser Ala Ser Ser Tyr
            665                 670                 675

acc cgt gca tcg cat agc gca gtg agt ctt atc ggt tct ggt gcc atg   2179
Thr Arg Ala Ser His Ser Ala Val Ser Leu Ile Gly Ser Gly Ala Met
        680                 685                 690

aac ttt gtg tac tgg ttc tct gca atg tcc ctg atg ggt agc ttc atc   2227
Asn Phe Val Tyr Trp Phe Ser Ala Met Ser Leu Met Gly Ser Phe Ile
    695                 700                 705

gtg atc ggt atc ggt tac gcc ggt gcc atg ctg ttt aat acg att cga   2275
Val Ile Gly Ile Gly Tyr Ala Gly Ala Met Leu Phe Asn Thr Ile Arg
710                 715                 720                 725

cgc acg ctg tcg ctc att ggt gcc gtt cct ttt gct gcg atg ggc ttt   2323
Arg Thr Leu Ser Leu Ile Gly Ala Val Pro Phe Ala Ala Met Gly Phe
                730                 735                 740

att gct ggt gtt gcc aag gtc att gtg tac acc atc gct atg ctc gta   2371
Ile Ala Gly Val Ala Lys Val Ile Val Tyr Thr Ile Ala Met Leu Val
            745                 750                 755

gag gtt atc gga acg atc att ttg tac cag ctc att acc cgg ttc ttg   2419
Glu Val Ile Gly Thr Ile Ile Leu Tyr Gln Leu Ile Thr Arg Phe Leu
        760                 765                 770

atg gct gta cca gca ctc ttt gaa caa cct ttg gct gat tcc tta agt   2467
Met Ala Val Pro Ala Leu Phe Glu Gln Pro Leu Ala Asp Ser Leu Ser
    775                 780                 785

agt aac gag agt gct gag ctg gtt gcc ggt gct ggt atg ggg cta gtc   2515
```

```
Ser Asn Glu Ser Ala Glu Leu Val Ala Gly Ala Gly Met Gly Leu Val
790                 795                 800                 805

ggt atg gca cta gct acc tca ggc aac tgg gcg att gcc ggc atg gtg   2563
Gly Met Ala Leu Ala Thr Ser Gly Asn Trp Ala Ile Ala Gly Met Val
                810                 815                 820

atc aca gtg gcc tca tcc atg ggg gtc atc atc ttc acg att att gcg   2611
Ile Thr Val Ala Ser Ser Met Gly Val Ile Ile Phe Thr Ile Ile Ala
            825                 830                 835

atg aag gtg cgc gga tct ttg gta tca ggt gtc gat gaa acc gtg acc   2659
Met Lys Val Arg Gly Ser Leu Val Ser Gly Val Asp Glu Thr Val Thr
        840                 845                 850

agt gtt att aac cgc ttc ttg gat aca cag gtc tct tct gca ggt gct   2707
Ser Val Ile Asn Arg Phe Leu Asp Thr Gln Val Ser Ser Ala Gly Ala
    855                 860                 865

acc tct ggt gac ggc atg atg cgt cgt gca gcc gca acg ggt ctt ggt   2755
Thr Ser Gly Asp Gly Met Met Arg Arg Ala Ala Ala Thr Gly Leu Gly
870                 875                 880                 885

att ggt gcg aca cat atg gta ctc aac cgt gat ggt gac ggt ggt gga   2803
Ile Gly Ala Thr His Met Val Leu Asn Arg Asp Gly Asp Gly Gly Gly
                890                 895                 900

tct gat tca ggc tct ggt gga tca ggt ggc ggt agc gat tca ggc ttg   2851
Ser Asp Ser Gly Ser Gly Gly Ser Gly Gly Gly Ser Asp Ser Gly Leu
            905                 910                 915

ggt gag aag gct gct ggt ctg gcg aag gtt gtc aca act gtg gct ggt   2899
Gly Glu Lys Ala Ala Gly Leu Ala Lys Val Val Thr Thr Val Ala Gly
        920                 925                 930

gcc gga tta gtc ggt aag tat gct acg gat gcg ctc gat aat tat gca   2947
Ala Gly Leu Val Gly Lys Tyr Ala Thr Asp Ala Leu Asp Asn Tyr Ala
    935                 940                 945

gat ggc gtt atc aac ggc gac ggt gat ggt gcg ttc gca gca ggt ggt   2995
Asp Gly Val Ile Asn Gly Asp Gly Asp Gly Ala Phe Ala Ala Gly Gly
950                 955                 960                 965

gac gct acc gtt gat ggc gac tat gta gca gat gga gat gca att gct   3043
Asp Ala Thr Val Asp Gly Asp Tyr Val Ala Asp Gly Asp Ala Ile Ala
                970                 975                 980

tct gct gat gct aac gct gat ttt gta gac ggt gtt gtt gat ggt gct   3091
Ser Ala Asp Ala Asn Ala Asp Phe Val Asp Gly Val Val Asp Gly Ala
            985                 990                 995

ggt cgc gcg tca ttt agc aat gct gcg tat agc tcc gat gga acc act   3139
Gly Arg Ala Ser Phe Ser Asn Ala Ala Tyr Ser Ser Asp Gly Thr Thr
        1000                1005                1010

ctc gac ggt gag ggt gcg agc gtt gat gca cag ggt aac ccg ctt cat   3187
Leu Asp Gly Glu Gly Ala Ser Val Asp Ala Gln Gly Asn Pro Leu His
    1015                1020                1025

gct gat ggc aca cca atg agt gct gct gaa gct gaa atg aag atg gct   3235
Ala Asp Gly Thr Pro Met Ser Ala Ala Glu Ala Glu Met Lys Met Ala
```

```
1030                1035                1040                1045

ggt ctg agc tcg tca gga acc atg atg gag aaa tct ggt gtg aaa tcg   3283
Gly Leu Ser Ser Ser Gly Thr Met Met Glu Lys Ser Gly Val Lys Ser
                1050                1055                1060

agt ggc att acc act gca gcg gat gtc atg gac gat cag tct ctg gca   3331
Ser Gly Ile Thr Thr Ala Ala Asp Val Met Asp Asp Gln Ser Leu Ala
            1065                1070                1075

agc agt gtc act gag tct ggt ctg tcc aag att cca gac acc tat ggt   3379
Ser Ser Val Thr Glu Ser Gly Leu Ser Lys Ile Pro Asp Thr Tyr Gly
        1080                1085                1090

gca gat gtc tcg ggt gct gcg ggc aca gtc gga act acc ggt gct gat   3427
Ala Asp Val Ser Gly Ala Ala Gly Thr Val Gly Thr Thr Gly Ala Asp
    1095                1100                1105

tac agt gcg acc gat tca agc gca ggt ctg aac atg agc gag gct gca   3475
Tyr Ser Ala Thr Asp Ser Ser Ala Gly Leu Asn Met Ser Glu Ala Ala
1110                1115                1120                1125

ttg cag agt ggc acc cca atg ggc gct ctc gct ggt gga tct gtg tcg   3523
Leu Gln Ser Gly Thr Pro Met Gly Ala Leu Ala Gly Gly Ser Val Ser
                1130                1135                1140

agt tcc gat cag gcc atg aat gac gca gct ctt cag att gca gcg tct   3571
Ser Ser Asp Gln Ala Met Asn Asp Ala Ala Leu Gln Ile Ala Ala Ser
            1145                1150                1155

cag ggt ctt gca cca gca ggt tcc ata gct ggt atg gag caa ctt agt   3619
Gln Gly Leu Ala Pro Ala Gly Ser Ile Ala Gly Met Glu Gln Leu Ser
        1160                1165                1170

gct caa gcc act gaa gca cct gct gga aag gcc ggc aag cag ctt ggc   3667
Ala Gln Ala Thr Glu Ala Pro Ala Gly Lys Ala Gly Lys Gln Leu Gly
    1175                1180                1185

gat ctt tct ggc tca gcg ctc aat act cag ctg gcg tcc atg gga cag   3715
Asp Leu Ser Gly Ser Ala Leu Asn Thr Gln Leu Ala Ser Met Gly Gln
1190                1195                1200                1205

cag gta ggt gac agt gtg aac agc gct tat gct gca ggc ggt atg ggt   3763
Gln Val Gly Asp Ser Val Asn Ser Ala Tyr Ala Ala Gly Gly Met Gly
                1210                1215                1220

ggt gtt gat gtg gct ggc aag gtc acc gag gca gca cag cac ttg tct   3811
Gly Val Asp Val Ala Gly Lys Val Thr Glu Ala Ala Gln His Leu Ser
            1225                1230                1235

cag gtt cca ggt cag att cag aat gct gtg acc aat gcg gat gct ggt   3859
Gln Val Pro Gly Gln Ile Gln Asn Ala Val Thr Asn Ala Asp Ala Gly
        1240                1245                1250

tcc tct ggc gca agc ttt ggt cag atg gca cag ggg gca gct ggt att   3907
Ser Ser Gly Ala Ser Phe Gly Gln Met Ala Gln Gly Ala Ala Gly Ile
    1255                1260                1265

gcc ggt gtc gca ggt gtg atc ggt gca gcg ggc gca gca agc tct gca   3955
Ala Gly Val Ala Gly Val Ile Gly Ala Ala Gly Ala Ala Ser Ser Ala
1270                1275                1280                1285
```

```
gca caa ggc gca ggt act gtc cag ggt gcg atg ggt aat gct gca gct   4003
Ala Gln Gly Ala Gly Thr Val Gln Gly Ala Met Gly Asn Ala Ala Ala
                1290                1295                1300

ggt gcg gga atg atc aac aac gct gtt tcc ggt gga gct act ggc tca   4051
Gly Ala Gly Met Ile Asn Asn Ala Val Ser Gly Gly Ala Thr Gly Ser
            1305                1310                1315

aca ggt gcc gca cat gtg gtc aat gca tca cat gga cca gtg gcg cct   4099
Thr Gly Ala Ala His Val Val Asn Ala Ser His Gly Pro Val Ala Pro
        1320                1325                1330

ggt cag gct cac tac caa gag tct ggt cat gca caa gca ttt gtg cag   4147
Gly Gln Ala His Tyr Gln Glu Ser Gly His Ala Gln Ala Phe Val Gln
    1335                1340                1345

aac aac cag gcc aac acc gcg cac aca gca aac acg cgt gca ccg tca   4195
Asn Asn Gln Ala Asn Thr Ala His Thr Ala Asn Thr Arg Ala Pro Ser
1350                1355                1360                1365

tca gct caa att atg ggc gcg aac gtt gct ggc tca ctg gca tca cag   4243
Ser Ala Gln Ile Met Gly Ala Asn Val Ala Gly Ser Leu Ala Ser Gln
                1370                1375                1380

gct gta cga gga atc ggt cag cct ggt cag atg ggt gct aat gtt cgc   4291
Ala Val Arg Gly Ile Gly Gln Pro Gly Gln Met Gly Ala Asn Val Arg
            1385                1390                1395

gac gcg atg ggt ggc agc gga cgc tct ggt ggc cgt ggt gga gca act   4339
Asp Ala Met Gly Gly Ser Gly Arg Ser Gly Gly Arg Gly Gly Ala Thr
        1400                1405                1410

caa ggc ggt cga ggc gca cag cgc agc ggt gtc agt gct aag aac ggt   4387
Gln Gly Gly Arg Gly Ala Gln Arg Ser Gly Val Ser Ala Lys Asn Gly
    1415                1420                1425

atc cgt gca cag cga ggt cag aag cct tct gtg acc ggc cag gcg atg   4435
Ile Arg Ala Gln Arg Gly Gln Lys Pro Ser Val Thr Gly Gln Ala Met
1430                1435                1440                1445

aat gca gca atg cgt tca gca gcg gta agc ggt cgc atg gca aac atg   4483
Asn Ala Ala Met Arg Ser Ala Ala Val Ser Gly Arg Met Ala Asn Met
                1450                1455                1460

gac ggc aac agt gta ggt ggc act gaa gca gat cca cag cag ggg agt   4531
Asp Gly Asn Ser Val Gly Gly Thr Glu Ala Asp Pro Gln Gln Gly Ser
            1465                1470                1475

ggc gta acc gag aag ggt gat aaa ggc gtt aaa tagcgtgtaa aacacaatga 4584
Gly Val Thr Glu Lys Gly Asp Lys Gly Val Lys
        1480                1485

ccg                                                               4587
```

<210> 772
<211> 1488
<212> PRT
<213> Corynebacterium glutamicum

<400> 772

```
Val Thr Ala Thr Val Leu Glu Pro Gln Pro Val Gln Leu Ser Glu Gln
 1               5                  10                  15

Asp Val Asp Ala Glu Ile Ala Arg Met Glu Leu Lys His Asn Arg His
            20                  25                  30

Lys Thr Trp Arg Arg Arg Thr Met Ala Val Val Met Thr Leu Leu Ile
        35                  40                  45

Ser Val Gly Leu Ser Phe Gly Ala Phe Gly Asn Lys Glu Arg Glu Ala
    50                  55                  60

Asn Ala Phe Ala Ser Ala Ile Ile Ala Gln Val Val Gly Ala Met Gly
65                  70                  75                  80

Glu Val Ala Phe Glu Ala Ile Cys Pro Ser Asp Gly Asp Thr Glu Met
                85                  90                  95

Leu Leu Lys Cys Ile Thr Glu Asn Leu Gly Glu Met His Ile Ile Glu
            100                 105                 110

Lys Cys Leu Glu Ala Glu Asp Val Leu Lys Cys Phe Tyr Asp Ala Lys
        115                 120                 125

Asn Glu Glu Gln Arg Lys Glu Gln Asn Leu Asp Lys Ala Pro Asp Tyr
    130                 135                 140

Ser Met Tyr Arg Met Ala Ser Ala Met Ala Ser Phe Tyr Gly Asn Gly
145                 150                 155                 160

Arg Ala Ala Thr Ala Gly Val Glu Glu Gly Gly Pro Asn Glu Phe Leu
                165                 170                 175

Asp Ser Glu Asp Ala Gly Leu Lys Val Trp Glu Gly Ile Leu Ser Lys
            180                 185                 190

Ala Ala Asn Gly Gly Asn Val Leu Gly Tyr Ala Asp Ala Lys His Asn
        195                 200                 205

Glu Asp Ser Gly Trp Phe Phe Gly Asn Gly Val Ala Asn Asn Glu Lys
    210                 215                 220

Thr Tyr Ser Tyr Asp Ser Leu Ala Asp His Ala Phe Gln Gly Pro Tyr
225                 230                 235                 240

His Phe Ala Leu Phe Gly Ala Thr Leu Ser Gly Leu Gly Phe Asp Ser
                245                 250                 255

Ser Lys Ala Glu Asp Ser Gln Thr Asp Phe Ala Gln Arg Lys Gly Met
            260                 265                 270

Gly Tyr Ala Met Met Ile Ala Tyr Ile Ile Ser Gly Gly Ile Asp Leu
        275                 280                 285

Val Phe Asn Thr Val Leu Asn Ile Leu Ser Thr Ile Asn Pro Phe Arg
    290                 295                 300

Leu Leu Val Gly Pro Val Ser Gln Asn Thr Asn Lys Thr Phe Thr Glu
305                 310                 315                 320
```

```
Asn Met Ala Gly Gly Gln Thr Thr Glu Gly Thr Pro Phe Glu Gly Met
                325                 330                 335

Thr Asp Phe Phe Gly Leu Ile Tyr Asn Trp Ser Val Thr Val Gly Trp
            340                 345                 350

Leu Ile Gly Ile Pro Val Ser Ile Gly Leu Phe Met Met Gly Ala Leu
        355                 360                 365

Met Phe Arg Arg Met Asp Lys Gly Ser Ala Phe Lys Lys Val Val Ile
    370                 375                 380

Arg Val Val Tyr Gly Val Val Gly Leu Pro Leu Leu Gly Val Ser Tyr
385                 390                 395                 400

Thr Gly Ala Leu Asp Ser Phe Leu Asp Ser Gly Ser Ser Thr Ser Ala
                405                 410                 415

Gly Ser Asn Ala Thr Lys Ile Val Leu Ser Thr Tyr Val Asp Phe Gln
            420                 425                 430

Ser Trp Ala Glu Asn Thr Arg Met Arg Val Pro Asp Lys Val Thr Leu
        435                 440                 445

Ala Trp Ser Leu Glu Asp Gln Ala Pro Thr Gly Gln Ser Met Arg Met
    450                 455                 460

Val Arg Asn Ser Ala Leu Glu Ile Asn Ala Gln Ser Asn Glu Ser Phe
465                 470                 475                 480

Thr Thr Phe Lys Asn Pro Gly Ser Met Asp Leu Gly Tyr Ser Met Asp
                485                 490                 495

Trp Met Glu Lys Met Ala Asp Pro Ala Asn Ser Gly Thr Asp Gly Thr
            500                 505                 510

Ser Ser Ser Ser Ala Thr Thr Ile Phe Gln Gly Thr Ile Ala Leu Leu
        515                 520                 525

Ser Arg Tyr Ile Asp Asn Asp Ser Ile Ser Ser Gly Ser Phe Glu Thr
    530                 535                 540

Ser Ile Arg Ser Ala Met Glu Ser Leu Thr Ser Lys Glu Gly Ser Gly
545                 550                 555                 560

Glu Ala Val Ala Gly Gly Asp Val Met Ala Trp Val Thr Gly Tyr Asn
                565                 570                 575

Thr Ala Ser Gly Leu Asn Glu Ile Thr Ala Ala Glu Leu Ala Asp Ala
            580                 585                 590

Asn Asn Pro Leu Leu Glu Val Ser Asp Ser Ala Gly Leu Gln Gly Arg
        595                 600                 605

Pro Ile Asp Arg Asn Ala Val Ser Phe Lys Ser Gly Asp Ala Thr Ala
    610                 615                 620

Ser Cys Asn Asn Ser Val Val Thr Gly Ser Arg Ala Val Val Gly Asp
625                 630                 635                 640

Tyr Arg Ser Asp Cys Asn Met Ser Pro Leu Thr Met Tyr Asn Phe Leu
```

```
                645                 650                 655

Asn Thr Ser Phe His Pro Ala Asp Ala Ser Val Phe Ser Thr Ser Thr
            660                 665                 670

Ser Ala Ser Ser Tyr Thr Arg Ala Ser His Ser Ala Val Ser Leu Ile
        675                 680                 685

Gly Ser Gly Ala Met Asn Phe Val Tyr Trp Phe Ser Ala Met Ser Leu
    690                 695                 700

Met Gly Ser Phe Ile Val Ile Gly Ile Gly Tyr Ala Gly Ala Met Leu
705                 710                 715                 720

Phe Asn Thr Ile Arg Arg Thr Leu Ser Leu Ile Gly Ala Val Pro Phe
                725                 730                 735

Ala Ala Met Gly Phe Ile Ala Gly Val Ala Lys Val Ile Val Tyr Thr
            740                 745                 750

Ile Ala Met Leu Val Glu Val Ile Gly Thr Ile Ile Leu Tyr Gln Leu
        755                 760                 765

Ile Thr Arg Phe Leu Met Ala Val Pro Ala Leu Phe Glu Gln Pro Leu
    770                 775                 780

Ala Asp Ser Leu Ser Ser Asn Glu Ser Ala Glu Leu Val Ala Gly Ala
785                 790                 795                 800

Gly Met Gly Leu Val Gly Met Ala Leu Ala Thr Ser Gly Asn Trp Ala
                805                 810                 815

Ile Ala Gly Met Val Ile Thr Val Ala Ser Ser Met Gly Val Ile Ile
            820                 825                 830

Phe Thr Ile Ile Ala Met Lys Val Arg Gly Ser Leu Val Ser Gly Val
        835                 840                 845

Asp Glu Thr Val Thr Ser Val Ile Asn Arg Phe Leu Asp Thr Gln Val
    850                 855                 860

Ser Ser Ala Gly Ala Thr Ser Gly Asp Gly Met Met Arg Arg Ala Ala
865                 870                 875                 880

Ala Thr Gly Leu Gly Ile Gly Ala Thr His Met Val Leu Asn Arg Asp
                885                 890                 895

Gly Asp Gly Gly Gly Ser Asp Ser Gly Ser Gly Gly Ser Gly Gly Gly
            900                 905                 910

Ser Asp Ser Gly Leu Gly Glu Lys Ala Ala Gly Leu Ala Lys Val Val
        915                 920                 925

Thr Thr Val Ala Gly Ala Gly Leu Val Gly Lys Tyr Ala Thr Asp Ala
    930                 935                 940

Leu Asp Asn Tyr Ala Asp Gly Val Ile Asn Gly Asp Gly Asp Gly Ala
945                 950                 955                 960

Phe Ala Ala Gly Gly Asp Ala Thr Val Asp Gly Asp Tyr Val Ala Asp
                965                 970                 975
```

```
Gly Asp Ala Ile Ala Ser Ala Asp Ala Asn Ala Asp Phe Val Asp Gly
            980                 985                 990

Val Val Asp Gly Ala Gly Arg Ala Ser Phe Ser Asn Ala Ala Tyr Ser
        995                 1000                1005

Ser Asp Gly Thr Thr Leu Asp Gly Glu Gly Ala Ser Val Asp Ala Gln
    1010                1015                1020

Gly Asn Pro Leu His Ala Asp Gly Thr Pro Met Ser Ala Ala Glu Ala
1025                1030                1035                1040

Glu Met Lys Met Ala Gly Leu Ser Ser Ser Gly Thr Met Met Glu Lys
                1045                1050                1055

Ser Gly Val Lys Ser Ser Gly Ile Thr Thr Ala Ala Asp Val Met Asp
            1060                1065                1070

Asp Gln Ser Leu Ala Ser Ser Val Thr Glu Ser Gly Leu Ser Lys Ile
        1075                1080                1085

Pro Asp Thr Tyr Gly Ala Asp Val Ser Gly Ala Ala Gly Thr Val Gly
    1090                1095                1100

Thr Thr Gly Ala Asp Tyr Ser Ala Thr Asp Ser Ser Ala Gly Leu Asn
1105                1110                1115                1120

Met Ser Glu Ala Ala Leu Gln Ser Gly Thr Pro Met Gly Ala Leu Ala
                1125                1130                1135

Gly Gly Ser Val Ser Ser Ser Asp Gln Ala Met Asn Asp Ala Ala Leu
            1140                1145                1150

Gln Ile Ala Ala Ser Gln Gly Leu Ala Pro Ala Gly Ser Ile Ala Gly
        1155                1160                1165

Met Glu Gln Leu Ser Ala Gln Ala Thr Glu Ala Pro Ala Gly Lys Ala
    1170                1175                1180

Gly Lys Gln Leu Gly Asp Leu Ser Gly Ser Ala Leu Asn Thr Gln Leu
1185                1190                1195                1200

Ala Ser Met Gly Gln Gln Val Gly Asp Ser Val Asn Ser Ala Tyr Ala
                1205                1210                1215

Ala Gly Gly Met Gly Gly Val Asp Val Ala Gly Lys Val Thr Glu Ala
            1220                1225                1230

Ala Gln His Leu Ser Gln Val Pro Gly Gln Ile Gln Asn Ala Val Thr
        1235                1240                1245

Asn Ala Asp Ala Gly Ser Ser Gly Ala Ser Phe Gly Gln Met Ala Gln
    1250                1255                1260

Gly Ala Ala Gly Ile Ala Gly Val Ala Gly Val Ile Gly Ala Ala Gly
1265                1270                1275                1280

Ala Ala Ser Ser Ala Ala Gln Gly Ala Gly Thr Val Gln Gly Ala Met
                1285                1290                1295
```

```
Gly Asn Ala Ala Ala Gly Ala Gly Met Ile Asn Asn Ala Val Ser Gly
            1300                1305                1310

Gly Ala Thr Gly Ser Thr Gly Ala Ala His Val Val Asn Ala Ser His
        1315                1320                1325

Gly Pro Val Ala Pro Gly Gln Ala His Tyr Gln Glu Ser Gly His Ala
    1330                1335                1340

Gln Ala Phe Val Gln Asn Asn Gln Ala Asn Thr Ala His Thr Ala Asn
1345                1350                1355                1360

Thr Arg Ala Pro Ser Ser Ala Gln Ile Met Gly Ala Asn Val Ala Gly
                1365                1370                1375

Ser Leu Ala Ser Gln Ala Val Arg Gly Ile Gly Gln Pro Gly Gln Met
            1380                1385                1390

Gly Ala Asn Val Arg Asp Ala Met Gly Gly Ser Gly Arg Ser Gly Gly
        1395                1400                1405

Arg Gly Gly Ala Thr Gln Gly Gly Arg Gly Ala Gln Arg Ser Gly Val
    1410                1415                1420

Ser Ala Lys Asn Gly Ile Arg Ala Gln Arg Gly Gln Lys Pro Ser Val
1425                1430                1435                1440

Thr Gly Gln Ala Met Asn Ala Ala Met Arg Ser Ala Ala Val Ser Gly
                1445                1450                1455

Arg Met Ala Asn Met Asp Gly Asn Ser Val Gly Gly Thr Glu Ala Asp
            1460                1465                1470

Pro Gln Gln Gly Ser Gly Val Thr Glu Lys Gly Asp Lys Gly Val Lys
        1475                1480                1485
```

<210> 773
<211> 916
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(916)
<223> FRXA00739

<400> 773

```
ttaaagtttc tatattccat tctaaaataa ctttgaattg gggattaatg aaacttttta 60

agcaattgtt taaaacgaat attgaggggg tggcgggcaa gtg act gcg aca gtt   115
                                        Val Thr Ala Thr Val
                                          1               5

tta gaa ccg caa cct gta cag ctt agt gag cag gac gta gat gct gag   163
Leu Glu Pro Gln Pro Val Gln Leu Ser Glu Gln Asp Val Asp Ala Glu
                 10                  15                  20
```

```
att gcg cgc atg gag ctt aaa cac aac cga cac aag acg tgg cga cgc   211
Ile Ala Arg Met Glu Leu Lys His Asn Arg His Lys Thr Trp Arg Arg
             25                  30                  35

cga acg atg gct gtt gtc atg acg ctc ttg atc tca gtg ggt ttg agc   259
Arg Thr Met Ala Val Val Met Thr Leu Leu Ile Ser Val Gly Leu Ser
         40                  45                  50

ttt ggt gcg ttt ggt aac aag gaa cgt gaa gct aat gct ttc gcc agc   307
Phe Gly Ala Phe Gly Asn Lys Glu Arg Glu Ala Asn Ala Phe Ala Ser
     55                  60                  65

gct att att gcc cag gtt gtc ggt gct atg ggc gag gtt gcc ttt gaa   355
Ala Ile Ile Ala Gln Val Val Gly Ala Met Gly Glu Val Ala Phe Glu
 70                  75                  80                  85

gcg att tgt ccc agt gat ggt gac acc gag atg ctt ctt aag tgc atc   403
Ala Ile Cys Pro Ser Asp Gly Asp Thr Glu Met Leu Leu Lys Cys Ile
                 90                  95                 100

acc gag aac tta ggt gaa atg cac att atc gag aag tgt ctc gaa gca   451
Thr Glu Asn Leu Gly Glu Met His Ile Ile Glu Lys Cys Leu Glu Ala
            105                 110                 115

gaa gat gtc ttg aag tgc ttc tac gat gcg aaa aac gaa gag caa cgt   499
Glu Asp Val Leu Lys Cys Phe Tyr Asp Ala Lys Asn Glu Glu Gln Arg
        120                 125                 130

aaa gaa cag aac ctt gat aaa gcc cct gat tac tcc atg tac cgt atg   547
Lys Glu Gln Asn Leu Asp Lys Ala Pro Asp Tyr Ser Met Tyr Arg Met
    135                 140                 145

gcc tct gcg atg gca tcg ttc tat ggc aat ggt cgg gca gct act gcc   595
Ala Ser Ala Met Ala Ser Phe Tyr Gly Asn Gly Arg Ala Ala Thr Ala
150                 155                 160                 165

ggt gta gag gaa ggc gga ccg aac gag ttc ctc gat tct gag gac gcc   643
Gly Val Glu Glu Gly Gly Pro Asn Glu Phe Leu Asp Ser Glu Asp Ala
                170                 175                 180

ggt ctt aag gtg tgg gag ggc att ctc agt aag gcc gcc aac gga ggc   691
Gly Leu Lys Val Trp Glu Gly Ile Leu Ser Lys Ala Ala Asn Gly Gly
            185                 190                 195

aat gtc ctt ggt tat gct gac gcg aaa cac aac gag gac tct ggt tgg   739
Asn Val Leu Gly Tyr Ala Asp Ala Lys His Asn Glu Asp Ser Gly Trp
        200                 205                 210

ttc ttt ggt aat ggt gtt gcc aac aac gag aaa acg tac tcc tat gat   787
Phe Phe Gly Asn Gly Val Ala Asn Asn Glu Lys Thr Tyr Ser Tyr Asp
    215                 220                 225

tct cta gct gat cat gcc ttt caa ggg cct tat cac ttt gca tta ttt   835
Ser Leu Ala Asp His Ala Phe Gln Gly Pro Tyr His Phe Ala Leu Phe
230                 235                 240                 245

ggc gcg aca ctg agt ggc tta ggc ttt gat agc tca aag gcg gag gat   883
Gly Ala Thr Leu Ser Gly Leu Gly Phe Asp Ser Ser Lys Ala Glu Asp
                250                 255                 260

tcg cag act gat ttt gct cag cgt aag ggc atg                      916
```

```
Ser Gln Thr Asp Phe Ala Gln Arg Lys Gly Met
            265                 270


<210> 774
<211> 272
<212> PRT
<213> Corynebacterium glutamicum

<400> 774
Val Thr Ala Thr Val Leu Glu Pro Gln Pro Val Gln Leu Ser Glu Gln
  1               5                  10                  15

Asp Val Asp Ala Glu Ile Ala Arg Met Glu Leu Lys His Asn Arg His
             20                  25                  30

Lys Thr Trp Arg Arg Arg Thr Met Ala Val Val Met Thr Leu Leu Ile
         35                  40                  45

Ser Val Gly Leu Ser Phe Gly Ala Phe Gly Asn Lys Glu Arg Glu Ala
     50                  55                  60

Asn Ala Phe Ala Ser Ala Ile Ile Ala Gln Val Val Gly Ala Met Gly
 65                  70                  75                  80

Glu Val Ala Phe Glu Ala Ile Cys Pro Ser Asp Gly Asp Thr Glu Met
                 85                  90                  95

Leu Leu Lys Cys Ile Thr Glu Asn Leu Gly Glu Met His Ile Ile Glu
            100                 105                 110

Lys Cys Leu Glu Ala Glu Asp Val Leu Lys Cys Phe Tyr Asp Ala Lys
        115                 120                 125

Asn Glu Glu Gln Arg Lys Glu Gln Asn Leu Asp Lys Ala Pro Asp Tyr
    130                 135                 140

Ser Met Tyr Arg Met Ala Ser Ala Met Ala Ser Phe Tyr Gly Asn Gly
145                 150                 155                 160

Arg Ala Ala Thr Ala Gly Val Glu Glu Gly Gly Pro Asn Glu Phe Leu
                165                 170                 175

Asp Ser Glu Asp Ala Gly Leu Lys Val Trp Glu Gly Ile Leu Ser Lys
            180                 185                 190

Ala Ala Asn Gly Gly Asn Val Leu Gly Tyr Ala Asp Ala Lys His Asn
        195                 200                 205

Glu Asp Ser Gly Trp Phe Phe Gly Asn Gly Val Ala Asn Asn Glu Lys
    210                 215                 220

Thr Tyr Ser Tyr Asp Ser Leu Ala Asp His Ala Phe Gln Gly Pro Tyr
225                 230                 235                 240

His Phe Ala Leu Phe Gly Ala Thr Leu Ser Gly Leu Gly Phe Asp Ser
                245                 250                 255

Ser Lys Ala Glu Asp Ser Gln Thr Asp Phe Ala Gln Arg Lys Gly Met
            260                 265                 270
```

<210> 775
<211> 2083
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2083)
<223> FRXA01587

<400> 775
catttagact ggtcggtgga cccgttctta gaatactaac aagacattca ctgagaatat 60

ggctggtggg cagaccacag aaggaacacc gcttggagga atg act gat ttc ttc 115
Met Thr Asp Phe Phe
1 5

ggg ttg atc tat aac tgg tca gtg act gtg ggc tgg ctc atc ggt att 163
Gly Leu Ile Tyr Asn Trp Ser Val Thr Val Gly Trp Leu Ile Gly Ile
10 15 20

cct gtc tcc att ggt ctg ttt atg atg ggt gcg ttg atg ttt cga cgc 211
Pro Val Ser Ile Gly Leu Phe Met Met Gly Ala Leu Met Phe Arg Arg
25 30 35

atg gac aag gga tca gcg ttt aaa aag gtt gtt atc cgc gtc gtg tac 259
Met Asp Lys Gly Ser Ala Phe Lys Lys Val Val Ile Arg Val Val Tyr
40 45 50

ggt gtc gtt ggc ctg cca ctg ctt ggt gtc tct tat acc ggt gcg ctg 307
Gly Val Val Gly Leu Pro Leu Leu Gly Val Ser Tyr Thr Gly Ala Leu
55 60 65

gat tcc ttc ctc gac agc ggt agt tcc aca agt gct gga tca aat gcg 355
Asp Ser Phe Leu Asp Ser Gly Ser Ser Thr Ser Ala Gly Ser Asn Ala
70 75 80 85

aca aag att gtg ttg tcc acc tac gtg gat ttc caa tca tgg gca gaa 403
Thr Lys Ile Val Leu Ser Thr Tyr Val Asp Phe Gln Ser Trp Ala Glu
90 95 100

aac acc cgt atg cgt gtt cct gac aaa gta aca ctg gcg tgg agt ctg 451
Asn Thr Arg Met Arg Val Pro Asp Lys Val Thr Leu Ala Trp Ser Leu
105 110 115

gag gat cag gcg cca aca ggg cag tcc atg cgg atg gta cgc aat tcg 499
Glu Asp Gln Ala Pro Thr Gly Gln Ser Met Arg Met Val Arg Asn Ser
120 125 130

gcg ttg gaa att aat gct caa tca aat gag agt ttt act act ttt aag 547
Ala Leu Glu Ile Asn Ala Gln Ser Asn Glu Ser Phe Thr Thr Phe Lys
135 140 145

aat cca ggt tcc atg gat cta ggc tat agc atg gac tgg atg gaa aag 595
Asn Pro Gly Ser Met Asp Leu Gly Tyr Ser Met Asp Trp Met Glu Lys
150 155 160 165

```
atg gcg gat cca gcc aat tct ggc acc gat ggg acc tca tca agt tcg   643
Met Ala Asp Pro Ala Asn Ser Gly Thr Asp Gly Thr Ser Ser Ser Ser
                170                 175                 180

gcg acg act att ttc cag gga acc atc gcg cta ctg agt cgt tat atc   691
Ala Thr Thr Ile Phe Gln Gly Thr Ile Ala Leu Leu Ser Arg Tyr Ile
            185                 190                 195

gac aac gac agt atc tcc tct ggc agt ttc gaa acc tct att cga agt   739
Asp Asn Asp Ser Ile Ser Ser Gly Ser Phe Glu Thr Ser Ile Arg Ser
        200                 205                 210

gcg atg gaa tct ttg acc tcg aaa gag gga agt ggc gaa gct gtt gcc   787
Ala Met Glu Ser Leu Thr Ser Lys Glu Gly Ser Gly Glu Ala Val Ala
    215                 220                 225

ggt ggt gat gta atg gcc tgg gtt act ggt tac aac aca gcc tct ggt   835
Gly Gly Asp Val Met Ala Trp Val Thr Gly Tyr Asn Thr Ala Ser Gly
230                 235                 240                 245

ctt aat gag atc act gct gct gaa tta gct gat gcg aac aat cca ttg   883
Leu Asn Glu Ile Thr Ala Ala Glu Leu Ala Asp Ala Asn Asn Pro Leu
                250                 255                 260

ctt gag gtc agc gac tca gct ggt ctg cag gga cga cct att gac cgc   931
Leu Glu Val Ser Asp Ser Ala Gly Leu Gln Gly Arg Pro Ile Asp Arg
            265                 270                 275

aat gcg gtg tca ttt aaa tct ggt gat gcg aca gcg tca tgc aac aac   979
Asn Ala Val Ser Phe Lys Ser Gly Asp Ala Thr Ala Ser Cys Asn Asn
        280                 285                 290

tca gtc gtg aca ggt tct cgt gct gtg gtc ggg gac tac cga agt gac  1027
Ser Val Val Thr Gly Ser Arg Ala Val Val Gly Asp Tyr Arg Ser Asp
    295                 300                 305

tgc aat atg tcg ccc ttg acg atg tac aac ttc ctc aac acc tca ttc  1075
Cys Asn Met Ser Pro Leu Thr Met Tyr Asn Phe Leu Asn Thr Ser Phe
310                 315                 320                 325

cat cca gct gat gca agt gtc ttt tct acg tcc act tct gcg tca agc  1123
His Pro Ala Asp Ala Ser Val Phe Ser Thr Ser Thr Ser Ala Ser Ser
                330                 335                 340

tac acc cgt gca tcg cat agc gca gtg agt ctt atc ggt tct ggt gcc  1171
Tyr Thr Arg Ala Ser His Ser Ala Val Ser Leu Ile Gly Ser Gly Ala
            345                 350                 355

atg aac ttt gtg tac tgg ttc tct gca atg tcc ctg atg ggt agc ttc  1219
Met Asn Phe Val Tyr Trp Phe Ser Ala Met Ser Leu Met Gly Ser Phe
        360                 365                 370

atc gtg atc ggt atc ggt tac gcc ggt gcc atg ctg ttt aat acg att  1267
Ile Val Ile Gly Ile Gly Tyr Ala Gly Ala Met Leu Phe Asn Thr Ile
    375                 380                 385

cga cgc acg ctg tcg ctc att ggt gcc gtt cct ttt gct gcg atg ggc  1315
Arg Arg Thr Leu Ser Leu Ile Gly Ala Val Pro Phe Ala Ala Met Gly
390                 395                 400                 405

ttt att gct ggt gtt gcc aag gtc att gtg tac acc atc gct atg ctc  1363
```

```
Phe Ile Ala Gly Val Ala Lys Val Ile Val Tyr Thr Ile Ala Met Leu
                410                 415                 420

gta gag gtt atc gga acg atc att ttg tac cag ctc att acc cgg ttc   1411
Val Glu Val Ile Gly Thr Ile Ile Leu Tyr Gln Leu Ile Thr Arg Phe
            425                 430                 435

ttg atg gct gta cca gca ctc ttt gaa caa cct ttg gct gat tcc tta   1459
Leu Met Ala Val Pro Ala Leu Phe Glu Gln Pro Leu Ala Asp Ser Leu
        440                 445                 450

agt agt aac gag agt gct gag ctg gtt gcc ggt gct ggt atg ggg cta   1507
Ser Ser Asn Glu Ser Ala Glu Leu Val Ala Gly Ala Gly Met Gly Leu
    455                 460                 465

gtc ggt atg gca cta gct acc tca ggc aac tgg gcg att gcc ggc atg   1555
Val Gly Met Ala Leu Ala Thr Ser Gly Asn Trp Ala Ile Ala Gly Met
470                 475                 480                 485

gtg atc aca gtg gcc tca tcc atg ggg gtc atc atc ttc acg att att   1603
Val Ile Thr Val Ala Ser Ser Met Gly Val Ile Ile Phe Thr Ile Ile
                490                 495                 500

gcg atg aag gtg cgc gga tct ttg gta tca ggt gtc gat gaa acc gtg   1651
Ala Met Lys Val Arg Gly Ser Leu Val Ser Gly Val Asp Glu Thr Val
            505                 510                 515

acc agt gtt att aac cgc ttc ttg gat aca cag gtc tct tct gca ggt   1699
Thr Ser Val Ile Asn Arg Phe Leu Asp Thr Gln Val Ser Ser Ala Gly
        520                 525                 530

gct acc tct ggt gac ggc atg atg cgt cgt gca gcc gca acg ggt ctt   1747
Ala Thr Ser Gly Asp Gly Met Met Arg Arg Ala Ala Ala Thr Gly Leu
    535                 540                 545

ggt att ggt gcg aca cat atg gta ctc aac cgt gat ggt gac ggt ggt   1795
Gly Ile Gly Ala Thr His Met Val Leu Asn Arg Asp Gly Asp Gly Gly
550                 555                 560                 565

gga tct gat tca ggc tct ggt gga tca ggt ggc ggt agc gat tca ggc   1843
Gly Ser Asp Ser Gly Ser Gly Gly Ser Gly Gly Gly Ser Asp Ser Gly
                570                 575                 580

ttg ggt gag aag gct gct ggt ctg gcg aag gtt gtc aca act gtg gct   1891
Leu Gly Glu Lys Ala Ala Gly Leu Ala Lys Val Val Thr Thr Val Ala
            585                 590                 595

ggt gcc gga tta gtc ggt aag tat gct acg gat gcg ctc gat aat tat   1939
Gly Ala Gly Leu Val Gly Lys Tyr Ala Thr Asp Ala Leu Asp Asn Tyr
        600                 605                 610

gca gat ggc gtt atc aac ggc gac ggt gat ggt gcg ttc gca gca ggt   1987
Ala Asp Gly Val Ile Asn Gly Asp Gly Asp Gly Ala Phe Ala Ala Gly
    615                 620                 625

ggt gac gct acc gtt gat ggc gac tat gta gca gat gga gat gca att   2035
Gly Asp Ala Thr Val Asp Gly Asp Tyr Val Ala Asp Gly Asp Ala Ile
630                 635                 640                 645

gct tct gct gat gct aac gct gat ttt gta gac ggg gtt gct gat ggt   2083
Ala Ser Ala Asp Ala Asn Ala Asp Phe Val Asp Gly Val Ala Asp Gly
```

650 655 660

<210> 776
<211> 661
<212> PRT
<213> Corynebacterium glutamicum

<400> 776
Met Thr Asp Phe Phe Gly Leu Ile Tyr Asn Trp Ser Val Thr Val Gly
1 5 10 15

Trp Leu Ile Gly Ile Pro Val Ser Ile Gly Leu Phe Met Met Gly Ala
20 25 30

Leu Met Phe Arg Arg Met Asp Lys Gly Ser Ala Phe Lys Lys Val Val
35 40 45

Ile Arg Val Val Tyr Gly Val Val Gly Leu Pro Leu Leu Gly Val Ser
50 55 60

Tyr Thr Gly Ala Leu Asp Ser Phe Leu Asp Ser Gly Ser Ser Thr Ser
65 70 75 80

Ala Gly Ser Asn Ala Thr Lys Ile Val Leu Ser Thr Tyr Val Asp Phe
85 90 95

Gln Ser Trp Ala Glu Asn Thr Arg Met Arg Val Pro Asp Lys Val Thr
100 105 110

Leu Ala Trp Ser Leu Glu Asp Gln Ala Pro Thr Gly Gln Ser Met Arg
115 120 125

Met Val Arg Asn Ser Ala Leu Glu Ile Asn Ala Gln Ser Asn Glu Ser
130 135 140

Phe Thr Thr Phe Lys Asn Pro Gly Ser Met Asp Leu Gly Tyr Ser Met
145 150 155 160

Asp Trp Met Glu Lys Met Ala Asp Pro Ala Asn Ser Gly Thr Asp Gly
165 170 175

Thr Ser Ser Ser Ser Ala Thr Thr Ile Phe Gln Gly Thr Ile Ala Leu
180 185 190

Leu Ser Arg Tyr Ile Asp Asn Asp Ser Ile Ser Ser Gly Ser Phe Glu
195 200 205

Thr Ser Ile Arg Ser Ala Met Glu Ser Leu Thr Ser Lys Glu Gly Ser
210 215 220

Gly Glu Ala Val Ala Gly Gly Asp Val Met Ala Trp Val Thr Gly Tyr
225 230 235 240

Asn Thr Ala Ser Gly Leu Asn Glu Ile Thr Ala Ala Glu Leu Ala Asp
245 250 255

Ala Asn Asn Pro Leu Leu Glu Val Ser Asp Ser Ala Gly Leu Gln Gly
260 265 270

Arg Pro Ile Asp Arg Asn Ala Val Ser Phe Lys Ser Gly Asp Ala Thr

```
        275                 280                 285

Ala Ser Cys Asn Asn Ser Val Val Thr Gly Ser Arg Ala Val Val Gly
    290                 295                 300

Asp Tyr Arg Ser Asp Cys Asn Met Ser Pro Leu Thr Met Tyr Asn Phe
305                 310                 315                 320

Leu Asn Thr Ser Phe His Pro Ala Asp Ala Ser Val Phe Ser Thr Ser
                325                 330                 335

Thr Ser Ala Ser Ser Tyr Thr Arg Ala Ser His Ser Ala Val Ser Leu
            340                 345                 350

Ile Gly Ser Gly Ala Met Asn Phe Val Tyr Trp Phe Ser Ala Met Ser
        355                 360                 365

Leu Met Gly Ser Phe Ile Val Ile Gly Ile Gly Tyr Ala Gly Ala Met
    370                 375                 380

Leu Phe Asn Thr Ile Arg Arg Thr Leu Ser Leu Ile Gly Ala Val Pro
385                 390                 395                 400

Phe Ala Ala Met Gly Phe Ile Ala Gly Val Ala Lys Val Ile Val Tyr
                405                 410                 415

Thr Ile Ala Met Leu Val Glu Val Ile Gly Thr Ile Ile Leu Tyr Gln
            420                 425                 430

Leu Ile Thr Arg Phe Leu Met Ala Val Pro Ala Leu Phe Glu Gln Pro
        435                 440                 445

Leu Ala Asp Ser Leu Ser Ser Asn Glu Ser Ala Glu Leu Val Ala Gly
    450                 455                 460

Ala Gly Met Gly Leu Val Gly Met Ala Leu Ala Thr Ser Gly Asn Trp
465                 470                 475                 480

Ala Ile Ala Gly Met Val Ile Thr Val Ala Ser Ser Met Gly Val Ile
                485                 490                 495

Ile Phe Thr Ile Ile Ala Met Lys Val Arg Gly Ser Leu Val Ser Gly
            500                 505                 510

Val Asp Glu Thr Val Thr Ser Val Ile Asn Arg Phe Leu Asp Thr Gln
        515                 520                 525

Val Ser Ser Ala Gly Ala Thr Ser Gly Asp Gly Met Met Arg Arg Ala
    530                 535                 540

Ala Ala Thr Gly Leu Gly Ile Gly Ala Thr His Met Val Leu Asn Arg
545                 550                 555                 560

Asp Gly Asp Gly Gly Gly Ser Asp Ser Gly Ser Gly Gly Ser Gly Gly
                565                 570                 575

Gly Ser Asp Ser Gly Leu Gly Glu Lys Ala Ala Gly Leu Ala Lys Val
            580                 585                 590

Val Thr Thr Val Ala Gly Ala Gly Leu Val Gly Lys Tyr Ala Thr Asp
        595                 600                 605
```

```
Ala Leu Asp Asn Tyr Ala Asp Gly Val Ile Asn Gly Asp Gly Asp Gly
    610                 615                 620

Ala Phe Ala Ala Gly Gly Asp Ala Thr Val Asp Gly Asp Tyr Val Ala
625                 630                 635                 640

Asp Gly Asp Ala Ile Ala Ser Ala Asp Ala Asn Ala Asp Phe Val Asp
                645                 650                 655

Gly Val Ala Asp Gly
            660
```

<210> 777
<211> 1541
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1518)
<223> FRXA01761

<400> 777

```
gct gat gct aac gct gat ttt gta gac ggt gtt gtt gat ggt gct ggt   48
Ala Asp Ala Asn Ala Asp Phe Val Asp Gly Val Val Asp Gly Ala Gly
  1               5                  10                  15

cgc gcg tca ttt agc aat gct gcg tat agc tcc gat gga acc act ctc   96
Arg Ala Ser Phe Ser Asn Ala Ala Tyr Ser Ser Asp Gly Thr Thr Leu
             20                  25                  30

gac ggt gag ggt gcg agc gtt gat gca cag ggt aac ccg ctt cat gct   144
Asp Gly Glu Gly Ala Ser Val Asp Ala Gln Gly Asn Pro Leu His Ala
         35                  40                  45

gat ggc aca cca atg agt gct gct gaa gct gaa atg aag atg gct ggt   192
Asp Gly Thr Pro Met Ser Ala Ala Glu Ala Glu Met Lys Met Ala Gly
     50                  55                  60

ctg agc tcg tca gga acc atg atg gag aaa tct ggt gtg aaa tcg agt   240
Leu Ser Ser Ser Gly Thr Met Met Glu Lys Ser Gly Val Lys Ser Ser
 65                  70                  75                  80

ggc att acc act gca gcg gat gtc atg gac gat cag tct ctg gca agc   288
Gly Ile Thr Thr Ala Ala Asp Val Met Asp Asp Gln Ser Leu Ala Ser
                 85                  90                  95

agt gtc act gag tct ggt ctg tcc aag att cca gac acc tat ggt gca   336
Ser Val Thr Glu Ser Gly Leu Ser Lys Ile Pro Asp Thr Tyr Gly Ala
            100                 105                 110

gat gtc tcg ggt gct gcg ggc aca gtc gga act acc ggt gct gat tac   384
Asp Val Ser Gly Ala Ala Gly Thr Val Gly Thr Thr Gly Ala Asp Tyr
        115                 120                 125

agt gcg acc gat tca agc gca ggt ctg aac atg agc gag gct gca ttg   432
Ser Ala Thr Asp Ser Ser Ala Gly Leu Asn Met Ser Glu Ala Ala Leu
    130                 135                 140
```

```
cag agt ggc acc cca atg ggc gct ctc gct ggt gga tct gtg tcg agt   480
Gln Ser Gly Thr Pro Met Gly Ala Leu Ala Gly Gly Ser Val Ser Ser
145                 150                 155                 160

tcc gat cag gcc atg aat gac gca gct ctt cag att gca gcg tct cag   528
Ser Asp Gln Ala Met Asn Asp Ala Ala Leu Gln Ile Ala Ala Ser Gln
                165                 170                 175

ggt ctt gca cca gca ggt tcc ata gct ggt atg gag caa ctt agt gct   576
Gly Leu Ala Pro Ala Gly Ser Ile Ala Gly Met Glu Gln Leu Ser Ala
            180                 185                 190

caa gcc act gaa gca cct gct gga aag gcc ggc aag cag ctt ggc gat   624
Gln Ala Thr Glu Ala Pro Ala Gly Lys Ala Gly Lys Gln Leu Gly Asp
        195                 200                 205

ctt tct ggc tca gcg ctc aat act cag ctg gcg tcc atg gga cag cag   672
Leu Ser Gly Ser Ala Leu Asn Thr Gln Leu Ala Ser Met Gly Gln Gln
    210                 215                 220

gta ggt gac agt gtg aac agc gct tat gct gca ggc ggt atg ggt ggt   720
Val Gly Asp Ser Val Asn Ser Ala Tyr Ala Ala Gly Gly Met Gly Gly
225                 230                 235                 240

gtt gat gtg gct ggc aag gtc acc gag gca gca cag cac ttg tct cag   768
Val Asp Val Ala Gly Lys Val Thr Glu Ala Ala Gln His Leu Ser Gln
                245                 250                 255

gtt cca ggt cag att cag aat gct gtg acc aat gcg gat gct ggt tcc   816
Val Pro Gly Gln Ile Gln Asn Ala Val Thr Asn Ala Asp Ala Gly Ser
            260                 265                 270

tct ggc gca agc ttt ggt cag atg gca cag ggg gca gct ggt att gcc   864
Ser Gly Ala Ser Phe Gly Gln Met Ala Gln Gly Ala Ala Gly Ile Ala
        275                 280                 285

ggt gtc gca ggt gtg atc ggt gca gcg ggc gca gca agc tct gca gca   912
Gly Val Ala Gly Val Ile Gly Ala Ala Gly Ala Ala Ser Ser Ala Ala
    290                 295                 300

caa ggc gca ggt act gtc cag ggt gcg atg ggt aat gct gca gct ggt   960
Gln Gly Ala Gly Thr Val Gln Gly Ala Met Gly Asn Ala Ala Ala Gly
305                 310                 315                 320

gcg gga atg atc aac aac gct gtt tcc ggt gga gct act ggc tca aca  1008
Ala Gly Met Ile Asn Asn Ala Val Ser Gly Gly Ala Thr Gly Ser Thr
                325                 330                 335

ggt gcc gca cat gtg gtc aat gca tca cat gga cca gtg gcg cct ggt  1056
Gly Ala Ala His Val Val Asn Ala Ser His Gly Pro Val Ala Pro Gly
            340                 345                 350

cag gct cac tac caa gag tct ggt cat gca caa gca ttt gtg cag aac  1104
Gln Ala His Tyr Gln Glu Ser Gly His Ala Gln Ala Phe Val Gln Asn
        355                 360                 365

aac cag gcc aac acc gcg cac aca gca aac acg cgt gca ccg tca tca  1152
Asn Gln Ala Asn Thr Ala His Thr Ala Asn Thr Arg Ala Pro Ser Ser
    370                 375                 380

gct caa att atg ggc gcg aac gtt gct ggc tca ctg gca tca cag gct  1200
```

```
Ala Gln Ile Met Gly Ala Asn Val Ala Gly Ser Leu Ala Ser Gln Ala
385                 390                 395                 400

gta cga gga atc ggt cag cct ggt cag atg ggt gct aat gtt cgc gac   1248
Val Arg Gly Ile Gly Gln Pro Gly Gln Met Gly Ala Asn Val Arg Asp
                405                 410                 415

gcg atg ggt ggc agc gga cgc tct ggt ggc cgt ggt gga gca act caa   1296
Ala Met Gly Gly Ser Gly Arg Ser Gly Gly Arg Gly Gly Ala Thr Gln
            420                 425                 430

ggc ggt cga ggc gca cag cgc agc ggt gtc agt gct aag aac ggt atc   1344
Gly Gly Arg Gly Ala Gln Arg Ser Gly Val Ser Ala Lys Asn Gly Ile
        435                 440                 445

cgt gca cag cga ggt cag aag cct tct gtg acc ggc cag gcg atg aat   1392
Arg Ala Gln Arg Gly Gln Lys Pro Ser Val Thr Gly Gln Ala Met Asn
    450                 455                 460

gca gca atg cgt tca gca gcg gta agc ggt cgc atg gca aac atg gac   1440
Ala Ala Met Arg Ser Ala Ala Val Ser Gly Arg Met Ala Asn Met Asp
465                 470                 475                 480

ggc aac agt gta ggt ggc act gaa gca gat cca cag cag ggg agt ggc   1488
Gly Asn Ser Val Gly Gly Thr Glu Ala Asp Pro Gln Gln Gly Ser Gly
                485                 490                 495

gta acc gag aag ggt gat aaa ggc gtt aaa tagcgtgtaa aacacaatga     1538
Val Thr Glu Lys Gly Asp Lys Gly Val Lys
            500                 505

ccg                                                               1541


<210> 778
<211> 506
<212> PRT
<213> Corynebacterium glutamicum

<400> 778
Ala Asp Ala Asn Ala Asp Phe Val Asp Gly Val Val Asp Gly Ala Gly
  1               5                  10                  15

Arg Ala Ser Phe Ser Asn Ala Ala Tyr Ser Ser Asp Gly Thr Thr Leu
             20                  25                  30

Asp Gly Glu Gly Ala Ser Val Asp Ala Gln Gly Asn Pro Leu His Ala
         35                  40                  45

Asp Gly Thr Pro Met Ser Ala Ala Glu Ala Glu Met Lys Met Ala Gly
     50                  55                  60

Leu Ser Ser Ser Gly Thr Met Met Glu Lys Ser Gly Val Lys Ser Ser
 65                  70                  75                  80

Gly Ile Thr Thr Ala Ala Asp Val Met Asp Asp Gln Ser Leu Ala Ser
                 85                  90                  95

Ser Val Thr Glu Ser Gly Leu Ser Lys Ile Pro Asp Thr Tyr Gly Ala
            100                 105                 110
```

```
Asp Val Ser Gly Ala Ala Gly Thr Val Gly Thr Thr Gly Ala Asp Tyr
        115                 120                 125

Ser Ala Thr Asp Ser Ser Ala Gly Leu Asn Met Ser Glu Ala Ala Leu
    130                 135                 140

Gln Ser Gly Thr Pro Met Gly Ala Leu Ala Gly Gly Ser Val Ser Ser
145                 150                 155                 160

Ser Asp Gln Ala Met Asn Asp Ala Ala Leu Gln Ile Ala Ala Ser Gln
                165                 170                 175

Gly Leu Ala Pro Ala Gly Ser Ile Ala Gly Met Glu Gln Leu Ser Ala
            180                 185                 190

Gln Ala Thr Glu Ala Pro Ala Gly Lys Ala Gly Lys Gln Leu Gly Asp
        195                 200                 205

Leu Ser Gly Ser Ala Leu Asn Thr Gln Leu Ala Ser Met Gly Gln Gln
    210                 215                 220

Val Gly Asp Ser Val Asn Ser Ala Tyr Ala Ala Gly Gly Met Gly Gly
225                 230                 235                 240

Val Asp Val Ala Gly Lys Val Thr Glu Ala Ala Gln His Leu Ser Gln
                245                 250                 255

Val Pro Gly Gln Ile Gln Asn Ala Val Thr Asn Ala Asp Ala Gly Ser
            260                 265                 270

Ser Gly Ala Ser Phe Gly Gln Met Ala Gln Gly Ala Ala Gly Ile Ala
        275                 280                 285

Gly Val Ala Gly Val Ile Gly Ala Ala Gly Ala Ala Ser Ser Ala Ala
    290                 295                 300

Gln Gly Ala Gly Thr Val Gln Gly Ala Met Gly Asn Ala Ala Ala Gly
305                 310                 315                 320

Ala Gly Met Ile Asn Asn Ala Val Ser Gly Gly Ala Thr Gly Ser Thr
                325                 330                 335

Gly Ala Ala His Val Val Asn Ala Ser His Gly Pro Val Ala Pro Gly
            340                 345                 350

Gln Ala His Tyr Gln Glu Ser Gly His Ala Gln Ala Phe Val Gln Asn
        355                 360                 365

Asn Gln Ala Asn Thr Ala His Thr Ala Asn Thr Arg Ala Pro Ser Ser
    370                 375                 380

Ala Gln Ile Met Gly Ala Asn Val Ala Gly Ser Leu Ala Ser Gln Ala
385                 390                 395                 400

Val Arg Gly Ile Gly Gln Pro Gly Gln Met Gly Ala Asn Val Arg Asp
                405                 410                 415

Ala Met Gly Gly Ser Gly Arg Ser Gly Gly Arg Gly Gly Ala Thr Gln
            420                 425                 430

Gly Gly Arg Gly Ala Gln Arg Ser Gly Val Ser Ala Lys Asn Gly Ile
```

```
        435                 440                 445

Arg Ala Gln Arg Gly Gln Lys Pro Ser Val Thr Gly Gln Ala Met Asn
    450                 455                 460

Ala Ala Met Arg Ser Ala Ala Val Ser Gly Arg Met Ala Asn Met Asp
465                 470                 475                 480

Gly Asn Ser Val Gly Gly Thr Glu Ala Asp Pro Gln Gln Gly Ser Gly
                485                 490                 495

Val Thr Glu Lys Gly Asp Lys Gly Val Lys
            500                 505


<210> 779
<211> 1065
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1042)
<223> RXN01765

<400> 779
gcagtccgtc ggtgtcgttt tccctgaact gccggcagag cttcagccac aaatcccagt 60

caaggcataa caccgcacac caagaatttt aggaggggtc atg agc aac aac gta   115
                                              Met Ser Asn Asn Val
                                                1               5

gtg aaa tat gag tgc gcg gtc gac gcc gac aac att gtc gca gtc gat   163
Val Lys Tyr Glu Cys Ala Val Asp Ala Asp Asn Ile Val Ala Val Asp
                10                  15                  20

atg cat gtg cac ttg gaa gtc gac agc tgc gga cac aaa tcg atg ccg   211
Met His Val His Leu Glu Val Asp Ser Cys Gly His Lys Ser Met Pro
            25                  30                  35

gca gac atc atg gcg gca tcc tcg aag tac ttt aag acc gcg gaa cga   259
Ala Asp Ile Met Ala Ala Ser Ser Lys Tyr Phe Lys Thr Ala Glu Arg
        40                  45                  50

act ccc tca gca gat gcc att gct gat att tat agg gaa cac aag atg   307
Thr Pro Ser Ala Asp Ala Ile Ala Asp Ile Tyr Arg Glu His Lys Met
    55                  60                  65

gcg gcg gtg gtt ttc acc atc gat gcg cgg acc caa atg ggg cat ctg   355
Ala Ala Val Val Phe Thr Ile Asp Ala Arg Thr Gln Met Gly His Leu
70                  75                  80                  85

ccg aac tcg att gat gat ttg gtg gca agc tgt gcc cgc aac aat gac   403
Pro Asn Ser Ile Asp Asp Leu Val Ala Ser Cys Ala Arg Asn Asn Asp
                90                  95                  100

gtg ctg atc cct ttt ggc agt gtg gat cct cgt acc ggc gag gac gcg   451
Val Leu Ile Pro Phe Gly Ser Val Asp Pro Arg Thr Gly Glu Asp Ala
            105                 110                 115

ctg gtg gaa gct cgc cga cag gtg gaa gaa ctc ggg gtg cga ggc ttc   499
```

```
Leu Val Glu Ala Arg Arg Gln Val Glu Glu Leu Gly Val Arg Gly Phe
        120                 125                 130

aaa ttc cat cca tcg gtt caa gga ttc gac cca tcc gcg cca gag ttc   547
Lys Phe His Pro Ser Val Gln Gly Phe Asp Pro Ser Ala Pro Glu Phe
    135                 140                 145

tac cca ctg tgg gaa ttg ctc gaa agt ttt gga ttg cca tgc gtg ttc   595
Tyr Pro Leu Trp Glu Leu Leu Glu Ser Phe Gly Leu Pro Cys Val Phe
150                 155                 160                 165

cat acc gga caa aac ggc atg ggt gca ggt ctt cca ggt ggt cga ggc   643
His Thr Gly Gln Asn Gly Met Gly Ala Gly Leu Pro Gly Gly Arg Gly
                170                 175                 180

att aag ctg cgc ttc tcc aac cca atg ttg ctt gat gat gtt gcg gcg   691
Ile Lys Leu Arg Phe Ser Asn Pro Met Leu Leu Asp Asp Val Ala Ala
            185                 190                 195

gac ttc ccg aac ctg acc atc atc atg gcg cac cct tct gtt cct tgg   739
Asp Phe Pro Asn Leu Thr Ile Ile Met Ala His Pro Ser Val Pro Trp
        200                 205                 210

cag gat gag gct aac tcg att gcc acc cac aag gcc aat gtg ttc att   787
Gln Asp Glu Ala Asn Ser Ile Ala Thr His Lys Ala Asn Val Phe Ile
    215                 220                 225

gat ctt tcc ggc tgg tcg ccg aag tat ttc cca gag tct ttg gtc aga   835
Asp Leu Ser Gly Trp Ser Pro Lys Tyr Phe Pro Glu Ser Leu Val Arg
230                 235                 240                 245

cag tcc aat aac gtg cta tcc aag aag gtg ctg ttt ggc acg gac ttc   883
Gln Ser Asn Asn Val Leu Ser Lys Lys Val Leu Phe Gly Thr Asp Phe
                250                 255                 260

ccg ctg att acc cca gag aaa tgg ctt gcg gct ttc gcg aat ctg cca   931
Pro Leu Ile Thr Pro Glu Lys Trp Leu Ala Ala Phe Ala Asn Leu Pro
            265                 270                 275

ctg aag gat gag gtt cgt ccg gga atc ctc aaa gac aat gcg gtg aag   979
Leu Lys Asp Glu Val Arg Pro Gly Ile Leu Lys Asp Asn Ala Val Lys
        280                 285                 290

gta ctt ggc cta gcc gct agc act gag cgc gga tct caa gca gaa aag   1027
Val Leu Gly Leu Ala Ala Ser Thr Glu Arg Gly Ser Gln Ala Glu Lys
    295                 300                 305

gtc gtg caa cat gcg tgatcccatt caaggtgctg tta                    1065
Val Val Gln His Ala
310
```

<210> 780
<211> 314
<212> PRT
<213> Corynebacterium glutamicum

<400> 780

```
Met Ser Asn Asn Val Val Lys Tyr Glu Cys Ala Val Asp Ala Asp Asn
  1               5                  10                  15
```

Ile Val Ala Val Asp Met His Val His Leu Glu Val Asp Ser Cys Gly
20 25 30

His Lys Ser Met Pro Ala Asp Ile Met Ala Ala Ser Ser Lys Tyr Phe
35 40 45

Lys Thr Ala Glu Arg Thr Pro Ser Ala Asp Ala Ile Ala Asp Ile Tyr
50 55 60

Arg Glu His Lys Met Ala Ala Val Val Phe Thr Ile Asp Ala Arg Thr
65 70 75 80

Gln Met Gly His Leu Pro Asn Ser Ile Asp Asp Leu Val Ala Ser Cys
85 90 95

Ala Arg Asn Asn Asp Val Leu Ile Pro Phe Gly Ser Val Asp Pro Arg
100 105 110

Thr Gly Glu Asp Ala Leu Val Glu Ala Arg Arg Gln Val Glu Glu Leu
115 120 125

Gly Val Arg Gly Phe Lys Phe His Pro Ser Val Gln Gly Phe Asp Pro
130 135 140

Ser Ala Pro Glu Phe Tyr Pro Leu Trp Glu Leu Leu Glu Ser Phe Gly
145 150 155 160

Leu Pro Cys Val Phe His Thr Gly Gln Asn Gly Met Gly Ala Gly Leu
165 170 175

Pro Gly Gly Arg Gly Ile Lys Leu Arg Phe Ser Asn Pro Met Leu Leu
180 185 190

Asp Asp Val Ala Ala Asp Phe Pro Asn Leu Thr Ile Ile Met Ala His
195 200 205

Pro Ser Val Pro Trp Gln Asp Glu Ala Asn Ser Ile Ala Thr His Lys
210 215 220

Ala Asn Val Phe Ile Asp Leu Ser Gly Trp Ser Pro Lys Tyr Phe Pro
225 230 235 240

Glu Ser Leu Val Arg Gln Ser Asn Asn Val Leu Ser Lys Lys Val Leu
245 250 255

Phe Gly Thr Asp Phe Pro Leu Ile Thr Pro Glu Lys Trp Leu Ala Ala
260 265 270

Phe Ala Asn Leu Pro Leu Lys Asp Glu Val Arg Pro Gly Ile Leu Lys
275 280 285

Asp Asn Ala Val Lys Val Leu Gly Leu Ala Ala Ser Thr Glu Arg Gly
290 295 300

Ser Gln Ala Glu Lys Val Val Gln His Ala
305 310

<210> 781
<211> 1065
<212> DNA

<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1042)
<223> FRXA01765

<400> 781
gcagtccgtc ggtgtcgttt tccctgaact gccggcagag cttcagccac aaatcccagt 60

caaggcataa caccgcacac caagaatttt aggaggggtc atg agc aac aac gta 115
Met Ser Asn Asn Val
1 5

gtg aaa tat gag tgc gcg gtc gac gcc gac aac att gtc gca gtc gat 163
Val Lys Tyr Glu Cys Ala Val Asp Ala Asp Asn Ile Val Ala Val Asp
10 15 20

atg cat gtg cac ttg gaa gtc gac agc tgc gga cac aaa tcg atg ccg 211
Met His Val His Leu Glu Val Asp Ser Cys Gly His Lys Ser Met Pro
25 30 35

gca gac atc atg gcg gca tcc tcg aag tac ttt aag acc gcg gaa cga 259
Ala Asp Ile Met Ala Ala Ser Ser Lys Tyr Phe Lys Thr Ala Glu Arg
40 45 50

act ccc tca gca gat gcc att gct gat att tat agg gaa cac aag atg 307
Thr Pro Ser Ala Asp Ala Ile Ala Asp Ile Tyr Arg Glu His Lys Met
55 60 65

gcg gcg gtg gtt ttc acc atc gat gcg cgg acc caa atg ggg cat ctg 355
Ala Ala Val Val Phe Thr Ile Asp Ala Arg Thr Gln Met Gly His Leu
70 75 80 85

ccg aac tcg att gat gat ttg gtg gca agc tgt gcc cgc aac aat gac 403
Pro Asn Ser Ile Asp Asp Leu Val Ala Ser Cys Ala Arg Asn Asn Asp
90 95 100

gtg ctg atc cct ttt ggc agt gtg gat cct cgt acc ggc gag gac gcg 451
Val Leu Ile Pro Phe Gly Ser Val Asp Pro Arg Thr Gly Glu Asp Ala
105 110 115

ctg gtg gaa gct cgc cga cag gtg gaa gaa ctc ggg gtg cga ggc ttc 499
Leu Val Glu Ala Arg Arg Gln Val Glu Glu Leu Gly Val Arg Gly Phe
120 125 130

aaa ttc cat cca tcg gtt caa gga ttc gac cca tcc gcg cca gag ttc 547
Lys Phe His Pro Ser Val Gln Gly Phe Asp Pro Ser Ala Pro Glu Phe
135 140 145

tac cca ctg tgg gaa ttg ctc gaa agt ttt gga ttg cca tgc gtg ttc 595
Tyr Pro Leu Trp Glu Leu Leu Glu Ser Phe Gly Leu Pro Cys Val Phe
150 155 160 165

cat acc gga caa aac ggc atg ggt gca ggt ctt cca ggt ggt cga ggc 643
His Thr Gly Gln Asn Gly Met Gly Ala Gly Leu Pro Gly Gly Arg Gly
170 175 180

att aag ctg cgc ttc tcc aac cca atg ttg ctt gat gat gtt gcg gcg 691
Ile Lys Leu Arg Phe Ser Asn Pro Met Leu Leu Asp Asp Val Ala Ala
185 190 195

```
gac ttc ccg aac ctg acc atc atc atg gcg cac cct tct gtt cct tgg   739
Asp Phe Pro Asn Leu Thr Ile Ile Met Ala His Pro Ser Val Pro Trp
        200                 205                 210

cag gat gag gct aac tcg att gcc acc cac aag gcc aat gtg ttc att   787
Gln Asp Glu Ala Asn Ser Ile Ala Thr His Lys Ala Asn Val Phe Ile
    215                 220                 225

gat ctt tcc ggc tgg tcg ccg aag tat ttc cca gag tct ttg gtc aga   835
Asp Leu Ser Gly Trp Ser Pro Lys Tyr Phe Pro Glu Ser Leu Val Arg
230                 235                 240                 245

cag tcc aat aac gtg cta tcc aag aag gtg ctg ttt ggc acg gac ttc   883
Gln Ser Asn Asn Val Leu Ser Lys Lys Val Leu Phe Gly Thr Asp Phe
                250                 255                 260

ccg ctg att acc cca gag aaa tgg ctt gcg gct ttc gcg aat ctg cca   931
Pro Leu Ile Thr Pro Glu Lys Trp Leu Ala Ala Phe Ala Asn Leu Pro
            265                 270                 275

ctg aag gat gag gtt cgt ccg gga atc ctc aaa gac aat gcg gtg aag   979
Leu Lys Asp Glu Val Arg Pro Gly Ile Leu Lys Asp Asn Ala Val Lys
        280                 285                 290

gta ctt ggc cta gcc gct agc act gag cgc gga tct caa gca gaa aag   1027
Val Leu Gly Leu Ala Ala Ser Thr Glu Arg Gly Ser Gln Ala Glu Lys
    295                 300                 305

gtc gtg caa cat gcg tgatcccatt caaggtgctg tta                    1065
Val Val Gln His Ala
310
```

<210> 782
<211> 314
<212> PRT
<213> Corynebacterium glutamicum

<400> 782

```
Met Ser Asn Asn Val Val Lys Tyr Glu Cys Ala Val Asp Ala Asp Asn
  1               5                  10                  15

Ile Val Ala Val Asp Met His Val His Leu Glu Val Asp Ser Cys Gly
             20                  25                  30

His Lys Ser Met Pro Ala Asp Ile Met Ala Ala Ser Ser Lys Tyr Phe
         35                  40                  45

Lys Thr Ala Glu Arg Thr Pro Ser Ala Asp Ala Ile Ala Asp Ile Tyr
     50                  55                  60

Arg Glu His Lys Met Ala Ala Val Val Phe Thr Ile Asp Ala Arg Thr
 65                  70                  75                  80

Gln Met Gly His Leu Pro Asn Ser Ile Asp Asp Leu Val Ala Ser Cys
                 85                  90                  95

Ala Arg Asn Asn Asp Val Leu Ile Pro Phe Gly Ser Val Asp Pro Arg
            100                 105                 110
```

```
Thr Gly Glu Asp Ala Leu Val Glu Ala Arg Arg Gln Val Glu Glu Leu
        115                 120                 125

Gly Val Arg Gly Phe Lys Phe His Pro Ser Val Gln Gly Phe Asp Pro
    130                 135                 140

Ser Ala Pro Glu Phe Tyr Pro Leu Trp Glu Leu Leu Glu Ser Phe Gly
145                 150                 155                 160

Leu Pro Cys Val Phe His Thr Gly Gln Asn Gly Met Gly Ala Gly Leu
                165                 170                 175

Pro Gly Gly Arg Gly Ile Lys Leu Arg Phe Ser Asn Pro Met Leu Leu
            180                 185                 190

Asp Asp Val Ala Ala Asp Phe Pro Asn Leu Thr Ile Ile Met Ala His
        195                 200                 205

Pro Ser Val Pro Trp Gln Asp Glu Ala Asn Ser Ile Ala Thr His Lys
    210                 215                 220

Ala Asn Val Phe Ile Asp Leu Ser Gly Trp Ser Pro Lys Tyr Phe Pro
225                 230                 235                 240

Glu Ser Leu Val Arg Gln Ser Asn Asn Val Leu Ser Lys Lys Val Leu
                245                 250                 255

Phe Gly Thr Asp Phe Pro Leu Ile Thr Pro Glu Lys Trp Leu Ala Ala
            260                 265                 270

Phe Ala Asn Leu Pro Leu Lys Asp Glu Val Arg Pro Gly Ile Leu Lys
        275                 280                 285

Asp Asn Ala Val Lys Val Leu Gly Leu Ala Ala Ser Thr Glu Arg Gly
    290                 295                 300

Ser Gln Ala Glu Lys Val Val Gln His Ala
305                 310
```

Sequence Listing Page 970 of 1000

<210> 783
<211> 588
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(565)
<223> RXN01767

<400> 783
acaccagccc tccacaagag cgtcgaagca atctacgctt cgacgctctt tttttcacta 60

```
cctactcatc ccccacataa gaaaaaaaga cgacaccacc atg att gac cat aaa   115
                                            Met Ile Asp His Lys
                                              1               5

ctg tgg ttt aac aca gta acc aac aac gcc tct gtc cga gaa gct gca   163
Leu Trp Phe Asn Thr Val Thr Asn Asn Ala Ser Val Arg Glu Ala Ala
                 10                  15                  20
```

```
gga aaa tgc gac ata ccc atc aga acg ctc aac gag cag ctt aac cgt   211
Gly Lys Cys Asp Ile Pro Ile Arg Thr Leu Asn Glu Gln Leu Asn Arg
            25                  30                  35

cga ata ctc cct gaa aag acc gtc atc gct cta gca cgc gct tat gat   259
Arg Ile Leu Pro Glu Lys Thr Val Ile Ala Leu Ala Arg Ala Tyr Asp
        40                  45                  50

ctc tca cct gtt gat gcg ctc gtt cgc acc gga cac ctc acc gaa gaa   307
Leu Ser Pro Val Asp Ala Leu Val Arg Thr Gly His Leu Thr Glu Glu
    55                  60                  65

gag gct ggt agt cgt gaa gaa gat gcc agc cca gat tca gct gac gac   355
Glu Ala Gly Ser Arg Glu Glu Asp Ala Ser Pro Asp Ser Ala Asp Asp
70                  75                  80                  85

tac cct acc tgg gca ctg aac tcg cac ctt gac tat ggc att ctc gga   403
Tyr Pro Thr Trp Ala Leu Asn Ser His Leu Asp Tyr Gly Ile Leu Gly
                90                  95                  100

gct ttt ggc gac atc gct gaa gaa gta aac agc gaa aga gtt aac cgc   451
Ala Phe Gly Asp Ile Ala Glu Glu Val Asn Ser Glu Arg Val Asn Arg
            105                 110                 115

gac aac gcc ata gag caa att cgc gca tgg ctc gac gag ctt cca ggc   499
Asp Asn Ala Ile Glu Gln Ile Arg Ala Trp Leu Asp Glu Leu Pro Gly
        120                 125                 130

agc cta ttc aac aac ctc cgc agc act aaa aca ggc tac atc gaa cta   547
Ser Leu Phe Asn Asn Leu Arg Ser Thr Lys Thr Gly Tyr Ile Glu Leu
    135                 140                 145

ttc gag acc tat ctc gat taaacccaac cagcacaaca ata                588
Phe Glu Thr Tyr Leu Asp
150                 155
```

<210> 784
<211> 155
<212> PRT
<213> Corynebacterium glutamicum

<400> 784

```
Met Ile Asp His Lys Leu Trp Phe Asn Thr Val Thr Asn Asn Ala Ser
  1               5                  10                  15

Val Arg Glu Ala Ala Gly Lys Cys Asp Ile Pro Ile Arg Thr Leu Asn
            20                  25                  30

Glu Gln Leu Asn Arg Arg Ile Leu Pro Glu Lys Thr Val Ile Ala Leu
        35                  40                  45

Ala Arg Ala Tyr Asp Leu Ser Pro Val Asp Ala Leu Val Arg Thr Gly
    50                  55                  60

His Leu Thr Glu Glu Glu Ala Gly Ser Arg Glu Glu Asp Ala Ser Pro
65                  70                  75                  80

Asp Ser Ala Asp Asp Tyr Pro Thr Trp Ala Leu Asn Ser His Leu Asp
                85                  90                  95
```

```
Tyr Gly Ile Leu Gly Ala Phe Gly Asp Ile Ala Glu Glu Val Asn Ser
            100                 105                 110

Glu Arg Val Asn Arg Asp Asn Ala Ile Glu Gln Ile Arg Ala Trp Leu
        115                 120                 125

Asp Glu Leu Pro Gly Ser Leu Phe Asn Asn Leu Arg Ser Thr Lys Thr
    130                 135                 140

Gly Tyr Ile Glu Leu Phe Glu Thr Tyr Leu Asp
145                 150                 155


<210> 785
<211> 436
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(436)
<223> FRXA01767

<400> 785
acaccagccc tccacaagag cgtcgaagca atctacgctt cgacgctctt tttttcacta 60

cctactcatc ccccacataa gaaaaaaaga cgacaccacc atg att gac cat aaa   115
                                            Met Ile Asp His Lys
                                              1               5

ctg tgg ttt aac aca gta acc aac aac gcc tct gtc cga gaa gct gca   163
Leu Trp Phe Asn Thr Val Thr Asn Asn Ala Ser Val Arg Glu Ala Ala
                10                  15                  20

gga aaa tgc gac ata ccc atc aga acg ctc aac gag cag ctt aac cgt   211
Gly Lys Cys Asp Ile Pro Ile Arg Thr Leu Asn Glu Gln Leu Asn Arg
            25                  30                  35

cga ata ctc cct gaa aag acc gtc atc gct cta gca cgc gct tat gat   259
Arg Ile Leu Pro Glu Lys Thr Val Ile Ala Leu Ala Arg Ala Tyr Asp
        40                  45                  50

ctc tca cct gtt gat gcg ctc gtt cgc acc gga cac ctc acc gaa gaa   307
Leu Ser Pro Val Asp Ala Leu Val Arg Thr Gly His Leu Thr Glu Glu
    55                  60                  65

gag gct ggt agt cgt gaa gaa gat gcc agc cca gat tca gct gac gac   355
Glu Ala Gly Ser Arg Glu Glu Asp Ala Ser Pro Asp Ser Ala Asp Asp
70                  75                  80                  85

tac cct acc tgg gca ctg aac tcg cac ctt gac tat ggc att ctc gga   403
Tyr Pro Thr Trp Ala Leu Asn Ser His Leu Asp Tyr Gly Ile Leu Gly
                90                  95                  100

gct ttt ggc gac atc gct gaa gaa gta aac agc                      436
Ala Phe Gly Asp Ile Ala Glu Glu Val Asn Ser
            105                 110


<210> 786
<211> 112
```

<212> PRT
<213> Corynebacterium glutamicum

<400> 786
Met Ile Asp His Lys Leu Trp Phe Asn Thr Val Thr Asn Asn Ala Ser
1 5 10 15

Val Arg Glu Ala Ala Gly Lys Cys Asp Ile Pro Ile Arg Thr Leu Asn
20 25 30

Glu Gln Leu Asn Arg Arg Ile Leu Pro Glu Lys Thr Val Ile Ala Leu
35 40 45

Ala Arg Ala Tyr Asp Leu Ser Pro Val Asp Ala Leu Val Arg Thr Gly
50 55 60

His Leu Thr Glu Glu Glu Ala Gly Ser Arg Glu Glu Asp Ala Ser Pro
65 70 75 80

Asp Ser Ala Asp Asp Tyr Pro Thr Trp Ala Leu Asn Ser His Leu Asp
85 90 95

Tyr Gly Ile Leu Gly Ala Phe Gly Asp Ile Ala Glu Glu Val Asn Ser
100 105 110

<210> 787
<211> 564
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(541)
<223> RXN01769

<400> 787
attttcaaca accaggacta aaacacctgc tgctgttgag cgcttctcac acatcatcct 60

cacaaccccg ttgcagcacc agcataaatc tatattcgct gtg acg ggg ttg ttg 115
Val Thr Gly Leu Leu
1 5

ggg cgc gcc cca cat tca ctc ttt ttc ccg att ggt ttc tac tac aca 163
Gly Arg Ala Pro His Ser Leu Phe Phe Pro Ile Gly Phe Tyr Tyr Thr
10 15 20

ccc atg acc tct att act act acc gat acc ccg cta tat aca gca ctg 211
Pro Met Thr Ser Ile Thr Thr Thr Asp Thr Pro Leu Tyr Thr Ala Leu
25 30 35

ccc cat acc cgt atc tct gat gcg gaa ttg ttg aca cca aca aca act 259
Pro His Thr Arg Ile Ser Asp Ala Glu Leu Leu Thr Pro Thr Thr Thr
40 45 50

gtg cac gag att ctc gtt tac gga ccg gct gag tgc cca ggg tgt aca 307
Val His Glu Ile Leu Val Tyr Gly Pro Ala Glu Cys Pro Gly Cys Thr
55 60 65

```
gca acg ctt gac ttc ttt gca cgc aaa aac atg ccg gcc acc aaa gtc   355
Ala Thr Leu Asp Phe Phe Ala Arg Lys Asn Met Pro Ala Thr Lys Val
 70                  75                  80                  85

act gta gct gcc ggt gat gta gca cat acc tac atc acc caa gac tta   403
Thr Val Ala Ala Gly Asp Val Ala His Thr Tyr Ile Thr Gln Asp Leu
                 90                  95                 100

ggt tat ctc caa gca ccg att gtc act gtc cgt atc agt tcc tct gct   451
Gly Tyr Leu Gln Ala Pro Ile Val Thr Val Arg Ile Ser Ser Ser Ala
            105                 110                 115

tct aac cac gac aac gaa cac aac acc cag atc ctg cac tgg tcc ggc   499
Ser Asn His Asp Asn Glu His Asn Thr Gln Ile Leu His Trp Ser Gly
        120                 125                 130

gtt aat cgc tac ctc atg cag gca ctc tcc cgt act cat ttc           541
Val Asn Arg Tyr Leu Met Gln Ala Leu Ser Arg Thr His Phe
    135                 140                 145

tagaaaggtt tttcccgtca tgt                                        564
```

<210> 788
<211> 147
<212> PRT
<213> Corynebacterium glutamicum

<400> 788

```
Val Thr Gly Leu Leu Gly Arg Ala Pro His Ser Leu Phe Phe Pro Ile
  1               5                  10                  15

Gly Phe Tyr Tyr Thr Pro Met Thr Ser Ile Thr Thr Thr Asp Thr Pro
             20                  25                  30

Leu Tyr Thr Ala Leu Pro His Thr Arg Ile Ser Asp Ala Glu Leu Leu
         35                  40                  45

Thr Pro Thr Thr Thr Val His Glu Ile Leu Val Tyr Gly Pro Ala Glu
     50                  55                  60

Cys Pro Gly Cys Thr Ala Thr Leu Asp Phe Phe Ala Arg Lys Asn Met
 65                  70                  75                  80

Pro Ala Thr Lys Val Thr Val Ala Ala Gly Asp Val Ala His Thr Tyr
                 85                  90                  95

Ile Thr Gln Asp Leu Gly Tyr Leu Gln Ala Pro Ile Val Thr Val Arg
            100                 105                 110

Ile Ser Ser Ser Ala Ser Asn His Asp Asn Glu His Asn Thr Gln Ile
        115                 120                 125

Leu His Trp Ser Gly Val Asn Arg Tyr Leu Met Gln Ala Leu Ser Arg
    130                 135                 140

Thr His Phe
145
```

<210> 789
<211> 552
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(529)
<223> FRXA01769

<400> 789
caggactaaa acacctgctg ctgttgagcg cttctcacac atcatcctca caaccccgtt 60

gcagcaccag cataaatcta tattcgctgt gacggggttg ttg ggg cgc gcc cca 115
Leu Gly Arg Ala Pro
1 5

cat tca ctc ttt ttc ccg att ggt ttc tac tac aca ccc atg acc tct 163
His Ser Leu Phe Phe Pro Ile Gly Phe Tyr Tyr Thr Pro Met Thr Ser
10 15 20

att act act acc gat acc ccg cta tat aca gca ctg ccc cat acc cgt 211
Ile Thr Thr Thr Asp Thr Pro Leu Tyr Thr Ala Leu Pro His Thr Arg
25 30 35

atc tct gat gcg gaa ttg ttg aca cca aca aca act gtg cac gag att 259
Ile Ser Asp Ala Glu Leu Leu Thr Pro Thr Thr Thr Val His Glu Ile
40 45 50

ctc gtt tac gga ccg gct gag tgc cca ggg tgt aca gca acg ctt gac 307
Leu Val Tyr Gly Pro Ala Glu Cys Pro Gly Cys Thr Ala Thr Leu Asp
55 60 65

ttc ttt gca cgc aaa aac atg ccg gcc acc aaa gtc act gta gct gcc 355
Phe Phe Ala Arg Lys Asn Met Pro Ala Thr Lys Val Thr Val Ala Ala
70 75 80 85

ggt gat gta gca cat acc tac atc acc caa gac tta ggt tat ctc caa 403
Gly Asp Val Ala His Thr Tyr Ile Thr Gln Asp Leu Gly Tyr Leu Gln
90 95 100

gca ccg att gtc act gtc cgt atc agt tcc tct gct tct aac cac gac 451
Ala Pro Ile Val Thr Val Arg Ile Ser Ser Ser Ala Ser Asn His Asp
105 110 115

aac gaa cac aac acc cag atc ctg cac tgg tcc ggc gtt aat cgc tac 499
Asn Glu His Asn Thr Gln Ile Leu His Trp Ser Gly Val Asn Arg Tyr
120 125 130

ctc atg cag gca ctc tcc cgt act cat ttc tagaaaggtt tttcccgtca 549
Leu Met Gln Ala Leu Ser Arg Thr His Phe
135 140

tgt 552

<210> 790
<211> 143
<212> PRT
<213> Corynebacterium glutamicum

<400> 790
Leu Gly Arg Ala Pro His Ser Leu Phe Phe Pro Ile Gly Phe Tyr Tyr
1 5 10 15

Thr Pro Met Thr Ser Ile Thr Thr Thr Asp Thr Pro Leu Tyr Thr Ala
20 25 30

Leu Pro His Thr Arg Ile Ser Asp Ala Glu Leu Leu Thr Pro Thr Thr
35 40 45

Thr Val His Glu Ile Leu Val Tyr Gly Pro Ala Glu Cys Pro Gly Cys
50 55 60

Thr Ala Thr Leu Asp Phe Phe Ala Arg Lys Asn Met Pro Ala Thr Lys
65 70 75 80

Val Thr Val Ala Ala Gly Asp Val Ala His Thr Tyr Ile Thr Gln Asp
85 90 95

Leu Gly Tyr Leu Gln Ala Pro Ile Val Thr Val Arg Ile Ser Ser Ser
100 105 110

Ala Ser Asn His Asp Asn Glu His Asn Thr Gln Ile Leu His Trp Ser
115 120 125

Gly Val Asn Arg Tyr Leu Met Gln Ala Leu Ser Arg Thr His Phe
130 135 140

<210> 791
<211> 825
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(802)
<223> RXN01771

<400> 791
tgccccgctg ttggtggttc cggagcggcg ataatcgcta aacgtttgag gtgattgtat 60

gggtattttc aggtcgcggt cgcaggattt tgggtggagc atg cac cag gct ggc 115
Met His Gln Ala Gly
1 5

cag ctc atc aat gat ccc agt cag ggt ctg tgg cgc act tct gcc ctg 163
Gln Leu Ile Asn Asp Pro Ser Gln Gly Leu Trp Arg Thr Ser Ala Leu
10 15 20

cgc tcg ccg gtt gct cgg gtt gga cat gcc gtg ttg cgc cag cgt gcc 211
Arg Ser Pro Val Ala Arg Val Gly His Ala Val Leu Arg Gln Arg Ala
25 30 35

ggt gag atc tcg cgc atg caa ggt cgt gag ttt tct cgc cct ggg gat 259
Gly Glu Ile Ser Arg Met Gln Gly Arg Glu Phe Ser Arg Pro Gly Asp
40 45 50

cag ttc cga cag gta gat ttg cgc agg cga ctg att cag gtc cat ccc 307
Gln Phe Arg Gln Val Asp Leu Arg Arg Arg Leu Ile Gln Val His Pro
55 60 65

```
caa tca att cct aca gcg gat gcg atg gcc gta acc atc acc atg gcg   355
Gln Ser Ile Pro Thr Ala Asp Ala Met Ala Val Thr Ile Thr Met Ala
 70                  75                  80                  85

ctc acc gct gcc acg att gat ccg gtg aag ttc gtc gcg gat tca cag   403
Leu Thr Ala Ala Thr Ile Asp Pro Val Lys Phe Val Ala Asp Ser Gln
                90                  95                 100

aac ccg gat gaa gag att tat ttg gca gct cag atc gca ttg cgg gaa   451
Asn Pro Asp Glu Glu Ile Tyr Leu Ala Ala Gln Ile Ala Leu Arg Glu
            105                 110                 115

atg gtt atc gct atg cct ttg gag gat ttc atc ggg gtg cgc att gat   499
Met Val Ile Ala Met Pro Leu Glu Asp Phe Ile Gly Val Arg Ile Asp
        120                 125                 130

cta gag cct gtt ttg gtg gct gct caa gct gct gcg aag aat gtg ggc   547
Leu Glu Pro Val Leu Val Ala Ala Gln Ala Ala Ala Lys Asn Val Gly
    135                 140                 145

gtg gaa gtc tcg tca atc ttg ctg aag gat ctg aat ctt ccc cag gag   595
Val Glu Val Ser Ser Ile Leu Leu Lys Asp Leu Asn Leu Pro Gln Glu
150                 155                 160                 165

tac tcg gga gcg ttg cag gaa tcg atc gtt gcg aaa att caa gcc gaa   643
Tyr Ser Gly Ala Leu Gln Glu Ser Ile Val Ala Lys Ile Gln Ala Glu
                170                 175                 180

act gat ctg gaa cgt gca cga aat gaa gtg aaa act acc cgt gct cga   691
Thr Asp Leu Glu Arg Ala Arg Asn Glu Val Lys Thr Thr Arg Ala Arg
            185                 190                 195

ctt gcc agc gcg aaa gtg ttg gag caa aat ccg att ctt gcc aaa att   739
Leu Ala Ser Ala Lys Val Leu Glu Gln Asn Pro Ile Leu Ala Lys Ile
        200                 205                 210

cgg atg att gaa gcg ctc cca ccg gga tcc aca att gag gtt cgg gag   787
Arg Met Ile Glu Ala Leu Pro Pro Gly Ser Thr Ile Glu Val Arg Glu
    215                 220                 225

ggt gac tca aag gca taaagttgcc catttcggtg ccc                    825
Gly Asp Ser Lys Ala
230
```

<210> 792
<211> 234
<212> PRT
<213> Corynebacterium glutamicum

<400> 792

```
Met His Gln Ala Gly Gln Leu Ile Asn Asp Pro Ser Gln Gly Leu Trp
  1               5                  10                  15

Arg Thr Ser Ala Leu Arg Ser Pro Val Ala Arg Val Gly His Ala Val
             20                  25                  30

Leu Arg Gln Arg Ala Gly Glu Ile Ser Arg Met Gln Gly Arg Glu Phe
         35                  40                  45
```

```
Ser Arg Pro Gly Asp Gln Phe Arg Gln Val Asp Leu Arg Arg Arg Leu
     50                  55                  60

Ile Gln Val His Pro Gln Ser Ile Pro Thr Ala Asp Ala Met Ala Val
 65                  70                  75                  80

Thr Ile Thr Met Ala Leu Thr Ala Ala Thr Ile Asp Pro Val Lys Phe
                 85                  90                  95

Val Ala Asp Ser Gln Asn Pro Asp Glu Glu Ile Tyr Leu Ala Ala Gln
            100                 105                 110

Ile Ala Leu Arg Glu Met Val Ile Ala Met Pro Leu Glu Asp Phe Ile
        115                 120                 125

Gly Val Arg Ile Asp Leu Glu Pro Val Leu Val Ala Ala Gln Ala Ala
    130                 135                 140

Ala Lys Asn Val Gly Val Glu Val Ser Ser Ile Leu Leu Lys Asp Leu
145                 150                 155                 160

Asn Leu Pro Gln Glu Tyr Ser Gly Ala Leu Gln Glu Ser Ile Val Ala
                165                 170                 175

Lys Ile Gln Ala Glu Thr Asp Leu Glu Arg Ala Arg Asn Glu Val Lys
            180                 185                 190

Thr Thr Arg Ala Arg Leu Ala Ser Ala Lys Val Leu Glu Gln Asn Pro
        195                 200                 205

Ile Leu Ala Lys Ile Arg Met Ile Glu Ala Leu Pro Pro Gly Ser Thr
    210                 215                 220

Ile Glu Val Arg Glu Gly Asp Ser Lys Ala
225                 230


<210> 793
<211> 825
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(802)
<223> FRXA01771

<400> 793
tgccccgctg ttggtggttc cggagcggcg ataatcgcta aacgtttgag gtgattgtat 60

gggtattttc aggtcgcggt cgcaggattt tgggtggagc atg cac cag gct ggc   115
                                            Met His Gln Ala Gly
                                              1               5

cag ctc atc aat gat ccc agt cag ggt ctg tgg cgc act tct gcc ctg   163
Gln Leu Ile Asn Asp Pro Ser Gln Gly Leu Trp Arg Thr Ser Ala Leu
                 10                  15                  20

cgc tcg ccg gtt gct cgg gtt gga cat gcc gtg ttg cgc cag cgt gcc   211
Arg Ser Pro Val Ala Arg Val Gly His Ala Val Leu Arg Gln Arg Ala
             25                  30                  35
```

```
ggt gag atc tcg cgc atg caa ggt cgt gag ttt tct cgc cct ggg gat   259
Gly Glu Ile Ser Arg Met Gln Gly Arg Glu Phe Ser Arg Pro Gly Asp
         40                  45                  50

cag ttc cga cag gta gat ttg cgc agg cga ctg att cag gtc cat ccc   307
Gln Phe Arg Gln Val Asp Leu Arg Arg Arg Leu Ile Gln Val His Pro
     55                  60                  65

caa tca att cct aca gcg gat gcg atg gcc gta acc atc acc atg gcg   355
Gln Ser Ile Pro Thr Ala Asp Ala Met Ala Val Thr Ile Thr Met Ala
 70                  75                  80                  85

ctc acc gct gcc acg att gat ccg gtg aag ttc gtc gcg gat tca cag   403
Leu Thr Ala Ala Thr Ile Asp Pro Val Lys Phe Val Ala Asp Ser Gln
                 90                  95                 100

aac ccg gat gaa gag att tat ttg gca gct cag atc gca ttg cgg gaa   451
Asn Pro Asp Glu Glu Ile Tyr Leu Ala Ala Gln Ile Ala Leu Arg Glu
            105                 110                 115

atg gtt atc gct atg cct ttg gag gat ttc atc ggg gtg cgc att gat   499
Met Val Ile Ala Met Pro Leu Glu Asp Phe Ile Gly Val Arg Ile Asp
        120                 125                 130

cta gag cct gtt ttg gtg gct gct caa gct gct gcg aag aat gtg ggc   547
Leu Glu Pro Val Leu Val Ala Ala Gln Ala Ala Ala Lys Asn Val Gly
    135                 140                 145

gtg gaa gtc tcg tca atc ttg ctg aag gat ctg aat ctt ccc cag gag   595
Val Glu Val Ser Ser Ile Leu Leu Lys Asp Leu Asn Leu Pro Gln Glu
150                 155                 160                 165

tac tcg gga gcg ttg cag gaa tcg atc gtt gcg aaa att caa gcc gaa   643
Tyr Ser Gly Ala Leu Gln Glu Ser Ile Val Ala Lys Ile Gln Ala Glu
                170                 175                 180

act gat ctg gaa cgt gca cga aat gaa gtg aaa act acc cgt gct cga   691
Thr Asp Leu Glu Arg Ala Arg Asn Glu Val Lys Thr Thr Arg Ala Arg
            185                 190                 195

ctt gcc agc gcg aaa gtg ttg gag caa aat ccg att ctt gcc aaa att   739
Leu Ala Ser Ala Lys Val Leu Glu Gln Asn Pro Ile Leu Ala Lys Ile
        200                 205                 210

cgg atg att gaa gcg ctc cca ccg gga tcc aca att gag gtt cgg gag   787
Arg Met Ile Glu Ala Leu Pro Pro Gly Ser Thr Ile Glu Val Arg Glu
    215                 220                 225

ggt gac tca aag gca taaagttgcc catttcggtg ccc                    825
Gly Asp Ser Lys Ala
230
```

<210> 794
<211> 234
<212> PRT
<213> Corynebacterium glutamicum

<400> 794
Met His Gln Ala Gly Gln Leu Ile Asn Asp Pro Ser Gln Gly Leu Trp

```
  1               5                  10                  15

Arg Thr Ser Ala Leu Arg Ser Pro Val Ala Arg Val Gly His Ala Val
            20                  25                  30

Leu Arg Gln Arg Ala Gly Glu Ile Ser Arg Met Gln Gly Arg Glu Phe
        35                  40                  45

Ser Arg Pro Gly Asp Gln Phe Arg Gln Val Asp Leu Arg Arg Arg Leu
    50                  55                  60

Ile Gln Val His Pro Gln Ser Ile Pro Thr Ala Asp Ala Met Ala Val
65                  70                  75                  80

Thr Ile Thr Met Ala Leu Thr Ala Ala Thr Ile Asp Pro Val Lys Phe
                85                  90                  95

Val Ala Asp Ser Gln Asn Pro Asp Glu Glu Ile Tyr Leu Ala Ala Gln
            100                 105                 110

Ile Ala Leu Arg Glu Met Val Ile Ala Met Pro Leu Glu Asp Phe Ile
        115                 120                 125

Gly Val Arg Ile Asp Leu Glu Pro Val Leu Val Ala Ala Gln Ala Ala
    130                 135                 140

Ala Lys Asn Val Gly Val Glu Val Ser Ser Ile Leu Leu Lys Asp Leu
145                 150                 155                 160

Asn Leu Pro Gln Glu Tyr Ser Gly Ala Leu Gln Glu Ser Ile Val Ala
                165                 170                 175

Lys Ile Gln Ala Glu Thr Asp Leu Glu Arg Ala Arg Asn Glu Val Lys
            180                 185                 190

Thr Thr Arg Ala Arg Leu Ala Ser Ala Lys Val Leu Glu Gln Asn Pro
        195                 200                 205

Ile Leu Ala Lys Ile Arg Met Ile Glu Ala Leu Pro Pro Gly Ser Thr
    210                 215                 220

Ile Glu Val Arg Glu Gly Asp Ser Lys Ala
225                 230
```

<210> 795
<211> 849
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(826)
<223> RXN01774

<400> 795
ctgcgcaaga agagaaaaaa caacgacagc gaagctgcgt tcgggcgaat cggcgataat 60

cacacaccac tcttcctgag agaatcctga ggtcatcacc atg tca ccg aac ttc 115
                                                Met Ser Pro Asn Phe
                                                  1   5

```
caa gct cgc ggt act act gcg ccc act gtt gct ttg tcc atg cgc cag   163
Gln Ala Arg Gly Thr Thr Ala Pro Thr Val Ala Leu Ser Met Arg Gln
                10                  15                  20

atc gcg cac atc cgt gaa gaa att aag aaa tca cca ctc gct gct tcc   211
Ile Ala His Ile Arg Glu Glu Ile Lys Lys Ser Pro Leu Ala Ala Ser
            25                  30                  35

gtt ttc atc aca ccc acc acc aaa caa atg gtt gtc cga gat cta gaa   259
Val Phe Ile Thr Pro Thr Thr Lys Gln Met Val Val Arg Asp Leu Glu
        40                  45                  50

tca ctg ttc cag cag ctc tac cac aca gat cta cct gaa cca tcc atc   307
Ser Leu Phe Gln Gln Leu Tyr His Thr Asp Leu Pro Glu Pro Ser Ile
    55                  60                  65

aaa gac agt ggt ctt atc agt gct atc ggc tct agc gcc ggc aat acc   355
Lys Asp Ser Gly Leu Ile Ser Ala Ile Gly Ser Ser Ala Gly Asn Thr
70                  75                  80                  85

aat aat cca gca ctc gcc cta gaa act cag atg gct tac cac ctg gtg   403
Asn Asn Pro Ala Leu Ala Leu Glu Thr Gln Met Ala Tyr His Leu Val
                90                  95                  100

ctt gct atg cac cac acc gat gtt gct acc tgg cac aag gtg gtg acc   451
Leu Ala Met His His Thr Asp Val Ala Thr Trp His Lys Val Val Thr
            105                 110                 115

aaa aac atc acc gaa tct gct gct gca caa gat gct gcg gtc gag cac   499
Lys Asn Ile Thr Glu Ser Ala Ala Ala Gln Asp Ala Ala Val Glu His
        120                 125                 130

agt gct aaa tac gat gct gtg tac gat gcc gca caa ctt atg ggc atc   547
Ser Ala Lys Tyr Asp Ala Val Tyr Asp Ala Ala Gln Leu Met Gly Ile
    135                 140                 145

act gtt gag gaa ggt aat gtc ggt agc atc gct att gcc ttt agc aca   595
Thr Val Glu Glu Gly Asn Val Gly Ser Ile Ala Ile Ala Phe Ser Thr
150                 155                 160                 165

gca cgt gca gac ggt aaa tct gat tgg tgt gtt tcc ggc atc agc cgc   643
Ala Arg Ala Asp Gly Lys Ser Asp Trp Cys Val Ser Gly Ile Ser Arg
                170                 175                 180

tac atc gag gtc acc gaa gcc ttg gat gct gcg cga gct gtc act aaa   691
Tyr Ile Glu Val Thr Glu Ala Leu Asp Ala Ala Arg Ala Val Thr Lys
            185                 190                 195

aat act gat gcg ctc aat aaa act gct cta cca gac gtg cag ccg gcg   739
Asn Thr Asp Ala Leu Asn Lys Thr Ala Leu Pro Asp Val Gln Pro Ala
        200                 205                 210

ccg gtt gtg cat tca gca cag ttc atg aac aag tcc gca cac gat cat   787
Pro Val Val His Ser Ala Gln Phe Met Asn Lys Ser Ala His Asp His
    215                 220                 225

ggg gtt aat act gcg gaa aaa gat caa cca acc ctg ttt taaaagactg    836
Gly Val Asn Thr Ala Glu Lys Asp Gln Pro Thr Leu Phe
230                 235                 240
```

tccatttaac aac 849

<210> 796
<211> 242
<212> PRT
<213> Corynebacterium glutamicum

<400> 796

```
Met Ser Pro Asn Phe Gln Ala Arg Gly Thr Thr Ala Pro Thr Val Ala
  1               5                  10                  15

Leu Ser Met Arg Gln Ile Ala His Ile Arg Glu Glu Ile Lys Lys Ser
             20                  25                  30

Pro Leu Ala Ala Ser Val Phe Ile Thr Pro Thr Thr Lys Gln Met Val
         35                  40                  45

Val Arg Asp Leu Glu Ser Leu Phe Gln Gln Leu Tyr His Thr Asp Leu
     50                  55                  60

Pro Glu Pro Ser Ile Lys Asp Ser Gly Leu Ile Ser Ala Ile Gly Ser
 65                  70                  75                  80

Ser Ala Gly Asn Thr Asn Asn Pro Ala Leu Ala Leu Glu Thr Gln Met
                 85                  90                  95

Ala Tyr His Leu Val Leu Ala Met His His Thr Asp Val Ala Thr Trp
            100                 105                 110

His Lys Val Val Thr Lys Asn Ile Thr Glu Ser Ala Ala Ala Gln Asp
        115                 120                 125

Ala Ala Val Glu His Ser Ala Lys Tyr Asp Ala Val Tyr Asp Ala Ala
    130                 135                 140

Gln Leu Met Gly Ile Thr Val Glu Glu Gly Asn Val Gly Ser Ile Ala
145                 150                 155                 160

Ile Ala Phe Ser Thr Ala Arg Ala Asp Gly Lys Ser Asp Trp Cys Val
                165                 170                 175

Ser Gly Ile Ser Arg Tyr Ile Glu Val Thr Glu Ala Leu Asp Ala Ala
            180                 185                 190

Arg Ala Val Thr Lys Asn Thr Asp Ala Leu Asn Lys Thr Ala Leu Pro
        195                 200                 205

Asp Val Gln Pro Ala Pro Val Val His Ser Ala Gln Phe Met Asn Lys
    210                 215                 220

Ser Ala His Asp His Gly Val Asn Thr Ala Glu Lys Asp Gln Pro Thr
225                 230                 235                 240

Leu Phe
```

<210> 797
<211> 883
<212> DNA

<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(883)
<223> FRXA01774

<400> 797
ctgcgcaaga agagaaaaaa caacgacagc gaagctgcgt tcgggcgaat cggcgataat 60

cacacaccac tcttcctgag agaatcctga ggtcatcacc atg tca ccg aac ttc 115
Met Ser Pro Asn Phe
1 5

caa gct cgc ggt act act gcg ccc act gtt gct ttg tcc atg cgc cag 163
Gln Ala Arg Gly Thr Thr Ala Pro Thr Val Ala Leu Ser Met Arg Gln
10 15 20

atc gcg cac atc cgt gaa gaa att aag aaa tca cca ctc gct gct tcc 211
Ile Ala His Ile Arg Glu Glu Ile Lys Lys Ser Pro Leu Ala Ala Ser
25 30 35

gtt ttc atc aca ccc acc acc aaa caa atg gtt gtc cga gat cta gaa 259
Val Phe Ile Thr Pro Thr Thr Lys Gln Met Val Val Arg Asp Leu Glu
40 45 50

tca ctg ttc cag cag ctc tac cac aca gat cta cct gaa cca tcc atc 307
Ser Leu Phe Gln Gln Leu Tyr His Thr Asp Leu Pro Glu Pro Ser Ile
55 60 65

aaa gac agt ggt ctt atc agt gct atc ggc tct agc gcc ggc aat acc 355
Lys Asp Ser Gly Leu Ile Ser Ala Ile Gly Ser Ser Ala Gly Asn Thr
70 75 80 85

aat aat cca gca ctc gcc cta gaa act cag atg gct tac cac ctg gtg 403
Asn Asn Pro Ala Leu Ala Leu Glu Thr Gln Met Ala Tyr His Leu Val
90 95 100

ctt gct atg cac cac acc gat gtt gct acc tgg cac aag gtg gtg acc 451
Leu Ala Met His His Thr Asp Val Ala Thr Trp His Lys Val Val Thr
105 110 115

aaa aac atc acc gaa tct gct gct gca caa gat gct gcg gtc gag cac 499
Lys Asn Ile Thr Glu Ser Ala Ala Ala Gln Asp Ala Ala Val Glu His
120 125 130

agt gct aaa tac gat gct gtg tac gat gcc gca caa ctt atg ggc atc 547
Ser Ala Lys Tyr Asp Ala Val Tyr Asp Ala Ala Gln Leu Met Gly Ile
135 140 145

act gtt gag gaa ggt aat gtc ggt agc atc gct att gcc ttt agc aca 595
Thr Val Glu Glu Gly Asn Val Gly Ser Ile Ala Ile Ala Phe Ser Thr
150 155 160 165

gca cgt gca gac ggt aaa tct gat tgg tgt gtt tcc ggc atc agc cgc 643
Ala Arg Ala Asp Gly Lys Ser Asp Trp Cys Val Ser Gly Ile Ser Arg
170 175 180

tac atc gag gtc acc gaa gcc ttg gat gct gcg cga gct gtc act aaa 691
Tyr Ile Glu Val Thr Glu Ala Leu Asp Ala Ala Arg Ala Val Thr Lys
185 190 195

```
aat act gat gcg ctc aat aaa act gct cta cca gac gtg cag ccg gcg   739
Asn Thr Asp Ala Leu Asn Lys Thr Ala Leu Pro Asp Val Gln Pro Ala
        200                 205                 210

ccg gtt gtg cat tca gca cag ttc atg aac aag tcc gca cac gat cat   787
Pro Val Val His Ser Ala Gln Phe Met Asn Lys Ser Ala His Asp His
    215                 220                 225

ggg gtt aat act gcg gaa aaa gat caa cca acc tgt tta aag act gtg   835
Gly Val Asn Thr Ala Glu Lys Asp Gln Pro Thr Cys Leu Lys Thr Val
230                 235                 240                 245

cat tta caa cca cat cgt tac ccc cga aca ggc ttt aag gct att caa   883
His Leu Gln Pro His Arg Tyr Pro Arg Thr Gly Phe Lys Ala Ile Gln
                250                 255                 260
```

<210> 798
<211> 261
<212> PRT
<213> Corynebacterium glutamicum

<400> 798

```
Met Ser Pro Asn Phe Gln Ala Arg Gly Thr Thr Ala Pro Thr Val Ala
  1               5                  10                  15

Leu Ser Met Arg Gln Ile Ala His Ile Arg Glu Glu Ile Lys Lys Ser
             20                  25                  30

Pro Leu Ala Ala Ser Val Phe Ile Thr Pro Thr Thr Lys Gln Met Val
         35                  40                  45

Val Arg Asp Leu Glu Ser Leu Phe Gln Gln Leu Tyr His Thr Asp Leu
     50                  55                  60

Pro Glu Pro Ser Ile Lys Asp Ser Gly Leu Ile Ser Ala Ile Gly Ser
 65                  70                  75                  80

Ser Ala Gly Asn Thr Asn Asn Pro Ala Leu Ala Leu Glu Thr Gln Met
                 85                  90                  95

Ala Tyr His Leu Val Leu Ala Met His His Thr Asp Val Ala Thr Trp
            100                 105                 110

His Lys Val Val Thr Lys Asn Ile Thr Glu Ser Ala Ala Ala Gln Asp
        115                 120                 125

Ala Ala Val Glu His Ser Ala Lys Tyr Asp Ala Val Tyr Asp Ala Ala
    130                 135                 140

Gln Leu Met Gly Ile Thr Val Glu Glu Gly Asn Val Gly Ser Ile Ala
145                 150                 155                 160

Ile Ala Phe Ser Thr Ala Arg Ala Asp Gly Lys Ser Asp Trp Cys Val
                165                 170                 175

Ser Gly Ile Ser Arg Tyr Ile Glu Val Thr Glu Ala Leu Asp Ala Ala
            180                 185                 190

Arg Ala Val Thr Lys Asn Thr Asp Ala Leu Asn Lys Thr Ala Leu Pro
```

```
        195                 200                 205

Asp Val Gln Pro Ala Pro Val Val His Ser Ala Gln Phe Met Asn Lys
    210                 215                 220

Ser Ala His Asp His Gly Val Asn Thr Ala Glu Lys Asp Gln Pro Thr
225                 230                 235                 240

Cys Leu Lys Thr Val His Leu Gln Pro His Arg Tyr Pro Arg Thr Gly
                245                 250                 255

Phe Lys Ala Ile Gln
            260


<210> 799
<211> 816
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(793)
<223> RXN01787

<400> 799
cagaagcacg tattttcttc ttaactcgca cctcatctgg tgtgggtttt tttgcatttt 60

ttacacaccc cactccacac acactcgcaa aggattcatc atg agc aac aat gct   115
                                        Met Ser Asn Asn Ala
                                          1               5

ctt tta gta gca aac gaa gcc gac atc ggt ctc tac ctc cac tgg aat   163
Leu Leu Val Ala Asn Glu Ala Asp Ile Gly Leu Tyr Leu His Trp Asn
                10                  15                  20

ggt ggt cgc gac tcg att gag gcg ttt ctc gcc tac gcc gca tac gcg   211
Gly Gly Arg Asp Ser Ile Glu Ala Phe Leu Ala Tyr Ala Ala Tyr Ala
            25                  30                  35

cag tta cca ccc atc aac gaa aat aac gat tgg ttg cca ccg ttt att   259
Gln Leu Pro Pro Ile Asn Glu Asn Asn Asp Trp Leu Pro Pro Phe Ile
        40                  45                  50

act gtg ctg aag aac ttc ttc ggc aat gat ggt tct ggc gtc tac ctc   307
Thr Val Leu Lys Asn Phe Phe Gly Asn Asp Gly Ser Gly Val Tyr Leu
    55                  60                  65

gaa cct gtc aat cag gat tat ctc gac ggc atc gac tat gac aac ggt   355
Glu Pro Val Asn Gln Asp Tyr Leu Asp Gly Ile Asp Tyr Asp Asn Gly
70                  75                  80                  85

gtt tac atg ctt gac gat tat gag atc act gag cgt att aat cca ccc   403
Val Tyr Met Leu Asp Asp Tyr Glu Ile Thr Glu Arg Ile Asn Pro Pro
                90                  95                  100

gct gtt gag caa gac tcc cac gat ctc cac gac atg ttg atc aaa att   451
Ala Val Glu Gln Asp Ser His Asp Leu His Asp Met Leu Ile Lys Ile
            105                 110                 115

gat aaa gct caa cca cct gtc gat caa ctc ggg agt ttt ctc cat ggc   499
```

```
Asp Lys Ala Gln Pro Pro Val Asp Gln Leu Gly Ser Phe Leu His Gly
        120                 125                 130

cta gag acc tct gtc gca gat ttg ggg gtt ggt gat cgc gta ttt ttg   547
Leu Glu Thr Ser Val Ala Asp Leu Gly Val Gly Asp Arg Val Phe Leu
    135                 140                 145

cca cgt ttt agc acc ttt gat aag aaa ctc ggt cgc tac cgc atc cac   595
Pro Arg Phe Ser Thr Phe Asp Lys Lys Leu Gly Arg Tyr Arg Ile His
150                 155                 160                 165

act gtt ctc gga ttc gct gag aac gat ccg ttt aac cct atg acc agc   643
Thr Val Leu Gly Phe Ala Glu Asn Asp Pro Phe Asn Pro Met Thr Ser
                170                 175                 180

agc gag cga ttt aaa ggt aag ccc tat gtc gat atg ttc gac aat caa   691
Ser Glu Arg Phe Lys Gly Lys Pro Tyr Val Asp Met Phe Asp Asn Gln
            185                 190                 195

gac aac gcc ttt aac cca aat tcc tat atc act aca gat acc gtg cgc   739
Asp Asn Ala Phe Asn Pro Asn Ser Tyr Ile Thr Thr Asp Thr Val Arg
        200                 205                 210

atc gtt gtc gat cct gta ccg gaa act aat ccc gac gat gag aaa gca   787
Ile Val Val Asp Pro Val Pro Glu Thr Asn Pro Asp Asp Glu Lys Ala
    215                 220                 225

gga cgc tagccatgtc tcgcagctac ccc                                816
Gly Arg
230


<210> 800
<211> 231
<212> PRT
<213> Corynebacterium glutamicum

<400> 800
Met Ser Asn Asn Ala Leu Leu Val Ala Asn Glu Ala Asp Ile Gly Leu
  1               5                  10                  15

Tyr Leu His Trp Asn Gly Gly Arg Asp Ser Ile Glu Ala Phe Leu Ala
             20                  25                  30

Tyr Ala Ala Tyr Ala Gln Leu Pro Pro Ile Asn Glu Asn Asn Asp Trp
         35                  40                  45

Leu Pro Pro Phe Ile Thr Val Leu Lys Asn Phe Phe Gly Asn Asp Gly
     50                  55                  60

Ser Gly Val Tyr Leu Glu Pro Val Asn Gln Asp Tyr Leu Asp Gly Ile
 65                  70                  75                  80

Asp Tyr Asp Asn Gly Val Tyr Met Leu Asp Asp Tyr Glu Ile Thr Glu
                 85                  90                  95

Arg Ile Asn Pro Pro Ala Val Glu Gln Asp Ser His Asp Leu His Asp
            100                 105                 110

Met Leu Ile Lys Ile Asp Lys Ala Gln Pro Pro Val Asp Gln Leu Gly
        115                 120                 125
```

```
Ser Phe Leu His Gly Leu Glu Thr Ser Val Ala Asp Leu Gly Val Gly
    130                 135                 140

Asp Arg Val Phe Leu Pro Arg Phe Ser Thr Phe Asp Lys Lys Leu Gly
145                 150                 155                 160

Arg Tyr Arg Ile His Thr Val Leu Gly Phe Ala Glu Asn Asp Pro Phe
                165                 170                 175

Asn Pro Met Thr Ser Ser Glu Arg Phe Lys Gly Lys Pro Tyr Val Asp
            180                 185                 190

Met Phe Asp Asn Gln Asp Asn Ala Phe Asn Pro Asn Ser Tyr Ile Thr
        195                 200                 205

Thr Asp Thr Val Arg Ile Val Val Asp Pro Val Pro Glu Thr Asn Pro
    210                 215                 220

Asp Asp Glu Lys Ala Gly Arg
225                 230
```

Sequence Listing - Page 987 - Date Saved: 2004-12-20

<210> 801
<211> 377
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(354)
<223> FRXA01787

<400> 801

```
acc gag aaa att gat aaa gct caa cca cct gtc gat caa ctc ggg agt   48
Thr Glu Lys Ile Asp Lys Ala Gln Pro Pro Val Asp Gln Leu Gly Ser
  1               5                  10                  15

ttt ctc cat ggc cta gag acc tct gtc gca gat ttg ggg gtt ggt gat   96
Phe Leu His Gly Leu Glu Thr Ser Val Ala Asp Leu Gly Val Gly Asp
             20                  25                  30

cgc gta ttt ttg cca cgt ttt agc acc ttt gat aag aaa ctc ggt cgc  144
Arg Val Phe Leu Pro Arg Phe Ser Thr Phe Asp Lys Lys Leu Gly Arg
         35                  40                  45

tac cgc atc cac act gtt ctc gga ttc gct gag aac gat ccg ttt aac  192
Tyr Arg Ile His Thr Val Leu Gly Phe Ala Glu Asn Asp Pro Phe Asn
     50                  55                  60

cct atg acc agc agc gag cga ttt aaa ggt aag ccc tat gtc gat atg  240
Pro Met Thr Ser Ser Glu Arg Phe Lys Gly Lys Pro Tyr Val Asp Met
 65                  70                  75                  80

ttc gac aat caa gac aac gcc ttt aac cca aat tcc tat atc act aca  288
Phe Asp Asn Gln Asp Asn Ala Phe Asn Pro Asn Ser Tyr Ile Thr Thr
                 85                  90                  95

gat acc gtg cgc atc gtt gtc gat cct gta ccg gaa act aat ccc gac  336
Asp Thr Val Arg Ile Val Val Asp Pro Val Pro Glu Thr Asn Pro Asp
            100                 105                 110
```

```
gat gag aaa gca gga cgc tagccatgtc tcgcagctac ccc                  377
Asp Glu Lys Ala Gly Arg
        115


<210> 802
<211> 118
<212> PRT
<213> Corynebacterium glutamicum

<400> 802
Thr Glu Lys Ile Asp Lys Ala Gln Pro Pro Val Asp Gln Leu Gly Ser
  1               5                  10                  15

Phe Leu His Gly Leu Glu Thr Ser Val Ala Asp Leu Gly Val Gly Asp
             20                  25                  30

Arg Val Phe Leu Pro Arg Phe Ser Thr Phe Asp Lys Lys Leu Gly Arg
         35                  40                  45

Tyr Arg Ile His Thr Val Leu Gly Phe Ala Glu Asn Asp Pro Phe Asn
     50                  55                  60

Pro Met Thr Ser Ser Glu Arg Phe Lys Gly Lys Pro Tyr Val Asp Met
 65                  70                  75                  80

Phe Asp Asn Gln Asp Asn Ala Phe Asn Pro Asn Ser Tyr Ile Thr Thr
                 85                  90                  95

Asp Thr Val Arg Ile Val Val Asp Pro Val Pro Glu Thr Asn Pro Asp
            100                 105                 110

Asp Glu Lys Ala Gly Arg
        115


<210> 803
<211> 897
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(874)
<223> RXN01796

<400> 803
atgtaactcg atcaggtgga aatgcccgca aaagtggcgg cggtggccga gggatggccg 60

ttggtgcggc atcggtggcc tgctactagt cgggctcttc ttg ctc ctt ggc ggt   115
                                        Leu Leu Leu Gly Gly
                                          1               5

aac cct gcc gag atc gac cag gtt tta ggt ggc gat caa acc cag atc   163
Asn Pro Ala Glu Ile Asp Gln Val Leu Gly Gly Asp Gln Thr Gln Ile
                10                  15                  20

gag tct gga gag tcc acc gga gcc ggc gac ttt gat cac tgc caa acc   211
Glu Ser Gly Glu Ser Thr Gly Ala Gly Asp Phe Asp His Cys Gln Thr
            25                  30                  35
```

```
ggc gca gat gcc aac gcc agt gat gat tgt cgc ctt tac tac acc tca   259
Gly Ala Asp Ala Asn Ala Ser Asp Asp Cys Arg Leu Tyr Tyr Thr Ser
         40                  45                  50

ttc tcc gtc aat gaa atg tgg cag act ttg ctt cca gct cag gct ggt   307
Phe Ser Val Asn Glu Met Trp Gln Thr Leu Leu Pro Ala Gln Ala Gly
     55                  60                  65

atc gaa tac acc gag ccg aca ttg act ctt ttc aaa aac tcc acc caa   355
Ile Glu Tyr Thr Glu Pro Thr Leu Thr Leu Phe Lys Asn Ser Thr Gln
 70                  75                  80                  85

acc ggc tgc ggt ttc gct tct gcg tcc act ggg ccg ttt tac tgt ccg   403
Thr Gly Cys Gly Phe Ala Ser Ala Ser Thr Gly Pro Phe Tyr Cys Pro
                 90                  95                 100

tca gac caa gat gct tat ttt gac ttg act ttc ttc gat cag atg cgt   451
Ser Asp Gln Asp Ala Tyr Phe Asp Leu Thr Phe Phe Asp Gln Met Arg
            105                 110                 115

cag ttc ggt gca gaa aac gcc ccg ctt gcc cag atg tac atc gtg gcg   499
Gln Phe Gly Ala Glu Asn Ala Pro Leu Ala Gln Met Tyr Ile Val Ala
        120                 125                 130

cac gag tac ggc cac cac gtc caa aac ctc gag ggc aca ctc gga ctg   547
His Glu Tyr Gly His His Val Gln Asn Leu Glu Gly Thr Leu Gly Leu
    135                 140                 145

tcc aat tac aac gat ccg ggc gct gat tcc aac gcc gtc aag atc gag   595
Ser Asn Tyr Asn Asp Pro Gly Ala Asp Ser Asn Ala Val Lys Ile Glu
150                 155                 160                 165

ttg cag gcc gat tgc tac gca ggc att tgg gct aat cac tcc agc gaa   643
Leu Gln Ala Asp Cys Tyr Ala Gly Ile Trp Ala Asn His Ser Ser Glu
                170                 175                 180

ggc ccg gat ccg cta ctc caa ccc atc acc gaa tct gag cta gat tcc   691
Gly Pro Asp Pro Leu Leu Gln Pro Ile Thr Glu Ser Glu Leu Asp Ser
            185                 190                 195

gct ctc ctt gct gca agc gcc gtg ggc gac gac aat atc cag caa cga   739
Ala Leu Leu Ala Ala Ser Ala Val Gly Asp Asp Asn Ile Gln Gln Arg
        200                 205                 210

tcc ggt ggc gat gtc aat cct gaa agc tgg act cac ggc tca tcg cag   787
Ser Gly Gly Asp Val Asn Pro Glu Ser Trp Thr His Gly Ser Ser Gln
    215                 220                 225

cag cgc aaa gac gcg ttc ctc gcc ggc tac aac acc ggc cag atg agc   835
Gln Arg Lys Asp Ala Phe Leu Ala Gly Tyr Asn Thr Gly Gln Met Ser
230                 235                 240                 245

gcc tgc gac ttc ctc ggc cgg ggc gtc tac aac gac gct taaagcattg    884
Ala Cys Asp Phe Leu Gly Arg Gly Val Tyr Asn Asp Ala
                250                 255

cttttcgacg tct                                                   897
```

<210> 804

<211> 258
<212> PRT
<213> Corynebacterium glutamicum

<400> 804
Leu Leu Leu Gly Gly Asn Pro Ala Glu Ile Asp Gln Val Leu Gly Gly
1 5 10 15

Asp Gln Thr Gln Ile Glu Ser Gly Glu Ser Thr Gly Ala Gly Asp Phe
20 25 30

Asp His Cys Gln Thr Gly Ala Asp Ala Asn Ala Ser Asp Asp Cys Arg
35 40 45

Leu Tyr Tyr Thr Ser Phe Ser Val Asn Glu Met Trp Gln Thr Leu Leu
50 55 60

Pro Ala Gln Ala Gly Ile Glu Tyr Thr Glu Pro Thr Leu Thr Leu Phe
65 70 75 80

Lys Asn Ser Thr Gln Thr Gly Cys Gly Phe Ala Ser Ala Ser Thr Gly
85 90 95

Pro Phe Tyr Cys Pro Ser Asp Gln Asp Ala Tyr Phe Asp Leu Thr Phe
100 105 110

Phe Asp Gln Met Arg Gln Phe Gly Ala Glu Asn Ala Pro Leu Ala Gln
115 120 125

Met Tyr Ile Val Ala His Glu Tyr Gly His His Val Gln Asn Leu Glu
130 135 140

Gly Thr Leu Gly Leu Ser Asn Tyr Asn Asp Pro Gly Ala Asp Ser Asn
145 150 155 160

Ala Val Lys Ile Glu Leu Gln Ala Asp Cys Tyr Ala Gly Ile Trp Ala
165 170 175

Asn His Ser Ser Glu Gly Pro Asp Pro Leu Leu Gln Pro Ile Thr Glu
180 185 190

Ser Glu Leu Asp Ser Ala Leu Leu Ala Ala Ser Ala Val Gly Asp Asp
195 200 205

Asn Ile Gln Gln Arg Ser Gly Gly Asp Val Asn Pro Glu Ser Trp Thr
210 215 220

His Gly Ser Ser Gln Gln Arg Lys Asp Ala Phe Leu Ala Gly Tyr Asn
225 230 235 240

Thr Gly Gln Met Ser Ala Cys Asp Phe Leu Gly Arg Gly Val Tyr Asn
245 250 255

Asp Ala

<210> 805
<211> 506
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(483)
<223> FRXA01796

<400> 805
```
ttt tac tgt ccg tca gac caa gat gct tat gtt gac ttg act ttg ttc   48
Phe Tyr Cys Pro Ser Asp Gln Asp Ala Tyr Val Asp Leu Thr Leu Phe
  1               5                  10                  15

gat cag atg cgt cag ttc ggt gca gaa aac gcc ccg ctt gcc cag atg   96
Asp Gln Met Arg Gln Phe Gly Ala Glu Asn Ala Pro Leu Ala Gln Met
             20                  25                  30

tac atc gtg gcg cac gag tac ggc cac cac gtc caa aac ctc gag ggc   144
Tyr Ile Val Ala His Glu Tyr Gly His His Val Gln Asn Leu Glu Gly
         35                  40                  45

aca ctc gga ctg tcc aat tac aac gat ccg ggc gct gat tcc aac gcc   192
Thr Leu Gly Leu Ser Asn Tyr Asn Asp Pro Gly Ala Asp Ser Asn Ala
     50                  55                  60

gtc aag atc gag ttg cag gcc gat tgc tac gca ggc att tgg gct aat   240
Val Lys Ile Glu Leu Gln Ala Asp Cys Tyr Ala Gly Ile Trp Ala Asn
 65                  70                  75                  80

cac tcc agc gaa ggc ccg gat ccg cta ctc caa ccc atc acc gaa tct   288
His Ser Ser Glu Gly Pro Asp Pro Leu Leu Gln Pro Ile Thr Glu Ser
                 85                  90                  95

gag cta gat tcc gct ctc ctt gct gca agc gcc gtg ggc gac gac aat   336
Glu Leu Asp Ser Ala Leu Leu Ala Ala Ser Ala Val Gly Asp Asp Asn
            100                 105                 110

atc cag caa cga tcc ggt ggc gat gtc aat cct gaa agc tgg act cac   384
Ile Gln Gln Arg Ser Gly Gly Asp Val Asn Pro Glu Ser Trp Thr His
        115                 120                 125

ggc tca tcg cag cag cgc aaa gac gcg ttc ctc gcc ggc tac aac acc   432
Gly Ser Ser Gln Gln Arg Lys Asp Ala Phe Leu Ala Gly Tyr Asn Thr
    130                 135                 140

ggc cag atg agc gcc tgc gac ttc ctc ggc cgg ggc gtc tac aac gac   480
Gly Gln Met Ser Ala Cys Asp Phe Leu Gly Arg Gly Val Tyr Asn Asp
145                 150                 155                 160

gct taaagcattg cttttcgacg tct                                     506
Ala
```

<210> 806
<211> 161
<212> PRT
<213> Corynebacterium glutamicum

<400> 806
```
Phe Tyr Cys Pro Ser Asp Gln Asp Ala Tyr Val Asp Leu Thr Leu Phe
  1               5                  10                  15
```

```
Asp Gln Met Arg Gln Phe Gly Ala Glu Asn Ala Pro Leu Ala Gln Met
            20                  25                  30

Tyr Ile Val Ala His Glu Tyr Gly His His Val Gln Asn Leu Glu Gly
        35                  40                  45

Thr Leu Gly Leu Ser Asn Tyr Asn Asp Pro Gly Ala Asp Ser Asn Ala
    50                  55                  60

Val Lys Ile Glu Leu Gln Ala Asp Cys Tyr Ala Gly Ile Trp Ala Asn
65                  70                  75                  80

His Ser Ser Glu Gly Pro Asp Pro Leu Leu Gln Pro Ile Thr Glu Ser
                85                  90                  95

Glu Leu Asp Ser Ala Leu Leu Ala Ala Ser Ala Val Gly Asp Asp Asn
            100                 105                 110

Ile Gln Gln Arg Ser Gly Gly Asp Val Asn Pro Glu Ser Trp Thr His
        115                 120                 125

Gly Ser Ser Gln Gln Arg Lys Asp Ala Phe Leu Ala Gly Tyr Asn Thr
    130                 135                 140

Gly Gln Met Ser Ala Cys Asp Phe Leu Gly Arg Gly Val Tyr Asn Asp
145                 150                 155                 160

Ala
```

<210> 807
<211> 1083
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1060)
<223> RXN01803

<400> 807

```
ctagcggaaa ggctttagcg acaaggcttt ttgcatgttt taatgcaggg aatattaact 60

ttttgttaat ctctgaccat tgaccttgta cgcttaaaac atg cga aag aaa aaa   115
                                              Met Arg Lys Lys Lys
                                                1               5

gac ggt caa aat ctc cca gac ttc cgg aaa aat ccg cca aag ctg gat   163
Asp Gly Gln Asn Leu Pro Asp Phe Arg Lys Asn Pro Pro Lys Leu Asp
                10                  15                  20

aaa aag gct tat gaa aaa gaa cta aaa aga ctt caa gcc gaa ctc gtc   211
Lys Lys Ala Tyr Glu Lys Glu Leu Lys Arg Leu Gln Ala Glu Leu Val
            25                  30                  35

gat ttg caa caa tgg gtt gtg gaa acc ggt gcg cgc gtg gtc atc gtc   259
Asp Leu Gln Gln Trp Val Val Glu Thr Gly Ala Arg Val Val Ile Val
        40                  45                  50

atg gaa ggc cgc gac gcc gct ggt aaa ggt tct gcg atc aag cgc att   307
```

```
Met Glu Gly Arg Asp Ala Ala Gly Lys Gly Ser Ala Ile Lys Arg Ile
     55                  60                  65

acg cag tac ctc aac ccc cgg tcc gca agg atc gaa gcg ctg ccc acc   355
Thr Gln Tyr Leu Asn Pro Arg Ser Ala Arg Ile Glu Ala Leu Pro Thr
 70                  75                  80                  85

cca aac tct cgg gaa aaa ggg cag tgg tat ttc cag cgc tac atc gaa   403
Pro Asn Ser Arg Glu Lys Gly Gln Trp Tyr Phe Gln Arg Tyr Ile Glu
                90                  95                 100

aaa ttg ccg act gct ggt gag atc gtt atc ttt gac cgc tcc tgg tac   451
Lys Leu Pro Thr Ala Gly Glu Ile Val Ile Phe Asp Arg Ser Trp Tyr
            105                 110                 115

aac cgt gca gga gtc gag cgc gtc atg gga ttt tgc acc tcc cag gag   499
Asn Arg Ala Gly Val Glu Arg Val Met Gly Phe Cys Thr Ser Gln Glu
        120                 125                 130

tac cgc cga ttc ctt cac cag gca cca atc ttt gaa cgc ctg ttg gtg   547
Tyr Arg Arg Phe Leu His Gln Ala Pro Ile Phe Glu Arg Leu Leu Val
    135                 140                 145

gaa gat ggc att cac ctg cgt aaa tac tgg ttc tct gta tct gat gaa   595
Glu Asp Gly Ile His Leu Arg Lys Tyr Trp Phe Ser Val Ser Asp Glu
150                 155                 160                 165

gag cag att gag cgt ttc gaa gac cgc ctg agc gat ccg ctg cgc cgg   643
Glu Gln Ile Glu Arg Phe Glu Asp Arg Leu Ser Asp Pro Leu Arg Arg
                170                 175                 180

tgg aag ttg tcg cca atg gat tta caa tcg atc acc cgc tgg gaa gat   691
Trp Lys Leu Ser Pro Met Asp Leu Gln Ser Ile Thr Arg Trp Glu Asp
            185                 190                 195

tac tca cgc gca aaa gat gag atg ttc atc cac acg gac atc ccg tca   739
Tyr Ser Arg Ala Lys Asp Glu Met Phe Ile His Thr Asp Ile Pro Ser
        200                 205                 210

gca ccg tgg tac acg gtg gaa tct gag gac aag aag cgt tcc cgc atc   787
Ala Pro Trp Tyr Thr Val Glu Ser Glu Asp Lys Lys Arg Ser Arg Ile
    215                 220                 225

aac gtc att tcg cat ctg ctc tcg acg att cct tat gag aag atc gat   835
Asn Val Ile Ser His Leu Leu Ser Thr Ile Pro Tyr Glu Lys Ile Asp
230                 235                 240                 245

cgt cca ttg ccg gaa atc cct cat cgc cca gat tct gaa tct gat tat   883
Arg Pro Leu Pro Glu Ile Pro His Arg Pro Asp Ser Glu Ser Asp Tyr
                250                 255                 260

gta cgt ccc cct cgc gat gag ttc cgt tat gtt cca gat gtg gca gca   931
Val Arg Pro Pro Arg Asp Glu Phe Arg Tyr Val Pro Asp Val Ala Ala
            265                 270                 275

cac ttg gaa gaa gag cgc atc aag aaa gaa gaa aaa gcc aag aag gca   979
His Leu Glu Glu Glu Arg Ile Lys Lys Glu Glu Lys Ala Lys Lys Ala
        280                 285                 290

aag aag cca gct aag gct gca gga aag aac tcg gat aag cag aag tct  1027
Lys Lys Pro Ala Lys Ala Ala Gly Lys Asn Ser Asp Lys Gln Lys Ser
```

```
    295                 300                 305

tcc gga gga aaa ggc aag aag aag tcc aag aaa tagaacgcct tttaaggggt 1080
Ser Gly Gly Lys Gly Lys Lys Lys Ser Lys Lys
310                 315                 320

tga                                                               1083


<210> 808
<211> 320
<212> PRT
<213> Corynebacterium glutamicum

<400> 808
Met Arg Lys Lys Lys Asp Gly Gln Asn Leu Pro Asp Phe Arg Lys Asn
  1               5                  10                  15

Pro Pro Lys Leu Asp Lys Lys Ala Tyr Glu Lys Glu Leu Lys Arg Leu
             20                  25                  30

Gln Ala Glu Leu Val Asp Leu Gln Gln Trp Val Val Glu Thr Gly Ala
         35                  40                  45

Arg Val Val Ile Val Met Glu Gly Arg Asp Ala Ala Gly Lys Gly Ser
     50                  55                  60

Ala Ile Lys Arg Ile Thr Gln Tyr Leu Asn Pro Arg Ser Ala Arg Ile
 65                  70                  75                  80

Glu Ala Leu Pro Thr Pro Asn Ser Arg Glu Lys Gly Gln Trp Tyr Phe
                 85                  90                  95

Gln Arg Tyr Ile Glu Lys Leu Pro Thr Ala Gly Glu Ile Val Ile Phe
            100                 105                 110

Asp Arg Ser Trp Tyr Asn Arg Ala Gly Val Glu Arg Val Met Gly Phe
        115                 120                 125

Cys Thr Ser Gln Glu Tyr Arg Arg Phe Leu His Gln Ala Pro Ile Phe
    130                 135                 140

Glu Arg Leu Leu Val Glu Asp Gly Ile His Leu Arg Lys Tyr Trp Phe
145                 150                 155                 160

Ser Val Ser Asp Glu Glu Gln Ile Glu Arg Phe Glu Asp Arg Leu Ser
                165                 170                 175

Asp Pro Leu Arg Arg Trp Lys Leu Ser Pro Met Asp Leu Gln Ser Ile
            180                 185                 190

Thr Arg Trp Glu Asp Tyr Ser Arg Ala Lys Asp Glu Met Phe Ile His
        195                 200                 205

Thr Asp Ile Pro Ser Ala Pro Trp Tyr Thr Val Glu Ser Glu Asp Lys
    210                 215                 220

Lys Arg Ser Arg Ile Asn Val Ile Ser His Leu Leu Ser Thr Ile Pro
225                 230                 235                 240

Tyr Glu Lys Ile Asp Arg Pro Leu Pro Glu Ile Pro His Arg Pro Asp
```

```
                245                 250                 255

Ser Glu Ser Asp Tyr Val Arg Pro Pro Arg Asp Glu Phe Arg Tyr Val
            260                 265                 270

Pro Asp Val Ala Ala His Leu Glu Glu Glu Arg Ile Lys Lys Glu Glu
        275                 280                 285

Lys Ala Lys Lys Ala Lys Lys Pro Ala Lys Ala Ala Gly Lys Asn Ser
    290                 295                 300

Asp Lys Gln Lys Ser Ser Gly Gly Lys Gly Lys Lys Lys Ser Lys Lys
305                 310                 315                 320
```

<210> 809
<211> 1083
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1060)
<223> FRXA01803

<400> 809

```
ctagcggaaa ggctttagcg acaaggcttt ttgcatgttt taatgcaggg aatattaact 60

ttttgttaat ctctgaccat tgaccttgta cgcttaaaac atg cga aag aaa aaa   115
                                            Met Arg Lys Lys Lys
                                              1               5

gac ggt caa aat ctc cca gac ttc cgg aaa aat ccg cca aag ctg gat   163
Asp Gly Gln Asn Leu Pro Asp Phe Arg Lys Asn Pro Pro Lys Leu Asp
                 10                  15                  20

aaa aag gct tat gaa aaa gaa cta aaa aga ctt caa gcc gaa ctc gtc   211
Lys Lys Ala Tyr Glu Lys Glu Leu Lys Arg Leu Gln Ala Glu Leu Val
             25                  30                  35

gat ttg caa caa tgg gtt gtg gaa acc ggt gcg cgc gtg gtc atc gtc   259
Asp Leu Gln Gln Trp Val Val Glu Thr Gly Ala Arg Val Val Ile Val
         40                  45                  50

atg gaa ggc cgc gac gcc gct ggt aaa ggt tct gcg atc aag cgc att   307
Met Glu Gly Arg Asp Ala Ala Gly Lys Gly Ser Ala Ile Lys Arg Ile
     55                  60                  65

acg cag tac ctc aac ccc cgg tcc gca agg atc gaa gcg ctg ccc acc   355
Thr Gln Tyr Leu Asn Pro Arg Ser Ala Arg Ile Glu Ala Leu Pro Thr
 70                  75                  80                  85

cca aac tct cgg gaa aaa ggg cag tgg tat ttc cag cgc tac atc gaa   403
Pro Asn Ser Arg Glu Lys Gly Gln Trp Tyr Phe Gln Arg Tyr Ile Glu
                 90                  95                 100

aaa ttg ccg act gct ggt gag atc gtt atc ttt gac cgc tcc tgg tac   451
Lys Leu Pro Thr Ala Gly Glu Ile Val Ile Phe Asp Arg Ser Trp Tyr
```

```
            105                 110                 115

aac cgt gca gga gtc gag cgc gtc atg gga ttt tgc acc tcc cag gag   499
Asn Arg Ala Gly Val Glu Arg Val Met Gly Phe Cys Thr Ser Gln Glu
        120                 125                 130

tac cgc cga ttc ctt cac cag gca cca atc ttt gaa cgc ctg ttg gtg   547
Tyr Arg Arg Phe Leu His Gln Ala Pro Ile Phe Glu Arg Leu Leu Val
    135                 140                 145

gaa gat ggc att cac ctg cgt aaa tac tgg ttc tct gta tct gat gaa   595
Glu Asp Gly Ile His Leu Arg Lys Tyr Trp Phe Ser Val Ser Asp Glu
150                 155                 160                 165

gag cag att gag cgt ttc gaa gac cgc ctg agc gat ccg ctg cgc cgg   643
Glu Gln Ile Glu Arg Phe Glu Asp Arg Leu Ser Asp Pro Leu Arg Arg
                170                 175                 180

tgg aag ttg tcg cca atg gat tta caa tcg atc acc cgc tgg gaa gat   691
Trp Lys Leu Ser Pro Met Asp Leu Gln Ser Ile Thr Arg Trp Glu Asp
            185                 190                 195

tac tca cgc gca aaa gat gag atg ttc atc cac acg gac atc ccg tca   739
Tyr Ser Arg Ala Lys Asp Glu Met Phe Ile His Thr Asp Ile Pro Ser
        200                 205                 210

gca ccg tgg tac acg gtg gaa tct gag gac aag aag cgt tcc cgc atc   787
Ala Pro Trp Tyr Thr Val Glu Ser Glu Asp Lys Lys Arg Ser Arg Ile
    215                 220                 225

aac gtc att tcg cat ctg ctc tcg acg att cct tat gag aag atc gat   835
Asn Val Ile Ser His Leu Leu Ser Thr Ile Pro Tyr Glu Lys Ile Asp
230                 235                 240                 245

cgt cca ttg ccg gaa atc cct cat cgc cca gat tct gaa tct gat tat   883
Arg Pro Leu Pro Glu Ile Pro His Arg Pro Asp Ser Glu Ser Asp Tyr
                250                 255                 260

gta cgt ccc cct cgc gat gag ttc cgt tat gtt cca gat gtg gca gca   931
Val Arg Pro Pro Arg Asp Glu Phe Arg Tyr Val Pro Asp Val Ala Ala
            265                 270                 275

cac ttg gaa gaa gag cgc atc aag aaa gaa gaa aaa gcc aag aag gca   979
His Leu Glu Glu Glu Arg Ile Lys Lys Glu Glu Lys Ala Lys Lys Ala
        280                 285                 290

aag aag cca gct aag gct gca gga aag aac tcg gat aag cag aag tct   1027
Lys Lys Pro Ala Lys Ala Ala Gly Lys Asn Ser Asp Lys Gln Lys Ser
    295                 300                 305

tcc gga gga aaa ggc aag aag aag tcc aag aaa tagaacgcct tttaaggggt 1080
Ser Gly Gly Lys Gly Lys Lys Lys Ser Lys Lys
310                 315                 320

tga                                                               1083
```

<210> 810
<211> 320
<212> PRT
<213> Corynebacterium glutamicum

<400> 810

```
Met Arg Lys Lys Lys Asp Gly Gln Asn Leu Pro Asp Phe Arg Lys Asn
  1               5                  10                  15

Pro Pro Lys Leu Asp Lys Lys Ala Tyr Glu Lys Glu Leu Lys Arg Leu
            20                  25                  30

Gln Ala Glu Leu Val Asp Leu Gln Gln Trp Val Val Glu Thr Gly Ala
        35                  40                  45

Arg Val Val Ile Val Met Glu Gly Arg Asp Ala Ala Gly Lys Gly Ser
    50                  55                  60

Ala Ile Lys Arg Ile Thr Gln Tyr Leu Asn Pro Arg Ser Ala Arg Ile
65                  70                  75                  80

Glu Ala Leu Pro Thr Pro Asn Ser Arg Glu Lys Gly Gln Trp Tyr Phe
                85                  90                  95

Gln Arg Tyr Ile Glu Lys Leu Pro Thr Ala Gly Glu Ile Val Ile Phe
            100                 105                 110

Asp Arg Ser Trp Tyr Asn Arg Ala Gly Val Glu Arg Val Met Gly Phe
        115                 120                 125

Cys Thr Ser Gln Glu Tyr Arg Arg Phe Leu His Gln Ala Pro Ile Phe
    130                 135                 140

Glu Arg Leu Leu Val Glu Asp Gly Ile His Leu Arg Lys Tyr Trp Phe
145                 150                 155                 160

Ser Val Ser Asp Glu Glu Gln Ile Glu Arg Phe Glu Asp Arg Leu Ser
                165                 170                 175

Asp Pro Leu Arg Arg Trp Lys Leu Ser Pro Met Asp Leu Gln Ser Ile
            180                 185                 190

Thr Arg Trp Glu Asp Tyr Ser Arg Ala Lys Asp Glu Met Phe Ile His
        195                 200                 205

Thr Asp Ile Pro Ser Ala Pro Trp Tyr Thr Val Glu Ser Glu Asp Lys
    210                 215                 220

Lys Arg Ser Arg Ile Asn Val Ile Ser His Leu Leu Ser Thr Ile Pro
225                 230                 235                 240

Tyr Glu Lys Ile Asp Arg Pro Leu Pro Glu Ile Pro His Arg Pro Asp
                245                 250                 255

Ser Glu Ser Asp Tyr Val Arg Pro Pro Arg Asp Glu Phe Arg Tyr Val
            260                 265                 270

Pro Asp Val Ala Ala His Leu Glu Glu Glu Arg Ile Lys Lys Glu Glu
        275                 280                 285

Lys Ala Lys Lys Ala Lys Lys Pro Ala Lys Ala Ala Gly Lys Asn Ser
    290                 295                 300

Asp Lys Gln Lys Ser Ser Gly Gly Lys Gly Lys Lys Lys Ser Lys Lys
305                 310                 315                 320
```

<210> 811
<211> 1299
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1276)
<223> RXN01809

<400> 811
acaacacgac agttgtaact agtggtttca acaccattat cggtatgact cgtggcgact 60

cgtatctctc tgatgatctc gatgacctgg gttaaacccg atg aac gag cag gaa 115
Met Asn Glu Gln Glu
1 5

cga gaa gcc tta gag gat gct gcc ctt gag gaa gct gcc tta gcc gat 163
Arg Glu Ala Leu Glu Asp Ala Ala Leu Glu Glu Ala Ala Leu Ala Asp
10 15 20

gaa tta gct gca tta gag gct gaa gct ggc gta caa ggg tca gtc gag 211
Glu Leu Ala Ala Leu Glu Ala Glu Ala Gly Val Gln Gly Ser Val Glu
25 30 35

cct tat gac tat gca gca gac ctt gat gat gag gac gag ttt gat gag 259
Pro Tyr Asp Tyr Ala Ala Asp Leu Asp Asp Glu Asp Glu Phe Asp Glu
40 45 50

gac cct ttt gct cag gat gaa ccc cgt gac gct ggt ccg cta ggt gag 307
Asp Pro Phe Ala Gln Asp Glu Pro Arg Asp Ala Gly Pro Leu Gly Glu
55 60 65

ttg agc agt gat aac cat gtc tct gag gct gtt gct gaa gac act ggg 355
Leu Ser Ser Asp Asn His Val Ser Glu Ala Val Ala Glu Asp Thr Gly
70 75 80 85

aca agt aca gaa gag tct gca caa gag ggc agt cac gaa gag tcg gta 403
Thr Ser Thr Glu Glu Ser Ala Gln Glu Gly Ser His Glu Glu Ser Val
90 95 100

gac aat ccc cgt gat ttc acc ggc act gcg aca gcg gtg cga tct ttt 451
Asp Asn Pro Arg Asp Phe Thr Gly Thr Ala Thr Ala Val Arg Ser Phe
105 110 115

cga ccc aga ctt ccc gta ccc aat gca ctg cga cca gga cca ccc atc 499
Arg Pro Arg Leu Pro Val Pro Asn Ala Leu Arg Pro Gly Pro Pro Ile
120 125 130

cga aca caa ccg gca gtg aac acc gac ata gat gat ggc ggg caa gag 547
Arg Thr Gln Pro Ala Val Asn Thr Asp Ile Asp Asp Gly Gly Gln Glu
135 140 145

aat aca gct ggc gcg act gcc gca gat gtg ggg gcg gga gtg ttt ttt 595
Asn Thr Ala Gly Ala Thr Ala Ala Asp Val Gly Ala Gly Val Phe Phe
150 155 160 165

```
ggt acg cat ttt gag ctg gct ttt ggg cag gtt gat gtt cac cgc cac   643
Gly Thr His Phe Glu Leu Ala Phe Gly Gln Val Asp Val His Arg His
                170                 175                 180

ata agg cat gag cag gct atg cga gat gga cac cag gat ctc agc gtc   691
Ile Arg His Glu Gln Ala Met Arg Asp Gly His Gln Asp Leu Ser Val
            185                 190                 195

ttt gtc ggt gct gat ggg gcg atc atg ctg gaa gaa ctt aaa aat cgt   739
Phe Val Gly Ala Asp Gly Ala Ile Met Leu Glu Glu Leu Lys Asn Arg
        200                 205                 210

tac cag cgc cca ccg gag aac gag ccc cat gat gat gat gtc acc gaa   787
Tyr Gln Arg Pro Pro Glu Asn Glu Pro His Asp Asp Asp Val Thr Glu
    215                 220                 225

atg ata aag acc acc gag gaa aca gag aag gag aac gta gag atg gat   835
Met Ile Lys Thr Thr Glu Glu Thr Glu Lys Glu Asn Val Glu Met Asp
230                 235                 240                 245

cag gat ata gct gta gta gac aac gtt gat gaa cag gtt gtg gtg aca   883
Gln Asp Ile Ala Val Val Asp Asn Val Asp Glu Gln Val Val Val Thr
                250                 255                 260

cct gct cat gac gct gac agc gta gcg gtt gtt gct gaa cag gtc gtt   931
Pro Ala His Asp Ala Asp Ser Val Ala Val Val Ala Glu Gln Val Val
            265                 270                 275

gcg tca gaa cca acg cca gag ccg gta ccc aag gtt gag cac gta gag   979
Ala Ser Glu Pro Thr Pro Glu Pro Val Pro Lys Val Glu His Val Glu
        280                 285                 290

atg agt gtc gat cta gcg ggt gag act att aca ccg att gat cag gca  1027
Met Ser Val Asp Leu Ala Gly Glu Thr Ile Thr Pro Ile Asp Gln Ala
    295                 300                 305

att cgg tct ttt atg cag ctc aac ggt att gag cac agc gtg gtg ttg  1075
Ile Arg Ser Phe Met Gln Leu Asn Gly Ile Glu His Ser Val Val Leu
310                 315                 320                 325

cga cgc ttg ggg ctg atg act cag gtg gca cat aat aag gaa ctt gat  1123
Arg Arg Leu Gly Leu Met Thr Gln Val Ala His Asn Lys Glu Leu Asp
                330                 335                 340

gag gtc tac gct aag gca ctt gcc gag ggt gaa tcc cat gct cag cag  1171
Glu Val Tyr Ala Lys Ala Leu Ala Glu Gly Glu Ser His Ala Gln Gln
            345                 350                 355

cag cat gaa tta gaa gca gaa aat gaa cgg ctt aaa aaa gaa gtt gat  1219
Gln His Glu Leu Glu Ala Glu Asn Glu Arg Leu Lys Lys Glu Val Asp
        360                 365                 370

gcg ctc gct gca gag ctt agt gct gcg ttg atg ggc gag ggt ggt ggt  1267
Ala Leu Ala Ala Glu Leu Ser Ala Ala Leu Met Gly Glu Gly Gly Gly
    375                 380                 385

gat cat gac taaggccgtg acaccaattg tgg                           1299
Asp His Asp
390
```

<210> 812
<211> 392
<212> PRT
<213> Corynebacterium glutamicum

<400> 812
Met Asn Glu Gln Glu Arg Glu Ala Leu Glu Asp Ala Ala Leu Glu Glu
1 5 10 15

Ala Ala Leu Ala Asp Glu Leu Ala Ala Leu Glu Ala Glu Ala Gly Val
20 25 30

Gln Gly Ser Val Glu Pro Tyr Asp Tyr Ala Ala Asp Leu Asp Asp Glu
35 40 45

Asp Glu Phe Asp Glu Asp Pro Phe Ala Gln Asp Glu Pro Arg Asp Ala
50 55 60

Gly Pro Leu Gly Glu Leu Ser Ser Asp Asn His Val Ser Glu Ala Val
65 70 75 80

Ala Glu Asp Thr Gly Thr Ser Thr Glu Glu Ser Ala Gln Glu Gly Ser
85 90 95

His Glu Glu Ser Val Asp Asn Pro Arg Asp Phe Thr Gly Thr Ala Thr
100 105 110

Ala Val Arg Ser Phe Arg Pro Arg Leu Pro Val Pro Asn Ala Leu Arg
115 120 125

Pro Gly Pro Pro Ile Arg Thr Gln Pro Ala Val Asn Thr Asp Ile Asp
130 135 140

Asp Gly Gly Gln Glu Asn Thr Ala Gly Ala Thr Ala Ala Asp Val Gly
145 150 155 160

Ala Gly Val Phe Phe Gly Thr His Phe Glu Leu Ala Phe Gly Gln Val
165 170 175

Asp Val His Arg His Ile Arg His Glu Gln Ala Met Arg Asp Gly His
180 185 190

Gln Asp Leu Ser Val Phe Val Gly Ala Asp Gly Ala Ile Met Leu Glu
195 200 205

Glu Leu Lys Asn Arg Tyr Gln Arg Pro Pro Glu Asn Glu Pro His Asp
210 215 220

Asp Asp Val Thr Glu Met Ile Lys Thr Thr Glu Glu Thr Glu Lys Glu
225 230 235 240

Asn Val Glu Met Asp Gln Asp Ile Ala Val Val Asp Asn Val Asp Glu
245 250 255

Gln Val Val Val Thr Pro Ala His Asp Ala Asp Ser Val Ala Val Val
260 265 270

Ala Glu Gln Val Val Ala Ser Glu Pro Thr Pro Glu Pro Val Pro Lys
275 280 285

```
Val Glu His Val Glu Met Ser Val Asp Leu Ala Gly Glu Thr Ile Thr
    290                 295                 300

Pro Ile Asp Gln Ala Ile Arg Ser Phe Met Gln Leu Asn Gly Ile Glu
305                 310                 315                 320

His Ser Val Val Leu Arg Arg Leu Gly Leu Met Thr Gln Val Ala His
                325                 330                 335

Asn Lys Glu Leu Asp Glu Val Tyr Ala Lys Ala Leu Ala Glu Gly Glu
            340                 345                 350

Ser His Ala Gln Gln Gln His Glu Leu Glu Ala Glu Asn Glu Arg Leu
        355                 360                 365

Lys Lys Glu Val Asp Ala Leu Ala Ala Glu Leu Ser Ala Ala Leu Met
    370                 375                 380

Gly Glu Gly Gly Gly Asp His Asp
385                 390


<210> 813
<211> 586
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(586)
<223> FRXA01062

<400> 813
acaacacgac agttgtaact agtggtttca acaccattat cggtatgact cgtggcgact 60

cgtatctctc tgatgatctc gatgacctgg gttaaacccg atg aac gag cag gaa   115
                                            Met Asn Glu Gln Glu
                                              1               5

cga gaa gcc tta gag gat gct gcc ctt gag gaa gct gcc tta gcc gat   163
Arg Glu Ala Leu Glu Asp Ala Ala Leu Glu Glu Ala Ala Leu Ala Asp
                10                  15                  20

gaa tta gct gca tta gag gct gaa gct ggc gta caa ggg tca gtc gag   211
Glu Leu Ala Ala Leu Glu Ala Glu Ala Gly Val Gln Gly Ser Val Glu
            25                  30                  35

cct tat gac tat gca gca gac ctt gat gat gag gac gag ttt gat gag   259
Pro Tyr Asp Tyr Ala Ala Asp Leu Asp Asp Glu Asp Glu Phe Asp Glu
        40                  45                  50

gac cct ttt gct cag gat gaa ccc cgt gac gct ggt ccg cta ggt gag   307
Asp Pro Phe Ala Gln Asp Glu Pro Arg Asp Ala Gly Pro Leu Gly Glu
    55                  60                  65

ttg agc agt gat aac cat gtc tct gag gct gtt gct gaa gac act ggg   355
Leu Ser Ser Asp Asn His Val Ser Glu Ala Val Ala Glu Asp Thr Gly
70                  75                  80                  85

aca agt aca gaa gag tct gca caa gag ggc agt cac gaa gag tcg gta   403
Thr Ser Thr Glu Glu Ser Ala Gln Glu Gly Ser His Glu Glu Ser Val
```

```
                90                  95                 100

gac aat ccc cgt gat ttc acc ggc act gcg aca gcg gtg cga tct ttt   451
Asp Asn Pro Arg Asp Phe Thr Gly Thr Ala Thr Ala Val Arg Ser Phe
            105                 110                 115

cga ccc aga ctt ccc gta ccc aat gca ctg cga cca gga cca ccc atc   499
Arg Pro Arg Leu Pro Val Pro Asn Ala Leu Arg Pro Gly Pro Pro Ile
        120                 125                 130

cga aca caa ccg gca gtg aac acc gac ata tat gat ggc ggg caa gag   547
Arg Thr Gln Pro Ala Val Asn Thr Asp Ile Tyr Asp Gly Gly Gln Glu
    135                 140                 145

aat aca gct ggc gcg act gcc gca gat gtg ggg gcg gga               586
Asn Thr Ala Gly Ala Thr Ala Ala Asp Val Gly Ala Gly
150                 155                 160
```

<210> 814
<211> 162
<212> PRT
<213> Corynebacterium glutamicum

<400> 814

```
Met Asn Glu Gln Glu Arg Glu Ala Leu Glu Asp Ala Ala Leu Glu Glu
  1               5                  10                  15

Ala Ala Leu Ala Asp Glu Leu Ala Ala Leu Glu Ala Glu Ala Gly Val
             20                  25                  30

Gln Gly Ser Val Glu Pro Tyr Asp Tyr Ala Ala Asp Leu Asp Asp Glu
         35                  40                  45

Asp Glu Phe Asp Glu Asp Pro Phe Ala Gln Asp Glu Pro Arg Asp Ala
     50                  55                  60

Gly Pro Leu Gly Glu Leu Ser Ser Asp Asn His Val Ser Glu Ala Val
 65                  70                  75                  80

Ala Glu Asp Thr Gly Thr Ser Thr Glu Glu Ser Ala Gln Glu Gly Ser
                 85                  90                  95

His Glu Glu Ser Val Asp Asn Pro Arg Asp Phe Thr Gly Thr Ala Thr
            100                 105                 110

Ala Val Arg Ser Phe Arg Pro Arg Leu Pro Val Pro Asn Ala Leu Arg
        115                 120                 125

Pro Gly Pro Pro Ile Arg Thr Gln Pro Ala Val Asn Thr Asp Ile Tyr
    130                 135                 140

Asp Gly Gly Gln Glu Asn Thr Ala Gly Ala Thr Ala Ala Asp Val Gly
145                 150                 155                 160

Ala Gly
```

<210> 815
<211> 659

<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(636)
<223> FRXA01809

<400> 815

```
cac ata agg cat gag cag gct atg cga gat gga cac cag gat ctc agc   48
His Ile Arg His Glu Gln Ala Met Arg Asp Gly His Gln Asp Leu Ser
  1               5                  10                  15

gtc ttt gtc ggt gct gat ggg gcg atc atg ctg gaa gaa ctt aaa aat   96
Val Phe Val Gly Ala Asp Gly Ala Ile Met Leu Glu Glu Leu Lys Asn
             20                  25                  30

cgt tac cag cgc cca ccg gag aac gag ccc cat gat gat gat gtc acc   144
Arg Tyr Gln Arg Pro Pro Glu Asn Glu Pro His Asp Asp Asp Val Thr
         35                  40                  45

gaa atg ata aag acc acc gag gaa aca gag aag gag aac gta gag atg   192
Glu Met Ile Lys Thr Thr Glu Glu Thr Glu Lys Glu Asn Val Glu Met
     50                  55                  60

gat cag gat ata gct gta gta gac aac gtt gat gaa cag gtt gtg gtg   240
Asp Gln Asp Ile Ala Val Val Asp Asn Val Asp Glu Gln Val Val Val
 65                  70                  75                  80

aca cct gct cat gac gct gac agc gta gcg gtt gtt gct gaa cag gtc   288
Thr Pro Ala His Asp Ala Asp Ser Val Ala Val Val Ala Glu Gln Val
                 85                  90                  95

gtt gcg tca gaa cca acg cca gag ccg gta ccc aag gtt gag cac gta   336
Val Ala Ser Glu Pro Thr Pro Glu Pro Val Pro Lys Val Glu His Val
            100                 105                 110

gag atg agt gtc gat cta gcg ggt gag act att aca ccg att gat cag   384
Glu Met Ser Val Asp Leu Ala Gly Glu Thr Ile Thr Pro Ile Asp Gln
        115                 120                 125

gca att cgg tct ttt atg cag ctc aac ggt att gag cac agc gtg gtg   432
Ala Ile Arg Ser Phe Met Gln Leu Asn Gly Ile Glu His Ser Val Val
    130                 135                 140

ttg cga cgc ttg ggg ctg atg act cag gtg gca cat aat aag gaa ctt   480
Leu Arg Arg Leu Gly Leu Met Thr Gln Val Ala His Asn Lys Glu Leu
145                 150                 155                 160

gat gag gtc tac gct aag gca ctt gcc gag ggt gaa tcc cat gct cag   528
Asp Glu Val Tyr Ala Lys Ala Leu Ala Glu Gly Glu Ser His Ala Gln
                165                 170                 175

cag cag cat gaa tta gaa gca gaa aat gaa cgg ctt aaa aaa gaa gtt   576
Gln Gln His Glu Leu Glu Ala Glu Asn Glu Arg Leu Lys Lys Glu Val
            180                 185                 190

gat gcg ctc gct gca gag ctt agt gct gcg ttg atg ggc gag ggt ggt   624
Asp Ala Leu Ala Ala Glu Leu Ser Ala Ala Leu Met Gly Glu Gly Gly
        195                 200                 205
```

ggt gat cat gac taaggccgtg acaccaattg tgg 659
Gly Asp His Asp
210

<210> 816
<211> 212
<212> PRT
<213> Corynebacterium glutamicum

<400> 816
His Ile Arg His Glu Gln Ala Met Arg Asp Gly His Gln Asp Leu Ser
1 5 10 15

Val Phe Val Gly Ala Asp Gly Ala Ile Met Leu Glu Glu Leu Lys Asn
20 25 30

Arg Tyr Gln Arg Pro Pro Glu Asn Glu Pro His Asp Asp Asp Val Thr
35 40 45

Glu Met Ile Lys Thr Thr Glu Glu Thr Glu Lys Glu Asn Val Glu Met
50 55 60

Asp Gln Asp Ile Ala Val Val Asp Asn Val Asp Glu Gln Val Val Val
65 70 75 80

Thr Pro Ala His Asp Ala Asp Ser Val Ala Val Val Ala Glu Gln Val
85 90 95

Val Ala Ser Glu Pro Thr Pro Glu Pro Val Pro Lys Val Glu His Val
100 105 110

Glu Met Ser Val Asp Leu Ala Gly Glu Thr Ile Thr Pro Ile Asp Gln
115 120 125

Ala Ile Arg Ser Phe Met Gln Leu Asn Gly Ile Glu His Ser Val Val
130 135 140

Leu Arg Arg Leu Gly Leu Met Thr Gln Val Ala His Asn Lys Glu Leu
145 150 155 160

Asp Glu Val Tyr Ala Lys Ala Leu Ala Glu Gly Glu Ser His Ala Gln
165 170 175

Gln Gln His Glu Leu Glu Ala Glu Asn Glu Arg Leu Lys Lys Glu Val
180 185 190

Asp Ala Leu Ala Ala Glu Leu Ser Ala Ala Leu Met Gly Glu Gly Gly
195 200 205

Gly Asp His Asp
210

<210> 817
<211> 804
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS

<222> (101)..(781)
<223> RXN01811

<400> 817
gaaggagaag agacattgtc tcaagaagag ctgacattag tcgcattgaa ttcttatgaa 60

aaaggagagt tgccaaagaa gaatatcatt atttgaaaac gtg ttt gaa ttt gat 115
Val Phe Glu Phe Asp
1 5

gat acc ttg gca aaa gat ata caa gta gac cgt acg tcc atg caa gta 163
Asp Thr Leu Ala Lys Asp Ile Gln Val Asp Arg Thr Ser Met Gln Val
10 15 20

ttc gaa gct tca gaa acc gtc aaa gaa gcg ata aaa gct tcg att gaa 211
Phe Glu Ala Ser Glu Thr Val Lys Glu Ala Ile Lys Ala Ser Ile Glu
25 30 35

caa gga cat act cgc tat ccg gtt atc tta gaa tca aaa gac aat gtt 259
Gln Gly His Thr Arg Tyr Pro Val Ile Leu Glu Ser Lys Asp Asn Val
40 45 50

tta ggt tat gtc acc ttg cca gat ttg atc aag caa tct tat aaa gat 307
Leu Gly Tyr Val Thr Leu Pro Asp Leu Ile Lys Gln Ser Tyr Lys Asp
55 60 65

gac cag ctg aca gta gaa cag ttg att gaa gag ccg atc gta aca act 355
Asp Gln Leu Thr Val Glu Gln Leu Ile Glu Glu Pro Ile Val Thr Thr
70 75 80 85

gaa acg atc cct ata aaa aaa tta ttg acg atc atg cga aaa aag gga 403
Glu Thr Ile Pro Ile Lys Lys Leu Leu Thr Ile Met Arg Lys Lys Gly
90 95 100

aag cat att gct atc tta aaa gat gaa tac gga ggg aca agc ggc tta 451
Lys His Ile Ala Ile Leu Lys Asp Glu Tyr Gly Gly Thr Ser Gly Leu
105 110 115

gtg acg att gaa gat att tta gaa gaa atc gtc ggg gaa atc cga gat 499
Val Thr Ile Glu Asp Ile Leu Glu Glu Ile Val Gly Glu Ile Arg Asp
120 125 130

gag aca gat ttg gac gaa gca ttg ata gcg gaa cag tca gat ggc tct 547
Glu Thr Asp Leu Asp Glu Ala Leu Ile Ala Glu Gln Ser Asp Gly Ser
135 140 145

tat atc atc tcc ggc aaa cta aca tta gat gat ttc cag cgt tat ttt 595
Tyr Ile Ile Ser Gly Lys Leu Thr Leu Asp Asp Phe Gln Arg Tyr Phe
150 155 160 165

cat gta gag att cca gag ttt gaa gaa acg aat ttt act aca ctt gcg 643
His Val Glu Ile Pro Glu Phe Glu Glu Thr Asn Phe Thr Thr Leu Ala
170 175 180

ggc ttt gct tct agc cga tat aaa gaa ata aaa gca gga aca atc att 691
Gly Phe Ala Ser Ser Arg Tyr Lys Glu Ile Lys Ala Gly Thr Ile Ile
185 190 195

gag att gca tca ttc cgt ttc acg gta tta gaa tac cag cat gca cat 739
Glu Ile Ala Ser Phe Arg Phe Thr Val Leu Glu Tyr Gln His Ala His
200 205 210

```
atc gat tat ttc aaa gta gag tcc acg gaa aga aaa aca gaa           781
Ile Asp Tyr Phe Lys Val Glu Ser Thr Glu Arg Lys Thr Glu
    215                 220                 225

taaaagaaaa aaggctgtga cat                                        804


<210> 818
<211> 227
<212> PRT
<213> Corynebacterium glutamicum

<400> 818
Val Phe Glu Phe Asp Asp Thr Leu Ala Lys Asp Ile Gln Val Asp Arg
  1               5                  10                  15

Thr Ser Met Gln Val Phe Glu Ala Ser Glu Thr Val Lys Glu Ala Ile
             20                  25                  30

Lys Ala Ser Ile Glu Gln Gly His Thr Arg Tyr Pro Val Ile Leu Glu
         35                  40                  45

Ser Lys Asp Asn Val Leu Gly Tyr Val Thr Leu Pro Asp Leu Ile Lys
     50                  55                  60

Gln Ser Tyr Lys Asp Asp Gln Leu Thr Val Glu Gln Leu Ile Glu Glu
 65                  70                  75                  80

Pro Ile Val Thr Thr Glu Thr Ile Pro Ile Lys Lys Leu Leu Thr Ile
                 85                  90                  95

Met Arg Lys Lys Gly Lys His Ile Ala Ile Leu Lys Asp Glu Tyr Gly
            100                 105                 110

Gly Thr Ser Gly Leu Val Thr Ile Glu Asp Ile Leu Glu Glu Ile Val
        115                 120                 125

Gly Glu Ile Arg Asp Glu Thr Asp Leu Asp Glu Ala Leu Ile Ala Glu
    130                 135                 140

Gln Ser Asp Gly Ser Tyr Ile Ile Ser Gly Lys Leu Thr Leu Asp Asp
145                 150                 155                 160

Phe Gln Arg Tyr Phe His Val Glu Ile Pro Glu Phe Glu Glu Thr Asn
                165                 170                 175

Phe Thr Thr Leu Ala Gly Phe Ala Ser Ser Arg Tyr Lys Glu Ile Lys
            180                 185                 190

Ala Gly Thr Ile Ile Glu Ile Ala Ser Phe Arg Phe Thr Val Leu Glu
        195                 200                 205

Tyr Gln His Ala His Ile Asp Tyr Phe Lys Val Glu Ser Thr Glu Arg
    210                 215                 220

Lys Thr Glu
225


<210> 819
```

<211> 789
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(766)
<223> RXN01813

<400> 819
gcgagaattc aagaaaacaa aacagatcaa agtaaggcaa caagtgagca acaaagttca 60

gaatccgaac caaggtggaa gcaagaactt cctctgggca atg gtg gcg atc gtc 115
Met Val Ala Ile Val
1 5

gtc gtt gca atc gtc gtc gtc ggc ttc atc gtc atc caa ggc cag ggc 163
Val Val Ala Ile Val Val Val Gly Phe Ile Val Ile Gln Gly Gln Gly
10 15 20

tca aaa gca gcc aag ctt ggt gac cgc gac tac gaa gac acc tct ttg 211
Ser Lys Ala Ala Lys Leu Gly Asp Arg Asp Tyr Glu Asp Thr Ser Leu
25 30 35

gca atg gaa gta ggc tcc gac tcc atc acg ctg acc tcc gca aac acc 259
Ala Met Glu Val Gly Ser Asp Ser Ile Thr Leu Thr Ser Ala Asn Thr
40 45 50

tcc gcc gac gca aag tcc gtg cag ctt ttt gaa gac ttc tcc tgc tct 307
Ser Ala Asp Ala Lys Ser Val Gln Leu Phe Glu Asp Phe Ser Cys Ser
55 60 65

cac tgc tcc gag ctc tcc ctc gcc acc gac gct gac atg aag act cag 355
His Cys Ser Glu Leu Ser Leu Ala Thr Asp Ala Asp Met Lys Thr Gln
70 75 80 85

atc gaa gac ggc aac ctg gtc gtc gaa atc aag cca ctg aac ttc ctt 403
Ile Glu Asp Gly Asn Leu Val Val Glu Ile Lys Pro Leu Asn Phe Leu
90 95 100

gac cgc gaa aac atc gac ggc cac tcc acc cac gca ttg gca gca gcc 451
Asp Arg Glu Asn Ile Asp Gly His Ser Thr His Ala Leu Ala Ala Ala
105 110 115

ctt gca gtg gca gac tcc aac gac gca acc ctc tac tgg aac ttc cgc 499
Leu Ala Val Ala Asp Ser Asn Asp Ala Thr Leu Tyr Trp Asn Phe Arg
120 125 130

gca ttc ctc atg gaa gat cag tcc gag atc tac aac cag tgg tcc gat 547
Ala Phe Leu Met Glu Asp Gln Ser Glu Ile Tyr Asn Gln Trp Ser Asp
135 140 145

gat gac ttc gca gac ggc gtt gaa gcc ctt ggc gca gac tcc tcc gta 595
Asp Asp Phe Ala Asp Gly Val Glu Ala Leu Gly Ala Asp Ser Ser Val
150 155 160 165

gta gac gca atc cga aac ggc gac aac atc cag cgc gca tac gac ctg 643
Val Asp Ala Ile Arg Asn Gly Asp Asn Ile Gln Arg Ala Tyr Asp Leu
170 175 180

gca acc gca aac ggt gaa gaa ctc act gaa gaa acc ggc agc ctg tcc 691

```
Ala Thr Ala Asn Gly Glu Glu Leu Thr Glu Glu Thr Gly Ser Leu Ser
            185                 190                 195

tca cca cgc gtc ctc cag gac ggc aag gat gtt gaa ggc aac atc tcc   739
Ser Pro Arg Val Leu Gln Asp Gly Lys Asp Val Glu Gly Asn Ile Ser
        200                 205                 210

gac tgg atc acc act gtt cta gct tct taaagaactg atctagaagg         786
Asp Trp Ile Thr Thr Val Leu Ala Ser
    215                 220

aaa                                                               789


<210> 820
<211> 222
<212> PRT
<213> Corynebacterium glutamicum

<400> 820
Met Val Ala Ile Val Val Val Ala Ile Val Val Val Gly Phe Ile Val
  1               5                  10                  15

Ile Gln Gly Gln Gly Ser Lys Ala Ala Lys Leu Gly Asp Arg Asp Tyr
             20                  25                  30

Glu Asp Thr Ser Leu Ala Met Glu Val Gly Ser Asp Ser Ile Thr Leu
         35                  40                  45

Thr Ser Ala Asn Thr Ser Ala Asp Ala Lys Ser Val Gln Leu Phe Glu
     50                  55                  60

Asp Phe Ser Cys Ser His Cys Ser Glu Leu Ser Leu Ala Thr Asp Ala
 65                  70                  75                  80

Asp Met Lys Thr Gln Ile Glu Asp Gly Asn Leu Val Val Glu Ile Lys
                 85                  90                  95

Pro Leu Asn Phe Leu Asp Arg Glu Asn Ile Asp Gly His Ser Thr His
            100                 105                 110

Ala Leu Ala Ala Ala Leu Ala Val Ala Asp Ser Asn Asp Ala Thr Leu
        115                 120                 125

Tyr Trp Asn Phe Arg Ala Phe Leu Met Glu Asp Gln Ser Glu Ile Tyr
    130                 135                 140

Asn Gln Trp Ser Asp Asp Asp Phe Ala Asp Gly Val Glu Ala Leu Gly
145                 150                 155                 160

Ala Asp Ser Ser Val Val Asp Ala Ile Arg Asn Gly Asp Asn Ile Gln
                165                 170                 175

Arg Ala Tyr Asp Leu Ala Thr Ala Asn Gly Glu Glu Leu Thr Glu Glu
            180                 185                 190

Thr Gly Ser Leu Ser Ser Pro Arg Val Leu Gln Asp Gly Lys Asp Val
        195                 200                 205

Glu Gly Asn Ile Ser Asp Trp Ile Thr Thr Val Leu Ala Ser
    210                 215                 220
```

<210> 821
<211> 730
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(730)
<223> FRXA01813

<400> 821
gcgagaattc aagaaaacaa aacagatcaa agtaaggcaa caagtgagca acaaagttca 60

gaatccgaac caaggtggaa gcaagaactt cctctgggca atg gtg gcg atc gtc 115
Met Val Ala Ile Val
1 5

gtc gtt gca atc gtc gtc gtc ggc ttc atc gtc atc caa ggc cag ggc 163
Val Val Ala Ile Val Val Val Gly Phe Ile Val Ile Gln Gly Gln Gly
10 15 20

tca aaa gca gcc aag ctt ggt gac cgc gac tac gaa gac acc tct ttg 211
Ser Lys Ala Ala Lys Leu Gly Asp Arg Asp Tyr Glu Asp Thr Ser Leu
25 30 35

gca atg gaa gta ggc tcc gac tcc atc acg ctg acc tcc gca aac acc 259
Ala Met Glu Val Gly Ser Asp Ser Ile Thr Leu Thr Ser Ala Asn Thr
40 45 50

tcc gcc gac gca aag tcc gtg cag ctt ttt gaa gac ttc tcc tgc tct 307
Ser Ala Asp Ala Lys Ser Val Gln Leu Phe Glu Asp Phe Ser Cys Ser
55 60 65

cac tgc tcc gag ctc tcc ctc gcc acc gac gct gac atg aag act cag 355
His Cys Ser Glu Leu Ser Leu Ala Thr Asp Ala Asp Met Lys Thr Gln
70 75 80 85

atc gaa gac ggc aac ctg gtc gtc gaa atc aag cca ctg aac ttc ctt 403
Ile Glu Asp Gly Asn Leu Val Val Glu Ile Lys Pro Leu Asn Phe Leu
90 95 100

gac cgc gaa aac atc gac ggc cac tcc acc cac gca ttg gca gca gcc 451
Asp Arg Glu Asn Ile Asp Gly His Ser Thr His Ala Leu Ala Ala Ala
105 110 115

ctt gca gtg gca gac tcc aac gac gca acc ctc tac tgg aac ttc cgc 499
Leu Ala Val Ala Asp Ser Asn Asp Ala Thr Leu Tyr Trp Asn Phe Arg
120 125 130

gca ttc ctc atg gaa gat cag tcc gag atc tac aac cag tgg tcc gat 547
Ala Phe Leu Met Glu Asp Gln Ser Glu Ile Tyr Asn Gln Trp Ser Asp
135 140 145

gat gac ttc gca gac ggc gtt gaa gcc ctt ggc gca gac tcc tcc gta 595
Asp Asp Phe Ala Asp Gly Val Glu Ala Leu Gly Ala Asp Ser Ser Val
150 155 160 165

gta gac gca atc cga acg gcg aca aca tcc agc gcg cat acg acc tgg 643
Val Asp Ala Ile Arg Thr Ala Thr Thr Ser Ser Ala His Thr Thr Trp

```
                170                 175                 180

caa ccg caa acg gtg aag aac tca ctg aag aaa ccg gca gcc tgt tct   691
Gln Pro Gln Thr Val Lys Asn Ser Leu Lys Lys Pro Ala Ala Cys Ser
            185                 190                 195

tac cac gcg ttc ttc aag acg gca agg atg ttg aag gca               730
Tyr His Ala Phe Phe Lys Thr Ala Arg Met Leu Lys Ala
        200                 205                 210


<210> 822
<211> 210
<212> PRT
<213> Corynebacterium glutamicum

<400> 822
Met Val Ala Ile Val Val Val Ala Ile Val Val Val Gly Phe Ile Val
  1               5                  10                  15

Ile Gln Gly Gln Gly Ser Lys Ala Ala Lys Leu Gly Asp Arg Asp Tyr
             20                  25                  30

Glu Asp Thr Ser Leu Ala Met Glu Val Gly Ser Asp Ser Ile Thr Leu
         35                  40                  45

Thr Ser Ala Asn Thr Ser Ala Asp Ala Lys Ser Val Gln Leu Phe Glu
     50                  55                  60

Asp Phe Ser Cys Ser His Cys Ser Glu Leu Ser Leu Ala Thr Asp Ala
 65                  70                  75                  80

Asp Met Lys Thr Gln Ile Glu Asp Gly Asn Leu Val Val Glu Ile Lys
                 85                  90                  95

Pro Leu Asn Phe Leu Asp Arg Glu Asn Ile Asp Gly His Ser Thr His
            100                 105                 110

Ala Leu Ala Ala Ala Leu Ala Val Ala Asp Ser Asn Asp Ala Thr Leu
        115                 120                 125

Tyr Trp Asn Phe Arg Ala Phe Leu Met Glu Asp Gln Ser Glu Ile Tyr
    130                 135                 140

Asn Gln Trp Ser Asp Asp Asp Phe Ala Asp Gly Val Glu Ala Leu Gly
145                 150                 155                 160

Ala Asp Ser Ser Val Val Asp Ala Ile Arg Thr Ala Thr Thr Ser Ser
                165                 170                 175

Ala His Thr Thr Trp Gln Pro Gln Thr Val Lys Asn Ser Leu Lys Lys
            180                 185                 190

Pro Ala Ala Cys Ser Tyr His Ala Phe Phe Lys Thr Ala Arg Met Leu
        195                 200                 205

Lys Ala
    210


<210> 823
```

<211> 915
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(892)
<223> RXN01815

<400> 823
gaatgaaaag aagtggtggc cgatgcttgg ctatctcagc ctgactttta cacttggata 60

ttctgctgtt tttctcggga tgcggctcta gaattgtaga atg aat cgt tca aca 115
Met Asn Arg Ser Thr
1 5

att tcc cca gtt gaa gcc cgc cag caa ttc cgc gca ggc ctt atc caa 163
Ile Ser Pro Val Glu Ala Arg Gln Gln Phe Arg Ala Gly Leu Ile Gln
10 15 20

ccc acc tcc ggc tgg tcc gcg ggt ttt gcc caa gcc aac ctc att tcc 211
Pro Thr Ser Gly Trp Ser Ala Gly Phe Ala Gln Ala Asn Leu Ile Ser
25 30 35

atg ccc cag gat ctg gct tat gat ttc ctg ctt ttt gct caa cgc aac 259
Met Pro Gln Asp Leu Ala Tyr Asp Phe Leu Leu Phe Ala Gln Arg Asn
40 45 50

ccc aag ccc tgc ccc atc ttg gaa gta tta aat gct ggc gaa acc ttc 307
Pro Lys Pro Cys Pro Ile Leu Glu Val Leu Asn Ala Gly Glu Thr Phe
55 60 65

ggc gga att ttc ggc tca aac gcc acc gaa gca gac atc cgc acc gac 355
Gly Gly Ile Phe Gly Ser Asn Ala Thr Glu Ala Asp Ile Arg Thr Asp
70 75 80 85

gcg ccc caa tac cgc att tac gca cac ggc gaa ctt atc gat tcc ccc 403
Ala Pro Gln Tyr Arg Ile Tyr Ala His Gly Glu Leu Ile Asp Ser Pro
90 95 100

gcc agc gcc gtc gat tat tgg cgc gac gac ctc gtc agt ttc atc atc 451
Ala Ser Ala Val Asp Tyr Trp Arg Asp Asp Leu Val Ser Phe Ile Ile
105 110 115

ggc tgc tcc ttt act ttt gaa cat ccc atg gtc caa gca ggc gtt ccc 499
Gly Cys Ser Phe Thr Phe Glu His Pro Met Val Gln Ala Gly Val Pro
120 125 130

gtc cgc cac ctc gag gcc ggc cgc aac gtc ccc atg tat gaa acc tca 547
Val Arg His Leu Glu Ala Gly Arg Asn Val Pro Met Tyr Glu Thr Ser
135 140 145

ctt gcc tgc cga cca gcc ggt tcc cta tca gga aac ctc gtg gtg tca 595
Leu Ala Cys Arg Pro Ala Gly Ser Leu Ser Gly Asn Leu Val Val Ser
150 155 160 165

ctg cgc atg atc ccc gca tcc caa gtc gcg gat gcc gtc cgc att acc 643
Leu Arg Met Ile Pro Ala Ser Gln Val Ala Asp Ala Val Arg Ile Thr
170 175 180

tcc cgc tac ccc gcg gtt cac gga gca cca gtc cac atc ggc gat cct 691

```
Ser Arg Tyr Pro Ala Val His Gly Ala Pro Val His Ile Gly Asp Pro
            185                 190                 195

tca ctg atc gga atc gat gac atc aac aac cct gat ttc ggc gat gcc   739
Ser Leu Ile Gly Ile Asp Asp Ile Asn Asn Pro Asp Phe Gly Asp Ala
        200                 205                 210

ccg ctg tcc gaa cca agc gac gtc ccc gtg ttt tgg gcc tgc gga gtt   787
Pro Leu Ser Glu Pro Ser Asp Val Pro Val Phe Trp Ala Cys Gly Val
    215                 220                 225

acc cct caa gca atg gtc atg tcc tcc aag cca ccg ctg gcg atc act   835
Thr Pro Gln Ala Met Val Met Ser Ser Lys Pro Pro Leu Ala Ile Thr
230                 235                 240                 245

cac gca ccc gga cac atg ctg atc acc gac gcc cca gat ctg gga ttc   883
His Ala Pro Gly His Met Leu Ile Thr Asp Ala Pro Asp Leu Gly Phe
                250                 255                 260

cag gtt cct taaacctgga tccaccgatg tga                            915
Gln Val Pro
```

[illegible]

<210> 824
<211> 264
<212> PRT
<213> Corynebacterium glutamicum

<400> 824

```
Met Asn Arg Ser Thr Ile Ser Pro Val Glu Ala Arg Gln Gln Phe Arg
  1               5                  10                  15

Ala Gly Leu Ile Gln Pro Thr Ser Gly Trp Ser Ala Gly Phe Ala Gln
             20                  25                  30

Ala Asn Leu Ile Ser Met Pro Gln Asp Leu Ala Tyr Asp Phe Leu Leu
         35                  40                  45

Phe Ala Gln Arg Asn Pro Lys Pro Cys Pro Ile Leu Glu Val Leu Asn
     50                  55                  60

Ala Gly Glu Thr Phe Gly Gly Ile Phe Gly Ser Asn Ala Thr Glu Ala
 65                  70                  75                  80

Asp Ile Arg Thr Asp Ala Pro Gln Tyr Arg Ile Tyr Ala His Gly Glu
                 85                  90                  95

Leu Ile Asp Ser Pro Ala Ser Ala Val Asp Tyr Trp Arg Asp Asp Leu
            100                 105                 110

Val Ser Phe Ile Ile Gly Cys Ser Phe Thr Phe Glu His Pro Met Val
        115                 120                 125

Gln Ala Gly Val Pro Val Arg His Leu Glu Ala Gly Arg Asn Val Pro
    130                 135                 140

Met Tyr Glu Thr Ser Leu Ala Cys Arg Pro Ala Gly Ser Leu Ser Gly
145                 150                 155                 160

Asn Leu Val Val Ser Leu Arg Met Ile Pro Ala Ser Gln Val Ala Asp
```

```
                165                 170                 175

Ala Val Arg Ile Thr Ser Arg Tyr Pro Ala Val His Gly Ala Pro Val
            180                 185                 190

His Ile Gly Asp Pro Ser Leu Ile Gly Ile Asp Asp Ile Asn Asn Pro
        195                 200                 205

Asp Phe Gly Asp Ala Pro Leu Ser Glu Pro Ser Asp Val Pro Val Phe
    210                 215                 220

Trp Ala Cys Gly Val Thr Pro Gln Ala Met Val Met Ser Ser Lys Pro
225                 230                 235                 240

Pro Leu Ala Ile Thr His Ala Pro Gly His Met Leu Ile Thr Asp Ala
                245                 250                 255

Pro Asp Leu Gly Phe Gln Val Pro
            260
```

<210> 825
<211> 915
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(892)
<223> FRXA01815

<400> 825

```
gaatgaaaag aagtggtggc cgatgcttgg ctatctcagc ctgactttta cacttggata 60

ttctgctgtt tttctcggga tgcggctcta gaattgtaga atg aat cgt tca aca   115
                                            Met Asn Arg Ser Thr
                                              1               5

att tcc cca gtt gaa gcc cgc cag caa ttc cgc gca ggc ctt atc caa   163
Ile Ser Pro Val Glu Ala Arg Gln Gln Phe Arg Ala Gly Leu Ile Gln
                 10                  15                  20

ccc acc tcc ggc tgg tcc gcg ggt ttt gcc caa gcc aac ctc att tcc   211
Pro Thr Ser Gly Trp Ser Ala Gly Phe Ala Gln Ala Asn Leu Ile Ser
             25                  30                  35

atg ccc cag gat ctg gct tat gat ttc ctg ctt ttt gct caa cgc aac   259
Met Pro Gln Asp Leu Ala Tyr Asp Phe Leu Leu Phe Ala Gln Arg Asn
         40                  45                  50

ccc aag ccc tgc ccc atc ttg gaa gta tta aat gct ggc gaa acc ttc   307
Pro Lys Pro Cys Pro Ile Leu Glu Val Leu Asn Ala Gly Glu Thr Phe
     55                  60                  65

ggc gga att ttc ggc tca aac gcc acc gaa gca gac atc cgc acc gac   355
Gly Gly Ile Phe Gly Ser Asn Ala Thr Glu Ala Asp Ile Arg Thr Asp
 70                  75                  80                  85

gcg ccc caa tac cgc att tac gca cac ggc gaa ctt atc gat tcc ccc   403
Ala Pro Gln Tyr Arg Ile Tyr Ala His Gly Glu Leu Ile Asp Ser Pro
                 90                  95                 100
```

```
gcc agc gcc gtc gat tat tgg cgc gac gac ctc gtc agt ttc atc atc   451
Ala Ser Ala Val Asp Tyr Trp Arg Asp Asp Leu Val Ser Phe Ile Ile
            105                 110                 115

ggc tgc tcc ttt act ttt gaa cat ccc atg gtc caa gca ggc gtt ccc   499
Gly Cys Ser Phe Thr Phe Glu His Pro Met Val Gln Ala Gly Val Pro
        120                 125                 130

gtc cgc cac ctc gag gcc ggc cgc aac gtc ccc atg tat gaa acc tca   547
Val Arg His Leu Glu Ala Gly Arg Asn Val Pro Met Tyr Glu Thr Ser
    135                 140                 145

ctt gcc tgc cga cca gcc ggt tcc cta tca gga aac ctc gtg gtg tca   595
Leu Ala Cys Arg Pro Ala Gly Ser Leu Ser Gly Asn Leu Val Val Ser
150                 155                 160                 165

ctg cgc atg atc ccc gca tcc caa gtc gcg gat gcc gtc cgc att acc   643
Leu Arg Met Ile Pro Ala Ser Gln Val Ala Asp Ala Val Arg Ile Thr
                170                 175                 180

tcc cgc tac ccc gcg gtt cac gga gca cca gtc cac atc ggc gat cct   691
Ser Arg Tyr Pro Ala Val His Gly Ala Pro Val His Ile Gly Asp Pro
            185                 190                 195

tca ctg atc gga atc gat gac atc aac aac cct gat ttc ggc gat gcc   739
Ser Leu Ile Gly Ile Asp Asp Ile Asn Asn Pro Asp Phe Gly Asp Ala
        200                 205                 210

ccg ctg tcc gaa cca agc gac gtc ccc gtg ttt tgg gcc tgc gga gtt   787
Pro Leu Ser Glu Pro Ser Asp Val Pro Val Phe Trp Ala Cys Gly Val
    215                 220                 225

acc cct caa gca atg gtc atg tcc tcc aag cca ccg ctg gcg atc act   835
Thr Pro Gln Ala Met Val Met Ser Ser Lys Pro Pro Leu Ala Ile Thr
230                 235                 240                 245

cac gca ccc gga cac atg ctg atc acc gac gcc cca gat ctg gga ttc   883
His Ala Pro Gly His Met Leu Ile Thr Asp Ala Pro Asp Leu Gly Phe
                250                 255                 260

cag gtt cct taaacctgga tccaccgatg tga                            915
Gln Val Pro
```

<210> 826
<211> 264
<212> PRT
<213> Corynebacterium glutamicum

<400> 826

```
Met Asn Arg Ser Thr Ile Ser Pro Val Glu Ala Arg Gln Gln Phe Arg
  1               5                  10                  15

Ala Gly Leu Ile Gln Pro Thr Ser Gly Trp Ser Ala Gly Phe Ala Gln
             20                  25                  30

Ala Asn Leu Ile Ser Met Pro Gln Asp Leu Ala Tyr Asp Phe Leu Leu
         35                  40                  45
```

```
Phe Ala Gln Arg Asn Pro Lys Pro Cys Pro Ile Leu Glu Val Leu Asn
     50                  55                  60

Ala Gly Glu Thr Phe Gly Gly Ile Phe Gly Ser Asn Ala Thr Glu Ala
 65                  70                  75                  80

Asp Ile Arg Thr Asp Ala Pro Gln Tyr Arg Ile Tyr Ala His Gly Glu
                 85                  90                  95

Leu Ile Asp Ser Pro Ala Ser Ala Val Asp Tyr Trp Arg Asp Asp Leu
            100                 105                 110

Val Ser Phe Ile Ile Gly Cys Ser Phe Thr Phe Glu His Pro Met Val
        115                 120                 125

Gln Ala Gly Val Pro Val Arg His Leu Glu Ala Gly Arg Asn Val Pro
    130                 135                 140

Met Tyr Glu Thr Ser Leu Ala Cys Arg Pro Ala Gly Ser Leu Ser Gly
145                 150                 155                 160

Asn Leu Val Val Ser Leu Arg Met Ile Pro Ala Ser Gln Val Ala Asp
                165                 170                 175

Ala Val Arg Ile Thr Ser Arg Tyr Pro Ala Val His Gly Ala Pro Val
            180                 185                 190

His Ile Gly Asp Pro Ser Leu Ile Gly Ile Asp Asp Ile Asn Asn Pro
        195                 200                 205

Asp Phe Gly Asp Ala Pro Leu Ser Glu Pro Ser Asp Val Pro Val Phe
    210                 215                 220

Trp Ala Cys Gly Val Thr Pro Gln Ala Met Val Met Ser Ser Lys Pro
225                 230                 235                 240

Pro Leu Ala Ile Thr His Ala Pro Gly His Met Leu Ile Thr Asp Ala
                245                 250                 255

Pro Asp Leu Gly Phe Gln Val Pro
            260
```

<210> 827
<211> 393
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(370)
<223> RXN01825

<400> 827
gtcaaggtag ctggcccggc aactgatacg ttaagctcaa acaagataag taccagttgc 60

tggggttttt ccaagacaat aaattatgaa ggtgtgaaca atg cca aag gca aga 115
                                                Met Pro Lys Ala Arg
                                                  1   5

gta act aaa aac gag acc gca ccg gtt tca agc aac cca agc gca aac 163

Val Thr Lys Asn Glu Thr Ala Pro Val Ser Ser Asn Pro Ser Ala Asn
10 15 20

cgc acc ccg gtt aag atc aat tcc gcc gga acc cca atg tgg tac aag 211
Arg Thr Pro Val Lys Ile Asn Ser Ala Gly Thr Pro Met Trp Tyr Lys
25 30 35

gtc atc atg ttt gcc ttc atg atc gtc ggc cta gcc tgg ttg atc att 259
Val Ile Met Phe Ala Phe Met Ile Val Gly Leu Ala Trp Leu Ile Ile
40 45 50

aac tac ctc gtg ggc cca cag atc cca ttc atg gct gat ctt ggt gca 307
Asn Tyr Leu Val Gly Pro Gln Ile Pro Phe Met Ala Asp Leu Gly Ala
55 60 65

tgg aac tat ggc atc ggc ttc ggt ctg atg atc atc ggc cta ctc atg 355
Trp Asn Tyr Gly Ile Gly Phe Gly Leu Met Ile Ile Gly Leu Leu Met
70 75 80 85

acc atg ggt tgg cgt taatccttca aaaaagtgac tgc 393
Thr Met Gly Trp Arg
90

<210> 828
<211> 90
<212> PRT
<213> Corynebacterium glutamicum

<400> 828
Met Pro Lys Ala Arg Val Thr Lys Asn Glu Thr Ala Pro Val Ser Ser
1 5 10 15

Asn Pro Ser Ala Asn Arg Thr Pro Val Lys Ile Asn Ser Ala Gly Thr
20 25 30

Pro Met Trp Tyr Lys Val Ile Met Phe Ala Phe Met Ile Val Gly Leu
35 40 45

Ala Trp Leu Ile Ile Asn Tyr Leu Val Gly Pro Gln Ile Pro Phe Met
50 55 60

Ala Asp Leu Gly Ala Trp Asn Tyr Gly Ile Gly Phe Gly Leu Met Ile
65 70 75 80

Ile Gly Leu Leu Met Thr Met Gly Trp Arg
85 90

<210> 829
<211> 393
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(370)
<223> FRXA01825

<400> 829
gtcaaggtag ctggcccggc aactgatacg ttaagctcaa acaagataag taccagttgc 60

```
tggggttttt ccaagacaat aaattatgaa ggtgtgaaca atg cca aag gca aga   115
                                            Met Pro Lys Ala Arg
                                              1               5

gta act aaa aac gag acc gca ccg gtt tca agc aac cca agc gca aac   163
Val Thr Lys Asn Glu Thr Ala Pro Val Ser Ser Asn Pro Ser Ala Asn
                 10                  15                  20

cgc acc ccg gtt aag atc aat tcc gcc gga acc cca atg tgg tac aag   211
Arg Thr Pro Val Lys Ile Asn Ser Ala Gly Thr Pro Met Trp Tyr Lys
             25                  30                  35

gtc atc atg ttt gcc ttc atg atc gtc ggc cta gcc tgg ttg atc att   259
Val Ile Met Phe Ala Phe Met Ile Val Gly Leu Ala Trp Leu Ile Ile
         40                  45                  50

aac tac ctc gtg ggc cca cag atc cca ttc atg gct gat ctt ggt gca   307
Asn Tyr Leu Val Gly Pro Gln Ile Pro Phe Met Ala Asp Leu Gly Ala
     55                  60                  65

tgg aac tat ggc atc ggc ttc ggt ctg atg atc atc ggc cta ctc atg   355
Trp Asn Tyr Gly Ile Gly Phe Gly Leu Met Ile Ile Gly Leu Leu Met
 70                  75                  80                  85

acc atg ggt tgg cgt taatccttca aaaaagtgac tgc                    393
Thr Met Gly Trp Arg
                 90
```

<210> 830
<211> 90
<212> PRT
<213> Corynebacterium glutamicum

<400> 830

```
Met Pro Lys Ala Arg Val Thr Lys Asn Glu Thr Ala Pro Val Ser Ser
  1               5                  10                  15

Asn Pro Ser Ala Asn Arg Thr Pro Val Lys Ile Asn Ser Ala Gly Thr
             20                  25                  30

Pro Met Trp Tyr Lys Val Ile Met Phe Ala Phe Met Ile Val Gly Leu
         35                  40                  45

Ala Trp Leu Ile Ile Asn Tyr Leu Val Gly Pro Gln Ile Pro Phe Met
     50                  55                  60

Ala Asp Leu Gly Ala Trp Asn Tyr Gly Ile Gly Phe Gly Leu Met Ile
 65                  70                  75                  80

Ile Gly Leu Leu Met Thr Met Gly Trp Arg
                 85                  90
```

<210> 831
<211> 585
<212> DNA
<213> Corynebacterium glutamicum

<220>

<221> CDS
<222> (101)..(562)
<223> RXN01831

<400> 831
cctgtggata attggttgtt ggctgatggt gatgtcatta cggtgggtca ttccaatatc 60

gaagttcgta ttgttagtcc ctagagggag aggttgatca atg gat tct ctg gtc 115
Met Asp Ser Leu Val
1 5

ctt ctt ggg ctt cgc atc gct ttg ctt gtg gtg ttg tgg ttt ttc gtc 163
Leu Leu Gly Leu Arg Ile Ala Leu Leu Val Val Leu Trp Phe Phe Val
10 15 20

ttg atg gcg ctg cgc gct atg agg gca gat ttg aaa gtg acg ggt caa 211
Leu Met Ala Leu Arg Ala Met Arg Ala Asp Leu Lys Val Thr Gly Gln
25 30 35

gcg tcg aca agc agc tcc tcc gtc gcg gca ccg cag ggc ctt gcc cgg 259
Ala Ser Thr Ser Ser Ser Ser Val Ala Ala Pro Gln Gly Leu Ala Arg
40 45 50

gct ttt aat cgc tcc agc ccg cct cgt ctt ttg acg gtg gtc gag ggc 307
Ala Phe Asn Arg Ser Ser Pro Pro Arg Leu Leu Thr Val Val Glu Gly
55 60 65

ccg ttg gcg ggc tcc tcg att gag gtg tcg gag gat atg acg atg ggc 355
Pro Leu Ala Gly Ser Ser Ile Glu Val Ser Glu Asp Met Thr Met Gly
70 75 80 85

cgt agc cct gag tgc acg ttt gtg gtg ggc gat gat tac gcc tcc ggc 403
Arg Ser Pro Glu Cys Thr Phe Val Val Gly Asp Asp Tyr Ala Ser Gly
90 95 100

atg cat gcg cgg gtg ttt aag cgt ggt tcg gag tgg ttt gtg gag gat 451
Met His Ala Arg Val Phe Lys Arg Gly Ser Glu Trp Phe Val Glu Asp
105 110 115

ctg gat tcg cgc aac ggc act ttt gtc ggt ggt acg cgc att gat cag 499
Leu Asp Ser Arg Asn Gly Thr Phe Val Gly Gly Thr Arg Ile Asp Gln
120 125 130

cct gag cag att gcg gtg ggc acg gat atc cgt att ggt cgt aca gca 547
Pro Glu Gln Ile Ala Val Gly Thr Asp Ile Arg Ile Gly Arg Thr Ala
135 140 145

gtg agg ctt gtt ccc tgatgttgaa acttaaatat gcg 585
Val Arg Leu Val Pro
150

<210> 832
<211> 154
<212> PRT
<213> Corynebacterium glutamicum

<400> 832
Met Asp Ser Leu Val Leu Leu Gly Leu Arg Ile Ala Leu Leu Val Val
1 5 10 15

```
Leu Trp Phe Phe Val Leu Met Ala Leu Arg Ala Met Arg Ala Asp Leu
            20                  25                  30

Lys Val Thr Gly Gln Ala Ser Thr Ser Ser Ser Ser Val Ala Ala Pro
        35                  40                  45

Gln Gly Leu Ala Arg Ala Phe Asn Arg Ser Ser Pro Pro Arg Leu Leu
    50                  55                  60

Thr Val Val Glu Gly Pro Leu Ala Gly Ser Ser Ile Glu Val Ser Glu
65                  70                  75                  80

Asp Met Thr Met Gly Arg Ser Pro Glu Cys Thr Phe Val Val Gly Asp
                85                  90                  95

Asp Tyr Ala Ser Gly Met His Ala Arg Val Phe Lys Arg Gly Ser Glu
            100                 105                 110

Trp Phe Val Glu Asp Leu Asp Ser Arg Asn Gly Thr Phe Val Gly Gly
        115                 120                 125

Thr Arg Ile Asp Gln Pro Glu Gln Ile Ala Val Gly Thr Asp Ile Arg
    130                 135                 140

Ile Gly Arg Thr Ala Val Arg Leu Val Pro
145                 150


<210> 833
<211> 585
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(562)
<223> FRXA01831

<400> 833
cctgtggata attggttgtt ggctgatggt gatgtcatta cggtgggtca ttccaatatc 60

gaagttcgta ttgttagtcc ctagagggag aggttgatca atg gat tct ctg gtc   115
                                            Met Asp Ser Leu Val
                                              1               5

ctt ctt ggg ctt cgc atc gct ttg ctt gtg gtg ttg tgg ttt ttc gtc   163
Leu Leu Gly Leu Arg Ile Ala Leu Leu Val Val Leu Trp Phe Phe Val
                10                  15                  20

ttg atg gcg ctg cgc gct atg agg gca gat ttg aaa gtg acg ggt caa   211
Leu Met Ala Leu Arg Ala Met Arg Ala Asp Leu Lys Val Thr Gly Gln
            25                  30                  35

gcg tcg aca agc agc tcc tcc gtc gcg gca ccg cag ggc ctt gcc cgg   259
Ala Ser Thr Ser Ser Ser Ser Val Ala Ala Pro Gln Gly Leu Ala Arg
        40                  45                  50

gct ttt aat cgc tcc agc ccg cct cgt ctt ttg acg gtg gtc gag ggc   307
Ala Phe Asn Arg Ser Ser Pro Pro Arg Leu Leu Thr Val Val Glu Gly
    55                  60                  65
```

```
ccg ttg gcg ggc tcc tcg att gag gtg tcg gag gat atg acg atg ggc   355
Pro Leu Ala Gly Ser Ser Ile Glu Val Ser Glu Asp Met Thr Met Gly
 70                  75                  80                  85

cgt agc cct gag tgc acg ttt gtg gtg ggc gat gat tac gcc tcc ggc   403
Arg Ser Pro Glu Cys Thr Phe Val Val Gly Asp Asp Tyr Ala Ser Gly
                90                  95                 100

atg cat gcg cgg gtg ttt aag cgt ggt tcg gag tgg ttt gtg gag gat   451
Met His Ala Arg Val Phe Lys Arg Gly Ser Glu Trp Phe Val Glu Asp
            105                 110                 115

ctg gat tcg cgc aac ggc act ttt gtc ggt ggt acg cgc att gat cag   499
Leu Asp Ser Arg Asn Gly Thr Phe Val Gly Gly Thr Arg Ile Asp Gln
        120                 125                 130

cct gag cag att gcg gtg ggc acg gat atc cgt att ggt cgt aca gca   547
Pro Glu Gln Ile Ala Val Gly Thr Asp Ile Arg Ile Gly Arg Thr Ala
    135                 140                 145

gtg agg ctt gtt ccc tgatgttgaa acttaaatat gcg                     585
Val Arg Leu Val Pro
150
```

Application Filed Electronically

<210> 834
<211> 154
<212> PRT
<213> Corynebacterium glutamicum

<400> 834

```
Met Asp Ser Leu Val Leu Leu Gly Leu Arg Ile Ala Leu Leu Val Val
  1               5                  10                  15

Leu Trp Phe Phe Val Leu Met Ala Leu Arg Ala Met Arg Ala Asp Leu
             20                  25                  30

Lys Val Thr Gly Gln Ala Ser Thr Ser Ser Ser Ser Val Ala Ala Pro
         35                  40                  45

Gln Gly Leu Ala Arg Ala Phe Asn Arg Ser Ser Pro Pro Arg Leu Leu
     50                  55                  60

Thr Val Val Glu Gly Pro Leu Ala Gly Ser Ser Ile Glu Val Ser Glu
 65                  70                  75                  80

Asp Met Thr Met Gly Arg Ser Pro Glu Cys Thr Phe Val Val Gly Asp
                 85                  90                  95

Asp Tyr Ala Ser Gly Met His Ala Arg Val Phe Lys Arg Gly Ser Glu
            100                 105                 110

Trp Phe Val Glu Asp Leu Asp Ser Arg Asn Gly Thr Phe Val Gly Gly
        115                 120                 125

Thr Arg Ile Asp Gln Pro Glu Gln Ile Ala Val Gly Thr Asp Ile Arg
    130                 135                 140

Ile Gly Arg Thr Ala Val Arg Leu Val Pro
145                 150
```

<210> 835
<211> 825
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(802)
<223> RXN01834

<400> 835
actaagaacg tgagcttggt ttcataatac cccccagggt attgttagcc aggtgattct 60

agcccttctt ggcggcctaa taataggcct acttcttggc atg ctc ggt ggt ggc 115
Met Leu Gly Gly Gly
1 5

ggt gcc atc ctt gcc att ccg ctg ctt att tat gga ttt tct ttt agc 163
Gly Ala Ile Leu Ala Ile Pro Leu Leu Ile Tyr Gly Phe Ser Phe Ser
10 15 20

gcc acg caa gct act gca gct tca tta atc atc atc gga ctt ggc gcc 211
Ala Thr Gln Ala Thr Ala Ala Ser Leu Ile Ile Ile Gly Leu Gly Ala
25 30 35

ctc att gga ctg atc agc caa tac gct gcc ggg cac gtc cgc ctt aaa 259
Leu Ile Gly Leu Ile Ser Gln Tyr Ala Ala Gly His Val Arg Leu Lys
40 45 50

gag ggt cta agc ttt ggc ctt tta ggg ttg gtc ggc tca ttt gtg ggc 307
Glu Gly Leu Ser Phe Gly Leu Leu Gly Leu Val Gly Ser Phe Val Gly
55 60 65

agt cac ctt gct agc aat atc ccc gat tcc cta ctc ctg agc ggc ttt 355
Ser His Leu Ala Ser Asn Ile Pro Asp Ser Leu Leu Leu Ser Gly Phe
70 75 80 85

gcc atc ctc acg ctc gtg gtg gcg ttg acc atg att tct aaa tta aga 403
Ala Ile Leu Thr Leu Val Val Ala Leu Thr Met Ile Ser Lys Leu Arg
90 95 100

agc acc cga gaa tac ata acc aga agg cca agc atc ctt gcc att gct 451
Ser Thr Arg Glu Tyr Ile Thr Arg Arg Pro Ser Ile Leu Ala Ile Ala
105 110 115

ctt agt gcc acc ggc gtg gga ttt ttg acg gga ttt ttt ggt gtg ggt 499
Leu Ser Ala Thr Gly Val Gly Phe Leu Thr Gly Phe Phe Gly Val Gly
120 125 130

ggc ggt ttt gcc att gtg cca gcc ttg att ttt gcg ctc ggt ttt tcc 547
Gly Gly Phe Ala Ile Val Pro Ala Leu Ile Phe Ala Leu Gly Phe Ser
135 140 145

atg cgg cag gct agc gcc act tcc cta gtg gtg atc gcc gtt aac agc 595
Met Arg Gln Ala Ser Ala Thr Ser Leu Val Val Ile Ala Val Asn Ser
150 155 160 165

gct att gcc atg gga ttt aga tat tcc gat ttg gca agt att gac tgg 643
Ala Ile Ala Met Gly Phe Arg Tyr Ser Asp Leu Ala Ser Ile Asp Trp
170 175 180

```
tca gtg atc tcg cca att atc atc acc acc gta ttg ggc gct ttt agt   691
Ser Val Ile Ser Pro Ile Ile Ile Thr Thr Val Leu Gly Ala Phe Ser
            185                 190                 195

ggc gta aaa cta gcc aaa aag gtc aaa gca tca tca ctg caa cta ggt   739
Gly Val Lys Leu Ala Lys Lys Val Lys Ala Ser Ser Leu Gln Leu Gly
        200                 205                 210

ttt gct ggc ttc ttg atc ttc att tcg atc tat atg gga ttt cag aat   787
Phe Ala Gly Phe Leu Ile Phe Ile Ser Ile Tyr Met Gly Phe Gln Asn
    215                 220                 225

ttc ccg gac ctt ttt taaaacttca aaatataccc ccc                    825
Phe Pro Asp Leu Phe
230
```

<210> 836
<211> 234
<212> PRT
<213> Corynebacterium glutamicum

<400> 836

```
Met Leu Gly Gly Gly Gly Ala Ile Leu Ala Ile Pro Leu Leu Ile Tyr
  1               5                  10                  15

Gly Phe Ser Phe Ser Ala Thr Gln Ala Thr Ala Ala Ser Leu Ile Ile
             20                  25                  30

Ile Gly Leu Gly Ala Leu Ile Gly Leu Ile Ser Gln Tyr Ala Ala Gly
         35                  40                  45

His Val Arg Leu Lys Glu Gly Leu Ser Phe Gly Leu Leu Gly Leu Val
     50                  55                  60

Gly Ser Phe Val Gly Ser His Leu Ala Ser Asn Ile Pro Asp Ser Leu
 65                  70                  75                  80

Leu Leu Ser Gly Phe Ala Ile Leu Thr Leu Val Val Ala Leu Thr Met
                 85                  90                  95

Ile Ser Lys Leu Arg Ser Thr Arg Glu Tyr Ile Thr Arg Arg Pro Ser
            100                 105                 110

Ile Leu Ala Ile Ala Leu Ser Ala Thr Gly Val Gly Phe Leu Thr Gly
        115                 120                 125

Phe Phe Gly Val Gly Gly Gly Phe Ala Ile Val Pro Ala Leu Ile Phe
    130                 135                 140

Ala Leu Gly Phe Ser Met Arg Gln Ala Ser Ala Thr Ser Leu Val Val
145                 150                 155                 160

Ile Ala Val Asn Ser Ala Ile Ala Met Gly Phe Arg Tyr Ser Asp Leu
                165                 170                 175

Ala Ser Ile Asp Trp Ser Val Ile Ser Pro Ile Ile Ile Thr Thr Val
            180                 185                 190

Leu Gly Ala Phe Ser Gly Val Lys Leu Ala Lys Lys Val Lys Ala Ser
```

```
        195                 200                 205

Ser Leu Gln Leu Gly Phe Ala Gly Phe Leu Ile Phe Ile Ser Ile Tyr
    210                 215                 220

Met Gly Phe Gln Asn Phe Pro Asp Leu Phe
225                 230


<210> 837
<211> 825
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(802)
<223> FRXA01834

<400> 837
actaagaacg tgagcttggt ttcataatac cccccagggt attgttagcc aggtgattct 60

agcccttctt ggcggcctaa taataggcct acttcttggc atg ctc ggt ggt ggc   115
                                              Met Leu Gly Gly Gly
                                                1               5

ggt gcc atc ctt gcc att ccg ctg ctt att tat gga ttt tct ttt agc   163
Gly Ala Ile Leu Ala Ile Pro Leu Leu Ile Tyr Gly Phe Ser Phe Ser
                10                  15                  20

gcc acg caa gct act gca gct tca tta atc atc atc gga ctt ggc gcc   211
Ala Thr Gln Ala Thr Ala Ala Ser Leu Ile Ile Ile Gly Leu Gly Ala
            25                  30                  35

ctc att gga ctg atc agc caa tac gct gcc ggg cac gtc cgc ctt aaa   259
Leu Ile Gly Leu Ile Ser Gln Tyr Ala Ala Gly His Val Arg Leu Lys
        40                  45                  50

gag ggt cta agc ttt ggc ctt tta ggg ttg gtc ggc tca ttt gtg ggc   307
Glu Gly Leu Ser Phe Gly Leu Leu Gly Leu Val Gly Ser Phe Val Gly
    55                  60                  65

agt cac ctt gct agc aat atc ccc gat tcc cta ctc ctg agc ggc ttt   355
Ser His Leu Ala Ser Asn Ile Pro Asp Ser Leu Leu Leu Ser Gly Phe
70                  75                  80                  85

gcc atc ctc acg ctc gtg gtg gcg ttg acc atg att tct aaa tta aga   403
Ala Ile Leu Thr Leu Val Val Ala Leu Thr Met Ile Ser Lys Leu Arg
                90                  95                  100

agc acc cga gaa tac ata acc aga agg cca agc atc ctt gcc att gct   451
Ser Thr Arg Glu Tyr Ile Thr Arg Arg Pro Ser Ile Leu Ala Ile Ala
            105                 110                 115

ctt agt gcc acc ggc gtg gga ttt ttg acg gga ttt ttt ggt gtg ggt   499
Leu Ser Ala Thr Gly Val Gly Phe Leu Thr Gly Phe Phe Gly Val Gly
        120                 125                 130

ggc ggt ttt gcc att gtg cca gcc ttg att ttt gcg ctc ggt ttt tcc   547
Gly Gly Phe Ala Ile Val Pro Ala Leu Ile Phe Ala Leu Gly Phe Ser
    135                 140                 145
```

```
atg cgg cag gct agc gcc act tcc cta gtg gtg atc gcc gtt aac agc   595
Met Arg Gln Ala Ser Ala Thr Ser Leu Val Val Ile Ala Val Asn Ser
150                 155                 160                 165

gct att gcc atg gga ttt aga tat tcc gat ttg gca agt att gac tgg   643
Ala Ile Ala Met Gly Phe Arg Tyr Ser Asp Leu Ala Ser Ile Asp Trp
                170                 175                 180

tca gtg atc tcg cca att atc atc acc acc gta ttg ggc gct ttt agt   691
Ser Val Ile Ser Pro Ile Ile Ile Thr Thr Val Leu Gly Ala Phe Ser
            185                 190                 195

ggc gta aaa cta gcc aaa aag gtc aaa gca tca tca ctg caa cta ggt   739
Gly Val Lys Leu Ala Lys Lys Val Lys Ala Ser Ser Leu Gln Leu Gly
        200                 205                 210

ttt gct ggc ttc ttg atc ttc att tcg atc tat atg gga ttt cag aat   787
Phe Ala Gly Phe Leu Ile Phe Ile Ser Ile Tyr Met Gly Phe Gln Asn
    215                 220                 225

ttc ccg gac ctt ttt taaaacttca aaatataccc ccc                     825
Phe Pro Asp Leu Phe
230
```

Application Filed with Sequence Listing

<210> 838
<211> 234
<212> PRT
<213> Corynebacterium glutamicum

<400> 838

```
Met Leu Gly Gly Gly Gly Ala Ile Leu Ala Ile Pro Leu Leu Ile Tyr
  1               5                  10                  15

Gly Phe Ser Phe Ser Ala Thr Gln Ala Thr Ala Ala Ser Leu Ile Ile
             20                  25                  30

Ile Gly Leu Gly Ala Leu Ile Gly Leu Ile Ser Gln Tyr Ala Ala Gly
         35                  40                  45

His Val Arg Leu Lys Glu Gly Leu Ser Phe Gly Leu Leu Gly Leu Val
     50                  55                  60

Gly Ser Phe Val Gly Ser His Leu Ala Ser Asn Ile Pro Asp Ser Leu
 65                  70                  75                  80

Leu Leu Ser Gly Phe Ala Ile Leu Thr Leu Val Val Ala Leu Thr Met
                 85                  90                  95

Ile Ser Lys Leu Arg Ser Thr Arg Glu Tyr Ile Thr Arg Arg Pro Ser
            100                 105                 110

Ile Leu Ala Ile Ala Leu Ser Ala Thr Gly Val Gly Phe Leu Thr Gly
        115                 120                 125

Phe Phe Gly Val Gly Gly Gly Phe Ala Ile Val Pro Ala Leu Ile Phe
    130                 135                 140

Ala Leu Gly Phe Ser Met Arg Gln Ala Ser Ala Thr Ser Leu Val Val
145                 150                 155                 160
```

```
Ile Ala Val Asn Ser Ala Ile Ala Met Gly Phe Arg Tyr Ser Asp Leu
               165                 170                 175

Ala Ser Ile Asp Trp Ser Val Ile Ser Pro Ile Ile Ile Thr Thr Val
            180                 185                 190

Leu Gly Ala Phe Ser Gly Val Lys Leu Ala Lys Lys Val Lys Ala Ser
        195                 200                 205

Ser Leu Gln Leu Gly Phe Ala Gly Phe Leu Ile Phe Ile Ser Ile Tyr
    210                 215                 220

Met Gly Phe Gln Asn Phe Pro Asp Leu Phe
225                 230


<210> 839
<211> 382
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(382)
<223> RXN01846

<400> 839
gtatttagga attgaaaccc actaaaaaac agactaagtt actaggtgat aacaaaagtt 60

gtttattact tatgggaata gtgtggaaag tagggtgaat atg tca att cct gga   115
                                            Met Ser Ile Pro Gly
                                              1               5


aat gtt agt tat gtt gca cag ggt ggc acc ggt tgg gat ggt gct gat   163
Asn Val Ser Tyr Val Ala Gln Gly Gly Thr Gly Trp Asp Gly Ala Asp
                 10                  15                  20

cag tac acc acg ggt gag agt tgg gat cta cag tcg ttc ctt gaa aac   211
Gln Tyr Thr Thr Gly Glu Ser Trp Asp Leu Gln Ser Phe Leu Glu Asn
             25                  30                  35

tcg act gac tac ctc atg att att ggt ggt tcg ctg ctg gca ctt gtt   259
Ser Thr Asp Tyr Leu Met Ile Ile Gly Gly Ser Leu Leu Ala Leu Val
         40                  45                  50

ggt ggt gct gct gtg att tgg ggc ttt gtc aac gtg atg cgc aag ctc   307
Gly Gly Ala Ala Val Ile Trp Gly Phe Val Asn Val Met Arg Lys Leu
     55                  60                  65

ttc ggt ggt cag agt ggt cag cag att cag tgg ttc acc act att ttg   355
Phe Gly Gly Gln Ser Gly Gln Gln Ile Gln Trp Phe Thr Thr Ile Leu
 70                  75                  80                  85

ctc atc att gtc ggt ggt gcg ttg cct                              382
Leu Ile Ile Val Gly Gly Ala Leu Pro
                 90


<210> 840
<211> 94
```

<212> PRT
<213> Corynebacterium glutamicum

<400> 840

```
Met Ser Ile Pro Gly Asn Val Ser Tyr Val Ala Gln Gly Gly Thr Gly
  1               5                  10                  15

Trp Asp Gly Ala Asp Gln Tyr Thr Thr Gly Glu Ser Trp Asp Leu Gln
             20                  25                  30

Ser Phe Leu Glu Asn Ser Thr Asp Tyr Leu Met Ile Ile Gly Gly Ser
         35                  40                  45

Leu Leu Ala Leu Val Gly Gly Ala Ala Val Ile Trp Gly Phe Val Asn
     50                  55                  60

Val Met Arg Lys Leu Phe Gly Gly Gln Ser Gly Gln Gln Ile Gln Trp
 65                  70                  75                  80

Phe Thr Thr Ile Leu Leu Ile Ile Val Gly Gly Ala Leu Pro
                 85                  90
```

<210> 841
<211> 358
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(358)
<223> FRXA01846

<400> 841

```
gtatttagga attgaaaccc actaaaaaac agactaagtt actaggtgat aacaaaagtt 60

gtttattact tatgggaata gtgtggaaag tagggtgaat atg tca att cct gga   115
                                            Met Ser Ile Pro Gly
                                              1               5

aat gtt agt tat gtt gca cag ggt ggc acc ggt tgg gat ggt gct gat   163
Asn Val Ser Tyr Val Ala Gln Gly Gly Thr Gly Trp Asp Gly Ala Asp
                 10                  15                  20

cag tac acc acg ggt gag agt tgg gat cta cag tcg ttc ctt gaa aac   211
Gln Tyr Thr Thr Gly Glu Ser Trp Asp Leu Gln Ser Phe Leu Glu Asn
             25                  30                  35

tcg act gac tac ctc atg att att ggt ggt tcg ctg ctg gca ctt gtt   259
Ser Thr Asp Tyr Leu Met Ile Ile Gly Gly Ser Leu Leu Ala Leu Val
         40                  45                  50

ggt ggt gct gct gtg att tgg ggc ttt gtc aac gtg atg cgc aag ctc   307
Gly Gly Ala Ala Val Ile Trp Gly Phe Val Asn Val Met Arg Lys Leu
     55                  60                  65

ttc ggt ggt cag agt ggt cag cag att cag tgg ttc acc act att ttg   355
Phe Gly Gly Gln Ser Gly Gln Gln Ile Gln Trp Phe Thr Thr Ile Leu
 70                  75                  80                  85

ctc                                                              358
```

Leu

<210> 842
<211> 86
<212> PRT
<213> Corynebacterium glutamicum

<400> 842
Met Ser Ile Pro Gly Asn Val Ser Tyr Val Ala Gln Gly Gly Thr Gly
1 5 10 15

Trp Asp Gly Ala Asp Gln Tyr Thr Thr Gly Glu Ser Trp Asp Leu Gln
20 25 30

Ser Phe Leu Glu Asn Ser Thr Asp Tyr Leu Met Ile Ile Gly Gly Ser
35 40 45

Leu Leu Ala Leu Val Gly Gly Ala Ala Val Ile Trp Gly Phe Val Asn
50 55 60

Val Met Arg Lys Leu Phe Gly Gly Gln Ser Gly Gln Gln Ile Gln Trp
65 70 75 80

Phe Thr Thr Ile Leu Leu
85

<210> 843
<211> 858
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(835)
<223> RXN01847

<400> 843
gacgtgtgat cataggtgac aaatataccc tctcaacttg gcttcgactg ccctgccccc 60

tcgatttaag aggcaaggct tttacagtat cctctcatgc atg ctt att gtg ttg 115
Met Leu Ile Val Leu
1 5

cct ccc tca gaa act aag acc cac ggc ggt tca gga aaa cct ctg gat 163
Pro Pro Ser Glu Thr Lys Thr His Gly Gly Ser Gly Lys Pro Leu Asp
10 15 20

ttt cac cat ttg agt ttc ccg tcg ctc acc aag gca cgc caa aca ata 211
Phe His His Leu Ser Phe Pro Ser Leu Thr Lys Ala Arg Gln Thr Ile
25 30 35

ctc gct gac ctg caa gct ttg gag gta gat gag gcg ctg aaa gtt ttg 259
Leu Ala Asp Leu Gln Ala Leu Glu Val Asp Glu Ala Leu Lys Val Leu
40 45 50

ggc att tct gaa aag ctc cgc cct gag gcc gaa tcc aat cgc gcg ctg 307
Gly Ile Ser Glu Lys Leu Arg Pro Glu Ala Glu Ser Asn Arg Ala Leu
55 60 65

```
gag acc agc cct acg atg cct gcg att ttt cgg tat tcc gga gtg ctt   355
Glu Thr Ser Pro Thr Met Pro Ala Ile Phe Arg Tyr Ser Gly Val Leu
 70                  75                  80                  85

tat gat gcg ctc gac gct gca acg ctg ccg gag aaa gca ctg gaa cgc   403
Tyr Asp Ala Leu Asp Ala Ala Thr Leu Pro Glu Lys Ala Leu Glu Arg
                90                  95                 100

ctc gcc atc ggc tcg gca ctt ttc ggc gtc atc cac gcc acc gat ccg   451
Leu Ala Ile Gly Ser Ala Leu Phe Gly Val Ile His Ala Thr Asp Pro
            105                 110                 115

atc ccg cat tac cgc ctg tcc ggc ggc aca aaa ctg ccc acc aaa agc   499
Ile Pro His Tyr Arg Leu Ser Gly Gly Thr Lys Leu Pro Thr Lys Ser
        120                 125                 130

ggc gag ctg ccc acc atg aag gcg cgt tgg ggc aca agc atc agc gaa   547
Gly Glu Leu Pro Thr Met Lys Ala Arg Trp Gly Thr Ser Ile Ser Glu
    135                 140                 145

gcg ctt atc gac gtc aac cag ctg gtg att gat ctt cgc agc ggg acc   595
Ala Leu Ile Asp Val Asn Gln Leu Val Ile Asp Leu Arg Ser Gly Thr
150                 155                 160                 165

tac caa cag ttg ggt cgc gta aaa gac gcc gtc acg gta cgc gtg gaa   643
Tyr Gln Gln Leu Gly Arg Val Lys Asp Ala Val Thr Val Arg Val Glu
                170                 175                 180

tca gtc atg gag gat ggc tcc cgc aaa gta gtc agc cac ttt aac aaa   691
Ser Val Met Glu Asp Gly Ser Arg Lys Val Val Ser His Phe Asn Lys
            185                 190                 195

cac tac aaa ggt gaa ctc gcc cgc gtg ctc gcg ctc tct gaa aaa gaa   739
His Tyr Lys Gly Glu Leu Ala Arg Val Leu Ala Leu Ser Glu Lys Glu
        200                 205                 210

gca cac acc gca gag gac gta atg agc att gcg cag gct gcg ggc ctt   787
Ala His Thr Ala Glu Asp Val Met Ser Ile Ala Gln Ala Ala Gly Leu
    215                 220                 225

gtg gtg gag gaa aac ccc aac cac aag gaa acc ctc act ctg gtt gtc   835
Val Val Glu Glu Asn Pro Asn His Lys Glu Thr Leu Thr Leu Val Val
230                 235                 240                 245

taggcgttaa tcaccatttt gat                                        858
```

<210> 844
<211> 245
<212> PRT
<213> Corynebacterium glutamicum

<400> 844

```
Met Leu Ile Val Leu Pro Pro Ser Glu Thr Lys Thr His Gly Gly Ser
  1               5                  10                  15

Gly Lys Pro Leu Asp Phe His His Leu Ser Phe Pro Ser Leu Thr Lys
             20                  25                  30

Ala Arg Gln Thr Ile Leu Ala Asp Leu Gln Ala Leu Glu Val Asp Glu
```

```
         35                  40                  45

Ala Leu Lys Val Leu Gly Ile Ser Glu Lys Leu Arg Pro Glu Ala Glu
     50                  55                  60

Ser Asn Arg Ala Leu Glu Thr Ser Pro Thr Met Pro Ala Ile Phe Arg
 65                  70                  75                  80

Tyr Ser Gly Val Leu Tyr Asp Ala Leu Asp Ala Ala Thr Leu Pro Glu
                 85                  90                  95

Lys Ala Leu Glu Arg Leu Ala Ile Gly Ser Ala Leu Phe Gly Val Ile
            100                 105                 110

His Ala Thr Asp Pro Ile Pro His Tyr Arg Leu Ser Gly Gly Thr Lys
        115                 120                 125

Leu Pro Thr Lys Ser Gly Glu Leu Pro Thr Met Lys Ala Arg Trp Gly
    130                 135                 140

Thr Ser Ile Ser Glu Ala Leu Ile Asp Val Asn Gln Leu Val Ile Asp
145                 150                 155                 160

Leu Arg Ser Gly Thr Tyr Gln Gln Leu Gly Arg Val Lys Asp Ala Val
                165                 170                 175

Thr Val Arg Val Glu Ser Val Met Glu Asp Gly Ser Arg Lys Val Val
            180                 185                 190

Ser His Phe Asn Lys His Tyr Lys Gly Glu Leu Ala Arg Val Leu Ala
        195                 200                 205

Leu Ser Glu Lys Glu Ala His Thr Ala Glu Asp Val Met Ser Ile Ala
    210                 215                 220

Gln Ala Ala Gly Leu Val Val Glu Glu Asn Pro Asn His Lys Glu Thr
225                 230                 235                 240

Leu Thr Leu Val Val
                245
```

<210> 845
<211> 809
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (52)..(786)
<223> FRXA01847

<400> 845

```
gccctgcccc ctcgatttaa gaggcaaggc ttttacagta tcctctcatg catg ctt   57
                                                          Met Leu
                                                            1

att gtg ttg cct ccc tca gaa act aag acc cac ggc ggt tca gga aaa   105
Ile Val Leu Pro Pro Ser Glu Thr Lys Thr His Gly Gly Ser Gly Lys
          5                  10                  15
```

```
cct ctg gat ttt cac cat ttg agt ttc ccg tcg ctc acc aag gca cgc   153
Pro Leu Asp Phe His His Leu Ser Phe Pro Ser Leu Thr Lys Ala Arg
     20                  25                  30

caa aca ata ctc gct gac ctg caa gct ttg gag gta gat gag gcg ctg   201
Gln Thr Ile Leu Ala Asp Leu Gln Ala Leu Glu Val Asp Glu Ala Leu
 35                  40                  45                  50

aaa gtt ttg ggc att tct gaa aag ctc cgc cct gag gcc gaa tcc aat   249
Lys Val Leu Gly Ile Ser Glu Lys Leu Arg Pro Glu Ala Glu Ser Asn
                 55                  60                  65

cgc gcg ctg gag acc agc cct acg atg cct gcg att ttt cgg tat tcc   297
Arg Ala Leu Glu Thr Ser Pro Thr Met Pro Ala Ile Phe Arg Tyr Ser
             70                  75                  80

gga gtg ctt tat gat gcg ctc gac gct gca acg ctg ccg gag aaa gca   345
Gly Val Leu Tyr Asp Ala Leu Asp Ala Ala Thr Leu Pro Glu Lys Ala
         85                  90                  95

ctg gaa cgc ctc gcc atc ggc tcg gca ctt ttc ggc gtc atc cac gcc   393
Leu Glu Arg Leu Ala Ile Gly Ser Ala Leu Phe Gly Val Ile His Ala
    100                 105                 110

acc gat ccg atc ccg cat tac cgc ctg tcc ggc ggc aca aaa ctg ccc   441
Thr Asp Pro Ile Pro His Tyr Arg Leu Ser Gly Gly Thr Lys Leu Pro
115                 120                 125                 130

acc aaa agc ggc gag ctg ccc acc atg aag gcg cgt tgg ggc aca agc   489
Thr Lys Ser Gly Glu Leu Pro Thr Met Lys Ala Arg Trp Gly Thr Ser
                135                 140                 145

atc agc gaa gcg ctt atc gac gtc aac cag ctg gtg att gat ctt cgc   537
Ile Ser Glu Ala Leu Ile Asp Val Asn Gln Leu Val Ile Asp Leu Arg
            150                 155                 160

agc ggg acc tac caa cag ttg ggt cgc gta aaa gac gcc gtc acg gta   585
Ser Gly Thr Tyr Gln Gln Leu Gly Arg Val Lys Asp Ala Val Thr Val
        165                 170                 175

cgc gtg gaa tca gtc atg gag gat ggc tcc cgc aaa gta gtc agc cac   633
Arg Val Glu Ser Val Met Glu Asp Gly Ser Arg Lys Val Val Ser His
    180                 185                 190

ttt aac aaa cac tac aaa ggt gaa ctc gcc cgc gtg ctc gcg ctc tct   681
Phe Asn Lys His Tyr Lys Gly Glu Leu Ala Arg Val Leu Ala Leu Ser
195                 200                 205                 210

gaa aaa gaa gca cac acc gca gag gac gta atg agc att gcg cag gct   729
Glu Lys Glu Ala His Thr Ala Glu Asp Val Met Ser Ile Ala Gln Ala
                215                 220                 225

gcg ggc ctt gtg gtg gag gaa aac ccc aac cac aag gaa acc ctc act   777
Ala Gly Leu Val Val Glu Glu Asn Pro Asn His Lys Glu Thr Leu Thr
            230                 235                 240

ctg gtt gtc taggcgttaa tcaccatttt gat                            809
Leu Val Val
        245
```

<210> 846
<211> 245
<212> PRT
<213> Corynebacterium glutamicum

<400> 846
Met Leu Ile Val Leu Pro Pro Ser Glu Thr Lys Thr His Gly Gly Ser
1 5 10 15

Gly Lys Pro Leu Asp Phe His His Leu Ser Phe Pro Ser Leu Thr Lys
20 25 30

Ala Arg Gln Thr Ile Leu Ala Asp Leu Gln Ala Leu Glu Val Asp Glu
35 40 45

Ala Leu Lys Val Leu Gly Ile Ser Glu Lys Leu Arg Pro Glu Ala Glu
50 55 60

Ser Asn Arg Ala Leu Glu Thr Ser Pro Thr Met Pro Ala Ile Phe Arg
65 70 75 80

Tyr Ser Gly Val Leu Tyr Asp Ala Leu Asp Ala Ala Thr Leu Pro Glu
85 90 95

Lys Ala Leu Glu Arg Leu Ala Ile Gly Ser Ala Leu Phe Gly Val Ile
100 105 110

His Ala Thr Asp Pro Ile Pro His Tyr Arg Leu Ser Gly Gly Thr Lys
115 120 125

Leu Pro Thr Lys Ser Gly Glu Leu Pro Thr Met Lys Ala Arg Trp Gly
130 135 140

Thr Ser Ile Ser Glu Ala Leu Ile Asp Val Asn Gln Leu Val Ile Asp
145 150 155 160

Leu Arg Ser Gly Thr Tyr Gln Gln Leu Gly Arg Val Lys Asp Ala Val
165 170 175

Thr Val Arg Val Glu Ser Val Met Glu Asp Gly Ser Arg Lys Val Val
180 185 190

Ser His Phe Asn Lys His Tyr Lys Gly Glu Leu Ala Arg Val Leu Ala
195 200 205

Leu Ser Glu Lys Glu Ala His Thr Ala Glu Asp Val Met Ser Ile Ala
210 215 220

Gln Ala Ala Gly Leu Val Val Glu Glu Asn Pro Asn His Lys Glu Thr
225 230 235 240

Leu Thr Leu Val Val
245

<210> 847
<211> 448
<212> DNA
<213> Corynebacterium glutamicum

<220>

<221> CDS
<222> (101)..(448)
<223> RXN01874

<400> 847
agtgtcggcg cgacgattgt gggcggtgct ttggcgtggc acgcagcagt ttggcatcac 60

agttccggag cgcaaaacgc ggtcagcctt tcgcgtcgca gtg atc gcg tat gtt 115
Val Ile Ala Tyr Val
1 5

gcc agc gcg tgc tgc ctg ccg ttt ggc gca ttt gcc gga gcg ttg ttg 163
Ala Ser Ala Cys Cys Leu Pro Phe Gly Ala Phe Ala Gly Ala Leu Leu
10 15 20

tcc aag gag ctg tcg gga cat ctc cag gaa cga gtc ctt ctc acc cac 211
Ser Lys Glu Leu Ser Gly His Leu Gln Glu Arg Val Leu Leu Thr His
25 30 35

acg gtg att aat ttt cta ggt ttc gtg gga ttt gct gcg ctc ggt tcg 259
Thr Val Ile Asn Phe Leu Gly Phe Val Gly Phe Ala Ala Leu Gly Ser
40 45 50

ctg tcg gtg ctg ttc gcc gcg att tgg cgc acc aaa att cgc cac aat 307
Leu Ser Val Leu Phe Ala Ala Ile Trp Arg Thr Lys Ile Arg His Asn
55 60 65

ttc acc ccg tgg tct gtg ggg atc atg gcg gtg agc ctg ccg atc atc 355
Phe Thr Pro Trp Ser Val Gly Ile Met Ala Val Ser Leu Pro Ile Ile
70 75 80 85

gtc acg ggc atc ctg ctc aac aac ggc tat gtc gcc gcc aca ggc ctg 403
Val Thr Gly Ile Leu Leu Asn Asn Gly Tyr Val Ala Ala Thr Gly Leu
90 95 100

gcc gcg tac gtg gca gca tgg ttg ctg gcc atg gtg ggg tgg ggg 448
Ala Ala Tyr Val Ala Ala Trp Leu Leu Ala Met Val Gly Trp Gly
105 110 115

<210> 848
<211> 116
<212> PRT
<213> Corynebacterium glutamicum

<400> 848
Val Ile Ala Tyr Val Ala Ser Ala Cys Cys Leu Pro Phe Gly Ala Phe
1 5 10 15

Ala Gly Ala Leu Leu Ser Lys Glu Leu Ser Gly His Leu Gln Glu Arg
20 25 30

Val Leu Leu Thr His Thr Val Ile Asn Phe Leu Gly Phe Val Gly Phe
35 40 45

Ala Ala Leu Gly Ser Leu Ser Val Leu Phe Ala Ala Ile Trp Arg Thr
50 55 60

Lys Ile Arg His Asn Phe Thr Pro Trp Ser Val Gly Ile Met Ala Val
65 70 75 80

```
Ser Leu Pro Ile Ile Val Thr Gly Ile Leu Leu Asn Asn Gly Tyr Val
                85                  90                  95

Ala Ala Thr Gly Leu Ala Ala Tyr Val Ala Ala Trp Leu Leu Ala Met
            100                 105                 110

Val Gly Trp Gly
        115
```

<210> 849
<211> 448
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(448)
<223> FRXA01874

<400> 849

```
agtgtcggcg cgacgattgt gggcggtgct ttggcgtggc acgcagcagt ttggcatcac 60

agttccggag cgcaaaacgc ggtcagcctt tcgcgtcgca gtg atc gcg tat gtt   115
                                            Val Ile Ala Tyr Val
                                              1               5

gcc agc gcg tgc tgc ctg ccg ttt ggc gca ttt gcc gga gcg ttg ttg   163
Ala Ser Ala Cys Cys Leu Pro Phe Gly Ala Phe Ala Gly Ala Leu Leu
                10                  15                  20

tcc aag gag ctg tcg gga cat ctc cag gaa cga gtc ctt ctc acc cac   211
Ser Lys Glu Leu Ser Gly His Leu Gln Glu Arg Val Leu Leu Thr His
            25                  30                  35

acg gtg att aat ttt cta ggt ttc gtg gga ttt gct gcg ctc ggt tcg   259
Thr Val Ile Asn Phe Leu Gly Phe Val Gly Phe Ala Ala Leu Gly Ser
        40                  45                  50

ctg tcg gtg ctg ttc gcc gcg att tgg cgc acc aaa att cgc cac aat   307
Leu Ser Val Leu Phe Ala Ala Ile Trp Arg Thr Lys Ile Arg His Asn
    55                  60                  65

ttc acc ccg tgg tct gtg ggg atc atg gcg gtg agc ctg ccg atc atc   355
Phe Thr Pro Trp Ser Val Gly Ile Met Ala Val Ser Leu Pro Ile Ile
70                  75                  80                  85

gtc acg ggc atc ctg ctc aac aac ggc tat gtc gcc gca cag gcc tgg   403
Val Thr Gly Ile Leu Leu Asn Asn Gly Tyr Val Ala Ala Gln Ala Trp
                90                  95                  100

ccg cgt acg tgg cag cat ggt tgc tgg cca tgg tgg ggt ggg gga       448
Pro Arg Thr Trp Gln His Gly Cys Trp Pro Trp Trp Gly Gly Gly
            105                 110                 115
```

<210> 850
<211> 116
<212> PRT
<213> Corynebacterium glutamicum

<400> 850
Val Ile Ala Tyr Val Ala Ser Ala Cys Cys Leu Pro Phe Gly Ala Phe
1 5 10 15

Ala Gly Ala Leu Leu Ser Lys Glu Leu Ser Gly His Leu Gln Glu Arg
20 25 30

Val Leu Leu Thr His Thr Val Ile Asn Phe Leu Gly Phe Val Gly Phe
35 40 45

Ala Ala Leu Gly Ser Leu Ser Val Leu Phe Ala Ala Ile Trp Arg Thr
50 55 60

Lys Ile Arg His Asn Phe Thr Pro Trp Ser Val Gly Ile Met Ala Val
65 70 75 80

Ser Leu Pro Ile Ile Val Thr Gly Ile Leu Leu Asn Asn Gly Tyr Val
85 90 95

Ala Ala Gln Ala Trp Pro Arg Thr Trp Gln His Gly Cys Trp Pro Trp
100 105 110

Trp Gly Gly Gly
115

<210> 851
<211> 969
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(946)
<223> RXN01875

<400> 851
aatcctatcc ctaaaaagtt tctaacaaaa gtattgcact tacttttttga tagtgctatc 60

ttcagttgtg tacttgaaac acacacgaat ggagcaagaa atg cgt att gca gta 115
Met Arg Ile Ala Val
1 5

act gga gca acg gga tct ttg ggt gga cat gtt gtg gat agt ctt cta 163
Thr Gly Ala Thr Gly Ser Leu Gly Gly His Val Val Asp Ser Leu Leu
10 15 20

aac aag ggc gtc gca gca tca gac atc gtt gcc att gtt cga aat gaa 211
Asn Lys Gly Val Ala Ala Ser Asp Ile Val Ala Ile Val Arg Asn Glu
25 30 35

gaa aag gca gca gac ctc aaa gcc cgt gga atc gct ctt ggt gtg gct 259
Glu Lys Ala Ala Asp Leu Lys Ala Arg Gly Ile Ala Leu Gly Val Ala
40 45 50

act ttt gaa gac gaa gcg gca ctg act gca gct ctt gaa ggt gtg gat 307
Thr Phe Glu Asp Glu Ala Ala Leu Thr Ala Ala Leu Glu Gly Val Asp
55 60 65

cgc ctt gtg ttt atc tct ggc agc gaa gtg ggg cag cgc gtt gcg cag 355
Arg Leu Val Phe Ile Ser Gly Ser Glu Val Gly Gln Arg Val Ala Gln

```
 70                  75                  80                  85

cac acc aat gtc atc aat gcc gct aaa gca gct ggc gtg aca ttc att   403
His Thr Asn Val Ile Asn Ala Ala Lys Ala Ala Gly Val Thr Phe Ile
                90                  95                 100

gca tac acc agc ttg ctc aac ctt ggt acc tca aag ctt gca ctt gct   451
Ala Tyr Thr Ser Leu Leu Asn Leu Gly Thr Ser Lys Leu Ala Leu Ala
            105                 110                 115

cca gag cac att gca acg gaa aag ctc ctg gca gaa agc ggc att gac   499
Pro Glu His Ile Ala Thr Glu Lys Leu Leu Ala Glu Ser Gly Ile Asp
        120                 125                 130

cac gcg ctg ctg cgc aat ggt tgg tac tgg gag aac tac gaa tct tca   547
His Ala Leu Leu Arg Asn Gly Trp Tyr Trp Glu Asn Tyr Glu Ser Ser
    135                 140                 145

att ggc gca gcg aag gcc acc ggg aag gta ttc ggc gca gct gaa ggc   595
Ile Gly Ala Ala Lys Ala Thr Gly Lys Val Phe Gly Ala Ala Glu Gly
150                 155                 160                 165

gca cgc gtt tcc gca gcc gca cgt aag gac tac gca gag gca gct gct   643
Ala Arg Val Ser Ala Ala Ala Arg Lys Asp Tyr Ala Glu Ala Ala Ala
                170                 175                 180

gtt gtc atc acc agc gac aac cag gca ggc aag gtc tat gag ctc gca   691
Val Val Ile Thr Ser Asp Asn Gln Ala Gly Lys Val Tyr Glu Leu Ala
            185                 190                 195

ggc gca cca gct ttg acc tac cca gag atc gca gct ggc att ggt gag   739
Gly Ala Pro Ala Leu Thr Tyr Pro Glu Ile Ala Ala Gly Ile Gly Glu
        200                 205                 210

gtc att ggt tct gag gca gaa tac gtc aac ctc tcc gtg gag gag tac   787
Val Ile Gly Ser Glu Ala Glu Tyr Val Asn Leu Ser Val Glu Glu Tyr
    215                 220                 225

caa aat gcg ctg gag cag gct ggc gtt cca gct gaa ttt gca gca ctt   835
Gln Asn Ala Leu Glu Gln Ala Gly Val Pro Ala Glu Phe Ala Ala Leu
230                 235                 240                 245

ctc gca ggc atg gat ccc atc att gca gag ggc gcg ctg tac tcc gac   883
Leu Ala Gly Met Asp Pro Ile Ile Ala Glu Gly Ala Leu Tyr Ser Asp
                250                 255                 260

agc acc gac cta cag gat ctc atc gga cgc ccg agc acc tca atc gtt   931
Ser Thr Asp Leu Gln Asp Leu Ile Gly Arg Pro Ser Thr Ser Ile Val
            265                 270                 275

gag gcc ctg agc tca taacctgcta ctcacctaaa atg                    969
Glu Ala Leu Ser Ser
        280
```

<210> 852
<211> 282
<212> PRT
<213> Corynebacterium glutamicum

<400> 852

```
Met Arg Ile Ala Val Thr Gly Ala Thr Gly Ser Leu Gly Gly His Val
  1               5                  10                  15

Val Asp Ser Leu Leu Asn Lys Gly Val Ala Ala Ser Asp Ile Val Ala
             20                  25                  30

Ile Val Arg Asn Glu Glu Lys Ala Ala Asp Leu Lys Ala Arg Gly Ile
         35                  40                  45

Ala Leu Gly Val Ala Thr Phe Glu Asp Glu Ala Ala Leu Thr Ala Ala
     50                  55                  60

Leu Glu Gly Val Asp Arg Leu Val Phe Ile Ser Gly Ser Glu Val Gly
 65                  70                  75                  80

Gln Arg Val Ala Gln His Thr Asn Val Ile Asn Ala Ala Lys Ala Ala
                 85                  90                  95

Gly Val Thr Phe Ile Ala Tyr Thr Ser Leu Leu Asn Leu Gly Thr Ser
            100                 105                 110

Lys Leu Ala Leu Ala Pro Glu His Ile Ala Thr Glu Lys Leu Leu Ala
        115                 120                 125

Glu Ser Gly Ile Asp His Ala Leu Leu Arg Asn Gly Trp Tyr Trp Glu
    130                 135                 140

Asn Tyr Glu Ser Ser Ile Gly Ala Ala Lys Ala Thr Gly Lys Val Phe
145                 150                 155                 160

Gly Ala Ala Glu Gly Ala Arg Val Ser Ala Ala Ala Arg Lys Asp Tyr
                165                 170                 175

Ala Glu Ala Ala Ala Val Val Ile Thr Ser Asp Asn Gln Ala Gly Lys
            180                 185                 190

Val Tyr Glu Leu Ala Gly Ala Pro Ala Leu Thr Tyr Pro Glu Ile Ala
        195                 200                 205

Ala Gly Ile Gly Glu Val Ile Gly Ser Glu Ala Glu Tyr Val Asn Leu
    210                 215                 220

Ser Val Glu Glu Tyr Gln Asn Ala Leu Glu Gln Ala Gly Val Pro Ala
225                 230                 235                 240

Glu Phe Ala Ala Leu Leu Ala Gly Met Asp Pro Ile Ile Ala Glu Gly
                245                 250                 255

Ala Leu Tyr Ser Asp Ser Thr Asp Leu Gln Asp Leu Ile Gly Arg Pro
            260                 265                 270

Ser Thr Ser Ile Val Glu Ala Leu Ser Ser
        275                 280
```

<210> 853
<211> 921
<212> DNA
<213> Corynebacterium glutamicum

<220>

<221> CDS
<222> (101)..(898)
<223> FRXA01875

<400> 853
ctwkcktsrs wtgtgtrsyw gawwmmcwyw cscagcatsr wgcwrgwwwy rmgkwktsca 60

syaaacwggr gtcartcscg gatctttggg tggacatgtt gtg gat agt ctt cta 115
Val Asp Ser Leu Leu
1 5

aac aag ggc gtc gca gca tca gac atc gtt gcc att gtt cga aat gaa 163
Asn Lys Gly Val Ala Ala Ser Asp Ile Val Ala Ile Val Arg Asn Glu
10 15 20

gaa aag gca gca gac ctc aaa gcc cgt gga atc gct ctt ggt gtg gct 211
Glu Lys Ala Ala Asp Leu Lys Ala Arg Gly Ile Ala Leu Gly Val Ala
25 30 35

act ttt gaa gac gaa gcg gca ctg act gca gct ctt gaa ggt gtg gat 259
Thr Phe Glu Asp Glu Ala Ala Leu Thr Ala Ala Leu Glu Gly Val Asp
40 45 50

cgc ctt gtg ttt atc tct ggc agc gaa gtg ggg cag cgc gtt gcg cag 307
Arg Leu Val Phe Ile Ser Gly Ser Glu Val Gly Gln Arg Val Ala Gln
55 60 65

cac acc aat gtc atc aat gcc gct aaa gca gct ggc gtg aca ttc att 355
His Thr Asn Val Ile Asn Ala Ala Lys Ala Ala Gly Val Thr Phe Ile
70 75 80 85

gca tac acc agc ttg ctc aac ctt ggt acc tca aag ctt gca ctt gct 403
Ala Tyr Thr Ser Leu Leu Asn Leu Gly Thr Ser Lys Leu Ala Leu Ala
90 95 100

cca gag cac att gca acg gaa aag ctc ctg gca gaa agc ggc att gac 451
Pro Glu His Ile Ala Thr Glu Lys Leu Leu Ala Glu Ser Gly Ile Asp
105 110 115

cac gcg ctg ctg cgc aat ggt tgg tac tgg gag aac tac gaa tct tca 499
His Ala Leu Leu Arg Asn Gly Trp Tyr Trp Glu Asn Tyr Glu Ser Ser
120 125 130

att ggc gca gcg aag gcc acc ggg aag gta ttc ggc gca gct gaa ggc 547
Ile Gly Ala Ala Lys Ala Thr Gly Lys Val Phe Gly Ala Ala Glu Gly
135 140 145

gca cgc gtt tcc gca gcc gca cgt aag gac tac gca gag gca gct gct 595
Ala Arg Val Ser Ala Ala Ala Arg Lys Asp Tyr Ala Glu Ala Ala Ala
150 155 160 165

gtt gtc atc acc agc gac aac cag gca ggc aag gtc tat gag ctc gca 643
Val Val Ile Thr Ser Asp Asn Gln Ala Gly Lys Val Tyr Glu Leu Ala
170 175 180

ggc gca cca gct ttg acc tac cca gag atc gca gct ggc att ggt gag 691
Gly Ala Pro Ala Leu Thr Tyr Pro Glu Ile Ala Ala Gly Ile Gly Glu
185 190 195

gtc att ggt tct gag gca gaa tac gtc aac ctc tcc gtg gag gag tac 739
Val Ile Gly Ser Glu Ala Glu Tyr Val Asn Leu Ser Val Glu Glu Tyr

```
        200                 205                 210

caa aat gcg ctg gag cag gct ggc gtt cca gct gaa ttt gca gca ctt   787
Gln Asn Ala Leu Glu Gln Ala Gly Val Pro Ala Glu Phe Ala Ala Leu
    215                 220                 225

ctc gca ggc atg gat ccc atc att gca gag ggc gcg ctg tac tcc gac   835
Leu Ala Gly Met Asp Pro Ile Ile Ala Glu Gly Ala Leu Tyr Ser Asp
230                 235                 240                 245

agc acc gac cta cag gat ctc atc gga cgc ccg agc acc tca atc gtt   883
Ser Thr Asp Leu Gln Asp Leu Ile Gly Arg Pro Ser Thr Ser Ile Val
                250                 255                 260

gag gcc ctg agc tca taacctgcta ctcacctaaa atg                    921
Glu Ala Leu Ser Ser
            265


<210> 854
<211> 266
<212> PRT
<213> Corynebacterium glutamicum

<400> 854
Val Asp Ser Leu Leu Asn Lys Gly Val Ala Ala Ser Asp Ile Val Ala
  1               5                  10                  15

Ile Val Arg Asn Glu Glu Lys Ala Ala Asp Leu Lys Ala Arg Gly Ile
             20                  25                  30

Ala Leu Gly Val Ala Thr Phe Glu Asp Glu Ala Ala Leu Thr Ala Ala
         35                  40                  45

Leu Glu Gly Val Asp Arg Leu Val Phe Ile Ser Gly Ser Glu Val Gly
     50                  55                  60

Gln Arg Val Ala Gln His Thr Asn Val Ile Asn Ala Ala Lys Ala Ala
 65                  70                  75                  80

Gly Val Thr Phe Ile Ala Tyr Thr Ser Leu Leu Asn Leu Gly Thr Ser
                 85                  90                  95

Lys Leu Ala Leu Ala Pro Glu His Ile Ala Thr Glu Lys Leu Leu Ala
            100                 105                 110

Glu Ser Gly Ile Asp His Ala Leu Leu Arg Asn Gly Trp Tyr Trp Glu
        115                 120                 125

Asn Tyr Glu Ser Ser Ile Gly Ala Ala Lys Ala Thr Gly Lys Val Phe
    130                 135                 140

Gly Ala Ala Glu Gly Ala Arg Val Ser Ala Ala Ala Arg Lys Asp Tyr
145                 150                 155                 160

Ala Glu Ala Ala Ala Val Val Ile Thr Ser Asp Asn Gln Ala Gly Lys
                165                 170                 175

Val Tyr Glu Leu Ala Gly Ala Pro Ala Leu Thr Tyr Pro Glu Ile Ala
            180                 185                 190
```

```
Ala Gly Ile Gly Glu Val Ile Gly Ser Glu Ala Glu Tyr Val Asn Leu
        195                 200                 205

Ser Val Glu Glu Tyr Gln Asn Ala Leu Glu Gln Ala Gly Val Pro Ala
    210                 215                 220

Glu Phe Ala Ala Leu Leu Ala Gly Met Asp Pro Ile Ile Ala Glu Gly
225                 230                 235                 240

Ala Leu Tyr Ser Asp Ser Thr Asp Leu Gln Asp Leu Ile Gly Arg Pro
                245                 250                 255

Ser Thr Ser Ile Val Glu Ala Leu Ser Ser
            260                 265


<210> 855
<211> 484
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(484)
<223> FRXA02734

<400> 855
aatcctatcc ctaaaaagtt tctaacaaaa gtattgcact tacttttttga tagtgctatc 60

ttcagttgtg tacttgaaac acacacgaat ggagcaagaa atg cgt att gca gta   115
                                              Met Arg Ile Ala Val
                                                1               5

act gga gca acg gga tct ttg ggt gga cat gtt gtg gat agt ctt cta   163
Thr Gly Ala Thr Gly Ser Leu Gly Gly His Val Val Asp Ser Leu Leu
                10                  15                  20

aac aag ggc gtc gca gca tca gac atc gtt gcc att gtt cga aat gaa   211
Asn Lys Gly Val Ala Ala Ser Asp Ile Val Ala Ile Val Arg Asn Glu
            25                  30                  35

gaa aag gca gca gac ctc aaa gcc cgt gga atc gct ctt ggt gtg gct   259
Glu Lys Ala Ala Asp Leu Lys Ala Arg Gly Ile Ala Leu Gly Val Ala
        40                  45                  50

act ttt gaa gac gaa acg gca ctg act gca gct ctt gaa ggt gtg gat   307
Thr Phe Glu Asp Glu Thr Ala Leu Thr Ala Ala Leu Glu Gly Val Asp
    55                  60                  65

cgc ctt gtg ttt atc tct ggc agc gaa gtg ggg cag cgc gtt gcg caa   355
Arg Leu Val Phe Ile Ser Gly Ser Glu Val Gly Gln Arg Val Ala Gln
70                  75                  80                  85

cac acc aat gtc atc aat gcc gct aaa gca act ggc gtg aca ttc att   403
His Thr Asn Val Ile Asn Ala Ala Lys Ala Thr Gly Val Thr Phe Ile
                90                  95                  100

gca tac acc agc ttg ctc aac ctt ggt cct caa agc ttg cac ttg ctc   451
Ala Tyr Thr Ser Leu Leu Asn Leu Gly Pro Gln Ser Leu His Leu Leu
            105                 110                 115
```

```
cag agc aca ttg caa ccg gaa aag ctc ctg gca                          484
Gln Ser Thr Leu Gln Pro Glu Lys Leu Leu Ala
        120                 125


<210> 856
<211> 128
<212> PRT
<213> Corynebacterium glutamicum

<400> 856
Met Arg Ile Ala Val Thr Gly Ala Thr Gly Ser Leu Gly Gly His Val
  1               5                  10                  15

Val Asp Ser Leu Leu Asn Lys Gly Val Ala Ala Ser Asp Ile Val Ala
             20                  25                  30

Ile Val Arg Asn Glu Glu Lys Ala Ala Asp Leu Lys Ala Arg Gly Ile
         35                  40                  45

Ala Leu Gly Val Ala Thr Phe Glu Asp Glu Thr Ala Leu Thr Ala Ala
     50                  55                  60

Leu Glu Gly Val Asp Arg Leu Val Phe Ile Ser Gly Ser Glu Val Gly
 65                  70                  75                  80

Gln Arg Val Ala Gln His Thr Asn Val Ile Asn Ala Ala Lys Ala Thr
                 85                  90                  95

Gly Val Thr Phe Ile Ala Tyr Thr Ser Leu Leu Asn Leu Gly Pro Gln
            100                 105                 110

Ser Leu His Leu Leu Gln Ser Thr Leu Gln Pro Glu Lys Leu Leu Ala
        115                 120                 125




<210> 857
<211> 1194
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1171)
<223> RXN01877

<400> 857
gtacccgtat tgtactaatt gtaattcccc ggagagggaa gaagtttaca tggcgcccca 60

tcagaagtca gggatcaacc ggatcaacag cacccgctcg gtg ccg ttg cgt ttg   115
                                            Val Pro Leu Arg Leu
                                              1               5

gct acc ggt ggc gtg ctc gcc acc ttg ctt atc ggc gga gtc acc gct   163
Ala Thr Gly Gly Val Leu Ala Thr Leu Leu Ile Gly Gly Val Thr Ala
                 10                  15                  20

gca gct acc aaa aag gac atc att gtt gat gtc aac ggc gag cag atg   211
```

```
Ala Ala Thr Lys Lys Asp Ile Ile Val Asp Val Asn Gly Glu Gln Met
            25                  30                  35

tcc cta gtg act atg tcc ggc act gtt gaa ggt gtg ctg gcg caa gct   259
Ser Leu Val Thr Met Ser Gly Thr Val Glu Gly Val Leu Ala Gln Ala
        40                  45                  50

ggt gtg gaa ctt ggt gac cag gac att gtt tcc cct tca ctg gat tca   307
Gly Val Glu Leu Gly Asp Gln Asp Ile Val Ser Pro Ser Leu Asp Ser
    55                  60                  65

tcc atc agt gat gaa gac act gtg act gtt cgt act gcc aag cag gtg   355
Ser Ile Ser Asp Glu Asp Thr Val Thr Val Arg Thr Ala Lys Gln Val
70                  75                  80                  85

gcg ctc gtg gtg gaa ggt caa atc caa aac gtg acc acc act gcg gtt   403
Ala Leu Val Val Glu Gly Gln Ile Gln Asn Val Thr Thr Thr Ala Val
                90                  95                  100

tcc gtg gag gac ctc ctg cag gaa gtc ggt ggc att acc ggt gct gat   451
Ser Val Glu Asp Leu Leu Gln Glu Val Gly Gly Ile Thr Gly Ala Asp
            105                 110                 115

gcg gtg gac gct gat ctt tca gag acc atc cca gaa tct ggt ttg aag   499
Ala Val Asp Ala Asp Leu Ser Glu Thr Ile Pro Glu Ser Gly Leu Lys
        120                 125                 130

gtg agt gtt acc aag ccg aag att att tcc atc aat gat ggt ggc aag   547
Val Ser Val Thr Lys Pro Lys Ile Ile Ser Ile Asn Asp Gly Gly Lys
    135                 140                 145

gtc act tac gtt tct ttg gca gct cag aac gta cag gaa gcc cta gag   595
Val Thr Tyr Val Ser Leu Ala Ala Gln Asn Val Gln Glu Ala Leu Glu
150                 155                 160                 165

ctg cgg gat att gag ctg ggt gct cag gac cgc att aat gtg cct ctg   643
Leu Arg Asp Ile Glu Leu Gly Ala Gln Asp Arg Ile Asn Val Pro Leu
                170                 175                 180

gat cag cag ctg aag aac aac gct gcg atc cag atc gac cgc gtt gac   691
Asp Gln Gln Leu Lys Asn Asn Ala Ala Ile Gln Ile Asp Arg Val Asp
            185                 190                 195

aac acc gaa atc act gaa act gtg tct ttc gat gct gag cca acc tac   739
Asn Thr Glu Ile Thr Glu Thr Val Ser Phe Asp Ala Glu Pro Thr Tyr
        200                 205                 210

gtg gat gat cca gaa gct cca gct ggc gat gaa act gtg gtc gaa gaa   787
Val Asp Asp Pro Glu Ala Pro Ala Gly Asp Glu Thr Val Val Glu Glu
    215                 220                 225

ggc gct cct gga acc aag gaa gtt act cgc acc gta aca acc gtt aat   835
Gly Ala Pro Gly Thr Lys Glu Val Thr Arg Thr Val Thr Thr Val Asn
230                 235                 240                 245

ggt cag gaa gaa tct tcc acg gtg atc aat gaa gtt gaa atc acc gca   883
Gly Gln Glu Glu Ser Ser Thr Val Ile Asn Glu Val Glu Ile Thr Ala
                250                 255                 260

gca aag cca gca acc att agc cgt ggc acc aaa act gtc gct gca aac   931
Ala Lys Pro Ala Thr Ile Ser Arg Gly Thr Lys Thr Val Ala Ala Asn
```

```
            265                 270                 275

tcc gtg tgg gat cag ctg gca cag tgt gaa tcc ggc gga aac tgg gca   979
Ser Val Trp Asp Gln Leu Ala Gln Cys Glu Ser Gly Gly Asn Trp Ala
        280                 285                 290

atc aac aca ggt aat ggc ttc tcc ggc ggc cta cag ttc cac cca cag   1027
Ile Asn Thr Gly Asn Gly Phe Ser Gly Gly Leu Gln Phe His Pro Gln
    295                 300                 305

acc tgg ctc gca tac ggt ggt gga gct ttc tcc ggt gac gct tcc ggt   1075
Thr Trp Leu Ala Tyr Gly Gly Gly Ala Phe Ser Gly Asp Ala Ser Gly
310                 315                 320                 325

gca agc cgt gaa cag caa atc tcc atc gca gaa aag gtt cag gct gca   1123
Ala Ser Arg Glu Gln Gln Ile Ser Ile Ala Glu Lys Val Gln Ala Ala
                330                 335                 340

caa ggt tgg gga gca tgg cct gct tgc acc gca agc ttg ggc atc cga   1171
Gln Gly Trp Gly Ala Trp Pro Ala Cys Thr Ala Ser Leu Gly Ile Arg
            345                 350                 355

tagtagaaat ctggcatcca ata                                        1194


<210> 858
<211> 357
<212> PRT
<213> Corynebacterium glutamicum

<400> 858
Val Pro Leu Arg Leu Ala Thr Gly Gly Val Leu Ala Thr Leu Leu Ile
  1               5                  10                  15

Gly Gly Val Thr Ala Ala Ala Thr Lys Lys Asp Ile Ile Val Asp Val
             20                  25                  30

Asn Gly Glu Gln Met Ser Leu Val Thr Met Ser Gly Thr Val Glu Gly
         35                  40                  45

Val Leu Ala Gln Ala Gly Val Glu Leu Gly Asp Gln Asp Ile Val Ser
     50                  55                  60

Pro Ser Leu Asp Ser Ser Ile Ser Asp Glu Asp Thr Val Thr Val Arg
 65                  70                  75                  80

Thr Ala Lys Gln Val Ala Leu Val Val Glu Gly Gln Ile Gln Asn Val
                 85                  90                  95

Thr Thr Thr Ala Val Ser Val Glu Asp Leu Leu Gln Glu Val Gly Gly
            100                 105                 110

Ile Thr Gly Ala Asp Ala Val Asp Ala Asp Leu Ser Glu Thr Ile Pro
        115                 120                 125

Glu Ser Gly Leu Lys Val Ser Val Thr Lys Pro Lys Ile Ile Ser Ile
    130                 135                 140

Asn Asp Gly Gly Lys Val Thr Tyr Val Ser Leu Ala Ala Gln Asn Val
145                 150                 155                 160
```

```
Gln Glu Ala Leu Glu Leu Arg Asp Ile Glu Leu Gly Ala Gln Asp Arg
                165                 170                 175

Ile Asn Val Pro Leu Asp Gln Gln Leu Lys Asn Asn Ala Ala Ile Gln
            180                 185                 190

Ile Asp Arg Val Asp Asn Thr Glu Ile Thr Glu Thr Val Ser Phe Asp
        195                 200                 205

Ala Glu Pro Thr Tyr Val Asp Asp Pro Glu Ala Pro Ala Gly Asp Glu
    210                 215                 220

Thr Val Val Glu Glu Gly Ala Pro Gly Thr Lys Glu Val Thr Arg Thr
225                 230                 235                 240

Val Thr Thr Val Asn Gly Gln Glu Glu Ser Ser Thr Val Ile Asn Glu
                245                 250                 255

Val Glu Ile Thr Ala Ala Lys Pro Ala Thr Ile Ser Arg Gly Thr Lys
            260                 265                 270

Thr Val Ala Ala Asn Ser Val Trp Asp Gln Leu Ala Gln Cys Glu Ser
        275                 280                 285

Gly Gly Asn Trp Ala Ile Asn Thr Gly Asn Gly Phe Ser Gly Gly Leu
    290                 295                 300

Gln Phe His Pro Gln Thr Trp Leu Ala Tyr Gly Gly Gly Ala Phe Ser
305                 310                 315                 320

Gly Asp Ala Ser Gly Ala Ser Arg Glu Gln Gln Ile Ser Ile Ala Glu
                325                 330                 335

Lys Val Gln Ala Ala Gln Gly Trp Gly Ala Trp Pro Ala Cys Thr Ala
            340                 345                 350

Ser Leu Gly Ile Arg
        355
```

Application Filed with the Patent Office

<210> 859
<211> 1188
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1165)
<223> FRXA01877

<400> 859
gtattgtact aattgtaatt ccccggagag ggaagaagtt tacatggcgc cccatcagaa 60

gtcagggatc aaccggatca acagcacccg ctcggtgccg ttg cgt ttg gct acc 115
                                          Leu Arg Leu Ala Thr
                                            1   5

ggt ggc gtg ctc gcc acc ttg ctt atc ggc gga gtc acc gct gca gct 163
Gly Gly Val Leu Ala Thr Leu Leu Ile Gly Gly Val Thr Ala Ala Ala
                10   15   20

```
acc aaa aag gac atc att gtt gat gtc aac ggc gag cag atg tcc cta   211
Thr Lys Lys Asp Ile Ile Val Asp Val Asn Gly Glu Gln Met Ser Leu
            25                  30                  35

gtg act atg tcc ggc act gtt gaa ggt gtg ctg gcg caa gct ggt gtg   259
Val Thr Met Ser Gly Thr Val Glu Gly Val Leu Ala Gln Ala Gly Val
        40                  45                  50

gaa ctt ggt gac cag gac att gtt tcc cct tca ctg gat tca tcc atc   307
Glu Leu Gly Asp Gln Asp Ile Val Ser Pro Ser Leu Asp Ser Ser Ile
    55                  60                  65

agt gat gaa gac act gtg act gtt cgt act gcc aag cag gtg gcg ctc   355
Ser Asp Glu Asp Thr Val Thr Val Arg Thr Ala Lys Gln Val Ala Leu
70                  75                  80                  85

gtg gtg gaa ggt caa atc caa aac gtg acc acc act gcg gtt tcc gtg   403
Val Val Glu Gly Gln Ile Gln Asn Val Thr Thr Thr Ala Val Ser Val
                90                  95                  100

gag gac ctc ctg cag gaa gtc ggt ggc att acc ggt gct gat gcg gtg   451
Glu Asp Leu Leu Gln Glu Val Gly Gly Ile Thr Gly Ala Asp Ala Val
            105                 110                 115

gac gct gat ctt tca gag acc atc cca gaa tct ggt ttg aag gtg agt   499
Asp Ala Asp Leu Ser Glu Thr Ile Pro Glu Ser Gly Leu Lys Val Ser
        120                 125                 130

gtt acc aag ccg aag att att tcc atc aat gat ggt ggc aag gtc act   547
Val Thr Lys Pro Lys Ile Ile Ser Ile Asn Asp Gly Gly Lys Val Thr
    135                 140                 145

tac gtt tct ttg gca gct cag aac gta cag gaa gcc cta gag ctg cgg   595
Tyr Val Ser Leu Ala Ala Gln Asn Val Gln Glu Ala Leu Glu Leu Arg
150                 155                 160                 165

gat att gag ctg ggt gct cag gac cgc att aat gtg cct ctg gat cag   643
Asp Ile Glu Leu Gly Ala Gln Asp Arg Ile Asn Val Pro Leu Asp Gln
                170                 175                 180

cag ctg aag aac aac gct gcg atc cag atc gac cgc gtt gac aac acc   691
Gln Leu Lys Asn Asn Ala Ala Ile Gln Ile Asp Arg Val Asp Asn Thr
            185                 190                 195

gaa atc act gaa act gtg tct ttc gat gct gag cca acc tac gtg gat   739
Glu Ile Thr Glu Thr Val Ser Phe Asp Ala Glu Pro Thr Tyr Val Asp
        200                 205                 210

gat cca gaa gct cca gct ggc gat gaa act gtg gtc gaa gaa ggc gct   787
Asp Pro Glu Ala Pro Ala Gly Asp Glu Thr Val Val Glu Glu Gly Ala
    215                 220                 225

cct gga acc aag gaa gtt act cgc acc gta aca acc gtt aat ggt cag   835
Pro Gly Thr Lys Glu Val Thr Arg Thr Val Thr Thr Val Asn Gly Gln
230                 235                 240                 245

gaa gaa tct tcc acg gtg atc aat gaa gtt gaa atc acc gca gca aag   883
Glu Glu Ser Ser Thr Val Ile Asn Glu Val Glu Ile Thr Ala Ala Lys
                250                 255                 260

cca gca acc att agc cgt ggc acc aaa act gtc gct gca aac tcc gtg   931
```

```
Pro Ala Thr Ile Ser Arg Gly Thr Lys Thr Val Ala Ala Asn Ser Val
            265                 270                 275

tgg gat cag ctg gca cag tgt gaa tcc ggc gga aac tgg gca atc aac   979
Trp Asp Gln Leu Ala Gln Cys Glu Ser Gly Gly Asn Trp Ala Ile Asn
        280                 285                 290

aca ggt aat ggc ttc tcc ggc ggc cta cag ttc cac cca cag acc tgg   1027
Thr Gly Asn Gly Phe Ser Gly Gly Leu Gln Phe His Pro Gln Thr Trp
    295                 300                 305

ctc gca tac ggt ggt gga gct ttc tcc ggt gac gct tcc ggt gca agc   1075
Leu Ala Tyr Gly Gly Gly Ala Phe Ser Gly Asp Ala Ser Gly Ala Ser
310                 315                 320                 325

cgt gaa cag caa atc tcc atc gca gaa aag gtt cag gct gca caa ggt   1123
Arg Glu Gln Gln Ile Ser Ile Ala Glu Lys Val Gln Ala Ala Gln Gly
                330                 335                 340

tgg gga gca tgg cct gct tgc acc gca agc ttg ggc atc cga           1165
Trp Gly Ala Trp Pro Ala Cys Thr Ala Ser Leu Gly Ile Arg
            345                 350                 355

tagtagaaat ctggcatcca ata                                        1188


<210> 860
<211> 355
<212> PRT
<213> Corynebacterium glutamicum

<400> 860
Leu Arg Leu Ala Thr Gly Gly Val Leu Ala Thr Leu Leu Ile Gly Gly
  1               5                  10                  15

Val Thr Ala Ala Ala Thr Lys Lys Asp Ile Ile Val Asp Val Asn Gly
             20                  25                  30

Glu Gln Met Ser Leu Val Thr Met Ser Gly Thr Val Glu Gly Val Leu
         35                  40                  45

Ala Gln Ala Gly Val Glu Leu Gly Asp Gln Asp Ile Val Ser Pro Ser
     50                  55                  60

Leu Asp Ser Ser Ile Ser Asp Glu Asp Thr Val Thr Val Arg Thr Ala
 65                  70                  75                  80

Lys Gln Val Ala Leu Val Val Glu Gly Gln Ile Gln Asn Val Thr Thr
                 85                  90                  95

Thr Ala Val Ser Val Glu Asp Leu Leu Gln Glu Val Gly Gly Ile Thr
            100                 105                 110

Gly Ala Asp Ala Val Asp Ala Asp Leu Ser Glu Thr Ile Pro Glu Ser
        115                 120                 125

Gly Leu Lys Val Ser Val Thr Lys Pro Lys Ile Ile Ser Ile Asn Asp
    130                 135                 140

Gly Gly Lys Val Thr Tyr Val Ser Leu Ala Ala Gln Asn Val Gln Glu
145                 150                 155                 160
```

```
Ala Leu Glu Leu Arg Asp Ile Glu Leu Gly Ala Gln Asp Arg Ile Asn
               165                 170                 175

Val Pro Leu Asp Gln Gln Leu Lys Asn Asn Ala Ala Ile Gln Ile Asp
            180                 185                 190

Arg Val Asp Asn Thr Glu Ile Thr Glu Thr Val Ser Phe Asp Ala Glu
        195                 200                 205

Pro Thr Tyr Val Asp Asp Pro Glu Ala Pro Ala Gly Asp Glu Thr Val
    210                 215                 220

Val Glu Glu Gly Ala Pro Gly Thr Lys Glu Val Thr Arg Thr Val Thr
225                 230                 235                 240

Thr Val Asn Gly Gln Glu Glu Ser Ser Thr Val Ile Asn Glu Val Glu
               245                 250                 255

Ile Thr Ala Ala Lys Pro Ala Thr Ile Ser Arg Gly Thr Lys Thr Val
            260                 265                 270

Ala Ala Asn Ser Val Trp Asp Gln Leu Ala Gln Cys Glu Ser Gly Gly
        275                 280                 285

Asn Trp Ala Ile Asn Thr Gly Asn Gly Phe Ser Gly Gly Leu Gln Phe
    290                 295                 300

His Pro Gln Thr Trp Leu Ala Tyr Gly Gly Gly Ala Phe Ser Gly Asp
305                 310                 315                 320

Ala Ser Gly Ala Ser Arg Glu Gln Gln Ile Ser Ile Ala Glu Lys Val
               325                 330                 335

Gln Ala Ala Gln Gly Trp Gly Ala Trp Pro Ala Cys Thr Ala Ser Leu
            340                 345                 350

Gly Ile Arg
        355
```

Sequence Listing - Page 1046 - 2010-12-20 09:44:56

<210> 861
<211> 1056
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1033)
<223> RXN01879

<400> 861
ctttgcgggc cgctgatatt gatccaacgc ttcgtggcga aaagcttgat gtcactgact 60

atgtgcgcct agctggggtg ttgcagcaaa aggatgagaa gtg aaa att acc gct 115
                                              Val Lys Ile Thr Ala
                                                1   5

aag gcg tgg gcg aaa acc aac ctg cat tta ggt gtg gga ccg gct cac 163
Lys Ala Trp Ala Lys Thr Asn Leu His Leu Gly Val Gly Pro Ala His
                10   15   20

```
gac gat gga ttt cac gag ctc atg acg gtg ttt caa acc att gat ctg   211
Asp Asp Gly Phe His Glu Leu Met Thr Val Phe Gln Thr Ile Asp Leu
            25                  30                  35

ttt gac acc gtc acc tta acc acc ctc gat gag gag ttg gtg gag gag   259
Phe Asp Thr Val Thr Leu Thr Thr Leu Asp Glu Glu Leu Val Glu Glu
        40                  45                  50

ggg agc gtc gtc aag caa tta tct gtg acc ggt gcc cgt ggc gtg cct   307
Gly Ser Val Val Lys Gln Leu Ser Val Thr Gly Ala Arg Gly Val Pro
    55                  60                  65

gag gac gcc agc aat ctt gcg tgg cgc gct gtg gat gcg ttg gtt aag   355
Glu Asp Ala Ser Asn Leu Ala Trp Arg Ala Val Asp Ala Leu Val Lys
70                  75                  80                  85

cgg cgc gcg gaa aag acg ccg ctg tct gca gtt tcg ctg cat att tcc   403
Arg Arg Ala Glu Lys Thr Pro Leu Ser Ala Val Ser Leu His Ile Ser
                90                  95                  100

aag ggg att ccg gtg gct ggc ggc atg gct ggc ggc tct gcg gat gcg   451
Lys Gly Ile Pro Val Ala Gly Gly Met Ala Gly Gly Ser Ala Asp Ala
            105                 110                 115

gct gcg aca ctg cgc gca gtg gat gcc tgg att ggg cct ttc ggc gag   499
Ala Ala Thr Leu Arg Ala Val Asp Ala Trp Ile Gly Pro Phe Gly Glu
        120                 125                 130

gac aca ttg ctg gag gtt gcc gcg gag ctc ggc tca gat gtg ccg ttt   547
Asp Thr Leu Leu Glu Val Ala Ala Glu Leu Gly Ser Asp Val Pro Phe
    135                 140                 145

tgc ctg ctt ggt ggc acc atg cgc ggt acc ggt cgc ggc gag cag ctg   595
Cys Leu Leu Gly Gly Thr Met Arg Gly Thr Gly Arg Gly Glu Gln Leu
150                 155                 160                 165

gta gat atg ttg acg cgc ggc aag cta cat tgg gtg gtg gcc gcg atg   643
Val Asp Met Leu Thr Arg Gly Lys Leu His Trp Val Val Ala Ala Met
                170                 175                 180

gcg cat ggc ctg tcc acg cct gag gta ttc aaa aag cat gat gag ctg   691
Ala His Gly Leu Ser Thr Pro Glu Val Phe Lys Lys His Asp Glu Leu
            185                 190                 195

aat ccg gaa tcg cat atg gat atc agc gac ctc agc gcc gca ctt ctc   739
Asn Pro Glu Ser His Met Asp Ile Ser Asp Leu Ser Ala Ala Leu Leu
        200                 205                 210

acc ggc aac acc gcc gag gtg ggg cag tgg ctg cac aat gat ctg acc   787
Thr Gly Asn Thr Ala Glu Val Gly Gln Trp Leu His Asn Asp Leu Thr
    215                 220                 225

agc gcc gca ctc agt ttg cgc cct gaa ctg cgc agc gtc ctc caa gaa   835
Ser Ala Ala Leu Ser Leu Arg Pro Glu Leu Arg Ser Val Leu Gln Glu
230                 235                 240                 245

ggc atc cgc tcc ggc gcg cat gca gga att gtc tcc ggc tcc ggc ccg   883
Gly Ile Arg Ser Gly Ala His Ala Gly Ile Val Ser Gly Ser Gly Pro
                250                 255                 260
```

```
acc acg gta ttc ttg tgc gaa tcg gag cac aaa gcg caa gac gtt aaa   931
Thr Thr Val Phe Leu Cys Glu Ser Glu His Lys Ala Gln Asp Val Lys
            265                 270                 275

gag gcg cta atc gac gcc ggc cag gtg tac gct gct tac acc gcc acc   979
Glu Ala Leu Ile Asp Ala Gly Gln Val Tyr Ala Ala Tyr Thr Ala Thr
        280                 285                 290

ggc cct gcg gcc tca acc gcc gac cag cgc ggc gca cac att ttg act   1027
Gly Pro Ala Ala Ser Thr Ala Asp Gln Arg Gly Ala His Ile Leu Thr
    295                 300                 305

gtt tca taataaagac aaacttaagt atc                                 1056
Val Ser
310
```

<210> 862
<211> 311
<212> PRT
<213> Corynebacterium glutamicum

<400> 862

```
Val Lys Ile Thr Ala Lys Ala Trp Ala Lys Thr Asn Leu His Leu Gly
  1               5                  10                  15

Val Gly Pro Ala His Asp Asp Gly Phe His Glu Leu Met Thr Val Phe
             20                  25                  30

Gln Thr Ile Asp Leu Phe Asp Thr Val Thr Leu Thr Thr Leu Asp Glu
         35                  40                  45

Glu Leu Val Glu Glu Gly Ser Val Val Lys Gln Leu Ser Val Thr Gly
     50                  55                  60

Ala Arg Gly Val Pro Glu Asp Ala Ser Asn Leu Ala Trp Arg Ala Val
 65                  70                  75                  80

Asp Ala Leu Val Lys Arg Arg Ala Glu Lys Thr Pro Leu Ser Ala Val
                 85                  90                  95

Ser Leu His Ile Ser Lys Gly Ile Pro Val Ala Gly Gly Met Ala Gly
            100                 105                 110

Gly Ser Ala Asp Ala Ala Ala Thr Leu Arg Ala Val Asp Ala Trp Ile
        115                 120                 125

Gly Pro Phe Gly Glu Asp Thr Leu Leu Glu Val Ala Ala Glu Leu Gly
    130                 135                 140

Ser Asp Val Pro Phe Cys Leu Leu Gly Gly Thr Met Arg Gly Thr Gly
145                 150                 155                 160

Arg Gly Glu Gln Leu Val Asp Met Leu Thr Arg Gly Lys Leu His Trp
                165                 170                 175

Val Val Ala Ala Met Ala His Gly Leu Ser Thr Pro Glu Val Phe Lys
            180                 185                 190

Lys His Asp Glu Leu Asn Pro Glu Ser His Met Asp Ile Ser Asp Leu
        195                 200                 205
```

```
Ser Ala Ala Leu Leu Thr Gly Asn Thr Ala Glu Val Gly Gln Trp Leu
    210                 215                 220

His Asn Asp Leu Thr Ser Ala Ala Leu Ser Leu Arg Pro Glu Leu Arg
225                 230                 235                 240

Ser Val Leu Gln Glu Gly Ile Arg Ser Gly Ala His Ala Gly Ile Val
                245                 250                 255

Ser Gly Ser Gly Pro Thr Thr Val Phe Leu Cys Glu Ser Glu His Lys
            260                 265                 270

Ala Gln Asp Val Lys Glu Ala Leu Ile Asp Ala Gly Gln Val Tyr Ala
        275                 280                 285

Ala Tyr Thr Ala Thr Gly Pro Ala Ala Ser Thr Ala Asp Gln Arg Gly
    290                 295                 300

Ala His Ile Leu Thr Val Ser
305                 310
```

Application Filed with the USPTO - Do Not Enter Into Computer

<210> 863
<211> 711
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(688)
<223> FRXA01879

<400> 863

```
ctttgcgggc cgctgatatt gatccaacgc ttcgtggcga aaagcttgat gtcactgact 60

atgtgcgcct agctggggtg ttgcagcaaa aggatgagaa gtg aaa att acc gct   115
                                              Val Lys Ile Thr Ala
                                                1               5

aag gcg tgg gcg aaa acc aac ctg cat tta ggt gtg gga ccg gct cac   163
Lys Ala Trp Ala Lys Thr Asn Leu His Leu Gly Val Gly Pro Ala His
                10                  15                  20

gac gat gga ttt cac gag ctc atg acg gtg ttt caa acc att gat ctg   211
Asp Asp Gly Phe His Glu Leu Met Thr Val Phe Gln Thr Ile Asp Leu
            25                  30                  35

ttt gac acc gtc acc tta acc acc ctc gat gag gag ttg gtg gag gag   259
Phe Asp Thr Val Thr Leu Thr Thr Leu Asp Glu Glu Leu Val Glu Glu
        40                  45                  50

ggg agc gtc gtc aag caa tta tct gtg acc ggt gcc cgt ggc gtg cct   307
Gly Ser Val Val Lys Gln Leu Ser Val Thr Gly Ala Arg Gly Val Pro
    55                  60                  65

gag gac gcc agc aat ctt gcg tgg cgc gct gtg gat gcg ttg gtt aag   355
Glu Asp Ala Ser Asn Leu Ala Trp Arg Ala Val Asp Ala Leu Val Lys
70                  75                  80                  85

cgg cgc gcg gaa aag acg ccg ctg tct gca gtt tcg ctg cat att tcc   403
```

```
Arg Arg Ala Glu Lys Thr Pro Leu Ser Ala Val Ser Leu His Ile Ser
                 90                  95                 100

aag ggg att ccg gtg gct ggc ggc atg gct ggc ggc tct gcg gat gcg   451
Lys Gly Ile Pro Val Ala Gly Gly Met Ala Gly Gly Ser Ala Asp Ala
            105                 110                 115

gct gcg aca ctg cgc gca gtg gat gcc tgg att ggg cct ttc ggc gag   499
Ala Ala Thr Leu Arg Ala Val Asp Ala Trp Ile Gly Pro Phe Gly Glu
        120                 125                 130

gac aca ttg ctg gag gtt gcc gcg gag ctc ggc tca gat gtg ccg ttt   547
Asp Thr Leu Leu Glu Val Ala Ala Glu Leu Gly Ser Asp Val Pro Phe
    135                 140                 145

tgc ctg ctt ggt ggc acc atg cgc ggt acc ggt cgc ggc gag cag ctg   595
Cys Leu Leu Gly Gly Thr Met Arg Gly Thr Gly Arg Gly Glu Gln Leu
150                 155                 160                 165

gta gat atg ttg acg cgc ggc aag cta cat tgg gtg gtg gcc gcg atg   643
Val Asp Met Leu Thr Arg Gly Lys Leu His Trp Val Val Ala Ala Met
                170                 175                 180

gcg cat ggc ctg tcc acc ctg agg tat tca aaa agc atg atg agc       688
Ala His Gly Leu Ser Thr Leu Arg Tyr Ser Lys Ser Met Met Ser
            185                 190                 195

tgaatccgga atcgcatatg gat                                        711


<210> 864
<211> 196
<212> PRT
<213> Corynebacterium glutamicum

<400> 864
Val Lys Ile Thr Ala Lys Ala Trp Ala Lys Thr Asn Leu His Leu Gly
  1               5                  10                  15

Val Gly Pro Ala His Asp Asp Gly Phe His Glu Leu Met Thr Val Phe
             20                  25                  30

Gln Thr Ile Asp Leu Phe Asp Thr Val Thr Leu Thr Thr Leu Asp Glu
         35                  40                  45

Glu Leu Val Glu Glu Gly Ser Val Val Lys Gln Leu Ser Val Thr Gly
     50                  55                  60

Ala Arg Gly Val Pro Glu Asp Ala Ser Asn Leu Ala Trp Arg Ala Val
 65                  70                  75                  80

Asp Ala Leu Val Lys Arg Arg Ala Glu Lys Thr Pro Leu Ser Ala Val
                 85                  90                  95

Ser Leu His Ile Ser Lys Gly Ile Pro Val Ala Gly Gly Met Ala Gly
            100                 105                 110

Gly Ser Ala Asp Ala Ala Ala Thr Leu Arg Ala Val Asp Ala Trp Ile
        115                 120                 125

Gly Pro Phe Gly Glu Asp Thr Leu Leu Glu Val Ala Ala Glu Leu Gly
```

```
    130                 135                 140

Ser Asp Val Pro Phe Cys Leu Leu Gly Gly Thr Met Arg Gly Thr Gly
145                 150                 155                 160

Arg Gly Glu Gln Leu Val Asp Met Leu Thr Arg Gly Lys Leu His Trp
                165                 170                 175

Val Val Ala Ala Met Ala His Gly Leu Ser Thr Leu Arg Tyr Ser Lys
            180                 185                 190

Ser Met Met Ser
        195


<210> 865
<211> 531
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(508)
<223> FRXA01880

<400> 865
agctcggctc agatgtgccg ttttgcctgc ttggtggcac catgcgcggt accggtcgcg 60

gcgagcagct ggtagatatg ttgacgcgcg gcaagctaca ttg ggt ggt ggc cgc   115
                                            Leu Gly Gly Gly Arg
                                              1               5

gat ggc gca tgg cct gtc cac cct gag gta ttc aaa aag cat gat gag   163
Asp Gly Ala Trp Pro Val His Pro Glu Val Phe Lys Lys His Asp Glu
                10                  15                  20

ctg aat ccg gaa tcg cat atg gat atc agc gac ctc agc gcc gca ctt   211
Leu Asn Pro Glu Ser His Met Asp Ile Ser Asp Leu Ser Ala Ala Leu
            25                  30                  35

ctc acc ggc aac acc gcc gag gtg ggg cag tgg ctg cac aat gat ctg   259
Leu Thr Gly Asn Thr Ala Glu Val Gly Gln Trp Leu His Asn Asp Leu
        40                  45                  50

acc agc gcc gca ctc agt ttg cgc cct gaa ctg cgc agc gtc ctc caa   307
Thr Ser Ala Ala Leu Ser Leu Arg Pro Glu Leu Arg Ser Val Leu Gln
    55                  60                  65

gaa ggc atc cgc tcc ggc gcg cat gca gga att gtc tcc ggc tcc ggc   355
Glu Gly Ile Arg Ser Gly Ala His Ala Gly Ile Val Ser Gly Ser Gly
70                  75                  80                  85

ccg acc acg gta ttc ttg tgc gaa tcg gag cac aaa gcg caa gac gtt   403
Pro Thr Thr Val Phe Leu Cys Glu Ser Glu His Lys Ala Gln Asp Val
                90                  95                  100

aaa gag gcg cta atc gac gcc ggc cag gtg tac gct gct tac acc gcc   451
Lys Glu Ala Leu Ile Asp Ala Gly Gln Val Tyr Ala Ala Tyr Thr Ala
            105                 110                 115

acc ggc cct gcg gcc tca acc gcc gac cag cgc ggc gca cac att ttg   499
```

```
Thr Gly Pro Ala Ala Ser Thr Ala Asp Gln Arg Gly Ala His Ile Leu
        120                 125                 130

act gtt tca taataaagac aaacttaagt atc                                  531
Thr Val Ser
    135


<210> 866
<211> 136
<212> PRT
<213> Corynebacterium glutamicum

<400> 866
Leu Gly Gly Gly Arg Asp Gly Ala Trp Pro Val His Pro Glu Val Phe
  1               5                  10                  15

Lys Lys His Asp Glu Leu Asn Pro Glu Ser His Met Asp Ile Ser Asp
             20                  25                  30

Leu Ser Ala Ala Leu Leu Thr Gly Asn Thr Ala Glu Val Gly Gln Trp
         35                  40                  45

Leu His Asn Asp Leu Thr Ser Ala Ala Leu Ser Leu Arg Pro Glu Leu
     50                  55                  60

Arg Ser Val Leu Gln Glu Gly Ile Arg Ser Gly Ala His Ala Gly Ile
 65                  70                  75                  80

Val Ser Gly Ser Gly Pro Thr Thr Val Phe Leu Cys Glu Ser Glu His
                 85                  90                  95

Lys Ala Gln Asp Val Lys Glu Ala Leu Ile Asp Ala Gly Gln Val Tyr
            100                 105                 110

Ala Ala Tyr Thr Ala Thr Gly Pro Ala Ala Ser Thr Ala Asp Gln Arg
        115                 120                 125

Gly Ala His Ile Leu Thr Val Ser
    130                 135


<210> 867
<211> 759
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(736)
<223> RXN01896

<400> 867
ttattgggca gctcttttgg accgcgaagt caccccgag ctgcgccaca gcattgctta 60

ttggatccgc gcgaaccaca tcaaacgcta gagtgattcc atg acg cat gcg atc   115
                                            Met Thr His Ala Ile
                                              1               5

ctc ttt gac ctc gac ggc acc ctc gtt gat cac gct tcc gcc gcc cgc   163
Leu Phe Asp Leu Asp Gly Thr Leu Val Asp His Ala Ser Ala Ala Arg
```

```
                10                  15                  20

gcc gcc ctg cac gcc tgg tcg ccg acc gtg ggc gtc gac acg gat gtt   211
Ala Ala Leu His Ala Trp Ser Pro Thr Val Gly Val Asp Thr Asp Val
            25                  30                  35

gag cgc tgg att gag ctg gat aag tgg ggt ttt gcc cgt ttt gag cgc   259
Glu Arg Trp Ile Glu Leu Asp Lys Trp Gly Phe Ala Arg Phe Glu Arg
        40                  45                  50

ggc gaa acc acg cat tta ggt cag cgg cgc gac cgc atc agg gcg tac   307
Gly Glu Thr Thr His Leu Gly Gln Arg Arg Asp Arg Ile Arg Ala Tyr
    55                  60                  65

ctc aac aga gag ctt gac gac gcc acc tgc gat gat att tac tcc ggc   355
Leu Asn Arg Glu Leu Asp Asp Ala Thr Cys Asp Asp Ile Tyr Ser Gly
70                  75                  80                  85

tac ctt aaa gca tat gag caa aac tgg act gcc tac ccc gat gcc aag   403
Tyr Leu Lys Ala Tyr Glu Gln Asn Trp Thr Ala Tyr Pro Asp Ala Lys
                90                  95                  100

ggc gtt ctc gat cgc gcg gta gcc acc ggt gcc cct gtg gga atc ctg   451
Gly Val Leu Asp Arg Ala Val Ala Thr Gly Ala Pro Val Gly Ile Leu
            105                 110                 115

acc aat ggc gca gcc ccc atg cag caa gac aag ctt gat cgc acc ggc   499
Thr Asn Gly Ala Ala Pro Met Gln Gln Asp Lys Leu Asp Arg Thr Gly
        120                 125                 130

ctt ggc ctg cca gaa ctc gtc atg ttg gcg gcg tcc act ctg gat tct   547
Leu Gly Leu Pro Glu Leu Val Met Leu Ala Ala Ser Thr Leu Asp Ser
    135                 140                 145

gcg aag cct cgc ccc gaa atg tat gcc cga gcg ctc acc cat ttg ggt   595
Ala Lys Pro Arg Pro Glu Met Tyr Ala Arg Ala Leu Thr His Leu Gly
150                 155                 160                 165

gcc cga acc gca aca att atc ggc gat gat tgg acc aac gat gtc gca   643
Ala Arg Thr Ala Thr Ile Ile Gly Asp Asp Trp Thr Asn Asp Val Ala
                170                 175                 180

gct ccc cgc gaa ctt ggc tgg aat gct ctc tat tta gat cgt tcc gga   691
Ala Pro Arg Glu Leu Gly Trp Asn Ala Leu Tyr Leu Asp Arg Ser Gly
            185                 190                 195

acc gat cca cgc gcc gat atc cac tcc ctg gat gaa ctc ttt cac       736
Thr Asp Pro Arg Ala Asp Ile His Ser Leu Asp Glu Leu Phe His
        200                 205                 210

taggctggcc tttattgttt ccg                                        759


<210> 868
<211> 212
<212> PRT
<213> Corynebacterium glutamicum

<400> 868
Met Thr His Ala Ile Leu Phe Asp Leu Asp Gly Thr Leu Val Asp His
  1               5                  10                  15
```

```
Ala Ser Ala Ala Arg Ala Ala Leu His Ala Trp Ser Pro Thr Val Gly
            20                  25                  30

Val Asp Thr Asp Val Glu Arg Trp Ile Glu Leu Asp Lys Trp Gly Phe
        35                  40                  45

Ala Arg Phe Glu Arg Gly Glu Thr Thr His Leu Gly Gln Arg Arg Asp
    50                  55                  60

Arg Ile Arg Ala Tyr Leu Asn Arg Glu Leu Asp Asp Ala Thr Cys Asp
65                  70                  75                  80

Asp Ile Tyr Ser Gly Tyr Leu Lys Ala Tyr Glu Gln Asn Trp Thr Ala
                85                  90                  95

Tyr Pro Asp Ala Lys Gly Val Leu Asp Arg Ala Val Ala Thr Gly Ala
            100                 105                 110

Pro Val Gly Ile Leu Thr Asn Gly Ala Ala Pro Met Gln Gln Asp Lys
        115                 120                 125

Leu Asp Arg Thr Gly Leu Gly Leu Pro Glu Leu Val Met Leu Ala Ala
    130                 135                 140

Ser Thr Leu Asp Ser Ala Lys Pro Arg Pro Glu Met Tyr Ala Arg Ala
145                 150                 155                 160

Leu Thr His Leu Gly Ala Arg Thr Ala Thr Ile Ile Gly Asp Asp Trp
                165                 170                 175

Thr Asn Asp Val Ala Ala Pro Arg Glu Leu Gly Trp Asn Ala Leu Tyr
            180                 185                 190

Leu Asp Arg Ser Gly Thr Asp Pro Arg Ala Asp Ile His Ser Leu Asp
        195                 200                 205

Glu Leu Phe His
    210
```

<210> 869
<211> 602
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(579)
<223> FRXA01896

<400> 869

```
gcc cgc gcc gcc ctg cac gcc tgg tcg ccg acc gtg ggc gtc gac acg   48
Ala Arg Ala Ala Leu His Ala Trp Ser Pro Thr Val Gly Val Asp Thr
  1               5                  10                  15

gat gtt gag cgc tgg att gag ctg gat aag tgg ggt ttt gcc cgt ttt   96
Asp Val Glu Arg Trp Ile Glu Leu Asp Lys Trp Gly Phe Ala Arg Phe
            20                  25                  30

gag cgc ggc gaa acc acg cat tta ggt cag cgg cgc gac cgc atc agg   144
```

```
Glu Arg Gly Glu Thr Thr His Leu Gly Gln Arg Arg Asp Arg Ile Arg
         35                  40                  45

gcg tac ctc aac aga gag ctt gac gac gcc acc tgc gat gat att tac   192
Ala Tyr Leu Asn Arg Glu Leu Asp Asp Ala Thr Cys Asp Asp Ile Tyr
     50                  55                  60

tcc ggc tac ctt aaa gca tat gag caa aac tgg act gcc tac ccc gat   240
Ser Gly Tyr Leu Lys Ala Tyr Glu Gln Asn Trp Thr Ala Tyr Pro Asp
 65                  70                  75                  80

gcc aag ggc gtt ctc gat cgc gcg gta gcc acc ggt gcc cct gtg gga   288
Ala Lys Gly Val Leu Asp Arg Ala Val Ala Thr Gly Ala Pro Val Gly
                 85                  90                  95

atc ctg acc aat ggc gca gcc ccc atg cag caa gac aag ctt gat cgc   336
Ile Leu Thr Asn Gly Ala Ala Pro Met Gln Gln Asp Lys Leu Asp Arg
            100                 105                 110

acc ggc ctt ggc ctg cca gaa ctc gtc atg ttg gcg gcg tcc act ctg   384
Thr Gly Leu Gly Leu Pro Glu Leu Val Met Leu Ala Ala Ser Thr Leu
        115                 120                 125

gat tct gcg aag cct cgc ccc gaa atg tat gcc cga gcg ctc acc cat   432
Asp Ser Ala Lys Pro Arg Pro Glu Met Tyr Ala Arg Ala Leu Thr His
    130                 135                 140

ttg ggt gcc cga acc gca aca att atc ggc gat gat tgg acc aac gat   480
Leu Gly Ala Arg Thr Ala Thr Ile Ile Gly Asp Asp Trp Thr Asn Asp
145                 150                 155                 160

gtc gca gct ccc cgc gaa ctt ggc tgg aat gct ctc tat tta gat cgt   528
Val Ala Ala Pro Arg Glu Leu Gly Trp Asn Ala Leu Tyr Leu Asp Arg
                165                 170                 175

tcc gga acc gat cca cgc gcc gat atc cac tcc ctg gat gaa ctc ttt   576
Ser Gly Thr Asp Pro Arg Ala Asp Ile His Ser Leu Asp Glu Leu Phe
            180                 185                 190

cac taggctggcc tttattgttt ccg                                    602
His
```

Sequence Listing - 2009-12-23 - 09:25:25

<210> 870
<211> 193
<212> PRT
<213> Corynebacterium glutamicum

<400> 870

```
Ala Arg Ala Ala Leu His Ala Trp Ser Pro Thr Val Gly Val Asp Thr
  1               5                  10                  15

Asp Val Glu Arg Trp Ile Glu Leu Asp Lys Trp Gly Phe Ala Arg Phe
             20                  25                  30

Glu Arg Gly Glu Thr Thr His Leu Gly Gln Arg Arg Asp Arg Ile Arg
         35                  40                  45

Ala Tyr Leu Asn Arg Glu Leu Asp Asp Ala Thr Cys Asp Asp Ile Tyr
     50                  55                  60
```

```
Ser Gly Tyr Leu Lys Ala Tyr Glu Gln Asn Trp Thr Ala Tyr Pro Asp
 65                  70                  75                  80

Ala Lys Gly Val Leu Asp Arg Ala Val Ala Thr Gly Ala Pro Val Gly
                 85                  90                  95

Ile Leu Thr Asn Gly Ala Ala Pro Met Gln Gln Asp Lys Leu Asp Arg
            100                 105                 110

Thr Gly Leu Gly Leu Pro Glu Leu Val Met Leu Ala Ala Ser Thr Leu
        115                 120                 125

Asp Ser Ala Lys Pro Arg Pro Glu Met Tyr Ala Arg Ala Leu Thr His
    130                 135                 140

Leu Gly Ala Arg Thr Ala Thr Ile Ile Gly Asp Asp Trp Thr Asn Asp
145                 150                 155                 160

Val Ala Ala Pro Arg Glu Leu Gly Trp Asn Ala Leu Tyr Leu Asp Arg
                165                 170                 175

Ser Gly Thr Asp Pro Arg Ala Asp Ile His Ser Leu Asp Glu Leu Phe
            180                 185                 190

His
```

Application Filed Electronically

<210> 871
<211> 909
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(886)
<223> RXN01899

<400> 871

```
cctcgcagca cttcgcgcag gcgaatccac agtggccgca accttgatca aagaacacat 60

cgaaggctac tacgaagaaa ccgctgccgc cgaggcctaa atg tcc cgc act ctg   115
                                               Met Ser Arg Thr Leu
                                                 1               5

tgg gcg gtt tca gat cta cac gtc acc ttc gcc caa aac caa aac acc   163
Trp Ala Val Ser Asp Leu His Val Thr Phe Ala Gln Asn Gln Asn Thr
                10                  15                  20

gtt gat gcc ctc atg ccg cag gac ccc ggc gac tgg ctg atc gtc gct   211
Val Asp Ala Leu Met Pro Gln Asp Pro Gly Asp Trp Leu Ile Val Ala
            25                  30                  35

ggc gat gta gca gag aaa atc ccc gat gtg gta cgt acc tta tcc gcg   259
Gly Asp Val Ala Glu Lys Ile Pro Asp Val Val Arg Thr Leu Ser Ala
        40                  45                  50

ctg gtc aaa cgc ttt gac acc gtg att tgg gtg ccg ggc aac cac gaa   307
Leu Val Lys Arg Phe Asp Thr Val Ile Trp Val Pro Gly Asn His Glu
    55                  60                  65
```

```
ctc ttc aac cgg aaa aca gac cgc gtc aac ggc aaa gcc cgc tac cga   355
Leu Phe Asn Arg Lys Thr Asp Arg Val Asn Gly Lys Ala Arg Tyr Arg
 70                  75                  80                  85

gca tta gtc gga caa ctc cga gcc atc ggc gtg atc acc ccc gaa gat   403
Ala Leu Val Gly Gln Leu Arg Ala Ile Gly Val Ile Thr Pro Glu Asp
                90                  95                 100

ccc tat ccg atc ttt ggt ggc gtc acc atc tgc cca ctt ttc aca ctt   451
Pro Tyr Pro Ile Phe Gly Gly Val Thr Ile Cys Pro Leu Phe Thr Leu
            105                 110                 115

tac gat tac tct ttc cgt ccc ctc ggc ctc acc gcg aaa caa gcc ctc   499
Tyr Asp Tyr Ser Phe Arg Pro Leu Gly Leu Thr Ala Lys Gln Ala Leu
        120                 125                 130

gcc caa gca aaa ata aag cta gac gac gaa cta gcc atc gcc ccc tac   547
Ala Gln Ala Lys Ile Lys Leu Asp Asp Glu Leu Ala Ile Ala Pro Tyr
    135                 140                 145

gta gac atc ccc gcc tgg tgc gcc gaa cga gtc acc tac aca gaa gac   595
Val Asp Ile Pro Ala Trp Cys Ala Glu Arg Val Thr Tyr Thr Glu Asp
150                 155                 160                 165

cgc cta aaa gcc acc aaa ggc cca aaa gtc ctg gtc aat cac tgg ccg   643
Arg Leu Lys Ala Thr Lys Gly Pro Lys Val Leu Val Asn His Trp Pro
                170                 175                 180

ctg gtc att gag ccc acc cac cgg ctc ttc caa aaa gac atc gcg ctg   691
Leu Val Ile Glu Pro Thr His Arg Leu Phe Gln Lys Asp Ile Ala Leu
            185                 190                 195

tgg tgt gga acc acc gcc acc agg gat tgg gcc gta cga ttc aac gct   739
Trp Cys Gly Thr Thr Ala Thr Arg Asp Trp Ala Val Arg Phe Asn Ala
        200                 205                 210

ctc atg gcc att cac ggt cac cta cat att cct gcc gaa acc cgc gtt   787
Leu Met Ala Ile His Gly His Leu His Ile Pro Ala Glu Thr Arg Val
    215                 220                 225

gat ggg gta agc cac gtg gag gtt tct ttg ggt tac ccc ttt gaa aaa   835
Asp Gly Val Ser His Val Glu Val Ser Leu Gly Tyr Pro Phe Glu Lys
230                 235                 240                 245

cac cca cct cac atg aag cgt ccg tgg ccg ttt ccg gtc atg cag att   883
His Pro Pro His Met Lys Arg Pro Trp Pro Phe Pro Val Met Gln Ile
                250                 255                 260

aac taactctgtt gcttaaatgg ggg                                    909
Asn
```

<210> 872
<211> 262
<212> PRT
<213> Corynebacterium glutamicum

<400> 872
Met Ser Arg Thr Leu Trp Ala Val Ser Asp Leu His Val Thr Phe Ala

```
  1               5                  10                  15

Gln Asn Gln Asn Thr Val Asp Ala Leu Met Pro Gln Asp Pro Gly Asp
            20                  25                  30

Trp Leu Ile Val Ala Gly Asp Val Ala Glu Lys Ile Pro Asp Val Val
        35                  40                  45

Arg Thr Leu Ser Ala Leu Val Lys Arg Phe Asp Thr Val Ile Trp Val
    50                  55                  60

Pro Gly Asn His Glu Leu Phe Asn Arg Lys Thr Asp Arg Val Asn Gly
65                  70                  75                  80

Lys Ala Arg Tyr Arg Ala Leu Val Gly Gln Leu Arg Ala Ile Gly Val
                85                  90                  95

Ile Thr Pro Glu Asp Pro Tyr Pro Ile Phe Gly Gly Val Thr Ile Cys
            100                 105                 110

Pro Leu Phe Thr Leu Tyr Asp Tyr Ser Phe Arg Pro Leu Gly Leu Thr
        115                 120                 125

Ala Lys Gln Ala Leu Ala Gln Ala Lys Ile Lys Leu Asp Asp Glu Leu
    130                 135                 140

Ala Ile Ala Pro Tyr Val Asp Ile Pro Ala Trp Cys Ala Glu Arg Val
145                 150                 155                 160

Thr Tyr Thr Glu Asp Arg Leu Lys Ala Thr Lys Gly Pro Lys Val Leu
                165                 170                 175

Val Asn His Trp Pro Leu Val Ile Glu Pro Thr His Arg Leu Phe Gln
            180                 185                 190

Lys Asp Ile Ala Leu Trp Cys Gly Thr Thr Ala Thr Arg Asp Trp Ala
        195                 200                 205

Val Arg Phe Asn Ala Leu Met Ala Ile His Gly His Leu His Ile Pro
    210                 215                 220

Ala Glu Thr Arg Val Asp Gly Val Ser His Val Glu Val Ser Leu Gly
225                 230                 235                 240

Tyr Pro Phe Glu Lys His Pro Pro His Met Lys Arg Pro Trp Pro Phe
                245                 250                 255

Pro Val Met Gln Ile Asn
            260
```

<210> 873
<211> 909
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(886)
<223> FRXA01899

<400> 873
cctcgcagca cttcgcgcag gcgaatccac agtggccgca accttgatca aagaacacat 60

cgaaggctac tacgaagaaa ccgctgccgc cgaggcctaa atg tcc cgc act ctg 115
Met Ser Arg Thr Leu
1 5

tgg gcg gtt tca gat cta cac gtc acc ttc gcc caa aac caa aac acc 163
Trp Ala Val Ser Asp Leu His Val Thr Phe Ala Gln Asn Gln Asn Thr
10 15 20

gtt gat gcc ctc atg ccg cag gac ccc ggc gac tgg ctg atc gtc gct 211
Val Asp Ala Leu Met Pro Gln Asp Pro Gly Asp Trp Leu Ile Val Ala
25 30 35

ggc gat gta gca gag aaa atc ccc gat gtg gta cgt acc tta tcc gcg 259
Gly Asp Val Ala Glu Lys Ile Pro Asp Val Val Arg Thr Leu Ser Ala
40 45 50

ctg gtc aaa cgc ttt gac acc gtg att tgg gtg ccg ggc aac cac gaa 307
Leu Val Lys Arg Phe Asp Thr Val Ile Trp Val Pro Gly Asn His Glu
55 60 65

ctc ttc aac cgg aaa aca gac cgc gtc aac ggc aaa gcc cgc tac cga 355
Leu Phe Asn Arg Lys Thr Asp Arg Val Asn Gly Lys Ala Arg Tyr Arg
70 75 80 85

gca tta gtc gga caa ctc cga gcc atc ggc gtg atc acc ccc gaa gat 403
Ala Leu Val Gly Gln Leu Arg Ala Ile Gly Val Ile Thr Pro Glu Asp
90 95 100

ccc tat ccg atc ttt ggt ggc gtc acc atc tgc cca ctt ttc aca ctt 451
Pro Tyr Pro Ile Phe Gly Gly Val Thr Ile Cys Pro Leu Phe Thr Leu
105 110 115

tac gat tac tct ttc cgt ccc ctc ggc ctc acc gcg aaa caa gcc ctc 499
Tyr Asp Tyr Ser Phe Arg Pro Leu Gly Leu Thr Ala Lys Gln Ala Leu
120 125 130

gcc caa gca aaa ata aag cta gac gac gaa cta gcc atc gcc ccc tac 547
Ala Gln Ala Lys Ile Lys Leu Asp Asp Glu Leu Ala Ile Ala Pro Tyr
135 140 145

gta gac atc ccc gcc tgg tgc gcc gaa cga gtc acc tac aca gaa gac 595
Val Asp Ile Pro Ala Trp Cys Ala Glu Arg Val Thr Tyr Thr Glu Asp
150 155 160 165

cgc cta aaa gcc acc aaa ggc cca aaa gtc ctg gtc aat cac tgg ccg 643
Arg Leu Lys Ala Thr Lys Gly Pro Lys Val Leu Val Asn His Trp Pro
170 175 180

ctg gtc att gag ccc acc cac cgg ctc ttc caa aaa gac atc gcg ctg 691
Leu Val Ile Glu Pro Thr His Arg Leu Phe Gln Lys Asp Ile Ala Leu
185 190 195

tgg tgt gga acc acc gcc acc agg gat tgg gcc gta cga ttc aac gct 739
Trp Cys Gly Thr Thr Ala Thr Arg Asp Trp Ala Val Arg Phe Asn Ala
200 205 210

ctc atg gcc att cac ggt cac cta cat att cct gcc gaa acc cgc gtt 787
Leu Met Ala Ile His Gly His Leu His Ile Pro Ala Glu Thr Arg Val

```
    215                 220                 225

gat ggg gta agc cac gtg gag gtt tct ttg ggt tac ccc ttt gaa aaa   835
Asp Gly Val Ser His Val Glu Val Ser Leu Gly Tyr Pro Phe Glu Lys
230                 235                 240                 245

cac cca cct cac atg aag cgt ccg tgg ccg ttt ccg gtc atg cag att   883
His Pro Pro His Met Lys Arg Pro Trp Pro Phe Pro Val Met Gln Ile
                250                 255                 260

aac taactctgtt gcttaaatgg ggg                                    909
Asn
```

<210> 874
<211> 262
<212> PRT
<213> Corynebacterium glutamicum

<400> 874

```
Met Ser Arg Thr Leu Trp Ala Val Ser Asp Leu His Val Thr Phe Ala
  1               5                  10                  15

Gln Asn Gln Asn Thr Val Asp Ala Leu Met Pro Gln Asp Pro Gly Asp
             20                  25                  30

Trp Leu Ile Val Ala Gly Asp Val Ala Glu Lys Ile Pro Asp Val Val
         35                  40                  45

Arg Thr Leu Ser Ala Leu Val Lys Arg Phe Asp Thr Val Ile Trp Val
     50                  55                  60

Pro Gly Asn His Glu Leu Phe Asn Arg Lys Thr Asp Arg Val Asn Gly
 65                  70                  75                  80

Lys Ala Arg Tyr Arg Ala Leu Val Gly Gln Leu Arg Ala Ile Gly Val
                 85                  90                  95

Ile Thr Pro Glu Asp Pro Tyr Pro Ile Phe Gly Gly Val Thr Ile Cys
            100                 105                 110

Pro Leu Phe Thr Leu Tyr Asp Tyr Ser Phe Arg Pro Leu Gly Leu Thr
        115                 120                 125

Ala Lys Gln Ala Leu Ala Gln Ala Lys Ile Lys Leu Asp Asp Glu Leu
    130                 135                 140

Ala Ile Ala Pro Tyr Val Asp Ile Pro Ala Trp Cys Ala Glu Arg Val
145                 150                 155                 160

Thr Tyr Thr Glu Asp Arg Leu Lys Ala Thr Lys Gly Pro Lys Val Leu
                165                 170                 175

Val Asn His Trp Pro Leu Val Ile Glu Pro Thr His Arg Leu Phe Gln
            180                 185                 190

Lys Asp Ile Ala Leu Trp Cys Gly Thr Thr Ala Thr Arg Asp Trp Ala
        195                 200                 205

Val Arg Phe Asn Ala Leu Met Ala Ile His Gly His Leu His Ile Pro
```

```
    210                 215                 220

Ala Glu Thr Arg Val Asp Gly Val Ser His Val Glu Val Ser Leu Gly
225                 230                 235                 240

Tyr Pro Phe Glu Lys His Pro Pro His Met Lys Arg Pro Trp Pro Phe
                245                 250                 255

Pro Val Met Gln Ile Asn
            260


<210> 875
<211> 1182
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1159)
<223> RXN01902

<400> 875
ggctggtccg aagtgcaaac cttcaacacc ggcacctacg gtgacaactg gaacttcctc 60

ttcttcggcg acacccagct gtacaacacc cactccaacc gtg cag aag aag tcc   115
                                    Val Gln Lys Lys Ser
                                      1               5

aga act ggg caa aca acc tgg aac ggc ggc cca cca atc gaa aac cca   163
Arg Thr Gly Gln Thr Thr Trp Asn Gly Gly Pro Pro Ile Glu Asn Pro
                10                  15                  20

gga acc tcc ttc atc ctc tcc gcg ggt gat cag gca aac cac tcc agc   211
Gly Thr Ser Phe Ile Leu Ser Ala Gly Asp Gln Ala Asn His Ser Ser
            25                  30                  35

tgg gac gag cac tcc gca tac atc tcc cca gaa acc ctg cgc aac tac   259
Trp Asp Glu His Ser Ala Tyr Ile Ser Pro Glu Thr Leu Arg Asn Tyr
        40                  45                  50

cgt ctg gcc gtg aac aat gga aac cac gac cag tac aac tac gac gcc   307
Arg Leu Ala Val Asn Asn Gly Asn His Asp Gln Tyr Asn Tyr Asp Ala
    55                  60                  65

tac aac gcg atg tac cca cgc cct aac cag gtc gat gag aac tac ttc   355
Tyr Asn Ala Met Tyr Pro Arg Pro Asn Gln Val Asp Glu Asn Tyr Phe
70                  75                  80                  85

ttc gag tac aac aat gca ctc ttc ctg tcc ctg gac tcc aac gac tac   403
Phe Glu Tyr Asn Asn Ala Leu Phe Leu Ser Leu Asp Ser Asn Asp Tyr
                90                  95                  100

ttg gac atc gac gac gac atc gca ttc ctt cgc gac acc gtc gca gca   451
Leu Asp Ile Asp Asp Asp Ile Ala Phe Leu Arg Asp Thr Val Ala Ala
            105                 110                 115

cac ggt gac gac aag gac tgg atc gtc ctg acc tac cac cat tcc act   499
His Gly Asp Asp Lys Asp Trp Ile Val Leu Thr Tyr His His Ser Thr
        120                 125                 130
```

```
ttc tcc cag gcc tac cac atg gat gac gct cgc att aag tac cag cgc   547
Phe Ser Gln Ala Tyr His Met Asp Asp Ala Arg Ile Lys Tyr Gln Arg
    135                 140                 145

gaa cgc ctc acc cca gtg atc tct gaa ctg aac gtt gac ttg gtt ctc   595
Glu Arg Leu Thr Pro Val Ile Ser Glu Leu Asn Val Asp Leu Val Leu
150                 155                 160                 165

ggt gga cac gac cac atc tac acc cgc tcc cac ctg atg aac ggc ttc   643
Gly Gly His Asp His Ile Tyr Thr Arg Ser His Leu Met Asn Gly Phe
                170                 175                 180

acc cca gtc gat gca ggc cgc gaa gca gtt gtc ggt gaa act ctg aac   691
Thr Pro Val Asp Ala Gly Arg Glu Ala Val Val Gly Glu Thr Leu Asn
            185                 190                 195

cct aag gcc ggc gaa gtt gtt tac ctt gca acc aac tct tcc tca ggc   739
Pro Lys Ala Gly Glu Val Val Tyr Leu Ala Thr Asn Ser Ser Ser Gly
        200                 205                 210

tcc aag ttc tac gac ttc tac gac ttc cag ctc ggc cag cgt tac gac   787
Ser Lys Phe Tyr Asp Phe Tyr Asp Phe Gln Leu Gly Gln Arg Tyr Asp
    215                 220                 225

acc gga ctg gat ttc cag gaa acc gtc gat cag aag aag atc cgc acc   835
Thr Gly Leu Asp Phe Gln Glu Thr Val Asp Gln Lys Lys Ile Arg Thr
230                 235                 240                 245

tac acc gca gtc tgg aac cag gac cag gtt cag gac tac acc aac gtt   883
Tyr Thr Ala Val Trp Asn Gln Asp Gln Val Gln Asp Tyr Thr Asn Val
                250                 255                 260

gaa ctg acc cca gaa ggc ctg act gtg acc act aag gac gca gtc tcc   931
Glu Leu Thr Pro Glu Gly Leu Thr Val Thr Thr Lys Asp Ala Val Ser
            265                 270                 275

ggc gag ctg gtt gac cag ttc acc ctg agc aag cag gac cgc gac gaa   979
Gly Glu Leu Val Asp Gln Phe Thr Leu Ser Lys Gln Asp Arg Asp Glu
        280                 285                 290

gaa tct gaa gtc cca gtt gaa gat gac aag gac gga gac aac gcg acc   1027
Glu Ser Glu Val Pro Val Glu Asp Asp Lys Asp Gly Asp Asn Ala Thr
    295                 300                 305

ggc tcc tcc aac ctt ggt cta gct gct atc ttg gct cca gtt ctg gcc   1075
Gly Ser Ser Asn Leu Gly Leu Ala Ala Ile Leu Ala Pro Val Leu Ala
310                 315                 320                 325

atc ttc ggt ttc gtc ggt gga ctc ttt gtt ggc ggc ggc tcc ctc gct   1123
Ile Phe Gly Phe Val Gly Gly Leu Phe Val Gly Gly Gly Ser Leu Ala
                330                 335                 340

gag ttc ttt gcc aac ctc ggc gtg aag atg cct ttc taatactgtc        1169
Glu Phe Phe Ala Asn Leu Gly Val Lys Met Pro Phe
            345                 350

tgagattcaa gca                                                   1182


<210> 876
<211> 353
```

<212> PRT
<213> Corynebacterium glutamicum

<400> 876

```
Val Gln Lys Lys Ser Arg Thr Gly Gln Thr Thr Trp Asn Gly Gly Pro
  1               5                  10                  15

Pro Ile Glu Asn Pro Gly Thr Ser Phe Ile Leu Ser Ala Gly Asp Gln
            20                  25                  30

Ala Asn His Ser Ser Trp Asp Glu His Ser Ala Tyr Ile Ser Pro Glu
        35                  40                  45

Thr Leu Arg Asn Tyr Arg Leu Ala Val Asn Asn Gly Asn His Asp Gln
    50                  55                  60

Tyr Asn Tyr Asp Ala Tyr Asn Ala Met Tyr Pro Arg Pro Asn Gln Val
65                  70                  75                  80

Asp Glu Asn Tyr Phe Phe Glu Tyr Asn Asn Ala Leu Phe Leu Ser Leu
                85                  90                  95

Asp Ser Asn Asp Tyr Leu Asp Ile Asp Asp Asp Ile Ala Phe Leu Arg
            100                 105                 110

Asp Thr Val Ala Ala His Gly Asp Asp Lys Asp Trp Ile Val Leu Thr
        115                 120                 125

Tyr His His Ser Thr Phe Ser Gln Ala Tyr His Met Asp Asp Ala Arg
    130                 135                 140

Ile Lys Tyr Gln Arg Glu Arg Leu Thr Pro Val Ile Ser Glu Leu Asn
145                 150                 155                 160

Val Asp Leu Val Leu Gly Gly His Asp His Ile Tyr Thr Arg Ser His
                165                 170                 175

Leu Met Asn Gly Phe Thr Pro Val Asp Ala Gly Arg Glu Ala Val Val
            180                 185                 190

Gly Glu Thr Leu Asn Pro Lys Ala Gly Glu Val Val Tyr Leu Ala Thr
        195                 200                 205

Asn Ser Ser Ser Gly Ser Lys Phe Tyr Asp Phe Tyr Asp Phe Gln Leu
    210                 215                 220

Gly Gln Arg Tyr Asp Thr Gly Leu Asp Phe Gln Glu Thr Val Asp Gln
225                 230                 235                 240

Lys Lys Ile Arg Thr Tyr Thr Ala Val Trp Asn Gln Asp Gln Val Gln
                245                 250                 255

Asp Tyr Thr Asn Val Glu Leu Thr Pro Glu Gly Leu Thr Val Thr Thr
            260                 265                 270

Lys Asp Ala Val Ser Gly Glu Leu Val Asp Gln Phe Thr Leu Ser Lys
        275                 280                 285

Gln Asp Arg Asp Glu Glu Ser Glu Val Pro Val Glu Asp Asp Lys Asp
    290                 295                 300
```

```
Gly Asp Asn Ala Thr Gly Ser Ser Asn Leu Gly Leu Ala Ala Ile Leu
305                 310                 315                 320

Ala Pro Val Leu Ala Ile Phe Gly Phe Val Gly Gly Leu Phe Val Gly
                325                 330                 335

Gly Gly Ser Leu Ala Glu Phe Phe Ala Asn Leu Gly Val Lys Met Pro
            340                 345                 350

Phe
```

<210> 877
<211> 887
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(864)
<223> FRXA01902

<400> 877

```
aac tac gac gcc tac aac gcg atg tac cca cgc cct aac cag gtc gat   48
Asn Tyr Asp Ala Tyr Asn Ala Met Tyr Pro Arg Pro Asn Gln Val Asp
  1               5                  10                  15

gag aac tac ttc ttc gag tac aac aat gca ctc ttc ctg tcc ctg gac   96
Glu Asn Tyr Phe Phe Glu Tyr Asn Asn Ala Leu Phe Leu Ser Leu Asp
             20                  25                  30

tcc aac gac tac ttg gac atc gac gac gac atc gca ttc ctt cgc gac   144
Ser Asn Asp Tyr Leu Asp Ile Asp Asp Asp Ile Ala Phe Leu Arg Asp
         35                  40                  45

acc gtc gca gca cac ggt gac gac aag gac tgg atc gtc ctg acc tac   192
Thr Val Ala Ala His Gly Asp Asp Lys Asp Trp Ile Val Leu Thr Tyr
     50                  55                  60

cac cat tcc act ttc tcc cag gcc tac cac atg gat gac gct cgc att   240
His His Ser Thr Phe Ser Gln Ala Tyr His Met Asp Asp Ala Arg Ile
 65                  70                  75                  80

aag tac cag cgc gaa cgc ctc acc cca gtg atc tct gaa ctg aac gtt   288
Lys Tyr Gln Arg Glu Arg Leu Thr Pro Val Ile Ser Glu Leu Asn Val
                 85                  90                  95

gac ttg gtt ctc ggt gga cac gac cac atc tac acc cgc tcc cac ctg   336
Asp Leu Val Leu Gly Gly His Asp His Ile Tyr Thr Arg Ser His Leu
            100                 105                 110

atg aac ggc ttc acc cca gtc gat gca ggc cgc gaa gca gtt gtc ggt   384
Met Asn Gly Phe Thr Pro Val Asp Ala Gly Arg Glu Ala Val Val Gly
        115                 120                 125

gaa act ctg aac cct aag gcc ggc gaa gtt gtt tac ctt gca acc aac   432
Glu Thr Leu Asn Pro Lys Ala Gly Glu Val Val Tyr Leu Ala Thr Asn
    130                 135                 140

tct tcc tca ggc tcc aag ttc tac gac ttc tac gac ttc cag ctc ggc   480
```

```
Ser Ser Ser Gly Ser Lys Phe Tyr Asp Phe Tyr Asp Phe Gln Leu Gly
145                 150                 155                 160

cag cgt tac gac acc gga ctg gat ttc cag gaa acc gtc gat cag aag   528
Gln Arg Tyr Asp Thr Gly Leu Asp Phe Gln Glu Thr Val Asp Gln Lys
                165                 170                 175

aag atc cgc acc tac acc gca gtc tgg aac cag gac cag gtt cag gac   576
Lys Ile Arg Thr Tyr Thr Ala Val Trp Asn Gln Asp Gln Val Gln Asp
            180                 185                 190

tac acc aac gtt gaa ctg acc cca gaa ggc ctg act gtg acc act aag   624
Tyr Thr Asn Val Glu Leu Thr Pro Glu Gly Leu Thr Val Thr Thr Lys
        195                 200                 205

gac gca gtc tcc ggc gag ctg gtt gac cag ttc acc ctg agc aag cag   672
Asp Ala Val Ser Gly Glu Leu Val Asp Gln Phe Thr Leu Ser Lys Gln
    210                 215                 220

gac cgc gac gaa gaa tct gaa gtc cca gtt gaa gat gac aag gac gga   720
Asp Arg Asp Glu Glu Ser Glu Val Pro Val Glu Asp Asp Lys Asp Gly
225                 230                 235                 240

gac aac gcg acc ggc tcc tcc aac ctt ggt cta gct gct atc ttg gct   768
Asp Asn Ala Thr Gly Ser Ser Asn Leu Gly Leu Ala Ala Ile Leu Ala
                245                 250                 255

cca gtt ctg gcc atc ttc ggt ttc gtc ggt gga ctc ttt gtt ggc ggc   816
Pro Val Leu Ala Ile Phe Gly Phe Val Gly Gly Leu Phe Val Gly Gly
            260                 265                 270

ggc tcc ctc gct gag ttc ttt gcc aac ctc ggc gtg aag atg cct ttc   864
Gly Ser Leu Ala Glu Phe Phe Ala Asn Leu Gly Val Lys Met Pro Phe
        275                 280                 285

taatactgtc tgagattcaa gca                                        887


<210> 878
<211> 288
<212> PRT
<213> Corynebacterium glutamicum

<400> 878
Asn Tyr Asp Ala Tyr Asn Ala Met Tyr Pro Arg Pro Asn Gln Val Asp
  1               5                  10                  15

Glu Asn Tyr Phe Phe Glu Tyr Asn Asn Ala Leu Phe Leu Ser Leu Asp
             20                  25                  30

Ser Asn Asp Tyr Leu Asp Ile Asp Asp Asp Ile Ala Phe Leu Arg Asp
         35                  40                  45

Thr Val Ala Ala His Gly Asp Asp Lys Asp Trp Ile Val Leu Thr Tyr
     50                  55                  60

His His Ser Thr Phe Ser Gln Ala Tyr His Met Asp Asp Ala Arg Ile
 65                  70                  75                  80

Lys Tyr Gln Arg Glu Arg Leu Thr Pro Val Ile Ser Glu Leu Asn Val
                 85                  90                  95
```